中国水产学会成立60周年

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第一专题：水产绿色健康养殖新技术新模式

翅碱蓬人工湿地构建及其在对虾养殖尾水净化中的应用

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摘要：通过构建翅碱蓬人工湿地研究其对南美白对虾养殖尾水的净化效果。本文以翅碱蓬人工湿地为处理组，无植被人工湿地为对照组，设置 0.05、0.15、0.25、0.35、0.45、0.55 m3·(m2·d) -1 水力负荷梯度进行试验，每组含三个平行。结果表明：在水力负荷条件较低时翅碱蓬人工湿地南美白对虾养殖尾水出水中 SS 与 TAN 含量显著低于无植被人工湿地 ($P < 0.05$)。当水力负荷为 0.05m3·(m2·d)-1 时翅碱蓬人工湿地中南美白对虾养殖尾水出水水质的 NO2--N、NO3--N、PO43--P 和 COD 含量最小依次为、0.18±0.02 mg/L、0.31±0.05 mg/L、0.03±0.02 mg/L、12.22±0.37 mg/L 显著低于无植被人工湿地 ($P < 0.05$)。本研究发现翅碱蓬人工湿地系统对养虾尾水具有较好的净化作用，在实际应用中建议选择较低的水力负荷条件以增强其净化效果。

关键词：翅碱蓬；人工湿地；南美白对虾；水产养殖尾水

Construction of Suaeda heteroptera artificial wetland and its application in the purification of shrimp aquaculture tail water

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Abstract： The purification effect of Suaeda heteroptera artificial wetland on the tail water of Penaeus vannamei culture was studied by constructing Suaeda heteroptera artificial wetland. In this paper, the Suaeda heteroptera artificial wetland was used as the treatment group, and the non-vegetated artificial wetland was used as the control group. The hydraulic load gradients of 0.05,0.15,0.25,0.35,0.45 and 0.55 m3 · (m2 · d) -1 were set up for the test. Each group contained three parallels. The results showed that the contents of SS and TAN in the effluent of Penaeus vannamei culture in Suaeda heteroptera constructed wetland were significantly lower than those in non-vegetation constructed wetland ($P < 0.05$). When the hydraulic load was 0.05 m3 · (m2 · d) -1, the contents of NO2-N, NO3-N, PO43-P and COD in the effluent of Penaeus vannamei aquaculture in Suaeda salsa constructed wetland were 0.18 ± 0.02 mg / L, 0.31 ± 0.05 mg / L, 0.03 ± 0.02 mg / L and 12.22 ± 0.37 mg / L, respectively, which were significantly lower than those in non-vegetated constructed wetland ($P < 0.05$). This study found that the Suaeda heteroptera constructed wetland system has a good purification effect on shrimp tail water. In practical application, it is recommended to select lower hydraulic load conditions to enhance its purification effect.

Key words: Suaeda heteroptera; artificial wetland; penaeus vannamei; aquaculture tail water

盐度驯化对雌性日本鳗鲡形态特征及性腺发育的影响

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摘要：为查明盐度驯化对 5 龄雌性日本鳗鲡（Anguilla japonica）形态特征及性腺发育的影响，本研究进行了 150 d 的模拟盐度驯化实验。结果显示，从盐度 0~35 依次驯化至 90 d 时，雌鳗的胸围、胸鳍指数、性体指数和肝脏指数随盐度的升高均显著增加（P<0.05）；而消化道指数和眼径指数随盐度的升高均无明显变化（P>0.05）。通过对卵巢切片观察发现，雌鳗的卵母细胞直径随盐度的升高显著上升（P<0.05）, 但卵母细胞始终处于脂肪泡时期。在盐度 35 中继续驯化后，发现雌鳗在第 90 d、120 d 和 150 d 的上述 7 项指标均不存在显著性差异（P>0.05）。同时实验还设置了同步盐度驯化的流水组。与静水组不同的是，流水组的卵母细胞直径均显著高于同一驯化盐度下的静水组（P<0.05），卵母细胞进入初级卵黄球时期。结果表明，盐度是雌性日本鳗鲡性腺发育的重要启动因子，流水刺激能够加速卵母细胞的发育。

关键词：日本鳗鲡；盐度驯化；形态特征；性腺发育

Effects of salinity acclimation on morphological characteristics and gonadal development of female Anguilla japonica

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Abstract： The effects of salinity acclimation on the morphological characteristics and gonadal development of 5-year-old female Japanese eels (Anguilla japonica) were investigated in this study. A 150-day salinity acclimation experiment was conducted to analyze the morphological features and gonadal development of female eels under different salinity conditions. The results showed that, as salinity increased from 0 to 35 over a period of 90 d (with 30 d of acclimation at salinities 15, 25, and 35, respectively), the pectoral circumference (PC), pectoral fin index (PI), gonadosomatic index (GSI), and liver index (LI) of female eels all significantly increased (P<0.05), while the digestive tract index (DTI) and eye diameter index (EI) showed no significant changes with increasing salinity (P>0.05). Ovarian histological observations revealed a significant increase in oocyte diameter (OD) with increasing salinity (P<0.05), although oocytes remained in the oil droplet stage. After continued acclimation at salinity 35, no significant differences were observed in the aforementioned seven indices at 90 d, 120 d, and 150 d (P>0.05). To investigate the impact of flowing water on female eel gonadal development, a concurrent flowing water group was also acclimated to varying salinities. The results showed that the trends of changes in seven indicators in the flowing water group of female Japanese eels during the entire salinity acclimation process were consistent with those of the still water group mentioned above. Except for oocyte diameter (OD), the other six indicators in the flowing water group at the same acclimation salinity level showed no significant differences compared to the still water group ($P>0.05$). The oocyte diameter (OD) in the flowing water group was significantly larger than in the still water group at the same salinity ($P<0.05$). After 30 d of acclimation at salinity 35, oocytes in the flowing water group entered the primary yolk globule stage, with an oocyte diameter of (161.97±7.46) μm, significantly larger than that of the still water group at (140.46±9.36) μm.These results indicate that salinity is a crucial triggering factor for the gonadal development of female Japanese eels, and the stimulation of flowing water accelerates oocyte development. The findings provide fundamental data and reference information for the reproductive biology research of Japanese eels.

Key words: Anguilla japonica; salinity acclimation; morphological characteristics; gonadal development

文蛤水平流养殖及营养成分特性研究

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摘要：通过现场试验方法探究了文蛤苗种水平流培育模式，并对其养殖成品文蛤营养成分进行了比较研究。结果表明，5 月份采捕规格壳长约 0.27cm，粒重约 0.005g 的滩涂文蛤苗种，采用水平流培育模式，当年文蛤平均壳长 2.62cm，相对增长率为 870.58%，平均粒重 4.50g，相对增长率为 44853.33%，成活率为 93%；水平流养殖（M1）成品文蛤软体组织中水分均显著高于滩涂养殖文蛤（M2），M2 粗脂肪显著高于 M1，粗蛋白除外套膜外，未呈现显著差异（P＞0.05）； M1 内脏团的必需氨基酸总量与非必需氨基酸总量的比值超 80%，显著高于 M2，且富含了更多的呈味氨基酸（P＜0.05）；棕榈油酸及硬脂酸在内脏团中含量最高，且 M1 显著高于 M2（P＜0.05）；M1 闭壳肌和斧足中的总糖含量更高；糖原在软体组织中均呈现 M1 显著高于 M2（P＜0.05）。水平流养殖模式提升了文蛤养殖效益，改善了文蛤的营养品质和口感。

关键词：水平流养殖；滩涂；文蛤；营养成分

Study on Horizontal Flow Culture and Nutrient Composition Characteristics of Meretrix meretrix system

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Abstract： The horizontal flow cultivation mode of clam seedlings was explored through on-site experimental methods, and a comparative study was conducted on the nutritional composition of clam products. The results showed that in May, the standard shell length was about 0.27cm, and the grain weight was about 0.005g. Using the horizontal flow cultivation mode, the average shell length of the clam was 2.62cm, the relative growth rate was 870.58%, the average grain weight was 4.50g, the relative growth rate was 44853.33%, and the survival rate was 93%; The water content in the soft tissue of the finished clam cultured in horizontal flow (M1) was significantly higher than that of the clam cultured in mudflat (M2), the crude fat of M2 was significantly higher than that of M1, and there was no significant difference in crude protein except for the coat film (P>0.05); The ratio of total essential amino acids to total non essential amino acids in M1 visceral mass exceeds 80%, significantly higher than that in M2, and is rich in more flavor amino acids (P<0.05); Palmitoleic acid and stearic acid have the highest content in visceral mass, and M1 is significantly higher than M2 (P<0.05); M1 has a higher total sugar content in the adductor muscle and foot of the axe; Glycogen levels in soft tissues were significantly higher in M1 than in M2 (P<0.05). The horizontal flow aquaculture model has improved the efficiency of clam farming, improved the nutritional quality and taste of clams.

Key words: Horizontal flow culture; mudflat clam; nutrient composition

循环水流速对黄河鲤（Cyprinus carpio haematopterus）生长性能和肌肉品质的影响

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摘要：为研究在循环水养殖中不同水流速度对黄河鲤（Cyprinus carpio haematopterus）生长性能和肌肉品质的影响，本实验选取 270 尾平均体长为（13.61±0.19）cm 的黄河鲤，将其平均分为三组：持续运动 S 组（1 bl/s，24 h/d），间歇运动 I 组（1 bl/s，8 h/d）和对照 C 组（0 bl/s），每组设置 3 个平行，每个平行 30 尾，进行为期 90 天的养殖实验。结果显示，S 组的增重率显著高于 C 组（$P < 0.05$）；S 组肌纤维密度显著大于其他两组；在氨基酸成分中，I 组中丝氨酸的含量显著高于 C 组，精氨酸含量显著高于 S 组（$P < 0.05$）；挥发性物质检测发现 I 组和 S 组具有刺激性气味物质含量极显著低于 C 组（$P < 0.01$）。以上结果表明，S 组黄河鲤生长速度更快，肌肉持水力更高、口感更好、蛋白含量更高、刺激性气味更小。本实验结果为循环水流速调控鱼类生长和肌肉品质提供一定的数据支持。

关键词：黄河鲤；循环水；流速；生长；肌肉品质

Effects of different water flow rates in recirculating aquaculture systems (RAS) on growth and muscle quality of Yellow River Carp (Cyprinus carpio haematopterus)

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Abstract：To investigate the effects of different water flow rates on the growth performance and muscle quality of Yellow River Carp (Cyprinus carpio haematopterus) in recirculating aquaculture systems (RAS). In this experiment, 270 Yellow River Carp with an average body length of (13.61±0.19) cm were selected for the study. They were equally divided into three groups: Sustained Exercise (SE, 1 bl/s，24 h/d)，Intermittent Exercise (IE, 1 bl/s，8 h/d), and Control Group (CG, 0 bl/s). Three replicates were set up in each group, each consisting of 30 fish, for a 90-day experiment. The results demonstrated a significant increase in the weight gain rate of SE compared to CG ($P < 0.05$). IE muscles exhibited a noticeable increase in muscle fiber density observed with increasing water flow. As to amino acids, IE had higher serine levels compared to CG, while SE had notably higher arginine levels ($P < 0.05$). Volatile substances were detected in both IE and SE. The content of compounds with unpleasant odors was significantly lower than that in CG ($P < 0.01$). The aforementioned results indicate that Yellow River Carp in the SE exhibited faster growth, better muscle water retention, improved taste, and higher protein content. The results of this experiment provide some data support for the regulation of fish growth and muscle quality in recirculating water culture.

Key words: Cyprinus carpio haematopterus; recirculating aquaculture systems (RAS); water flow rate; growth; muscle quality

火山石和细菌屋对锦鲤养殖池水质净化效果的对比研究

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摘要：为了比较火山石和细菌屋 2 种生物滤材对锦鲤养殖池的水质净化效果，分别设置火山石组、细菌屋组、空白对照组，在水泥池中开展了为期 7 周的循环水过滤养殖试验，养殖对象为同一亲本繁育的锦鲤苗种。试验结果显示，火山石的比表面积显著大于细菌屋的比表面积；火山石组和细菌屋组水体中的硝化细菌数量显著高于对照组，其中火山石组最高。试验结果表明，火山石更有利于硝化细菌的生长繁殖，是较好的锦鲤养殖池生物滤材。

关键词：火山石；细菌屋；锦鲤；水质净化；生物滤材

Comparative study on water purification effect of volcanic stone and bacteria house on brocade carp culture

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Abstract： In order to study the water purification effect of volcanic stone and bacteria house on brocade carp culture. Volcanic stone group, bacterial house group and blank control group were set in this study, and the brocade carp seedlings bred by the same parent were subjected to circulating water filtration culture. The results showed that the specific surface area of volcanic rocks was higher than that of bacteria houses. The number of nitrifying bacteria in the volcanic group and the bacterial house group were significantly higher than that in the control group, and the volcanic group was the highest. Because volcanic stone was a natural filter material, rich in mineral elements, and has a high specific surface area, it was more conducive to the growth and reproduction of nitrifying bacteria. Therefore, it was more suitable to select volcanic stone as a biological filter material.

Key words: volcanic stone; bacteria house; brocade carp; water purification; biofilter material

生态净养对去除大口黑鲈土腥味与提升营养成分的效果

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摘要：将池塘养殖的体质量 450-500 g 的商品大口黑鲈用清水清洗，置于室内循环微流水中净养，第 0、7、14、21 和 28 d 时采集背部肌肉，分别测定土腥味物质土臭素(GSM)和二甲基异莰醇(2-MIB)以及蛋白质、脂肪酸和氨基酸等营养成分含量，研究大口黑鲈在净养下鱼肉土腥味物质及营养成分的变化，探究该模式对鱼肉品质的提升效果。结果显示，在生态净养下，第 7 dGSM 和 2-MIB 的去除率分别为 48.7%和 81.70%，低于感官阈值；在净养前期，脂肪含量降低、蛋白质含量增加，而水分和灰分含量变化不显著 (P>0.05)；净养 7 d 左右，DHA 显著上升(P＜0.05)，油酸含量下降，提高了鱼肉脂肪酸价值；在整个过程中氨基酸总量、必需氨基酸和鲜味氨基酸呈上升趋势，但鱼肉的氨基酸评分随时间变化差异不显著(P>0.05)。研究表明，生态净养可以有效去除鱼肉土腥味，提升鱼肉品质，最适宜净养时间为 7 d。

关键词：生态净养；大口黑鲈；土腥味；营养成分；脂肪酸；氨基酸

Effect of Ecological Clean Water Holding on Removal of Earthy Odor and Improvement of Nutrient Compositions in Largemouth Bass （Micropterus salmoides）

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Abstract： Contents of geosmin(GSM)and2-Methylisoborneol(2-MIB) and nutritional compositions including protein, fatty acids and amino acids were determined in largemouth bass (Micropterus salmoides) with body weight of 450-500 g farmed in a marketable fish ponds and then held in clean water for 0, 7, 14, 21 and 28 days to evaluate the change in changes in contents of GSM and 2-MIB earthy odor and nutritional compositions of largemouth bass in clean water and to explore its effect on the improvement of fish flesh quality. The contents of GSM and were shown to be already below the sensory threshold at the 7th day during the clean water holding process, with removal rates of 48.7% for GSM and 81.70% for 2-MIB. There was decrease in fat content and increase in protein content in the early stage, without significant change in moisture and ash content. The content of DHA was found to be increased and C18:1n-9 decreased significantly at the 7th day(P＜0.05), improving the nutritional value of fat acids. Total amount of amino acids, essential amino acids and delicious amino acids were shown to be an upward trend throughout the process, while the amino acid scores were not significantly changed (P>0.05). In conclusion ecological clean water holding leads to effectively remove the earthy odor and the quality of fish flesh, with the optimal holding period of 7 days.

Key words: ecological purification; Micropterus salmoides; earthy smell; nutrient content; fatty acid; amino acid

摄食稻草和配合饲料对草鱼生长、血清生化指标、肌肉营养成分和肠道组织结构的影响

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摘要：为了验证摄食水稻秸秆对草鱼生长的影响，为稻鱼轮作提供理论依据。实验以平均初体质量为 55.36±0.52 g 的草鱼为研究对象。对照组(CF)投喂配合饲料，实验组是投喂处理后的干稻草 (DS) 和投喂新鲜稻草（FS），养殖周期为 60 天。实验结果显示：与 CF 组相比，DS 组和 FS 组的特定生长率、脏体比、肝体比、肠重比和肥满度均显著降低（P<0.05）。血清总蛋白和白蛋白在各组间的差异性显著（P<0.05），CF 组的球蛋白、总胆固醇、甘油三酯 和高密度脂蛋白胆固醇显著高于 DS 组和 FS 组（P<0.05）；CF 组和 DS 组的蛋白质含量高于 FS 组，DS 组和 FS 组脂肪极显著低于 CF 组（P<0.05）；与 DS 组相比，CF 组和 FS 组肠道结构较为完整。实验结果表明，与投喂配合饲料相比，投喂单一的水稻秸秆显著降低了草鱼生长性能和脂肪酸含量，投喂干稻草对草鱼肠道造成了一定损伤，降低了消化吸收能力。

关键词：草鱼；水稻秸秆；稻渔轮作

Effects of ingestion of rice straw and compound feeds on growth, serum biochemical indices, muscle nutrients and intestinal histology of grass carp (Ctenopharyngodon idella)

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Abstract：In order to verify the effect of ingesting rice straw on the growth of grass carp and to provide a theoretical basis for rice-fish rotation. The experiment was conducted on grass carp with an average initial body mass of 55.36±0.52 g. The control group (CF) was fed with compound feed. The control group (CF) was fed with compound feed, and the experimental group was fed with treated dry straw (DS) and fed with fresh straw (FS) with a 60-day culture cycle. The experimental results showed that specific growth rate, dirty body ratio, liver body ratio, gut weight ratio and fattening were significantly (P<0.05) lower in DS and FS groups compared to CF group. Total serum protein and albumin were significantly different between groups (P<0.05), and globulin, total cholesterol, triglyceride and HDL cholesterol were significantly higher in CF group than in DS and FS groups (P<0.05); protein content was higher in CF and DS groups than in FS group, and fat was extremely significantly lower in DS and FS groups than in CF group (P<0.05); and the specific growth rate was significantly higher in CF group compared to DS group (P<0.05); the specific growth rate was significantly higher in DS and FS groups compared to DS group (P<0.05). and FS groups had a more intact intestinal structure compared to the DS group. The experimental results showed that feeding single rice straw significantly reduced the growth performance and fatty acid content of grass carp compared with feeding compound feeds, and feeding dry rice straw caused some damage to the intestinal tract of grass carp and reduced the digestive and absorptive ability.

Key words: grass carp；rice straw；rice-fish rotation

盐碱胁迫对翘嘴鳜幼鱼生存、生长及生理变化的影响

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摘要：盐碱水在世界范围内分布广泛、储量丰富，对水产养殖业的发展和盐碱资源的综合利用起着至关重要的作用。本研究评估了翘嘴鳜急性盐碱胁迫耐受性以及长期盐碱胁迫下的生长和生理变化。急性胁迫下，翘嘴鳜 96h 半致死盐度和碳酸盐碱度分别为 13.92 和 13.44mmol/L。设置淡水（FW，对照组）、盐水（SW，盐度 5）和碱水组（AW，碳酸盐碱度 8mmol/L），研究翘嘴鳜长期盐碱胁迫下生存、生长及生理变化。结果表明，经过 60 d 养殖，盐度和碱度均不影响翘嘴鳜存活率，且 SW 组的生长性能明显优于 FW 组，与 FW 组相比，AW 组的肝体比较低，SW 组的肌肉含量显著提高。在生理指标分析中，AW 组表现出较高的 VHA 活性，而 SW 组的催乳素水平较低，对鳃组织进行电镜检测，发现盐度和碱度环境下鳃氯细胞形态与结构发生适应性变化。这些结果表明，翘嘴鳜具有良好的盐碱耐受性，在盐度 5 和碳酸盐碱度 8mmol/L 的水中表现出较好的生长性能。

关键词：盐度；碱度；鳜鱼；生长性能；生理调节

Effects of saline and alkaline stresses on survival, growth, and physiological responses in juvenile mandarin fish (Siniperca chuatsi)

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Abstract：Abstract: Saline-alkaline water, which is widely distributed and abundant worldwide, plays a critical role in the advancement of the aquaculture industry and the comprehensive utilization of saline-alkaline resources. This study evaluated the tolerance of mandarin fish (Siniperca chuatsi) to acute salinity and alkalinity while investigating the growth and physiological changes under chronic saline and alkaline stress. First, we estimated effects of acute salinity and alkalinity on mandarin fish （4.33 ± 0.31 g), the LC50 for 96 h of salinity and alkalinity was 13.92 and 13.44 mmol/L, respectively. Then, we measured the 60-d survival, growth performance and physiological responses of mandarin fish (22.53 ± 0.60 g) reared in freshwater (FW, the control group), saline water (SW; fixed salinity of 5) and alkaline water (AW; carbonate alkalinity of 8 mmol/L). The results revealed that both SW and AW groups neither affected the survival rate of mandarin fish, and the growth performance in SW group was significantly superior to FW group. Compared to the FW group， AW group demonstrated a lower hepatosomatic index and SW group showed a significantly higher meat content. In the analysis of physiological indicators, the AW group exhibited higher V-H+-ATPase (VHA) activity, while the SW group had lower prolactin (PRL) levels. The mitochondria-rich cells (MRCs) underwent morphological adaptations to saline and alkaline stress, highlighting their importance in osmotic regulation and acid-base balance. Our results suggested mandarin fish had good tolerance to salinity and alkalinity, and it was suitable for breeding in low saline and alkaline water, which suggested that saline-alkaline areas and agricultural irrigation water can be successfully utilized for sustainable aquaculture. This research will which expanding the understanding of the saline and alkaline tolerance in aquaculture organisms and offering theoretical support for the cultivation of mandarin fish in saline-alkaline water.

Key words: Salinity; Alkalinity; Siniperca chuatsi; Growth performance; Physiological Regulation

基于食物多样化构建食物丰容在黄姑鱼生长、免疫和抗氧化性能的影响

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摘要：食物丰容是环境丰容的一种重要表现形式，是一种全新的投喂手段，可通过改变食物的形式或种类、变换食物提供的方法和时间、增加食物提供的技巧等来构建，对改善动物身心健康、增强其自然行为能力和环境适应能力有重要作用。本文以黄姑鱼（Nibea albiflora）幼鱼为材料，选取配合饲料、冰鲜脊尾白虾和活沙蚕按特定比例组合成 3 种等氮能比的食谱，构建食物丰容，研究其对黄姑鱼的作用，养殖周期为 60 天。结果表明，与仅投喂配合饲料的鱼相比，经食物丰容强化后的鱼，增重率和存活率被显著提高，产出成本下降约 23%，胃、肝和前肠对食物中脂肪和蛋白质的消化吸收能力更强，血清、肝脏和脾脏中的与免疫和抗氧化相关的活性物质有显著提高。经脱水应激后，食物丰容组的鱼生理机能反应平稳，复水后恢复迅速。转录组分析表明，食物丰容主要影响了肝脏中代谢相关通路及脾脏中免疫和抗氧化相关通路。本研究可为黄姑鱼及其他鱼类养殖高质量发展提供参考。

关键词：食物丰容；黄姑鱼；生长；免疫；抗氧化性能

Effect of food enrichment based on diets diversity on the growth, immunity and antioxidant capacity of Nibea albiflora

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Abstract： Food enrichment, an important member of environment enrichment, is a novel feeding strategy which can be constructed by changing the form or type of food, adjusting the feeding time or feeding frequency, diversifying the methods of feeding or enriching the feeding tips based on animals' dietary characteristics, and it plays essential roles in improving the physical and mental health of animals, their natural behavior ability and environmental adaptability. In the current study, the juvenile Nibea albiflora was used and the commercial diet, the ice-fresh Exopalaemon carinicauda and the live Perinereis nuntia were selected to build three isonitrogen energy ratios recipes by special formulas so as to construct the food enrichment model then explore the effects of such a feeding strategy on the fish. The cultured period was 60 days. And the results demonstrated that compared to the fish simply fed with the commercial diet, the fish from the food enrichment group owned a higher weight gain and survival rate, and the output cost was declined with the ratio reached to 23%. Meanwhile, they also had stronger digestion and absorption of fat and protein in the stomach, liver and foregut, as well as higher activity of immunity and antioxidant in the serum, liver and spleen. A dehydration assay was conducted and the result displayed that after this stimulation, the physiological function of fish from the food enrichment group was stable and could recover quickly. The transcriptome results showed that such a feeding strategy could mainly affect the metabolism-related pathways in the liver and immune-related and antioxidant-related pathways in the spleen. Summary, our study can provide some reference for the high quality development of N. albiflora or other species culturing.

Key words: Food enrichment; Nibea albiflora; Growth; Immunity; Antioxidant capacity

摄食后急性低氧对黄颡鱼
呼吸代谢和消化的影响

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摘要：本实验以两种摄食状态的黄颡鱼为研究对象，进行 48 h 急性低氧暴露，主要研究摄食后急性低氧对黄颡鱼呼吸代谢和消化的影响。结果表明，摄食后急性低氧的黄颡鱼呼吸频率加快，耗氧率降低。鳃中 SDH 先升高后显著降低（$p < 0.05$），而 LDH 显著增加（$p < 0.05$）；缺氧诱导因子（hif-1α）表达水平显著升高（$p < 0.05$），下游编码基因 hk，pfkla，pkma 等糖酵解关键分子表达水平提高，关键酶（HK，PFK 和 PK）活性增加；同时，葡萄糖含量降低，乳酸含量增加，这说明黄颡鱼鳃中的代谢方式逐渐向无氧代谢转变，激活无氧糖酵解为体内提供能量。此外，黄颡鱼肝脏和肠中的消化酶活性（胰蛋白酶，脂肪酶，淀粉酶）降低，消化基因（trpsin, lipac, amylase）表达水平受到抑制，说明其消化能力的降低，这可能对其生长发育造成不利影响。本研究为鱼类健康养殖提供新的见解。

关键词：摄食，低氧；代谢；消化；黄颡鱼

Effects of acute hypoxic post-feeding condition on respiratory metabolism and digestion in yellow catfish (Pelteobagrus fulvidraco)

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Abstract： In this study, acute hypoxia was applied to two states of yellow catfish (Pelteobagrus fulvidraco) (non-feeding and feeding) for 48 h. We investigated the effects of acute hypoxia on the respiratory metabolism and digestive ability of yellow catfish (mean body length: 7.61 ± 0.52 cm). The results indicated that the respiratory frequency of yellow catfish under acute hypoxic post-feeding condition was rapidly accelerated and the oxygen consumption rate was reduced. The level of succinate dehydrogenase in the gills first increased and then significantly decreased ($p < 0.05$) and the level of lactate dehydrogenase significantly increased ($p < 0.05$). When the expression level of hypoxia-inducing factor was significantly increased ($p < 0.05$), the downstream coding genes (hexokinase 1 (hk1), phosphofructokinase (pfkla), and pyruvate kinase M1/2a (pkma)), key molecules of glycolysis, and the activity of crucial enzymes (hexokinase, phosphofructokinase, and pyruvate kinase) increased. At the same time, the glucose level dropped and the lactic acid level increased, indicating that the metabolic mode in the gills of yellow catfish under acute hypoxic post-feeding condition gradually changed to anaerobic, and the anaerobic glycolysis process was activated to provide the required energy for the body. In addition, we found that the activity of digestive enzymes (trypsin, lipase, and amylase) and expression levels of digestive genes (trypsin, lipase, and amylase) were inhibited in the liver and intestine of yellow catfish under the acute hypoxic post-feeding condition, indicating that their digestive ability was reduced. This may adversely affect growth and development. This study analyzed the effects of acute hypoxic post-feeding exposure on the respiratory metabolism and digestive capacity of yellow catfish, providing new insights into fish physiology and sustainable fish culture.

Key words: Feeding; Hypoxia; Metabolism; Digestion; Pelteobagrus fulvidraco

海水养殖中高密度下的慢性应激：

评估对虹鳟生长性能和脂质代谢的影响

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摘要：在海水养殖中，高养殖密度造成的长期应激损害了动物福利，并导致渔业产量下降。然而，以往大多数研究都是在淡水而非海水中评估高密度放养对虹鳟的影响。将虹鳟在圆形水箱中海水养殖 84 天，设置低密度（"LD"，9.15→22.00kg/m³）、中密度（"MD"，13.65→32.05kg/m³）和高密度（"HD"，27.31→52.24kg/m³）。评估了养殖密度对其生长性能和脂质代谢的影响。在海水养殖中，高密度的慢性应激会明显降低生长性能和饲养效率。在 HD 的肠道中，脂类消化能力增强，而血液中甘油三酯的浓度降低。此外，在 HD 肝脏观察到乙酰辅酶 A 羧化酶（ACC）和脂肪酸合成酶（FAS）减少，激素敏感脂肪酶（HSL）浓度增加，肝脏β氧化过程被激活。冗余分析表明，甘油和 HSL 可用作评估海水养殖鳟鱼生长性能的潜在标记。研究表明，长期高养殖密度会对虹鳟的生长性能产生负面影响，减少脂肪酸的从头合成，促进脂肪分解。

关键词：虹鳟；海水养殖；养殖密度；生长；脂质代谢

Effects of chronic stress from high stocking density in mariculture: evaluations of growth performance and lipid metabolism of rainbow trout (Oncorhychus mykiss)

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Abstract：Background: Global rainbow trout (Oncorhychus mykiss) production was around 1 million tons and inland aquaculture occupied about 70%. As the scarcity of freshwater resource, mariculture plays an important role in providing commercial trout production for high quality protein worldwide. In aquaculture, chronic stress due to high stocking density impaired animal welfare and results in declined fishery production with low protein quality. However, most of previous studies evaluated effects of high stocking density on trout in freshwater rather than seawater.

Methods: Juvenile trout were reared for 84 days in circular tanks under 3 stocking densities, including low density (“LD”, 9.15 kg/m³), moderate density (“MD”, 13.65 kg/m³) and high density (“HD”, 27.31 kg/m³) in seawater. The final densities of LD, MD and HD were 22.00, 32.05 and 52.24 kg/m³, respectively. Growth performance and lipid metabolism were evaluated.

Results: Growth performance and feeding efficiency was significantly reduced due to chronic stress of high density in mariculture. The gut digestive activity of lipids was promoted in the gut of HD, while the concentration of triglyceride was decreased in the blood. Furthermore, decreased Acetyl-CoA carboxylase (ACC) and fatty acid synthase (FAS), increased hormone sensitive lipase (HSL) concentration and activated hepatic β-oxidation process were observed in trout of HD. Redundancy analysis showed glycerol and HSL can be used as potential markers to evaluate growth performance of trout in mariculture.

Conclusion: We showed chronic high stocking density led to negative effects on growth performance, reduced de novo synthesis of fatty acids and enhanced lipolysis. Our study would provide a basis for understanding the growth and lipid metabolism of rainbow trout under chronic stress from stocking density in mariculture.

Key words: Rainbow trout; Mariculture; Stocking density; Growth; Lipid metabolism

消毒剂对草鱼肠道免疫及肠道菌群的影响

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摘要：肠道微生物组对维持鱼类健康稳态至关重要。消毒剂可以杀死重要的病原体并对鱼卵进行消毒，但它们对健康鱼类的免疫途径和肠道微生物组的影响尚不清楚。在这项研究中，我们在为期四周的试验中研究了两种消毒剂对草鱼转录组特征、免疫反应和肠道微生物群动态的影响。特别是用 80μg/L 戊二醛或 50μg/L 聚维酮碘对水进行消毒。我们发现戊二醛和聚维酮碘可诱导肠道氧化应激，并降低草鱼消化酶的功能。16S rDNA 高通量测序结果表明，经过消毒处理后，草鱼肠道微生物群的多样性降低。此外，转录组分析显示，消毒剂暴露改变了草鱼的免疫相关途径。与对照组相比，戊二醛组和聚维酮碘组均检测到组织病理学变化和细胞凋亡。总之，暴露于消毒剂会增加氧化应激，抑制免疫反应，导致细胞凋亡，并导致草鱼肠道菌群失调。

关键词：消毒剂；戊二醛；聚维酮碘；凋亡；草鱼

Long-term disinfectant influences on intestinal immunity and microbiome variation of grass carp

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Abstract： The gut microbiome is crucial in maintaining fish health homeostasis. Disinfectants can kill important pathogens and disinfect fish eggs, yet their effect on the immune pathways and intestinal microbiome in healthy fish remains unknown. In this study, we investigated the effects of two disinfectants on the transcriptome profiles, immunological response, and gut microbiota dynamics of grass carp over a four-week trial. In particular, aquatic water was disinfected with 80 μg/L glutaraldehyde or 50 μg/L povidone-iodine. We found that glutaraldehyde and povidone-iodine induced gut oxidative stress and depressed the function of grass carp digestive enzymes. The results of the 16S rDNA high-throughput sequencing identified a reduction in the diversity of grass carp gut microbiota following the disinfectant treatment. Moreover, transcriptome profiling revealed that disinfectant exposure altered the immune-related pathways of grass carp. Compared to the control group, histopathological changes and apoptosis were detected in both glutaraldehyde and povidone-iodine groups. In conclusion, exposure to disinfectants was observed to increase oxidative stress, suppress the immune response, cause apoptosis, and lead to dysbiosis of the intestinal flora in grass carp.

Key words: disinfectant; glutaraldehyde; povidone-iodine; apoptosis; grass carp

基于遥感和动态能量收支模型的山东长牡蛎养殖适宜性研究

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摘要：为了优化山东近海长牡蛎养殖的空间格局，本研究采用卫星遥感获取的海水表层温度、叶绿素浓度和悬浮颗粒物浓度数据，基于市场最为关注的牡蛎售卖指标，构建了山东半岛长牡蛎养殖适宜性市场导向评价模型（SMASM）。研究结果表明，桑沟湾全年的养殖适宜性都较高；莱州湾东部水体在春秋时节适合进行牡蛎的育肥养殖；崂山湾和长山岛附近适合进行稚贝的培育。模型结果与山东牡蛎实际年产值保持一致，总体呈增长趋势。其中，2019年牡蛎总产值低于前一年，是受到了超强台风利奇马的影响。本研究结果可以为山东半岛长牡蛎养殖规划提供有效的量化依据和理论基础。

关键词：长牡蛎；卫星遥感；动态能量收支；养殖适宜性指数；养殖区划管理

Remote Sensing and Dynamic Energy Budget-driven Crassostrea gigas aquaculture suitability assessment in Shandong Coastal

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Abstract： Managing the costal aquaculture area of Crassostrea gigas can increase the yield and reduce the losses caused by environment in Shandong. In this study, based on Dynamic Energy Budget (DEB) model, sea surface temperature, chlorophyll-a and total suspended sediment data obtained by remote sensing, were used to construct an evaluation model for C. gigas suitability assessment in Shandong Province. The results revealed that Sanggou Bay exhibited high aquaculture suitability throughout the whole year. Eastern of Laizhou Bay were suitable for oyster fattening during the spring and autumn seasons. Additionally, Laoshan Bay and Changshan Island coastal were suitable for the cultivation of oyster seedlings. Sudden drops in water temperature, red tides, and significant increases in turbidity can exert detrimental effects on oyster production, which has been evidenced to be influenced by Super Typhoon Lekima in 2019. The results of this study can provide effective quantification and scientific basis for C. gigas aquaculture suitability assessment in Shandong province.

Key words: Crassostrea gigas; satellite remote sensing; Dynamic Energy Budget (DEB); aquaculture suitability index; aquaculture zoning management

循环水养殖中流速对翘嘴鳜生长、抗氧化、免疫和肠道健康的影响研究

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摘要：流速被认为是影响鱼类生长和健康的重要因素之一，选择合适的流速对提高水产品质量和养殖经济效益具有重要作用。本实验以翘嘴鳜为研究对象，首次研究了循环水养殖中水流速度对其生长性能、抗氧化活性、免疫反应和肠道菌群的影响。结果表明，1.2bl/s 的高流速促进了翘嘴鳜的生长和消化，增加了粗蛋白质含量，抑制了脂肪沉积。0.8bl/s 的中流速丰富了翘嘴鳜的肠道群落丰富度。此外，翘嘴鳜在中、高流速条件下的食欲更为旺盛。然而，高流速会引起翘嘴鳜的应激，导致免疫力下降，增加死亡率和肠道疾病的风险。上述发现不仅能够为实际生产中的循环水养殖鳜鱼提供流速参考，同时为水产养殖中福利化、智能化、节能化的流速控制系统的研发提供理论依据，对推动鳜鱼工厂化养殖发展具有重要意义。

关键词：翘嘴鳜；流速；生长；免疫；肠道健康

Effects of flow velocity on the growth performance, antioxidant activity, immunity and intestinal health of Chinese Perch (Siniperca chuatsi) in recirculating aquaculture systems

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Abstract： Flow velocity is considered to be one of the important factors affecting the growth and health of fish, and choosing the appropriate flow velocity plays an important role in improving the quality of aquatic products and the economic benefits of aquaculture. In this study, the effects of water flow velocity on the growth performance, antioxidant activity, immune response and intestinal microbiota of Chinese Perch (Siniperca chuatsi) in recirculating aquaculture were studied for the first time. The results showed that the high flow velocity of 1.2 bl/s promoted the growth and digestion of Chinese Perch. The medium flow velocity of 0.8 bl/s enriched the intestinal community richness of Chinese Perch. In addition, the appetite of Chinese Perch was more vigorous under medium and high flow velocity conditions. However, high flow velocity can cause stress in Chinese Perch, leading to decreased immunity and increased mortality and the risk of intestinal disease. The above findings can not only provide a flow velocity reference for circulating water aquaculture Chinese Perch in actual production, but also provide a theoretical basis for the research and development of welfare, intelligence and energy saving flow rate control system in aquaculture, which is of great significance to promote the development of Chinese Perch factory aquaculture.

Key words: flow velocity; Chinese perch; growth performance; immunity; intestinal health

红毛菜陆基悬浮养殖技术研究

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摘要：考虑到传统海区浮筏养殖存在环境不可控、养殖周期有限、病敌害频发等问题，室内陆基悬浮养殖是未来大型藻类产业发展的一个重要方向。红毛菜是迄今为止报道的二十碳五烯酸（EPA）含量最高的大型高值海藻，其特殊的丝状结构，是最适合悬浮培养的藻种。本研究首次开展了红毛菜叶状体（原叶体）悬浮培养试验，以 50L 光生物反应器和 1000L 白色塑料桶为培养器具，日生长率最高达 18.18%·d-1 和 21.39%·d-1，远高于网帘的室内水泥池养殖和海区筏式养殖；确定了最佳环境条件，养殖周期从传统筏式养殖的 10-15 天缩短到 6-9 天。室内悬浮培养的红毛菜灰分和粗脂肪含量提高了 20.81%和 25.00%，新鉴定到 13 种微量脂肪酸，其中 n-7 不饱和脂肪酸含量随培养时间延长而增加。本研究技术空间利用效率高、养殖周期短、养成品无杂质，填补了大型藻类陆基可控悬浮养殖模式的空白，为水产 10 大优异种质资源的开发利用提供技术支撑。

关键词：红毛菜；陆基养殖；悬浮培养；海区筏式网帘养殖；高效光生物反应器养殖

Research on land-based suspension aquaculture of Bangia fuscopurpurea

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Abstract： Indoor land-based suspended cultivation is an important direction for the future development of macroalgae industry considering the issues of environmental uncontrollability, limited cultivation cycle, and frequent occurrence of diseases in traditional Sea-area raft net curtain aquaculture. Bangia fuscopurpurea is a large-value seaweed with the highest content of eicosapentaenoic acid (EPA) reported so far, and its unique filamentous structure makes it the most suitable species for suspended cultivation. In this study, we conducted the cultivation mode of suspension propagation in kelp phytotron glass room with temperature 9.0~22.0℃ during the period from December 9, 2021 to February 10, 2022． The results showed that the maximum average daily growth rate could reach 18.18%·d-1 and 21.39%·d-1 in the 50 L photobioreactor and 1 000 L culture tank， respectively， which the yield was much higher than that in indoor cement pond culture and marine raft culture. The optimal environmental conditions were determined, and the cultivation cycle was shortened from 10-15 days in traditional raft cultivation to 6-9 days. The ash and crude fat content of Bangia fuscopurpurea cultivated through indoor suspended cultivation increased by 20.81% and 25.00%, respectively. Thirteen types of trace fatty acids were newly identified, with the content of n-7 unsaturated fatty acids increasing with the prolongation of cultivation time. The high technical spatial utilization efficiency, short cultivation cycle, and impurity-free end products of this study fill the gap in large-scale controlled suspended cultivation models indoor for macroalgae, providing technical support for the development and utilization of the top 10 excellent aquatic germplasm resources.

Key words: Bangia fuscopurpurea; Land-based aquaculture; Suspension propagation; Sea-area raft net curtain aquaculture; Efficient photobioreactor aquaculture

水稻浮床对养殖池塘水质净化效果研究

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摘要：为研究水稻对养殖池塘水质净化效果和鱼类产量的影响，设计 2 个处理，分别为水稻浮床组（试验组），常规养殖组（对照组）。试验期间，定期检测两个试验池塘水质理化指标，试验结束后统计养殖鱼类产量、成活率及水稻产量。结果显示：试验组平均水温略低于对照组，透明度(SD)高于对照组；试验初期，试验组溶解氧(DO)含量高于对照组，中后期 DO 含量低于对照组。试验期间，水稻浮床对养殖池塘水体总磷(TP)、总氮(TN)、氨氮(NH4+-N)、亚硝酸盐氮(NO2--N)、化学耗氧量(CODMn)的平均去除率分别为 30.6%、29.6%、27.9%、21.0%和 15.6%。试验组不同养殖鱼类成活率均高于对照组，养殖鱼类产量 22 557.15 kg/hm2，浮床水稻产量 5 234.57 kg/hm2。

关键词：池塘养殖；浮床种稻；水质净化

Study on the Purification Effect of Rice Floating-Bed on Water Quality in Aquaculture Pond

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Abstract：In order to study the effect of rice on water purification and fish production in aquaculture ponds, two treatments were designed, namely, rice floating-bed group (experimental group) and conventional aquaculture group (control group).During the experiment, the physical and chemical indexes of water quality of the two experimental ponds were detected regularly, and the yield of cultured fish, survival rate and rice yield were counted after the experiment.The results showed that the average water temperature of the experimental group was slightly lower than that of the control group, and the transparency (SD) of the experimental group was higher than that of the control group.At the beginning of the experiment, the content of dissolved oxygen (DO) in the experiment group was higher than that in the control group, and the content of DO in the experiment group was lower than that in the control group at the middle and late stages.The average removal rates of TP, TN, NH4+-N, NO2--N and CODMn were 30. 6%, 29.6%, 27.9%, 21.0% and 15. 6% respectively.The survival rate of different cultured fish in the experimental group was higher than that in the control group, the yield of cultured fish was 22 557. 15 kg/hm2, and the yield of floating bed rice was 5 234. 57 kg/hm2.

Key words: Pond culture; Rice planting on floating bed; Water purification

响应面法优化雨生红球藻培养基

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摘要：雨生红球藻（Haematococcus pluvialis）是生产高值天然虾青素的优质藻种，优化培养基营养盐组成对提高藻细胞密度和虾青素产量具有重要意义。以雨生红球藻为受试藻株，以BG11为基础培养基，进行单因素试验筛选 NaNO3、MgSO4·7H2O、K2HPO4·3H2O 和 Na2CO3 共 4 种营养盐最适浓度范围，采用响应面法对培养基关键营养盐浓度进行优化，并进行验证试验。结果表明：雨生红球藻相对适宜营养盐 NaNO3、MgSO4·7H2O、K2HPO4·3H2O 和 Na2CO3 的质量浓度范围分别为 1500-2000、80-640、20-60 和 20-80 mg·L-1；对藻细胞生长的促进作用依次为 NaNO3、Na2CO3、K2HPO4·3H2O 和 MgSO4·7H2O；通过响应面法分析得到上述 4 种营养盐最佳盐浓度分别为 1556.42、51.43、42.18 和 358.59 mg·L-1，其中 K2H

关键词：雨生红球藻；培养基优化；响应面法

Optimization the Culture Medium of Haematococcus pluvialis by Response Surface Methodology

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Abstract： Haematococcus pluvialis is an excellent algae species for production natural astaxanthin. Optimizing the nutrients composition of the culture medium is important to improve the density of algal cells and astaxanthin content. A single-factor test was conducted to screen the optimal concentration range of NaNO3, MgSO4·7H2O, K2HPO4·3H2O and Na2CO3, and the medium was optimized using the response surface methodology and validation tests. The results showed that the mass concentration of NaNO3,MgSO4·7H2O,K2HPO4·3H2O and Na2CO3, were in the ranges of 1500-2000, 80-640, 20-60 and 20-80 mg·L-1, respectively. The most promoting effects on algal cell density were in the order of NaNO3, Na2CO3, K2HPO4·3H2O and MgSO4·7H2O, the optimal nutrient concentrations respectively were 1556.42 mg·L-1, 51.43 mg·L-1, 42.18 mg·L-1 and 358.59 mg·L-1. The interaction between K2HPO4·3H2O and MgSO4·7H2O was significant(P<0.05). Cultured H. pluvialis for 8 days in the optimized medium, the Fv/Fm of PSII and Chl-a content of the algae cells were 0.69 and 7268.97 μg·L-1, respectively, which were both significantly higher than the that in the control group, and the cell density was 3.53 × 105 mL-1, which was significantly higher than the control by 20.48 %(P<0.05).

Key words: Haematococcus pluvialis; Culture medium optimization; Response surface methodology

稻渔综合种养模式下养殖密度对鲤鱼肌肉抗氧化状态、氨基酸和脂肪酸组成的影响

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摘要：为探究稻鲤共作模式下不同养殖密度对鲤鱼(Cyprinus carpio)抗氧化状态、肌肉氨基酸和脂肪酸组成的影响，以初始体重为(105.83 ± 2.52) g 的鲤鱼为研究对象，在低密度(52.9 g/m3)、中密度(105.8/m3)和高密度(158.7 g/m3)三种密度中养殖 60 天。结果显示，与低密度组相比，高密度组中肌肉 T-AOC、GSH 和 GPx 的含量显著下降；此外，大部分氨基酸含量无显著变化，而 SFA、MUFA、n-3 PUFA 以及 n-6 PUFA 的含量显著增加。综上所述，稻-鲤共作模式下高养殖密度会对鲤鱼的抗氧化状态产生不利影响，并导致肌肉的脂肪酸含量发生改变。

关键词：稻鱼共作；鲤鱼；养殖密度；抗氧化状态；肌肉组成

Effects of stocking density on the antioxidant status, amino acid and fatty acid composition of Cyprinus carpio in Integrated Rice-Fish farming systems

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Abstract：To investigate the effects of stocking density on the antioxidant status, muscle amino acid and fatty acid composition of Cyprinus carpio in integrated rice-fish farming systems, the fish with an initial weight of (105.83 ± 2.52) g were reared at low density (LD, 52.9 g/m3), medium density (MD, 105.8/m3) and high density (HD, 158.7 g/m3) for 60 days. The results showed that the content of T-AOC, GSH and GPx in the HD group decreased significantly compared with the LD group. In addition, most amino acid levels did not change significantly, while SFA, MUFA, n-3 PUFA and n-6 PUFA increased significantly. Overall, our data indicated that the HD treatment adversely affected the antioxidant status and led to changes in the fatty acid content in the muscle of Cyprinus carpio in an integrated rice–fish farming system.

Key words: Integrated Rice-Fish Farming; Cyprinus carpio; Stocking Density; Antioxidant status; Muscle Composition

基于涡量矩定理草金幼鱼水动力特性分析

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摘要：鱼体推进机理及推进性能的研究是流体力学中的一个热点，自然界中的鱼类大多数通过身体尾鳍波动模式来产生更大的速度和推力，本文以短尾草金幼鱼为研究对象，利用数字粒子图像测速技术（PIV）和涡量矩定理，对鱼类前进转弯、转弯、后退三种运动状态进行追踪，完成速度、流场、涡量的测量。研究结果表明：不同运动状态下，运动学和水动力学差异明显，三种转弯运动过程中主要依靠正值涡量产生鱼类机动所需作用力且主要依靠尾鳍产生。相关研究结果对鲤科鱼类、其它鱼类运动机理的研究以及水下仿生模型的研究提供参考依据。

关键词：草金幼鱼；粒子图像处理技术；涡量矩定理；作用力；推进效率

Kinetic study of juvenile grass gold based on the vorticity moment theorem

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Abstract： In this paper, the juvenile bobtail golden fish is the research object, and the digital particle image velocity measurement (PIV) and vorticity moment theorem are used to track the three motion states of the fish forward turn, turn and retreat, and complete the measurement of velocity, flow field and vorticity. The results show that there are obvious differences in kinematics and hydrodynamics under different motion states, and the positive vorticity is mainly relied on the positive vorticity to generate the force required for fish maneuvering and the tail fin is mainly relied on during the three turning movements. The results of this study provide a reference for the study of the locomotion mechanism of carps and other fishes and the study of underwater biomimetic models.

Key words: Juvenile grass gold; particle image processing technology; eddy moment theorem; Effort; Advance efficiency

长江口养殖池塘微塑料赋存特征及生态效应

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摘要：为了解微塑料对养殖鱼类及养殖生产系统潜在的影响，我们对长江口淡水养殖池塘微塑料赋存特征进行了调查，在此基础上研究了其生态效应。结果显示，微塑料可在鱼类肠道、鳃和皮肤蓄积，改变共生微生物群落结构和多样性，导致肠道菌群功能紊乱，抑制消化吸收、刺激免疫反应，并通过菌群-肠-脑轴机制改变摄食和运动行为；进一步通过整合生物标志物，发现微塑料干扰氧化还原稳态和组织同位素周转，且这些效应能够被饥饿修饰，并通过引起鱼类氧化防御和色素沉积之间的分配权衡，降低了鱼类养殖品质；作为新生态位，发现微塑料不仅能够吸附重金属，还可作为微生物载体，通过选择性富集功能微生物导致与池塘环境介质中微生物群落发生显著分化，微塑料表面生物膜中参与氮转化的功能基因也发生了特性性富集，沉积塑料际 amoA、hao 基因丰度显著富集，而水体塑料际 nxrA、nxrB 基因丰度显著增加，从而差异促进了硝化过程，并增加了池塘氮转化中 N2O 的产生。

关键词：微塑料；养殖池塘；氮转化；温室气体

Occurrence characteristics and ecological effects of microplastics in aquaculture ponds of Yangtze River estuary

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Abstract： In order to understand the potential impacts of microplastics on cultured fish and aquaculture system, we investigated the occurrence characteristics of microplastics in freshwater aquaculture ponds in the Yangtze River Estuary, and then studied their ecological effects. The results showed that microplastics could accumulate in the gut, gill and skin of fish, change the structure and diversity of symbiotic microbial communities, lead to intestinal microbiota dysbiosis, inhibit digestion and absorption, stimulate immune response, and change feeding and exercise behavior through the microbiome-gut-brain axis. Further, by integrating biomarkers, it was found that microplastics interfered with REDOX homeostasis and tissue isotope turnover, and these effects could be modified by starvation, and reduced fish culture quality by causing a distributional tradeoff between oxidation defense and pigmentation. As a new ecological niche, it is found that microplastics can not only adsorb heavy metals, but also serve as microbial carriers. Through selective enrichment of functional microorganisms, significant differentiation occurred between microplastics and microbial communities in the pond environment medium. Functional genes involved in nitrogen conversion in the biofilm on the surface of microplastics also presented characteristic enrichment, and the abundance of amoA and hao genes was significantly enriched in the deposited plastics. The abundance of nxrA and nxrB genes in water plastisphere increased significantly, which promoted the nitrification process and increased the production of greenhouse gas N2O in the pond nitrogen conversion.

Key words: Microplastics; Aquaculture ponds; Nitrogen conversion; Greenhouse gas

茯苓多糖和黄芪多糖添加对长江鲟免疫应答和肠道菌群结构的影响研究

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摘要：为探明茯苓多糖和黄芪多糖添加对长江鲟生长、免疫的影响，本研究将长江鲟随机分为三组，分别给予常规饲料、常规饲料加茯苓多糖（200 mg/kg）和常规饲料加黄芪多糖（200 mg/kg）投喂，为期 14 天。研究结果显示，饲粮中添加黄芪多糖可显著提高长江鲟体重增长。与摄食常规饲料的个体相比，茯苓多糖和黄芪多糖添加可以提高摄食个体超氧化物歧化酶、溶菌酶、过氧化氢酶和谷胱甘肽过氧化物酶活性水平，同时降低丙二醛水平。此外，黄芪多糖添加可提升摄食个体两种炎症细胞因子（肿瘤坏死因子和免疫球蛋白 M）的基因表达水平。肠道菌群结构分析结果表明，黄芪多糖添加可提高摄食个体主要肠道菌群的丰度和多样性，茯苓多糖添加摄食个体的肠道微生物组成和常规饲料摄食个体有显著差异。本研究结果表明，饲粮中添加茯苓多糖和黄芪多糖可能加快长江鲟生长发育并提高炎症免疫响应，为鲟鱼人工育种中植物多糖添加的潜在应用提供了理论依据和数据参考。

关键词：达氏鲟；茯苓多糖；黄芪多糖；肠道微生物

Biological effects of Poria cocos and Astragalus polysaccharides on the immune responses and microbiome of Dabry' s sturgeons

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Abstract：This current study aims to examine the impact of Poria cocos (PP) and Astragalus polysaccharides (AP) in the diet on the antioxidant status, expression of immune-related genes, and the composition and potential functions of gut bacterial communities in Dabry's sturgeons. In this study, Dabry's sturgeons were subjected to random allocation into three groups and provided with diets consisting of normal food, PP-supplemented food (200 mg/kg), and AP-supplemented food (200 mg/kg) for a duration of 14 days. The inclusion of AP in the diet resulted in a significant increase in the final body weight of Dabry's sturgeon. Compared to individuals fed with a normal diet, those fed with diets containing PP and AP exhibited enhanced activity levels of superoxide dismutase, lysozyme, catalase, and glutathione peroxidase, while concurrently experiencing reduced levels of malondialdehyde. Furthermore, the group administered with AP exhibited elevated gene expression levels of two inflammatory cytokines, namely tumor necrosis factor alpha and immunoglobulin M, compared to the control group. Examination of the intestinal microbiota demonstrated that the consumption of AP enhanced the abundance and variety of the predominant gut microbiota in Dabry's sturgeons. The composition of the microbiota in the PP group differed significantly from that of the control group. The findings of our study suggest that the inclusion of PP and AP in the diet may have a positive impact on the growth, development, and inflammatory response of Dabry's sturgeons. These results offer valuable insights into the potential use of plant polysaccharide additives in the artificial breeding of sturgeons.

Key words: Dabry's sturgeon; Poria cocos; Astragalus; polysaccharide; gut microbiota

克氏原螯虾合理投喂问题的探讨

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摘要：当前，克氏原螯虾的饲料投喂普遍采用随机抛撒的方式，存在较大的盲目性；该虾养殖的饲料成本一般占整个生产成本的50-60%。如何合理投喂，减少饲料浪费，节省养殖成本，这是养殖者非常关心的一个重要问题。围绕克氏原螯虾合理投喂问题，我们研究了两种蛋白含量（26%、30%）的饲料和五个投喂水平对克氏原螯虾存活、生长及肌肉营养成份的影响，探讨了投饵区不同生境类型对克氏原螯虾摄食行为及摄食的影响，初步评估了克氏原螯虾对配合饲料的感知能力。主要研究结论如下：（1）投喂蛋白含量26%的饲料可以满足食用虾养殖对营养的需求，最适投喂水平为60%的饱食水平。（2）投饵区不同生境类型对搜索时间和摄食效率存在显著的影响，草丛和石砾生境不利于摄食；草丛密度越高，残饵率越高；这些表明饲料应投放在平坦且无草或草稀的底质上。（3）克氏原螯虾对配合饲料感知的最大距离为12m。

关键词：克氏原螯虾；营养需求；摄食水平；摄食行为；食物感知

Research on the aspect of reasonable feeding strategy in red swamp crayfish (Procambarus clarkii)

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Abstract： In order to establish the reasonable feeding strategy for Procambarus clarkii, we studied the effects of two dietary protein levels (26% and 30%) and five feeding levels (satiation, 80%, 60%, 40% and 20% satiations) on growth performance and muscle composition of juvenile P. clarkii, experimentally tested the effects of four habitat types (feed platform, sand, gravel and grass substrate) of feeding area on the foraging behaviors and consumption, and investigated the ability for perception of formulated feed in P. clarkii. Main conclusions were presented as follows: (1) The dietary protein content of 26% may meet the nutritional needs of juvenile P. clarkii, and the optimal feeding level was 80% of satiation level. (2) The habitat types had significant impacts on search time, consumption and residual feeds. The grass and gravel habitat were not conducive for P. clarkii to forage pellet feeds, in which the residual feed was significantly higher than that in feed platform; the higher the grass density of feeding area, the higher the residual feed. Those suggested that pellet feed should be cast on the flat and no or sparse grass substrate to increase feed utilization rate, not be placed on the uneven or dense grass substrate. (3) Maximum of spacing distance for P. clarkii to perceive pellet feed was estimated to be 12 m.

Key words: Red swamp crayfish (Procambarus clarkia); nutrient requirement; feeding level; foraging behavior; perception of food

稻–鲤(Cyprinus carpio)共作模式下养殖密度对鲤肝脏功能以及抗氧化状态的影响

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摘要：养殖密度是影响水产养殖产量的重要因素，放养密度过高会引起养殖动物的应激。为探究稻渔综合种养模式中养殖密度对鲤(Cyprinus carpio)肝脏的氧化应激和能量代谢的影响，本研究以鲤为研究对象，设置为低密度组(LD,10 尾，52.9g/m2)、中密度组(MD,20 尾，105.8g/m2)、高密度组(HD,30 尾，158.7g / m2)三个养殖密度进行饲养，养殖周期为 90d。结果表明，HD 组的超氧化物歧化酶(SOD)、谷胱甘肽(GSH)和丙二醛(MDA)水平均高于 LD 组。转录组分析显示，与 LD 组相比，HD 组的肝脏中有 1127 个基因上调，1423 个基因下调。在稻渔综合种养模式中，高养殖密度导致了鲤氧化应激和能量代谢的失调，这可能是鲤对不利环境胁迫的适应性反应。

关键词：稻鲤综合种养；转录组分析；氧化应激；养殖密度

Effect of culture density on liver function and antioxidant status of common carp under rice-carp (Cyprinuscarpio) co-cropping mode

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Abstract： Aquaculture density is an important factor affecting the yield of aquaculture. Too high stocking density will cause stress of cultured animals. In order to explore the effect of culture density on liver oxidative stress and energy metabolism of common carp (Cyprinuscarpio) in rice-fishing comprehensive culture model, common carp were divided into three groups: low density group (LD,10 tail, 52.9g/m2), medium density group (MD,20 tail, 105.8g/m2) and high density group (HD,30 tail, 158.7g/m2). The culture period was 90 days. The results showed that the levels of superoxide dismutase (SOD), glutathione (GSH) and malondialdehyde (MDA) in HD group were higher than those in LD group. Transcriptome analysis showed that compared with LD group, 1127 genes were up-regulated and 1423 genes were down-regulated in HD group. In the rice-fishing integrated cultivation model, high culture density led to the imbalance of oxidative stress and energy metabolism of common carp, which may be the adaptive response of common carp to adverse environmental stress.

Key words: Comprehensive cultivation of rice and common carp; Transcriptome analysis; Oxidative stress; Culture density

施肥对斑点叉尾鮰肠道菌群的影响

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摘要：为探究施肥对斑点叉尾鮰肠道菌群的影响，本研究对斑点叉尾鮰进行了为期 3 个月的养殖实验，实验分为 3 组：有机肥组(Y)，无机肥组(W)与对照组(D)。实验结束后，取出斑点叉尾鮰的肠道内容物，通过 16S rRNA 扩增子测序技检测斑点叉尾鮰肠道菌群组。结果显示，施肥后斑点叉尾鮰肠道菌群的多样性与丰度均有多降低。在门水平上，三组的优势菌群均为厚壁菌门(Firmicutes)、变形菌门(Proteobacteria)和拟杆菌门(Bacteroidetes)，与对照组相比，有机肥组和无机肥组中厚壁菌门 (Firmicutes)显著上升，与拟杆菌门(Bacteroidetes)的比值线性升高。在属水平上，与对照组相比，施肥组中以罗姆布茨菌属(Romboutsia)和苏黎世杆菌属(Turicibacter)为优势菌属，其中，无机肥组中链球菌属(Streptococcus)相对丰度显著上升(P＜0.05)，

关键词：斑点叉尾鮰；有机肥；无机肥

Effects of Fertilization the Intestinal Microbiota of Channel Catfish (Ictalurus punctatus)

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Abstract： In order to investigate the effects of fertilization on intestinal microbiota of Ictalurus punctatus, a three-month breeding experiment was carried out on I. punctatus, which was divided into three groups: organic fertilizer group (Y), inorganic fertilizer group (W) and control group (D), After the experiment, the intestinal contents of the I. punctatus were removed, and the intestinal microbiota of I. punctatus was detected by 16S rRNA amplification technique. The results showed that the diversity and abundance of intestinal microbiota were higher after fertilization. At the phylum level, the dominant bacteria groups of the three groups were Firmicutes, Proteobacteria and Bacteroidetes, Compared with the control group, Firmicutes increased significantly in both the organic and inorganic fertilizer groups. The ratio of Bacteroidetes to Bacteroidetes increased linearly. At the genus level, Romboutsia and Turicibacter were dominant bacteria in the fertilization group compared with the control group, and the relative abundance of Streptococcus in the inorganic fertilizer group was significantly increased ($P < 0.05$). The relative abundance of lactobacillus in the control group was higher than that in the inorganic fertilizer group ($P < 0.05$). According to the difference analysis of the flora among the three groups, the content of Lactobacillus in the intestinal tract of the inorganic fertilizer group was significantly increased, and the streptococcus in the intestinal healthy organic, fertilizer group was significantly down-regulated and the streptococcus in the regulated I. punctatus was significantly reduced, and the I. punctatus was decreased The results show that the application of organic and inorganic fertilizer in aquaculture can effectively promote the healthy growth of fish. This study provides a theory for the green and healthy culture of I. punctatus.

Key words: Ictalurus punctatus; Organic fertilizer; Inorganic fertilizer

健康与患病黄鳝菌群组成比较

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摘要：为了解健康与患病黄鳝菌群组成差异。采集源于相同养殖条件的健康（H）与患病（B）黄鳝体表粘液（N）、肠道粘膜（C）和健康黄鳝肠道内容物（I），采用 Illumina 高通量测序方法分析其中的微生物组成。结果：HN Alpha 多样性显著高于 BN（$P<0.05$），HC 与 BC 无显著性差异（$P>0.05$）。LefSe 分析发现 HC 组以梭杆菌门、鲸杆菌属、邻单胞菌属等为优势差异物种；BC 组以变形菌门、无色杆菌属、假单胞菌属等为优势差异物种。物种组成分析健康黄鳝梭杆菌门，鲸杆菌属、邻单胞菌属等菌群丰度较高，患病黄鳝变形菌门、厚壁菌门，气单胞菌属、Undibacterium 等菌群丰度较高。BugBase 表型预测发现患病黄鳝致病性细菌丰度升高。综上所述，健康黄鳝微生物多样性较高，梭杆菌门、鲸杆菌属等有益菌丰度较高；患病黄鳝微生物多样性较低，但变形菌门、气单胞菌属等致病性细菌丰度较高。

关键词：黄鳝；高通量测序；体表粘液、肠道粘膜；肠道内容物；BugBase 表型预测

Study on microbial composition of healthy vs diseased rice field eel Monopterus albus

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Abstract：In order to understand the composition and differences of intestinal microorganisms in healthy and diseased Monopterus albus.Illumina high-throughput sequencing was used to analyze the microbial composition of the body surface mucus (N), intestinal mucosa (C) and intestinal contents (I) of healthy (H) and diseased (B)Monopterus albus derived from the same breeding conditions.The results showed that the Alpha diversity of HN was significantly higher than that of BN group ($P<0.05$).There was no significant difference in Alpha diversity between HC and BC ($P>0.05$).LefSe analysis found that the HC group was dominated by Fusobacteria, Cetobacterium and Plesiomonas. In the BC group, Proteobacteria, Achromobacter and Pseudomonas were the dominant species.Analysis of species composition the abundance of Fusobacteria, Cetobacterium, and Plesiomonas in healthy Monopterus albus was higher, and the abundance of Proteobacteria, Firmicutes, Undibacterium, and Aeromonas in diseased Monopterus albus was higher.BugBase phenotype prediction showed that the abundance of pathogenic bacteria in diseased Monopterus albus increased.In summary, the microbial diversity of healthy Monopterus albus is high, and the abundance of beneficial bacteria such as Fusobacteria and Cetobacterium is high. The microbial diversity of diseased Monopterus albus decreased, but the abundance of pathogenic bacteria such as Proteobacteria and Aeromonas was higher.

Key words: Monopterus albus; high-throughput sequencing; body surface mucus; intestinal mucosa ; intestinal contents ; BugBase phenotype prediction

微塑料对大口黑鲈养殖池塘沉积物中温室气体产生及释放的影响机制

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摘要：作为一种新型污染物，微塑料通过渔业活动等途径进入到养殖水体中，能够为微生物提供附着基质并与之形成“塑料际”，能够影响沉积物中微生物的碳氮生化循环来影响温室气体的产生。本论文基于平面光极、同位素分析等技术，探究不同微塑料浓度下沉积物温室气体（一氧化二氮、二氧化碳和甲烷）的排放特征及产生途径。研究检测了不同微塑料浓度下温室气体的排放通量，其中一氧化二氮和二氧化碳呈现负排放趋势，而甲烷呈现正排放趋势。通过平面光极技术分析了沉积物-水界面溶解氧（DO）的扩散通量，微塑料添加组的 DO 扩散通量要比对照组更高。这些结果表明，大口黑鲈养殖池塘积累的微塑料改变了沉积物的理化性质，增加了溶解氧的扩散通量，改变了沉积物中温室气体的产生和释放。本研究为实现养殖池塘氮素减排，科学应对微塑料，推动水产养殖绿色发展做出贡献。

关键词：微塑料；养殖池塘；温室气体；沉积物

The Influence Mechanism of Microplastics on the Production and Release of Greenhouse Gases in Sediments of Large Mouth Black Perch Farming Ponds

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Abstract： As a new type of pollutant, microplastics enter aquaculture water bodies through fishing activities and other means, providing a substrate for microorganisms to adhere to and form a "plastic boundary" with them. They can affect the carbon and nitrogen biochemical cycling of microorganisms in sediment and affect the production of greenhouse gases. This paper explores the emission characteristics and production pathways of greenhouse gases (nitrous oxide, carbon dioxide, and methane) in sediment under different microplastic concentrations, based on techniques such as planar photoelectrode and isotope analysis. The study examined the emission flux of greenhouse gases under different microplastic concentrations, with nitrogen monoxide and carbon dioxide showing a negative emission trend, while methane showed a positive emission trend. The diffusion flux of dissolved oxygen (DO) at the sediment water interface was analyzed using planar photoelectrode technology. The DO diffusion flux of the microplastic addition group was higher than that of the control group. These results indicate that the accumulation of microplastics in largemouth bass aquaculture ponds has altered the physical and chemical properties of sediment, increased the diffusion flux of dissolved oxygen, and altered the production and release of greenhouse gases in sediment. This study contributes to achieving nitrogen reduction in aquaculture ponds, scientifically addressing microplastics, and promoting the green development of aquaculture.

Key words: Microplastics; Breeding ponds; Greenhouse gases; sediment

不同密度鲢鱼和大口黑鲈混养模式下池塘水质和底泥的比较研究同密度鲢鱼和大口黑鲈混养模式下池塘水质和底泥的比较研究

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摘要：为研究大口黑鲈和白鲢混养池塘水质和底泥的变化，在池塘搭建 12 个网箱，对照组为单养鲈鱼（72 条）、A 组（鲈鱼：鲢鱼=4.5:1）、B 组（鲈鱼：鲢鱼=9:1）、C 组（鲈鱼:鲢鱼=18:1），养殖时间为 8 周，每周从网箱中水和泥进行理化指标的测定，从而确定优质的混养比例。

试验结果显示，1-8 周对照组的总氮含量最高，B 组的总氮最低；总磷呈现递增趋势，对照组总磷含量较高，B 组总磷含量最低；亚硝对照组和 C 组较高，B 组最低；8 周时对照组和 C 组的氨氮含量高于 B 组。底泥的亚硝呈现波动趋势，B 组的亚硝含量从第四周开始高于其他组别，但无明显差异（P>0.05）；对照组的氨氮含量 1-8 周都低于其他组别，C 组氨氮较高，B 组次之。研究结果揭示，对照组的水质和其他组别相比较差，B 组的水质优于其他组别；对照组的底泥更为优质，B 组次之，C 组的底泥环境较差，因此 B 组（鲈鱼：鲢鱼=9:1）混养模式更适宜鱼的生存。

关键词：大口黑鲈；白鲢；理化指标；底泥；水质

Comparative Study on Pond Water Quality and Sediment under Different Density Silver Carp and Large Mouth Black Perch Mixed Culture Models

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Abstract：To study the changes in water quality and sediment in a mixed culture pond of largemouth black bass and silver carp, 12 net cages were constructed in the pond. The control group consisted of 72 single culture perch, A group (perch: silver carp=4.5:1), B group (perch: silver carp=9:1), and C group (perch: silver carp=18:1). The cultivation period was 8 weeks, and the physical and chemical indicators of the water and sediment in the cage were measured weekly to determine the high-quality mixed culture ratio.

The experimental results showed that the control group had the highest total nitrogen content from 1 to 8 weeks, while group B had the lowest total nitrogen content; The total phosphorus showed an increasing trend, with the control group having a higher total phosphorus content and the B group having the lowest total phosphorus content; The nitrite control group and group C were higher, while group B was the lowest; At 8 weeks, the ammonia nitrogen content in the control group and group C was higher than that in group B. The nitrite content in the sediment shows a fluctuating trend, and the nitrite content in Group B is higher than other groups from the fourth week onwards, but there is no significant difference (P>0.05); The ammonia nitrogen content of the control group was lower than other groups from 1 to 8 weeks, with Group C having a higher ammonia nitrogen content and Group B taking the second place. The research results revealed that the water quality of the control group was worse than that of other groups, while the water quality of Group B was better than that of other groups; The sediment of the control group is of higher quality, followed by Group B, and the sediment environment of Group C is poor. Therefore, the mixed culture mode of Group B (bass: silver carp=9:1) is more suitable for the survival of fish.

Key words: Large mouth bass; silver carp; physical and chemical indicators; sediment; water quality

菌藻共生体系对中间球海胆肠道菌群、免疫、生长和存活的影响

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摘要：为探究菌藻共生体系对中间球海胆肠道菌群、免疫、生长和存活的影响，本研究通过在聚乙烯波纹板上接种底栖硅藻、在水中加入光合细菌与枯草芽孢杆菌构建菌藻共生体系（菌藻组）。检测并比较了菌藻组与对照组间水质指标，水体、海胆肠道与波纹板菌群结构，以及实验结束时（35d）海胆吞噬作用相关免疫指标及生长性能的差异。结果表明：菌藻组波纹板上的优势菌为红螺菌科，优势藻为多管藻属、菱形藻属；菌藻组氨氮和亚硝酸盐含量均低于对照组。菌藻组养殖 1 周后，海胆肠道菌群与水体菌群的多样性和丰度均显著增加；水中优势菌为红螺菌科，而对照组为黄杆菌科。实验结束时，菌藻组海胆吞噬相关指标显著高于对照组，细胞凋亡率、坏死率与海胆死亡率均显著低于对照组。体重 SGR 较对照组提高 20 %。研究表明，菌藻共生体系能通过净化水质、改变养殖系统和肠道菌群结构、提高海胆免疫提高了海胆的生长速度和成活率，此结果为开发海胆健康养殖模式提供了新的思路。

关键词：菌藻共生体系；中间球海胆；生长；免疫指标；微生物群落

Effects of the bacteria-algal symbiosis system on gut microbiota, immunity, growth, and survival of sea urchins （Strongylocentrotus intermedius）

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Abstract：To investigate the effects of a bacteria-alga symbiosis on gut microbiota, immunity, growth and survival of sea urchin （Strongylocentrotus intermedius）, we cultured sea urchin in a bacteria-alga symbiosis constructed by seeding benthic diatoms on polyethylene rippled plates and adding photosynthetic bacteria and Bacillus subtilis to aquaculture water. The differences in water quality indicators, the bacteria composition of water, sea urchin gut and plate during the experiment, and the immune parameters related to phagocytosis, mortality and specific growth rate (SGR) of sea urchins at the end of the experiment (35 days) were detected and compared between the control group and bacteria-alga symbiosis group。The results showed that Rhodospirillaceae (31%) was the dominant bacteria on the plastic plate, and the dominant algae were Chordariaceae (34%), Melanothamnus (7%), and Nitzidina (7%). The contents of ammonia nitrogen and nitrite in the symbiotic system were lower than those in the control group, and the level of ammonia nitrogen was extremely significantly lower ($P < 0.01$). The diversity and abundance of sea urchin gut microbiota and water microbiota were significantly increased after 1 week in the bacteria-algae symbiosis system ($P < 0.05$). After 3 weeks, the diversity of bacteria in the water body was significantly lower than that in the control group, but the abundance was still significantly higher than that in the control group ($P < 0.05$). Rhodospirillaceae (69%) was the dominant bacteria in the water body of the bacteria-algae symbiosis system, while Flavobacteriaceae (56%) was the dominant bacteria in the control group. The composition of the dominant flora of sea urchin gut flora was similar to that of the control group, but the abundance was significantly higher than that of the control group ($P < 0.05$). The diversity and abundance of sea urchin gut microbiota and water microbiota were significantly increased after 1 week in the bacteria-algae symbiosis system ($P < 0.05$). After 3 weeks, the diversity of bacteria in the water body was significantly lower than that in the control group, but the abundance was still significantly higher than that in the control group ($P < 0.05$). Rhodospirillaceae (69%) was the dominant bacteria in the water body of the bacteria-algae symbiosis system, while Flavobacteriaceae (56%) was the dominant bacteria in the control group. The composition of the dominant flora of sea urchin intestinal flora was similar to that of the control group, but the abundance was significantly higher than that of the control group ($P < 0.05$). At the end of the experiment, the proportion of phagocytic, phagocytic rate, phagocytic index, and T-AOC activity of sea urchins in the bacterial-algal symbiosis group were significantly higher than those in the control group ($P < 0.05$), while the apoptosis rate and necrosis rate were significantly lower than those in the control group ($P < 0.05$). The mortality of sea urchins in the bacterial-algal symbiosis group (2.22±1.92%) was significantly lower than that in the control group (45.56±15.03%) ($P < 0.05$), and the SGR of sea urchins in the bacterial-algal symbiosis group was 20% higher than that in the control group ($P < 0.01$). Our results showed that the bacterial-algal symbiosis could improve the growth rate and survival rate of sea urchin Strongylocentrotus intermedius by purifying water quality, changing the structure of culture system and intestinal flora, and improving sea urchin immunity, which provided a new idea for the development of a healthy culture model of sea urchin S.intermedius

Key words: bacteria-algal symbiosis system; Strongylocentrotus intermedius; growth; immune parameter; microflora

内蒙古及周边内陆盐碱水对虾养殖产业现状与问题探讨

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摘要：盐碱水是一种特殊的养殖水资源。随着国家对内陆盐碱地综合开发的力度日渐加强，盐碱水渔业利用逐渐兴起。近年来，通过引进适合盐碱水环境的对虾品种，以及改进养殖设施和饲养管理技术，盐碱水对虾养殖产业在内蒙古及周边各省区迅速发展。本报告概况介绍了内蒙古对虾养殖产业的自然资源基础、养殖品种、模式、产业规模、生产成本、效益等现状，又从苗种、饲料等资源供应、病害防控、产品加工、市场销售等方面分析了产业发展中存在的问题，最后对我国北方内陆盐碱水对虾产业的可持续发展方向进行了探讨。

关键词：内蒙古；内陆；盐碱水；对虾养殖

Discussion on the status and problems of shrimp aquaculture with inland saline-alkine waters in Inner Mongolia and adjacent areas

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Abstract： Saline-alkali water is a special aquaculture water resource. With the strengthening of the comprehensive development of inland saline-alkali land, the utilization of saline-alkali water fishery is gradually rising. In recent years, through the introduction of prawn varieties for saline water environment, and improvement of facilities and farming technology, shrimp farming industry is rapidly developing in Inner Mongolia and the surrounding provinces. This report briefly introduces the status quo of natural resource base, breeding varieties, mode, industrial scale, production cost and benefits of shrimp aquaculture industry in Inner Mongolia, and analyzes the problems existing in the development of the industry from the aspects of supply of resources such as seedlings and feed, disease prevention and control, product processing and marketing. Finally, the sustainable development direction of inland shrimp aquaculture industry in north China was discussed.

Key words: Inner Mongolia; inland; saline-alkali water; shrimp aquaculture

厚颌鲂仔稚鱼消化系统发育与
胆囊收缩素和胰蛋白酶的反馈调节的相关性探究

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摘要：本文为研究厚颌鲂消化系统发育进程，仔稚鱼期胰蛋白酶（TRY）、胆囊收缩素（CCK）发生和变化情况，探讨三者相关性。以 1-50 日龄厚颌鲂为试验对象，利用 HE 染色、ELISA 等技术检测。研究发现：1 日龄仔鱼体重 1.07±0.04 mg，全长 4.51±0.152 mm；4 日龄开口；12 日龄肠道褶皱增加；30 日龄体长体重显著增长，肠道处于发育敏感期；42 日龄肠道、肝胰脏发育较完善；50 日龄稚鱼体重为 125.30±12.30 mg，体长为 20.99±3.14 mm。12 日龄前后 TRY 活性呈下降趋势，40 日龄肠道发育较完善后 TRY 活性呈上升趋势。1 日龄 CCK 浓度最低；30 日龄显著增加达到最大值。消化器官发育与体长体重增长正相关，CCK 对 TRY 进行负反馈调节。建议加强 12-42 日龄食物营养供应。通过本研究以期为厚颌鲂苗种工厂化培育提供理论参考。

关键词：厚颌鲂；仔稚鱼；组织切片；消化系统；胆囊收缩素；胰蛋白酶

The Correlation between Digestive System Cholecystokinin and Trypsin Feedback Regulation and Development in Megalobrama pellegrini Larve and Juvenile

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Abstract： The purpose of this study was to investigate the development of digestive system, the changes of trypsin (TRY) and cholecystokinin (CCK) in Megalobrama pellegrini larve and juvenile, and to explore the correlation among them. HE staining and ELISA were used to detect Megalobrama pellegrini from 1 to 50 days old. The results showed that the body weight of 1-day-old larve was 1.07±0.04 mg, and the total length was 4.51±0.152 mm. 4 days old opened the oropharyngeal cavity; Intestinal fold increased at 12 days of age; At 30 days of age, the body weight increased significantly, and the intestinal tract was in the developmental sensitive stage. The intestinal tract and hepatopancreas were well developed at 42 days of age. The body weight of the 50-day-old juvenile was 125.30±12.30 mg, and the body length was 20.99±3.14 mm. TRY activity decreased before and after 12 days of age, and increased after intestinal development was more complete at 40 days of age. The concentration of CCK was the lowest at 1 day of age. 30 days of age increased significantly to the maximum. Digestive organ development was positively correlated with body length and weight increase, and CCK negatively regulated TRY. It is recommended to strengthen the food nutrition supply for 12-42 days of age. Through this study, we hope to provide theoretical reference for the factory breeding of Megalobrama pellegrini larve and juvenile.

Key words: Megalobrama pellegrini; Larve and juvenile; Tissue slice; Digestive system; Cholecystokinin; Trypsin

繖房江蓠对循环水系统内珍珠龙胆石斑鱼混养水质调控分析

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摘要：为探讨繖房江蓠在循环水养殖模式中对水质的调控作用，本论文以珍珠龙胆石斑鱼循环水养殖为例，研究添加繖房江蓠后，水质变化及石斑鱼的生长情况。结果显示：①水质净化效果明显，实验组 YA 水体中氨氮、亚硝酸盐、磷酸盐质量浓度均低于对照组 YB（P＜0.05），YA 各质量浓度最终值分别为（2.484±0.079）、（0.020±0.01）、（0.558±0.117）mg/L；YB 最终值分别为（2.616±0.038）、（1.679±0.06），（1815±0.152）mg/L；②对珍珠龙胆石斑鱼生长有促进作用。相对于 YB 石斑鱼增重率、存活率达到了 32.02±0.58%、57.14 %，YA 石斑鱼的增重率、存活率达到了 67.37±7.58%、96.43%。研究结果表明循环水养殖模式下，添加大型海藻能有效的净化水质、促进主养对象及自我的生长。为实现绿色高效的循环水养殖提供基础参考。

关键词：繖房江蓠；珍珠龙胆石斑鱼，循环水养殖，水质

Analysis of water quality control of pearl gentian grouper mixed culture in Recirculating Aquaculture System by Gracilaria coronopifolia.

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Abstract： In order to explore the role of Apiaceae in regulating water quality in the Recirculating Aquaculture System, this thesis takes pearl gentian grouper recirculating water culture as an example to study the changes of the water quality of the recirculating water after the addition of the Gracilaria coronopifolia. ①The effect of water purification is obvious, pH value of the experimental group is higher than that of the control group, the mass concentration of ammonia nitrogen, nitrite and phosphate in the experimental group YA is lower than the control group YB (P＜0.05), the final values of the mass concentration of ammonia nitrogen, nitrite and phosphate in the experimental group YA are (2.484±0.079 mg/L), (0.020±0.01 mg/L), (0.558±0.117 mg/L); the final values of ammonia nitrogen, nitrite, and phosphate mass concentrations in control group YB were (2.616±0.038 mg/L), (1.679±0.06 mg/L), and (1815±0.152 mg/L), ②There was a promoting effect on the growth of pearl grouper. Compared with the control group YB grouper, the weight gain rate and survival rate reached 32.02±0.58% and 57.14%, and that of the experimental group YA grouper was higher than that of the control group (P ＜ 0.05), and the weight gain rate and survival rate reached 67.37±7.58% and 96.43%.The results of the study show that the addition of Gracilaria coronopifolia can not only effectively purify the water quality and promote the growth of the main aquaculture objects, but also self-growth under the Recirculating Aquaculture System. It provides a basic reference for the realization of green and efficient recirculating water aquaculture, and provides basic data and experience for the improvement and optimization of macroalgae recirculating water aquaculture mode.

Key words: Gracilaria coronopifolia; pearl gentian grouper; Recirculating Aquaculture System; water quality

短期禁食和单日投喂频率对厚颌鲂稚鱼消化系统组织学、胆囊收缩素(CCK)和胰蛋白酶(TRY)的影响

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摘要：本研究探讨厚颌鲂稚鱼在短期禁食及单日不同投喂频率下 CCK 与 TRY 的反馈。短期禁食试验以孵出后培养至 60 日龄的厚颌鲂（183.75±61.16 mg，20.74 ± 4.08 mm）为研究对象，结果表明：投喂组（FCG）体重、CCK、TRY 均高于禁食组（FTG）。FTG 中 TRY 和 CCK 在第 9 天达到最低值后呈现回升趋势，未见明显负反馈调节。肠绒毛膜上皮细胞损伤程度高于肝胰腺，上皮细胞受损明显。在单日投喂频率实验中，将 64 日龄稚鱼随机分为四个不同投喂次数组。结果表明：CCK 在单次投喂夜间具最小值，各组内有明显的闭环调节，禁食组的闭环终点前移，不同投喂频率对 CCK 和 TRY 日节律的长期波动没有直接影响，单次喂食可能导致饥饿感提前，每日 3 次喂食或更有利于厚颌鲂稚鱼生长。

关键词：厚颌鲂稚鱼；胆囊收缩素；胰蛋白酶；禁食；组织学

Effects of short-time fasting and feeding frequencies within 24 hours on histology, cholecystokinin and trypsin enzyme activities of digestive organs in juvenile black bream, Megalobrama pellegrini (Tchang, 1930)

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Abstract： This study investigated the feedback of cholecystokinin (CCK) and trypsin (TRY) in juvenile black bream, Megalobrama Pellegrini (Tchang, 1930) under short-term fasting and different feeding frequencies in a single day. The short-term fasting trial used juvenile M. Pellegrini (wet weight 183.75 ± 61.16 mg, total length 20.74 ± 4.08 mm) cultured in a recirculating aquaculture system (RAS) to 60 days after hatching as the research object. The normal feeding group (FCG) had higher body weight, CCK, and TRY compared to the fasting group (FTG). The FTG exhibited the lowest TRY and CCK content on the 9th fasting day, while the CCK content peaked on the 11th day. No noticeable negative feedback regulation was observed during the short-term fasting test for CCK and TRY. The degree of damage to the enterocytes cells was higher than that in the hepatopancreas, with the epithelial cells detaching from the striatum boundaries. In daily rhythm experiment, juveniles aged 64 days (DAH64) were randomly assigned to four groups in different feeding frequencies , Results revealed that in feeding only once group , CCK had a minimum value at nighttime; in groups twice, three times and fasting, there was a peak value during the nighttime in each group. The experiment demonstrated evident closed-loop adjustments in each of the treatment groups, with the closed-loop point shifted forward in fasting group. A single feeding may lead to early hunger, but feeding three times a day may be more conducive to the growth of juvenile M. Pellegrini.

Key words: Black bream juvenile; CCK; Trypsin; Fasting; Histology

第二专题：水产生物技术与遗传育种

凡纳滨对虾耐低盐家系免疫特性及适应机制的研究

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摘要：凡纳滨对虾是一种广泛分布且适应广盐性水环境的水生动物。已知低盐度会对凡纳滨对虾的抗病性和免疫力产生影响，但目前对不同遗传背景凡纳滨对虾对低盐度的适应机制了解甚少。因此，本研究旨在探讨凡纳滨对虾低盐耐家系（FG I/J）的免疫特性及其适应机理。研究中检测了低盐度（5‰）和自然盐度（24‰）下凡纳滨对虾 FG I/J 家系和对照家系的抗病性和免疫指标。同时，在盐度为 5‰时，对 FG I/J 家系和对照家系的肝胰腺转录组学进行了分析。研究结果显示，与对照家系相比，FG I/J 家系对副溶血弧菌表现出更强的耐受性，并且免疫能力和炎症反应显著增强。根据转录组学分析，与对照家系相比，FG I/J 家系中的能量代谢和免疫调节途径显著富集。综上所述，能量代谢能够为 FG I/J 家系在低盐条件下免疫调节提供更多的能量以应对长期低盐胁迫，因此表现出更强的耐受性。

关键词：凡纳滨对虾；低盐度；耐低盐家系；免疫；能量代谢

Studies on immunological characteristics and mechanism analysis of Litopenaeus vannamei low salt-tolerance family

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Abstract： Litopenaeus vannamei, a widely distributed euryhaline aquatic animal, is known to be affected by low salinity, which can impact its disease resistance and immunity. However, there is still a limited understanding of the adaptation mechanisms of Litopenaeus vannamei to low salinity in different genetic backgrounds. Therefore, this study aimed to investigate the immunity characteristics and mechanisms of the low salt-tolerant family (FG I/J) of Litopenaeus vannamei. The study examined the disease resistance and immune parameters (including total haemocyte count [THC], cell viability, lysozyme activity [LZM], phenoloxidase content [PO], interleukin-6 content [IL-6], and tumor necrosis factor-alpha content [TNF-α]) of the FG I/J and Control families of Litopenaeus vannamei under low salinity (5‰) and natural salinity (24‰). Additionally, hepatopancreas transcriptomics of the FG I/J and Control families were analyzed at a salinity of 5‰. The results demonstrated that the FG I/J family exhibited stronger tolerance to V. parahaemolyticus, as well as a more pronounced immune capacity and inflammatory response compared to the Control family. Transcriptome analysis revealed that energy metabolism and immune regulation pathways had significant enrichments. In summary, FG I/J families exhibit greater tolerance to long-term low-salt stress due to their ability to provide more energy for immune regulation.

Key words: Litopenaeus vannamei; Low salinity; low salt-tolerance family; Immunity; Energy metabolism

光强和光周期对克氏原螯虾生长、能量和脂质代谢的影响

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摘要：光照是影响水生动物生长的重要因素。目前，对水生动物生长发育的研究主要集中在光周期和光照强度等单一因素上。而在自然条件下，光周期的变化总是伴随着光照强度的波动。因此，本研究探讨了不同光照强度（600、1200、1800 lx）和光周期（4L：20D、14L：10D、24L：0D）对克氏原螯虾生长、能量和脂质代谢的影响。结果表明，光照强度与光周期之间的一次效应、二次效应和交互效应均显著（$P < 0.05$）。在 1200 lx 和 24L: 0D 条件下，克氏原螯虾的摄食率、特定生长率和特定增重率显著高于对照组（1200 lx 和 14L: 10D），也高于其他处理组。在 1200 lx 和 14L: 10D 条件下，克氏原螯虾能量和脂质代谢相关酶活性及相关基因表达水平明显高于对照组，也高于其他处理组。因此，适当的光照强度和延长光周期对克氏原螯虾的摄食、生长、能量和脂质代谢具有重要意义。

关键词：光照强度；光周期；生长；能量代谢；脂质代谢；克氏原螯虾

Effects of light intensity and photoperiod on growth, energy and lipid metabolism of Procambarus clarkii

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Abstract：Light is an important factor affecting the growth of aquatic animals. At present, the studies on the growth and development of aquatic animals were mainly focused on single factor such as photoperiod and light intensity. While under natural conditions, the change of photoperiod is always accompanied by the fluctuation of light intensity. Therefore, this study explored the effects of different light intensities (600, 1200, 1800 lx) and photoperiod (4L: 20D, 14L: 10D, 24L: 0D) on the growth, energy and lipid metabolism of Procambarus clarkii. The results showed that the linear effect, quadratic effect and interaction effect between light intensity and photoperiod were significant ($P < 0.05$). The feeding rate, specific growth rate and specific weight gain rate of P. clarkii under the condition of 1200 lx and 24L: 0D were significantly higher than that of the control group (1200 lx and 14L: 10D), and higher than that of other treatment groups. Under the condition of 1200 lx and 14L: 10D, energy and lipid metabolism-related enzyme activities and related gene expression levels of P. clarkii were significantly higher than those of the control group, and higher than those of other treatment groups. Therefore, proper light intensity and prolonged photoperiod are of great significance to the food intake, growth, energy and lipid metabolism of P. clarkii.

Key words: light intensity; photoperiod; growth; energy metabolism; lipid metabolism; Procambarus clarkii

虹鳟倍性鉴定 SSR 标记筛选与应用研究

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摘要：虹鳟是我国冷水性鱼类的主要养殖品种。与二倍体相比，虹鳟三倍体具有生长速度快、肉质好和不育等优点。目前，鉴定虹鳟倍性主要是通过流式细胞术进行 DNA 含量分析，但这种方法需要采集鱼类血液或组织样本，会对其造成伤害。为了实现利用微创方法收集样本鉴定虹鳟倍性，本研究利用 PCR 扩增以及电泳分离技术对 153 个微卫星标记(SSR 标记)进行分析，其中 139 个 SSR 标记能够在二倍体和三倍体中成功扩增，筛选出 132 个 SSR 标记具有多态性，最终鉴定出 7 个标记在三倍体中表现出较高的变异性。通过在 52 个已知倍性水平的参考样本和 48 个未知倍性的样本上进行验证，进一步从中筛选出 3 个 SSR 标记足以区分倍性水平，并且根据 3 个标记序列重新设计了 3 对具有良好稳定性的引物序列进行倍性分析应用。本研究所筛选的 SSR 标记解决了现有虹鳟倍性鉴定中存在的技术流程复杂、耗材昂贵的问题，并有助于不同倍性虹鳟的遗传多样性研究。

关键词：虹鳟；鲑科鱼类；微卫星；三倍体；倍性检测

Screening and Application of SSR Markers for Identification of Ploidy in Oncorhynchus mykiss

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Abstract: Rainbow trout (Oncorhynchus mykiss) is one of the world's most widely farmed cold-water economic fish. It is also the primary cold-water fish species in China. Since the 1960s, the rainbow trout germplasm has been introduced from North Korea, the United States, Denmark, and other countries, and a systematic study has been carried out on germplasm preservation, identification, breeding, and variety breeding. Compared with rainbow trout diploid, the triploid has the advantages of a high feed conversion rate, fast growth rate, and good meat quality. Moreover, the triploid gonadal hypoplasia can mitigate risks associated with high mortality and meat quality decline during spawning and avert the ecological risk of invasive alien species caused by breeding escape. Therefore, breeding triploid rainbow trout has more significant market and ecological benefits. As diploid and triploid rainbow trout are very similar in terms of morphology, it is difficult to distinguish the ploidy of rainbow trout by morphology alone. Currently, DNA content analysis by flow cytometry is the main method used to identify the ploidy of rainbow trout, but this method necessitates the collection of fish blood or tissue samples, and the body length of the fish to collect the blood must be at least 5 cm. Additionally, these sampling operations may harm the fish. This method also involves a delicate operation, complicated technical process, and expensive consumables, thus, the popularization and application of triploid identification of rainbow trout are greatly restricted. Considering the limitations of the technical test for the ploidy of rainbow trout, a minimally invasive and economical method with only a small amount of sampling is needed to identify and analyze the ploidy of rainbow trout in batches. Microsatellite markers (SSR markers) are simple repeated sequences widely distributed in eukaryotic genomes and have been widely used in ploidy and pedigree analyses of fish. The advantages of microsatellite (SSR) analysis include high reproducibility, low sample requirements, and rapid population genetic analysis. In order to achieve the use of a minimally invasive method to collect samples for trout ploidy identification, this study analyzed 153 SSR markers using PCR amplification and electrophoresis separation technology. Among them, 139 SSR markers could be successfully amplified in diploid and triploid, and 132 SSR markers were screened for polymorphism. Finally, seven markers showed high variability in triploid. By verifying 52 reference samples with a known ploidy level and 48 samples with an unknown ploidy level, three SSR markers (SSR1054, SSR1056, and SSR1468) were further screened to distinguish the ploidy level. Moreover, three pairs of primer sequences with good stability were redesigned according to the three marker sequences for ploidy analysis application. When SSR markers were selected for ploidy identification, amplification sites with high variability were preferred because they greatly improve the efficiency of SSR-assisted ploidy identification. Differentiation of the variability of amplification sites mainly considers the number of alleles expressed and the relative frequency of these alleles. Furthermore, having clear map bands that are easy to observe and analyze is an important criterion for screening high-quality specific SSR markers. Statistical clear map bands can correctly judge the allelic configuration at each locus, thus, determining the ploidy level of rainbow trout. However, when the number of microsatellite DNA alleles shown in the electrophoretic map was less than the maximum number of alleles that may occur at the ploidy level of the polyploid species, it was difficult to accurately judge the ploidy by direct observation of the number of alleles. In diploid individuals, highly heterozygous SSR amplifies at most two alleles at a given site. Similarly, three and four alleles can be observed in triploid and tetraploid individuals, respectively. However, in some rare cases, the actual number of alleles cannot be correctly determined by looking directly at the number of alleles. For example, individuals with unknown ploidy show multiple possible genotypes for two alleles, which can occur with both diploids (AB) and triploids (AAB or ABB). Therefore, this study combined the analysis results of multiple specific SSR markers to improve the accuracy of ploidy detection. In addition, this study found three specific labeling bands that can assist in the differentiation of diploid and triploid rainbow trout, namely, SSR1054-305bp, SSR1056-463bp, and SSR1468-363bp. These three specific markers will greatly improve the accuracy of using SSR markers to identify triploid rainbow trout. Microsatellite null alleles are another potential limitation in SSR ploidy identification, which can be eliminated or avoided by changing the binding site of primers and flanking sequences due to the failure of normal gene amplification due to mutations in SSR lateral sequences. Although the results of this study cannot eliminate the presence of null alleles in future samples, the present experimental data suggest that the frequency of null alleles is so low that their impact on polyploid identification is minimal. SSR markers screened in this study solve the existing problems of a complex technical process and expensive consumables in the identification of rainbow trout ploidy, providing a minimally invasive, economical, reliable, and batch-operable molecular method and contributing to the study of the genetic diversity of rainbow trout with different ploidy.

Key words: Rainbow trout; Salmonidae; Microsatellite; Triploid; Ploidy detection

通过对 mRNA 和 miRNA 的联合分析，揭示了南美白对虾（ Litopenaeus vannamei ）在急性碱度胁迫下的作用机制

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摘要：南美白对虾（Litopenaeus vannamei）是盐碱水中常见的养殖物种，而碱度胁迫被认为是虾的应激源之一。本研究中，我们旨在探讨在低碱（50 mg/L）和高碱（350 mg/L）条件下RNA-seq 对急性高碱胁迫的响应机制。我们鉴定出 215 个差异表达 miRNA（DEGs）和 35 个差异表达 miRNA（DEMs），其中 180 个 DEGs 和 28 个 DEMs 上调，35 个 DEGs 和 7 个 DEMs下调。DEGs 在碳水化合物的消化吸收、胰腺分泌、淀粉和蔗糖代谢、抗原加工和呈递以及谷胱甘肽代谢等途径中富集。参与溶酶体和离子转运途径的 DEMs 表达显著上调。同时获得了 42个被 DEMs 靶向的 DEGs。我们在南美白对虾中检测出一些碱度胁迫候选的基因和 miRNA，以及碱度胁迫相关基因的表达模式。其中大多数基因在离子调节、消化和免疫中的表达水平高，而在代谢中富集的基因表达水平下调。

关键词：盐碱水、碳酸盐碱度、碱度胁迫、miRNA-mRNA、稳态调节

Combined analysis of mRNA and miRNA reveals the mechanism of pacific white shrimp (Litopenaeus vannamei) under acute alkalinity stress

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Abstract： The pacific white shrimp (Litopenaeus vannamei) is now a more common aquaculture species in saline-alkali waters, while alkalinity stress is considered to be one of the stressors for shrimp. Thus, an understanding of the molecular response to alkalinity stress is critical for advancing the sustainability of culture in pacific white shrimp. In this study, we aimed to explore the response mechanism to acute high-alkaline stress by RNA-seq at low-alkaline (50 mg/L) and high-alkaline (350 mg/L). We identified 215 differentially expressed mRNAs (DEGs) and 35 differentially expressed miRNAs (DEMs), of which 180 DEGs and 28 DEMs were up-regulated, 35 DEGs and 7 DEMs were down-regulated, respectively. The DEGs were enriched in several pathways, including carbohydrate digestion and absorption, pancreatic secretion, starch and sucrose metabolism, antigen processing and presentation and glutathione metabolism. The DEMs involved in lysosome and ion transport related pathways were significantly up-regulated. We also achieved 42 DEGs, which were targeted by DEMs. miRNA-mRNA regulatory network was constructed by integrated analysis of miRNA-mRNA data. We detected several genes and miRNAs which were identified as candidate regulators of alkalinity stress, and expression patterns of key genes related to alkalinity stress in pacific white shrimp. Among these genes, the expression levels of most key genes enriched in ion regulation, digestion and immunity were increased, and the expression levels of genes enriched in metabolism were down-regulated. This research indicated that the homeostatic regulation and digestion changed significantly under acute alkaline stress, and the variations from metabolic and immunity can cope with the osmotic shock of alkalinity stress in pacific white shrimp. This study provides key clues for exploring the molecular mechanism of pacific white shrimp under acute alkalinity stress, and also gives scientific basis for the optimisation of saline-alkaline aquaculture technology.

Key words: saline-alkaline waters; carbonate alkalinity; alkalinity stress; miRNA-mRNA; homeostatic regulation

Nanog 基因对中华鳖雄性生殖细胞发育的调控机制

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摘要：Nanog 作为干细胞转录因子对哺乳动物干细胞的调控作用及机制已有广泛深入的研究，但关于龟鳖类干细胞的发育及 NANOG 的功能研究还极为有限。本研究以中华鳖为研究材料，我们分离和培养了中华鳖的精巢细胞。并且通过腺病毒感染鳖细胞的技术，在培养细胞里进行了 Nanog 基因的过表达和敲降研究，通过比较转录组分析开展 Nanog 调控精巢细胞发育分化的分子机制研究。结果表明，nanog 基因过表达对中华鳖精巢细胞的生长增殖具显著的影响，并对 Zar1l、Olfm1、Gpr3、Hsd17b3、Sox3、Bmp3、Rasd1 等基因有显著上调作用，对 Adcy8、Dio2、Itgb6、Pik3r1、Eml6、Tspan8、Wnt2b 等基因有显著下调作用。本研究一方面为解析 nanog 基因对生殖细胞发育分化作用及机制奠定基础，另一方面，能为龟鳖生殖细胞分离培养及定向分化研究提供技术与理论基础。

关键词：Nanog 基因；精巢细胞培养；腺病毒感染；基因过表达与敲降；转录组分析；中华鳖

The regulation mechanisms whereby nanog gene functions in male germ cells' development in the Chinese soft shelled turtle (Pelodiscus sinensis)

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Abstract： Nanog, as a stem cell transcription factor, has been well studied for its regulation mechanism behind the stem cells' development in mammals. However, because of the limitation of materials and the lack of stem cell lines in reptiles, especially in turtles, both the study on the development of stem cells and function analysis of NANOG were limited. In this study, we isolated and conducted an in vitro culture of testicular cells in the Chinese soft-shelled turtle. Moreover, by adenovirus infection, the nanog gene's overexpression and knockdown were conducted in the cultured cells. Likewise, the comparative analysis on cells' proliferation and transcriptome profiles were performed The results showed that the nanog gene overexpression could promoted the proliferation of the cultured testicular cells of the soft-shelled turtle, and significantly modulated a serial of genes, including up-regulating the genes, zar1l, olfm1, gpr3, hsd17b3, hox3, bmp3 and rasd1, while down-regulating the genes, adcy8, dio2, itgb6, pik3r1, eml6, tspan8, wnt2b, and so on. The present study can provide a basis for demonstrating the regulation mechanisms whereby the nanog gene play a role in germ cells' development and differentiation, also facillitate the germ cell culture and defined differentiation induction. More importantly, the findings of this study would benefit developing the techniques of turtles' germ cell manipulations, genetic preservation and innovation.

Key words: Nanog; culture of testicular cells; adenovirus infection; gene overexpression and knockdown; transcriptomic analysis; Pelodiscus sinensis

17 β –雌二醇诱导日本沼虾性别逆转和性腺转录组分析：机制、途径和潜在危害

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摘要：本研究通过对正常雄虾（M）、正常雌虾（FM）、性别逆转雄虾（RM）和未发生性别逆转的雄虾（NRM）进行性腺转录组分析，确定饲料中添加不同浓度的 17β-雌二醇是否能诱导日本沼虾的性别逆转，并筛选出与性别相关的基因。与对照组相比，40 天后，在变态后 25 天投喂 200mg/kg 的 17β-雌二醇性别比例最高（雌：雄）达到 2.22:1。组织学观察到了精巢和卵巢共存的现象。NRM 组的雄虾精巢发育较慢，且没有成熟的精子。RNA 测序显示，三个比较组分别存在 3702，3111 和 4978 个差异表达基因。视黄醇代谢和核苷酸切除修复途径分别被确定为性别逆转和精子成熟的关键途径。

关键词：17β-雌二醇，组织学观察，日本沼虾，性别比例，性别逆转，转录组

17β-Estradiol Induced Sex Reversal and Gonadal Transcriptome Analysis in the Oriental River Prawn (Macrobrachium nipponense): Mechanisms, Pathways, and Potential Harm

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Abstract： Sex reversal induced by 17β-estradiol (E2) has shown the potential possibility for monoculture technology development. The present study aimed to determine whether dietary supplementation with different concentrations of E2 could induce sex reversal in M. nipponense, and select the sex-related genes by performing the gonadal transcriptome analysis of normal male (M), normal female (FM), sex-reversed male prawns (RM), and unreversed male prawns (NRM). Histology, transcriptome analysis, and qPCR were performed to compare differences in gonad development, key metabolic pathways, and genes. Compared with the control, after 40 days, feeding E2 with 200 mg/kg at PL25 (PL: post-larvae developmental stage) resulted in the highest sex ratio (female: male) of 2.22:1. Histological observations demonstrated the co-existence of testis and ovaries in the same prawn. Male prawns from the NRM group exhibited slower testis development without mature sperm. RNA sequencing revealed 3702 differentially expressed genes (DEGs) between M vs. FM,3111 between M vs. RM, and 4978 between FM vs. NRM. Retinol metabolism and nucleotide excision repair pathways were identified as the key pathways for sex reversal and sperm maturation, respectively. Sperm gelatinase (SG) was not screened in M vs. NRM, corroborating the results of the slice D. In M vs. RM, reproduction-related genes such as cathepsin C (CatC), heat shock protein cognate (HSP), double-sex (Dsx), and gonadotropin-releasing hormone receptor (GnRH) were expressed differently from the other two groups, indicating that these are involved in the process of sex reversal. Exogenous E2 can induce sex reversal, providing valuable evidence for the establishment of monoculture in this species.

Key words: 17β-Estradiol; histological observations; Macrobrachium nipponense; sex ratio; sex reversal; transcriptome

中华鳖卵无介质孵化的开发与评价

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摘要：在人工条件下，成功且高效的孵化中华鳖卵是其产业化发展的重要一步。而现实需求对中华鳖卵传统的孵化模式提出了挑战。在这里，本研究开发了一种中华鳖卵无介质孵化的方法，并评估了其与传统蛭石孵化模式的区别以及光照对无介质孵化的影响。研究发现，与传统的蛭石孵化模式相比，无论是在恒温或波动的温度条件，无介质孵化对中华鳖卵的孵化率、幼体体重、背甲长、背甲宽、腹甲长、腹甲宽和翻身时间均没有显著影响。同时，在无介质孵化过程中，光照处理显著缩短了孵化期，并对幼体体重、背甲长、背甲宽、腹甲长和翻身时间产生了显著的负面影响。此外，本研究还首次报道了中华鳖卵同步孵化的现象。总之，我们的研究结果为改进中华鳖卵孵化方法提供了基础数据和新的见解。

关键词：中华鳖；无介质孵化；光照处理；幼体特征；卵的同步孵化

Development and evaluation of a medium-free incubation method for hatching Chinese soft-shelled turtle (Pelodiscus sinensis) eggs

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Abstract：In aquaculture, the traditional method for hatching Pelodiscus sinensis eggs needs further investigation. Here, we developed a medium-free incubation method for hatching P. sinensis eggs and evaluated its differences from the traditional vermiculite incubation method and the effects of light on it. We found that medium-free incubation had no significant effects on hatching success, body weight, carapace length, carapace width, plastron length, plastron width, and righting response time of P. sinensis compared with those under traditional vermiculite incubation, irrespective of thermostatic or fluctuating temperature conditions. Furthermore, light treatment significantly shortened the incubation period and negatively affected body weight, carapace length, carapace width, plastron length, and righting response time during medium-free incubation. Additionally, this study is the first to report the phenomenon of egg-hatching synchrony in P. sinensis. Overall, our results provide basic data and novel insights for improving the method for hatching P. sinensis eggs.

Key words: Pelodiscus sinensis; Medium-free incubation; Light exposure; Larval characteristics; Egg-hatching synchrony

中华绒螯蟹种质资源研究与新品种培育

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摘要：中华绒螯蟹（俗称河蟹）是我国的特有生物，而种质问题已是我国中华绒螯蟹产业发展的突出问题之一。我们在收集国内外绒螯蟹种质资源群体 500 余份的基础上，开展了种质资源研究，查明长江、黄河和辽河水系的绒螯蟹为中华绒螯蟹，广西南流江和广东珠江水系为合浦绒螯蟹，日本本岛为日本绒螯蟹；瓯江和闽江水系为中华绒螯蟹与合浦绒螯蟹的遗传混杂区，图们江水系和俄罗斯海参崴为中华绒螯蟹与日本绒螯蟹的遗传混杂区。建立了不同绒螯蟹种群从幼蟹到成蟹的形态量化判别函数，找到了三种绒螯蟹的生化和分子遗传标记，以及中华绒螯蟹不同种群的分子遗传渐渗标记，建立了从形态、生化遗传、分子遗传和基因组等方面鉴别绒螯蟹不同种群的方法。查明了中华绒螯蟹主要养殖种群的生长性能、性腺发育规律、生殖洄游特点与蜕壳特性。创建了“系内群体选育+系间配套杂交”河蟹配套系育种技术，培育出“江海 21”新品种（品种登记号 GS-02-003-2015）。

关键词：中华绒螯蟹；种质；遗传鉴别；品种

Germplasm resources studies and new variety selection of the Chinese mitten crab

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Abstract：Chinese mitten crab (commonly known as river crab) is a unique organism in China, and germplasm issues have become one of the prominent issues in the development of Chinese mitten crab industry. On the basis of more than 500 germplasm resources of Eriocheir sinensis, we carried out research on germplasm resources and found out that the mitten crab in the Yangtze, Yellow and Liaohe Rivers is Eriocheir sinensis, the crab in the Nanliujiang River in Guangxi and the Pearl River in Guangdong is Eriocheir hepunensis, and the crab in the main island of Japan is Eriocheir japonica. The Oujiang and Minjiang rivers are genetic hybrid regions of E. sinensis and E. hepunensis, while the Tumen river and Vladivostok in Russia are genetic hybrid regions of E. sinensis and E. japonica. We have established morphological discriminant technologies for different juvenile to adult populations of E. sinensis, and developed biochemical and molecular genetic markers for these three kinds of mitten crabs, as well as molecular genetic introgression markers for different populations of E. sinensis . We have identified the growth performance, gonadal development patterns, reproductive migration characteristics, and molting characteristics of the different populations of E. sinensis. We have created a breeding technology of "mass selection within strains and matching hybridization between strains" for Chinese mitten crab, and have developed a new variety of Chinese mitten crab "Jianghai 21" (variety number GS-02-003-2015)

Key words: Chinese mitten crab; Germplasm; Genetic identification; variety

干扰素调控因子 9 通过 PI3K–AKT 信号通路调控 Mx1 参与鲤(Cyprinus carpio)

上皮细胞抗 CyHV–3 过程

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摘要：干扰素调节因子 9 (IRF9)是参与先天免疫和适应性免疫的重要转录调节因子。鲤疱疹病毒-III 型(CyHV-3)是一种在养殖鲤鱼中造成广泛死亡和巨大经济损失的病毒。然而 IRF9 对鲤 CyHV-3 感染的影响尚未见报道。本研究中 CyHV-3 感染期间 IRF9 抑制病毒因子 TK 和 ORF72 的表达。IRF9 蛋白在 CyHV-3 感染的 CCF 细胞中被快速诱导。此外，CyHV-3 感染后，在过表达 IRF9 的 CCF 细胞中诱导了包括(IFNI、ISG15、Mx1 和 Viperin 基因的表达。CyHV-3 感染诱导 IRF9 过表达显著增加 Mx1、PI3K 基因表达和 AKT 蛋白表达($p<0.01$)。有趣的是，在 CyHV-3 感染 CCF 细胞期间，当 AKT 蛋白水平保持不变时，IRF9 并未显著影响 Mx1 基因的表达。这些结果表明 IRF9 在 CyHV-3 感染 CCF 细胞过程中通过 PI3K-AKT 信号通路上调 Mx1 的表达，从而抑制病毒复制。

关键词：IRF9；CyHV-3；CCF 细胞；Mx1；PI3K-AKT 信号通路

IRF9 inhibits CyHV-3 replication by regulating the PI3K-AKT signalling pathway in common carp (Cyprinus carpio) epithelial cells

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Abstract：Interferon regulatory factor 9 (IRF9) is an important transcriptional regulator involved in innate and adaptive immunity. Cyprinid herpesvirus-3 (CyHV-3) is a virus causing widespread death and great economic loss in farmed common carp (Cyprinus carpio). However, the effect of IRF9 on CyHV-3 infection in common carp has not been reported. In this study, during CyHV-3 infection, IRF9 overexpression in common carp fin epithelial (CCF) cells significantly reduced the expression of viral factor thymidine kinase (TK) and open reading frame 72 (ORF72), and knockdown of IRF9 produced the opposite results ($p<0.05$). In CCF cells. The IRF9 protein was expression in the nucleus and was rapidly induced in CCF cells by CyHV-3 infection. In addition, several genes associated with virus infection, including type I interferon (IFNI), IFN-stimulated gene 15 (ISG15), myxovirus resistance 1 (Mx1) and Viperin were induced in CCF cells overexpressing IRF9 upon CyHV-3 infection. IRF9 overexpression induced by CyHV-3 infection significantly increased the gene expression of Mx1 and phosphoinositide 3-kinase (PI3K) and the protein expression of protein kinase B (AKT) ($p<0.01$). Interestingly, IRF9 did not significantly affect Mx1 gene expression when AKT protein levels remained unchanged during CyHV-3 infection of CCF cells. These results indicated that IRF9 inhibited viral replication by upregulating the expression of Mx1 via the PI3K-AKT signalling pathway during CyHV-3 infection in CCF cells and provide some basis for the study of the antiviral molecular mechanisms of common carp.

Key words: IRF9; CyHV-3; CCF cells; Mx1; PI3K-AKT signalling pathway

MRFs 启动子多态性对尼罗罗非鱼生长的影响

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摘要：生肌调节因子基因家族(Myogenic regulatory factors，MRFs)参与机体肌肉的生长与调控，是研究动物生长的良好候选基因。本研究以尼罗罗非鱼为研究对象，探究 MRFs 基因家族启动子区域多态性与生长性状及基因表达量之间的关联，并检测不同基因型 mRNA 的表达量。结果表明： Myf5、Myf6、Myog、Myod1 与 Myod2 五个基因启动子区域存在 11 个多态性位点，其中 Myf5 基因存在 2 个 SNP 位点，Myf6 基因存在 5 个 SNP 位点，Myog 基因存在 1 个 SNP 位点，Myod1 基因存在 1 个 SNP 位点，Myod2 基因存在 2 个 SNP 位点，进一步将这些位点与生长性状进行关联性分析，结果发现 11 个位点中有 10 个位点与生长性状显著相关(P＜0.05)。实时荧光定量实验结果显示，Myf5 基因的 C-1323T 位点、Myf6 基因的 G-42T 位点与 Myog 基因的 A-304C 位点不同基因型的相对表达

关键词：尼罗罗非鱼；生肌调节因子基因家族；启动子；双荧光素酶；相对表达量

Promoter polymorphism in MRFs effect Nile tilapia growth traits

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Abstract： Myogenic regulatory factors (MRFs) are excellent candidate genes for studying animal growth as they play a crucial role in muscle growth and regulation. In this study, Nile Tilapia was chosen as the research subject to investigate the relationship between the polymorphism of the promoter region of MRFs gene family, growth traits, and gene expression level. The impact of SNP loci on promoter activity was determined using a dual-luciferase reporter assay. The results showed that there were 11 polymorphic loci in the promoter regions of Myf5, Myf6, Myog, Myod1 and Myod2 genes, among which there were 2 SNP loci in Myf5, 5 SNP loci in Myf6 and 1 SNP loci in Myog. Myod1 gene had one SNP loci, and Myod2 gene had two SNP loci. Further correlation analysis between these loci and growth traits showed that 10 of the 11 loci were significantly correlated with growth traits ($P < 0.05$). Through linkage disequilibrium analysis and double type construction, the results showed that there were 3, 4 and 1 diplotypes of Myf5, Myf6 and Myod2, respectively, which were closely related to growth traits, and further analysis found that these double types contained more dominant growth molecular markers than other combinations. Quantitative real-time PCR experiment results revealed significant variations in the relative expression levels of various genotypes at the C-1323T loci of the Myf5 gene, the G-42T loci of the Myf6 gene, and the A-304C loci of the Myog gene ($P < 0.05$). Dual-luciferase detection revealed that the promoter activity of the C-1323T mutant of the Myf5 gene differed significantly from that of the wild-type individuals ($P < 0.05$). The molecular markers identified from the promoter of the MRFs gene family show a significant correlation with the growth traits of Nile Tilapia. These markers can be considered as potential indicators in the growth and breeding of Tilapia.

Key words: Nile tilapia; Myogenic regulatory factor gene family; Promoter; Dominant growth traits; Dual-luciferase assay

海洋双壳贝类模式物种侏儒蛤-精子超低温冷冻保存技术研究

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摘要：精子超低温冷冻保存技术已在海洋经济双壳贝类中开展了研究以用于其种质资源保存。但针对由冷冻精子获得的后代/下一代的研究较少，而这方面的研究结果对精子种质资源冷冻库的建设非常重要。侏儒蛤是海水双壳贝类，已被当作模式生物用来阐释海水经济双壳贝类养殖方面的问题。其优势在于世代周期短，且整个生活周期都可在实验室进行。因此，本研究以侏儒蛤为研究对象，优化精子超低温冷冻保存主要步骤，拟开发侏儒蛤精子超低温冷冻保存技术用于研究冷冻精子受精获得的后代/下一代的表现，同时借鉴侏儒蛤精子超低温冷冻保存技术开发蛤仔类经济贝类精子超低温冷冻保存技术。实验结果显示，虽然解冻后精子结构和生理指标与对照组相比均发生了显著变化，但解冻后 D 型幼虫率仍可达 80%以上。因此本研究表明，侏儒蛤可作为模式生物用于研究精子超低温冷冻保存对海洋双壳贝类后代/下一代的影响，同时该方法对经济蛤仔类精子超低温冷冻保存技术开发提供有价值的参考。

关键词：侏儒蛤；精子；非程序超低温冷冻

Development of sperm cryopreservation technique in dwarf surfclam Mulinia lateralis-a model species for research in marine bivalve species

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Abstract： Understanding the performance of progeny/next generation produced from cryopreserved sperm is important for sperm cryobanking. However, this knowledge is limited in marine bivalve species. The Mulinia lateralis has been used as a model species for research in marine bivalve species aquaculture purposes. The advantages of this species involve short generation interval and techniques for culture can be conduced in laboratory. This study investigated key parameters to develop sperm cryopreservation technique in M. lateralis in order to use this species to understand the performance of progeny/next generation generated from cryopreserved sperm. Results showed that although data for sperm quality were significantly changed after cryopreservation, > 80% post-thaw D-larval rate was achieved. Thus, this study suggested that M. lateralis could be used as a model species to investigate the performance of progeny/next generation generated from cryopreserved sperm in marine bivalve species. Moreover, protocol developed from this study is valuable for development of same technique in economic cockle and clam species which has limited research.

Key words: Dwarf surfclam; Mulinia lateralis; Sperm cryopreservation; Non-programmable freezing technique

Rxr γ 在中华鳖性腺分化中的分子特征和潜在功能

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摘要：视黄素 X 受体（RXR）是配体依赖的核受体家族的成员之一。研究表明，RXRs 参与了脊椎动物的繁殖。然而，关于 RXRs 在龟鳖类中的功能的信息却鲜有报道。本研究克隆并分析了中华鳖的 Rxrγ cDNA 序列，并构建了多克隆抗体。RXRγ蛋白在中华鳖成熟和分化的性腺中均呈阳性信号。随后，利用短干扰 RNA（RNAi）技术证实了 Rxrγ基因在性腺分化中的功能。中华鳖 Rxrγ基因全长 cDNA 序列为 2152 bp，编码 407 个氨基酸，包含典型的核受体家族结构域，包括 DBD、LBD、AF1。此外，Rxrγ基因在中华鳖性腺分化过程中表现出二态性的表达模式。实时荧光定量 PCR 结果显示，Rxrγ基因在中华鳖卵巢中高表达。RNAi 处理增加了 ZZ 胚胎性腺中支持细胞的数量。此外，RNA 干扰还上调了胚胎性腺中雄性基因的表达。然而，雌性基因和减数分裂相关基因表达下降。结果表明，Rxrγ参与了中华鳖性腺的分化和发育。

关键词：中华鳖；视黄酸 X 受体γ；多克隆抗体；性腺分化；RNA 干扰

Molecular characterization and potential function of Rxrγ in gonadal differentiation of Chinese soft-shelled turtle (Pelodiscus sinensis)

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Abstract：Retinoid X receptor (RXR) is a member of the ligand-dependent nuclear receptor family. Previous studies revealed that RXRs are involved in reproduction in vertebrates. However, information on the function of RXRs in turtles is scarce. In this study, the Rxrγ cDNA sequence of Pelodiscus sinensis was cloned and analyzed, and a polyclonal antibody was constructed. RXRγ protein showed a positive signal in both mature and differentiated gonads of the turtle. Subsequently, the function of the Rxrγ gene in gonadal differentiation was confirmed using short interfering RNA (RNAi). The full-length cDNA sequence of the Rxrγ gene in P. sinensis was 2152 bp, encoding 407 amino acids and containing typical nuclear receptor family domains, including the DNA-binding domain (DBD), ligand-binding domain (LBD), and activation function 1 (AF1). Moreover, gonadal Ps-Rxrγ showed sexual dimorphism expression patterns in differentiated gonads. Real-time quantitative PCR results revealed that the Rxrγ gene was highly expressed in the turtle ovary. RNAi treatment increased the number of Sertoli cells in ZZ embryonic gonads. Furthermore, RNA interference upregulated Dmrt1 and Sox9 in ZZ and ZW embryonic gonads. However, Foxl2, Cyp19a1, Stra8, and Cyp26b1 were downregulated in embryonic gonads. The results indicated that Rxrγ participated in gonadal differentiation and development in P. sinensis.

Key words: Pelodiscus sinensis; Retinoid X receptor γ; Polyclonal antibody; Gonadal differentiation; RNA interference

中国梭鲈（Sander l ucioperca ）种质资源收集与遗传评价

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摘要：为了解和利用梭鲈种质资源，收集了新疆乌伦古湖(WL)、宁夏腾格里湖(TL)、乌苏里江抚远段(WS)、黑龙江黑河段(HR)的活体种质用于遗传选育，采集了兴凯湖(XL)和哈萨克斯坦的斋桑湖(ZL)群体的鳍条样本，基于微卫星标记对中国主要梭鲈种质资源开展了遗传评价。微卫星标记的分析结果显示中国梭鲈群体中，WL、TL、HR 群体处于高度多态水平(PIC≥0.5)，而 WR 和 XL 群体处于中度多态水平(0.25≤PIC<0.5)。另外，中国梭鲈群体的遗传多样性低于 ZL 群体(PIC=0.751)。梭鲈群体间具有中度遗传分化(FST=0.1897>0.15)，WL、TL、HR 3 个梭鲈群体与 XL 和 WR 群体具有高度显著的遗传分化，与 ZL 群体分化不显著。本研究对梭鲈种质资源的收集与遗传评价为种群保护和有效利用提供了依据。

关键词：梭鲈；微卫星；遗传资源; 遗传评价

pikeperch; microsatellite marker; genetic evaluation

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Abstract： The pikeperch (Sander lucioperca) is a native fish species in European and Asian river basins. Owing to its fast growth rate, strong adaptability, and high nutritional value, it has become a promising candidate species for aquaculture. However, information on the genetic background of these populations is still limited, hindering the protection and sustainable utilisation of genetic resources in China. In the present, a total of 92,162 pairs of microsatellite primers were designed. Among them, dinucleotide repeats were the most abundant microsatellites (81.47%), followed by trinucleotides (8.21%), tetranucleotides (7.59%), and pentanucleotide repeat microsatellites (2.73%). Of the 200 pairs of synthesised primers, 122 exhibited obvious repeat-length polymorphisms. Thirty polymorphic markers were selected to analyse the six populations of pike-perch. Among Chinese populations, the average number of alleles (Na) and effective alleles (Ne) per population varied from 2.333(WR) to 7.800(WL) and from 1.787(XL) to 4.435(WL), respectively. The observed heterozygosity (Ho) and polymorphism information content (PIC) ranged from 0.377(XL) to 0.796(TL) and from 0.304(XL) to 0.715(WL), respectively. The results showed that three populations were highly polymorphic (PIC≥0.5), two populations were moderately polymorphic (0.25≤PIC<0.5). In addition, the diversity in Chinese populations was lower than that in the ZL population (PIC=0.751). The FST estimated using the analysis of molecular variance (AMOVA) was 0.1897, indicating moderate levels of genetic differentiation among the populations. Results from the UPGMA dendrogram, structure analysis, and PCA analysis showed that the six populations of pikeperch were largely divided into two genetically distinct groups. The four populations, WL, TL, HR, and ZL, were highly significantly different from KL and WR in northeast China. These populations can be utilised for breeding programs to achieve substantial genetic variations in their descendants. Genetic diversity and structure analysis of populations will provide useful information for conservation management and effective utilisation of pikeperch.

Key words: Sander lucioperca; microsatellite markers; germplasm resource； genetic evaluation

南移仿刺参性腺发育形态组织学及其配子超微结构观察

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摘要：本研究在人工控温培育条件下取南移养殖仿刺参亲参进行解剖观察，固定仿刺参精巢、卵巢进行组织切片和和透射电镜观察。结果表明，采集的仿刺参性腺组织可划分为增殖期、发育期和成熟期 3 个发育时期，其中增殖期精巢性腺呈白色，生殖管壁上附着大量的精原细胞，透射电镜下精原细胞与基底膜相连接、呈长多边形；增殖期卵巢性腺为浅橙色，生殖管壁上附着有少量卵原细胞和卵黄发生前期卵母细胞，透射电镜下卵原细胞内染色质颗粒随机散布在核内；发育期精巢性腺呈乳黄色，生殖上皮有大量精母细胞和精子细胞，透射电镜下次级精母细胞出现尾部结构；发育期卵巢性腺生殖管中存在大量卵母细胞和卵黄发生前期卵母细胞；成熟期精巢呈乳白色，存在大量精子，生殖管直径为 1~5 mm；成熟期卵巢性腺呈橘红色，卵巢中充满卵子，透射电镜下卵径均大于 80 μm。本研究结果表明，在人工控温条件下可初步实现南移仿刺参的性腺促熟发育。

关键词：仿刺参；性腺发育；组织观察；超微结构

Histological observation and microscopic analysis of gonadal development of Apostichopus japonicus in the south of China

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Abstract： In this study, under the condition of artificial temperature control cultivation, the sea cucumbers cultured in the south of China were taken for anatomical observation. Samples were studied by tissue fixation, tissue section, and transmission electron microscopy. Results showed that the gonadal tissues of A. japonicus could be divided into three development stages proliferation, development, and maturity. The male gonads were in white color in the proliferation stage, while a large number of spermatogonia and spermatocytes were observed on the wall of the reproductive tube. Under the transmission electron microscope, the spermatogonia were connected with the basement membrane in the shape of a long polygon. The ovarian was light orange in the proliferative phase. A small number of oogonia and previtellogenic oocytes were observed on the wall of the reproductive tube. Chromatin particles with large electron density in oogonia were randomly distributed in the nucleus. Entering the developmental stage, most of the male gonads were milk-yellow, and a large number of spermatocytes and sperm cells were observed in the reproductive epithelium. The secondary spermatocytes appeared tail structure. There were a large number of oocytes and previtellogenic oocytes in the reproductive duct of ovarian gonads at the development stage. The mature gonads were milky white, and a large number of sperms were found. The reproductive tube was 1~5 mm in diameter. The gonads of the mature ovary were orange-red, and the ovaries were filled with eggs. The size of the eggs was more than 80 μm in diameter. The results of this study showed that the gonadal maturation of A. japonicus could be preliminarily realized under artificial temperature control.

Key words:：Apostichopus japonicus; gonadal development; histological observation; ultrastructure

金虎杂交斑与母本棕点石斑鱼低氧耐受能力分析

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摘 要：采用封闭式呼吸室测定棕点石斑鱼(Epinephelus fuscoguttatus)和金虎杂交斑(E. fuscoguttatus ♀ × E. tukula ♂)幼鱼的耗氧率与窒息点,在正常溶氧[(5.71±0.31) mg/L]和溶解氧下降至 4 mg/L、3 mg/L、2 mg/L、1 mg/L、0.4 mg/L 处 1 h 后以及恢复正常溶氧水平 3 h 后，采取棕点石斑鱼和金虎杂交斑幼鱼的肝脏组织，测定其部分抗氧化酶活性与能量利用相关的指标。结果表明：(1)在水温(31.18±0.38) ℃时金虎杂交斑的耗氧率为 0.16 mg/(g·h)，显著高于其母本棕点石斑鱼幼鱼($P<0.05$)；棕点石斑鱼与金虎杂交斑幼鱼的窒息点分别为 0.22 mg/L、0.24 mg/L，二者差异不显著；(2)溶解氧浓度下降和复氧的全过程中，棕点石斑鱼幼鱼肝脏中超氧化物歧化酶(superoxide dismutase

关键词：金虎杂交斑；棕点石斑鱼；低氧耐受能力

雅罗鱼杂交种及其双亲耐碱性能相关生理指标比较研究

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摘要：为探究杂交子代“雅龙 1 号”及其亲本达里湖瓦氏雅罗鱼(母本)和额尔齐斯河高体雅罗鱼(父本)的耐碱性能，对它们进行 7 d 的 50 mM 碳酸氢钠碱度胁迫实验，对与耐碱性能相关的生理指标及其基因表达进行了比较研究。发现母本鳃的钠-钾 ATP 酶活性及其对应基因的表达量均高于杂交种，显著高于父本(P<0.05)；血清碱性磷酸酶活性及鳃中 alpl 的表达量极显著低于其他两种鱼(P<0.0001)，表明其可能通过 AKP 去磷酸化作用，调控 NKA 酶活性，参与渗透压调节。母本的血氨及尿素氮含量极显著低于其他两种鱼，血清谷氨酸脱氢酶和谷氨酰胺合成酶，以及鳃相关基因表达量部分高于子代，均显著高于父本，表明母本通过合成氨中间代谢物和提高氨转运蛋白活性消耗体内的氨。这些生理指标与母本极强的耐碱性能显著相关，较好地遗传给了子代。本研究结果为鱼类耐碱性能的综合评价提供了理论依据，为雅罗鱼耐碱新品种选育及良种申报奠定了工作基础。

关键词：雅罗鱼；杂交种；耐碱性能；渗透压调节；氨代谢

A comparative study on physiological indexes related to alkali resistance of Leuciscus hybrids and their parents

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Abstract： To investigate the alkali resistance of the hybrids of Leuciscus and its parent Leuciscus waleckii (female parent) and Leuciscus idus (male parent) of the Irtysh River in Xinjiang, the alkalinity stress experiment of 50 mmol/L NaHCO3 was carried out on three experimental fish for 7 days. Several physiological indexes and corresponding gene expressions, which participate osmotic pressure regulation and ammonia metabolism and significantly related to alkali resistance, were compared and studied. The results showed that the Na+/K+ ATPase (NKA) activity and gene expression (ATPase α1-like and ATPase α3) of the gill tissues of the female parent with strong alkali resistance were higher than those of hybrids, and significantly higher than those of the male parent (P<0.05). The serum alkaline phosphatase (AKP) activity and the gene expression amount (alpl) of gill tissue were significantly lower than those of the other two fish (P<0.0001), indicating that the female parent may regulate NKA enzyme activity through AKP dephosphorylation and participate in osmotic pressure regulation under high alkaline stress. The detection of ammonia metabolism related indexes showed that the blood ammonia (Amon) and urea nitrogen (BUN) contents of the female parent were very significantly lower than those of the other two fish (P<0.0001), while the serum glutamate dehydrogenase (GDH) and glutamine synthetase (GS), as well as the expression of related genes in the gill tissue (glud, glul, Rhbg and Rhcg1) were mostly higher than those of hybrids, and significantly higher than those of the male parent (P<0.05), indicating that the female parent consumed ammonia in the body by synthesizing ammonia intermediate metabolites and increasing the activity of ammonia transporters. In summary, these physiological indexes were significantly related to the female parent's strong alkali resistance, and were well inherited to its hybrid offspring. The results of this study provide a theoretical basis for the comprehensive evaluation of the alkali resistance of fish, and lay a working foundation for the selection and breeding of new varieties of alkali resistance and the declaration of improved varieties of Leuciscus.

Key words: Leuciscus; Hybrids; Alkali resistance; Osmotic pressure regulation; Ammonia metabolism

不同水温条件对皱纹盘鲍三倍体生长性状的影响

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摘要：皱纹盘鲍三倍体具有较高的产业价值和广阔的应用前景，而适合三倍体生长的养殖条件仍不明确。因此，本研究比较了皱纹盘鲍二倍体和三倍体在三种恒温条件下(18°C, 22°C 和 26°C)养殖三个月的生长性状。结果表明，26°C组三倍体存活率显著高于二倍体，而其他两温度组三倍体存活率与二倍体相似。除 22°C 组壳宽和 26°C 组壳长外，皱纹盘鲍三倍体在各温度下生长性状均显著优于二倍体。其中足肌重的三倍体优势率分别为 81.44%(18°C)、76.21%(22°C)和 54.96%(26°C)。壳长和体重的特定增长率表明，22°C 组三倍体生长速度最快。通过 ABT 法对二倍体和三倍体的高温耐受性进行了测评，三倍体的 ABT 显著高于二倍体。足肌吸附力结果表明，三倍体的足肌吸附力强于二倍体。综上所述，本研究证实了皱纹盘鲍三倍体在出肉率性状上的三倍体优势，并确定了适合三倍体生长的温度范围。结果将为鲍养殖产业发展提供参考。

关键词：皱纹盘鲍；三倍体；生长；温度；出肉率

Changes in water temperature: the effect of triploid performance in Pacific abalone (Haliotis discus hannai)

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Abstract： The triploid Pacific abalone has significant industrial value and promising application prospects. However, it remains unclear which culture environment is ideal for maximizing the triploid advantages of Pacific abalone. To address this knowledge gap, this study investigated the characteristics of triploid Pacific abalone after three months of culture under three constant temperature conditions (18 °C, 22 °C, and 26 °C). The results showed that the survival rate of triploids in the 26 °C group was significantly higher than that of diploids ($P < 0.05$), while the survival rate of triploids in the other two groups was similar to that of diploids ($P > 0.05$). Except for the shell width of the 22 °C group and the shell length of the 26 °C group, triploid Pacific abalone exhibited significantly superior growth traits compared to diploids at all temperatures ($P < 0.05$). The most notable improvement was observed in the foot muscle weight trait, with a triploid advantage rate of 81.44% (18 °C), 76.21% (22 °C), and 54.96% (26 °C), respectively. The specific growth rate and gain ratio of shell length and body weight indicated that triploids grew the fastest in the 22°C group. Furthermore, the thermal resistance of diploids and triploids was evaluated through the Arrhenius break temperature (ABT) of cardiac performance. The results demonstrated that the ABT of triploids was significantly higher than that of diploids ($P < 0.05$, ABT2N = 30.81 ± 0.43 °C, ABT3N = 31.38 ± 0.72 °C). Both diploid and triploid foot adhesion forces were measured, and the results showed that triploid foot adhesion force was stronger than that of diploids ($P < 0.05$). Additionally, there was a significant positive correlation between foot adhesion force and meat yield traits (foot muscle weight, FMSI, FI) ($P < 0.05$). In summary, this study confirmed the triploid advantage in meat yield of Pacific abalone and identified a temperature range that maximizes their growth rate. Moreover, triploids exhibited improved thermal resistance and adhesion capacity compared to diploids with the increase of meat yield. The results of this study could serve as a reference for identifying a culture model suitable for triploid Pacific abalone and could promote the development of the triploid aquaculture industry.

Key words: Pacific abalone; triploid; growth; temperature; meat yield

CRISPR/cas9 诱导的 LEAP2 和 GHSR1a 基因敲除突变斑马鱼表现出生长异常和脂质代谢受损

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摘要：肝脏表达的抗菌肽 2 (LEAP2)最初被描述为抗菌肽，最近被认为为是生长激素促分泌素受体 1a (GHSR1a)的另一种配体。本研究通过禁食和再喂养实验发现斑马鱼中 LEAP2 的表达受饮食调节，并能拮抗胃饥饿素的作用。LEAP2 的缺失可促进斑马鱼肝脏 ghrelin 和大脑 GHSR1a 的上调，导致斑马鱼 AGRP 表达增加，食欲增强。此外，LEAP2 缺乏导致斑马鱼运动活动减少，导致具有 LEAP2-/-的成年雌性斑马鱼随着肝脏脂滴的增加而变得肥胖。GHSR1a 突变导致肝脏中 ghrelin 和 LEAP2 的表达降低。这种改变导致雄性斑马鱼更瘦，肝脂滴显著减少。综上所述，这些研究结果强调了 LEAP2 作为饱食欲因子在机体能量平衡调节中的重要意义，揭示了其通过与 GHSR1a 相互作用。

关键词：斑马鱼；LEAP2；GHSR1a；血糖；肥胖

CRISPR/Cas9-induced LEAP2 and GHSR1a knockout mutant zebrafish displayed abnormal growth and impaired lipid metabolism

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Abstract: Liver-expressed antimicrobial peptide 2 (LEAP2), originally described as an antimicrobial peptide, has recently been recognized as another ligand of growth hormone secretagogue receptor 1a (GHSR1a). LEAP2, acts both as an endogenous competitive antagonist of ghrelin and an inverse agonist of constitutive GHSR1a activity, which vigorously blocks ghrelin's effects on food intake and hormonal secretion in mice. In this study, fasting and refeeding experiments revealed that the expression of LEAP2 in zebrafish is diet-regulated and antagonizes the action of ghrelin. The absence of LEAP2 can promote the upregulation of ghrelin in the zebrafish liver and GHSR1a in the brain, leading to an increase in AGRP expression in zebrafish and enhanced appetite. Additionally, LEAP2 deficiency results in a reduction in zebrafish locomotor activity, causing adult female zebrafish with LEAP2-/- to become obese with an increase in liver lipid droplets. Mutation of GHSR1a leads to decreased expression of both ghrelin and LEAP2 in the liver. This alteration results in leaner male zebrafish with a significant reduction in liver lipid droplets. Taken together, these research findings underscore the significance of LEAP2 as a satiety factor in the regulation of organismal energy balance, revealing its pivotal role in energy metabolism regulation through interaction with GHSR1a.

Key words: Zebrafish; LEAP2; GHSR1a; Blood glucose; Fat

基于双壳张合行为的贝类生物活性监测方法研究

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摘要：我国是贝类产业大国，贝类健康评价方法的发展，对降低贝类养殖风险、提高养殖产量、提升育种效益具有重要意义。本研究开发了一种非侵入式的贝类双壳运动监测方法，通过设备加工制造，实现贝类行为原位监测。研究以我国北方重要养殖品种虾夷扇贝为例，在实验室下模拟贝类正常生存环境，通过每日 24 小时连续监测 31 天发现，扇贝双壳张合运动具有昼夜节律特点。且存活时间久的个体，其快速开合的双壳运动在其整个监测过程中的日分布更均匀，这提示我们双壳快速开合的速率指标是反映贝类活性的重要参数。进一步评估双壳开合运动与扇贝活力及死亡率的相关性发现，生存潜力预测系数与扇贝存活时间呈显著正相关，在此计算中，贝类双壳快速张合能力及壳宽（贝类厚度指标）是评估扇贝生存潜力重要的变量。本研究通过开发一种高效无损、能够反映贝类生存潜力的评价指标，聚焦贝类张合行为规律解析，提高了人们对双壳贝类贝壳张合行为的理解与认识。

关键词：扇贝；张合行为；生存潜力；生物监测

Research on monitoring methods of shellfish bioactivity based on bivalve valve movements.

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Abstract： China is a big country in shellfish industry, and the development of shellfish health evaluation methods is of great significance to reduce the risk of shellfish breeding, improve the production and improve the breeding benefit. In this study, a non-invasive method for monitoring valve movements was developed, and the behavior of shellfish was monitored in situ through equipment manufacturing. In this study, an important breeding species, Yesso scallop, in northern China was taken as an example, the normal living environment of shellfish was simulated in the laboratory, and it was found that the valve movements of scallops had the characteristics of circadian rhythm through continuous monitoring 24 hours a day for 31 days. The daily distribution of the rapid valve opening and closing movements of the long-lived individuals was more uniform during the whole monitoring process, suggesting that the rate of rapid opening and closing is an important parameter reflecting the activity of shellfish. Further evaluation of the correlation between bivalve opening and closing movement and scallop vitality showed that the prediction coefficient of survival potential was significantly positively correlated with the survival time of scallops. In this calculation, the rapid opening-closing ability of valve movements and shell width (shellfish thickness index) were important variables to evaluate the survival potential of scallops. By developing an efficient and non-destructive evaluation index that can reflect the survival potential of shellfish, this study focused on the analysis of shellfish valve behavior, and improved people's understanding of bivalve valve behavior.

Key words: Scallop; Valve movements; Survival potential; Biomonitoring

日本沼虾卵黄蛋白原基因 SNP 的筛选及其与卵巢发育的关系

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摘要：本研究首次对日本沼虾性腺指数与生长性状进行了相关分析。结果表明，“性快熟”对雌性日本沼虾的大小有显著的负面影响（p<0.01），对雄虾几乎没有影响（p>0.05）。之后基于日本沼虾卵黄蛋白原基于进行 SNP 筛选，共筛选到 31 个候选位点，其中有 6 个位点与雌虾性腺指数显著相关，位点 C+948A 中的 CC、G+1209A 中的 GG、A+1879G 中的 AG、T+4458A 中的 TT 和 AT、A+7080A 中的 AT 和 A+9435G 中的 AA 基因型与卵巢快速成熟显著相关。有 5 个 SNP 位点与雌性生长性状显著相关，其中 3 个与卵巢成熟显著相关（C+948A、T+4458A 和 A+9435G）。

关键词：日本沼虾；卵巢成熟；单核苷酸多态性；卵黄蛋白原

Identification SNPs in vitellogenin gene and their association with ovarian development and growth of Macrobrachium nipponense

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Abstract：In this study, the correlation analysis between gonadosomatic index and growth traits of M. nipponense was carried out for the first time. The results proved that short sexual maturity M. nipponense had a significant negatively effect on the female prawn size (p < 0.01) but had almost no effect on the male (p > 0.05). The full-length Vitellogenin gene of M. nipponense (Mn-Vg) were applied to detect polymorphism and the correlation between SNP and ovarian development. 31 candidate SNP loci of Mn-Vg were identified and the genetic diversity of these loci in the M. nipponense population was moderate polymorphism. The correlation between Mn-Vg SNPs and ovarian development was further investigated. 6 SNPs were significantly correlated with female GSI. The genotype CC in C+948A, GG in G+1209A, AG in A+1879G, TT and AT in T+4458A, AT in A+7080A and AA in A+9435G are significantly associated with rapid ovary maturation. Further statistical analysis results between SNPs and female growth index showed five SNP loci were significantly associated with female growth traits. Three of them significantly associated with ovarian maturation (C+948A, T+4458A and A+9435G).

Key words: Macrobrachium nipponense; ovary maturation; single nucleotide polymorphism; vitellogenin

日本沼虾琥珀酸脱氢酶复合物铁硫亚基 B 基因的鉴定和表征

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摘要：本研究采用定量聚合酶链反应(qPCR)、原位杂交、western-blot、RNA 干扰(RNAi)等方法，结合组织学观察，进一步深入分析了 Mn-SDHB 的功能。在不同发育阶段，Mn-SDHB 在不同组织中的表达水平最高的部位是精巢和幼虫后发育阶段 25 的雄性对虾，表明 SDHB 可能参与了日本沼虾雄性的性发育。原位杂交和 western-blot 分析表明 SDHB 在睾丸发育中起重要作用。原位杂交分析也表明 Mn-SDHB 在精巢发育中的潜在作用。注射 Mn-SDHB dsRNA 后，Mn-IAG 的表达降低，表明 SDHB 对日本沼虾 IAG 具有正向调节作用。因此，SDHB 参与了雄性精巢发育的机制。Mn-SDHB dsRNA 注射 10 d 后，精巢发育受到抑制，精子很少出现，说明 SDHB 对日本沼虾雄性精巢发育有积极影响。本研究突出了 SDHB 在日本沼虾的功能，为今后其他甲壳类动物雄性性发育的研究提供了新的思路。

关键词：日本沼虾；SDHB；qPCR 分析；RNA 干扰；精巢发育

Identifification and Characterization of the Succinate Dehydrogenase Complex Iron Sulfur Subunit B Gene in the Oriental River Prawn, Macrobrachium nipponense

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Abstract: In this study, the functions of Mn-SDHB were further analyzed in depth using quantitative polymerase chain reaction (qPCR), in situ hybridization, western-blot, and RNA interference (RNAi), combined with the histological observations. The full-genome sequence of Mn-SDHB was 54,608 bp at Chromosome 34, including 7 introns and 6 exons. The full-length cDNA sequence of Mn-SDHB was 1,268 base pairs (bp) long with an open reading frame of 807 bp, encoding for 268 amino acids. The highest expression level of Mn-SDHB in different tissues was observed in the testis, and male prawns at post-larval developmental stage 25 during different developmental stages, indicating that SDHB was potentially involved in the male sexual development in M. nipponense. In situ hybridization and western-blot analysis indicated that SDHB plays essential roles in the testis development. The in situ hybridization analysis also implies the potential roles of Mn-SDHB in ovarian development. The expressions of Mn-IAG were decreased after Mn-SDHB dsRNA injection, indicating SDHB has the positive regulatory effects on IAG in M. nipponese. Thus, SDHB was involved in the mechanism of the male sexual development. The testis development was inhibited, and sperms were rarely observed after 10 days of Mn-SDHB dsRNA injection, indicating SDHB has positive effects on the male sexual development in M. nipponense. This study highlights the functions of SDHB in M. nipponense, which provide new insights for the future studies of the male sexual development in other crustacean species.

Key words: Macrobrachium nipponense; SDHB; qPCR analysis; RNAi; male sexual development

首个无脊椎动物的 QRFP 样肽受体基因的克隆、特征分析及其在曼氏无针乌贼摄食中的作用研究

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摘要：头足类动物被认为是无脊椎动物神经系统进化的巅峰，它们的各种行为都受到多种神经肽-受体系统的调控。乌贼是头足类的代表物种之一，是研究神经肽-受体系统的良好模型。新发现的一类 G 蛋白偶联受体（QRFPR）是神经肽 QRFP 的内源性受体，其分布模式、结构特征及生物学功能在除脊索动物外的其他种类中未见报道。本研究在曼氏无针乌贼（Sepiella japonica）中克隆了首个无脊椎动物的 QRFP 样肽受体基因（Sj_QRFPLR）。生物信息分析及实验结果显示：1）Sj_QRFPLR 是 A 类 GPCR，属于 QRFPR 家族；2）QRFPR 在头足类物种中可能具有结构保守性；3）Sj_QRFPLR 在雌性乌贼脑的多个功能叶和成体许多外周组织中广泛分布，暗示其具有功能多样性；4）Sj_QRFPLR 可能在乌贼中具有促进食欲的功能。研究结果有助于我们深入研究 QRFP/QRFPR 系统及其他神经肽系统在低等无脊椎动物中的功能。

关键词：神经肽；26RFa/QRFP；QRFP 样肽受体；乌贼；曼氏无针无针

The first invertebrate QRFP-like peptide receptor gene in the cephalopod Sepiella japonica: identification, characterization and possible role in orexigenic activity

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Abstract： Various behaviors of the cephalopod are under the control of neuropeptide-receptor systems. As a representative specie in the cephalopod, Sepiella japonica is an excellent model to study peptidergic regulation. The novel identified receptor QRFPR is the endogenous receptor for the neuropeptide QRFP. The distribution pattern, structure, and biological actions of QRFPR have been largely described in vertebrate species, while no knowledge of QRFPR has been reported in invertebrate. Given this, we characterized the first invertebrate QRFP-like peptide receptor gene in the S. japonica, termed Sj_QRFPLR. Multiple alignments, phylogenetic analysis, and in vitro subcellular localization analysis indicated that Sj_QRFPLR is a class A GPCR and it belongs to the QRFPR family. Meanwhile, QRFPR is likely to be structurally conserved in cephalopod species. In situ hybridization and RT-PCR data revealed a widespread distribution pattern of Sj_QRFPLR in multiple function lobes of the female brain and numerous peripheral tissues in adults cuttlefish. Functional analysis indicated that Sj_QRFPLR is likely to exhibit orexigenic properties. Findings made here will contribute to our understanding of QRFPR and the peptidergic regulation of the QRFP/QRFPR system in invertebrates.

Key words: Neuropeptide; 26RFa/QRFP; QRFP-like peptide receptor; cuttlefish; Sepiella japonica

卵形鲳鲹 C4orf48 基因的克隆、功能分析及其在摄食和生殖中的作用

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摘要：C4ORF48 是近年来新发现的一种活性多肽，目前对其研究还处于初步阶段，特别是在鱼类中还未见研究报道。本研究克隆并分析了卵形鲳鲹 C4orf48 的 cDNA 序列，结果显示卵形鲳鲹 C4orf48 cDNA 开放阅读框为 273 bp，共计编码 90 个氨基酸，含有一个信号肽和一个推定的成熟肽。组织表达分析发现，卵形鲳鲹 C4orf48 在雄性的脑、垂体和心脏中表达量较高，而在雌性中则在脑、垂体和卵巢等组织中大量表达。食物剥夺实验结果显示，禁食 2 d 和 7 d 后下丘脑中的 C4orf48 mRNA 表达上调，并在重新投喂后恢复正常水平。此外，C4ORF48-17 多肽体内和体外给药可以显著增加卵形鲳鲹中 3 种 gnrh 亚型、lh 和 fsh mRNA 的表达水平，也可以显著刺激食欲调控相关的 agrp 和 npy 基因表达上调。我们的数据表明 C4ORF48 可能作为促食欲因子和促生殖因子参与卵形鲳鲹的摄食和生殖调控，为相关研究提供参考。

关键词：C4ORF48；摄食；生殖；卵形鲳鲹

Molecular Cloning and Functional Characterization of C4ORF48 in Golden Pompano (Trachinotus ovatus) and Its Role in Food Intake and Reproduction

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Abstract：C4ORF48 is a recently discovered polypeptide, and research on it is still in the preliminary stage, especially in fish. In this study, the cDNA sequence of the golden pompano C4orf48 was cloned and analyzed. The results showed that the open reading frame (ORF) of C4orf48 cDNA was 273 bp, encoding 90 amino acids. It contained a signal peptide and a predicted mature peptide. Sequence alignment and phylogenetic tree analysis showed that the C4ORF48 of the golden pompano was highly homologous to the C4ORF48 of the same order Perciformes, such as Seriola dumerili, Lates calcarifer, and Echeneis naucrates. Tissue expression analysis showed that C4orf48 in golden pompano was highly expressed in the male hypothalamus, pituitary, and heart. In females, it was highly expressed in the hypothalamus, pituitary, and ovary. The results of the food deprivation experiment showed that the expression of C4orf48 mRNA in the hypothalamus was upregulated after fasting for 2 d and 7 d, and returned to normal levels after refeeding. In addition, the administration of C4ORF48-17 peptides in vivo and in vitro significantly increased the expression levels of three gnrh subtypes, lh and fsh mRNA in golden pompano. It also significantly stimulated the upregulation of the agrp and npy genes, which are related to appetite regulation. Our data show that C4ORF48 plays a role in regulating food intake and reproduction in golden pompano as an orexigenic factor and reproductive promoting factor. This finding provides a theoretical foundation for further research in this field.

Key words: C4ORF48; feeding; reproduction; golden pompano

胆固醇 7–脱氢酶在日本沼虾卵巢成熟和蜕皮过程中的功能分析:为生殖蜕皮进程提供依据

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摘要：本研究通过生物信息学方法研究了胆固醇 7-脱氢酶基因的序列特征，通过 qPCR 研究了其在日本沼虾不同组织，卵巢发育不同时期及胚胎发育不同阶段的表达。通过 RNA 干扰方法，探究胆固醇 7-脱氢酶在日本沼虾性腺成熟和蜕皮中的功能。结果显示，干扰胆固醇 7-脱氢酶基因后，与对照组相比，实验组日本沼虾性腺发育显著受到抑制，蜕皮频率和蜕皮激素含量也显著降低。

关键词：日本沼虾；胆固醇 7-脱氢酶；蜕皮；性腺成熟

Function Analysis of Cholesterol 7-Desaturase in Ovarian Maturation and Molting in Macrobrachium nipponense: Providing Evidence for Reproductive Molting Progress

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Abstract： The function of cholesterol 7-desaturase in gonadal maturation and molting of Macrobrachium nipponense was investigated by RNA interference. The results showed that silencing cholesterol 7-desaturase gene, the gonadal development of Macrobrachium nipponense in the experimental group was significantly inhibited compared with the control group, and the frequency and content of molting hormone were also significantly reduced.

Key words: Macrobrachium nipponense; Cholesterol 7-desaturase; molting; ovarian maturation

MiRn–3 通过靶向凝溶胶蛋白抑制仿刺参体壁创伤愈合

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摘要：为了丰富我们对 miRn-3 在创伤愈合过程中的调控功能的认识，本研究以刺参为模型，克隆并表征了 miRn-3 的潜在靶基因 Gelsolin（AjGSN），验证了 miRn-3 与 AjGSN 的相互作用并探讨了 miRn-3/AjGSN 模体在刺参体壁创伤愈合中的作用。结果表明：1）AjGSN 全长 cDNA 为 2935 bp，在棘皮动物中具有较高的序列保守性；2）miRn-3 可与 AjGSN 的 3'UTR 结合，负向调控 AjGSN 的表达；3）过表达 miRn-3 和抑制表达 AjGSN 会抑制刺参体壁创伤愈合。

关键词：刺参；基因克隆；体壁创伤愈合；miRn-3/AjGSN 模体

MiRn-3 inhibits cutaneous wound healing by targeting gelsolin in the sea cucumber Apostichopus japonicus

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Abstract：To enrich our knowledge of the regulatory function of miRn-3 in the process of wound healing, the sea cucumber Apostichopus japonicus was used as a target model in this study. Gelsolin (AjGSN), a potential target gene of miRn-3, was cloned and characterized, and the interaction between miRn-3 and AjGSN was verified. The function of the miRn-3/AjGSN axis in regulating cutaneous wound healing was explored in the sea cucumber A. japonicus. The results showed that 1) the full-length cDNA of AjGSN was 2935 bp, with a high level of sequence conservation across the echinoderms; 2) miRn-3 could bind to the 3'UTR of AjGSN and negatively regulate the expression of AjGSN; 3) overexpression of miRn-3 and inhibition of the expression of AjGSN suppressed cutaneous wound healing in A. japonicus.

Key words: Apostichopus japonicus; Gene cloning; Cutaneous wound healing; miRn-3/AjGSN axis

红螯螯虾雌雄间性个体表型分选

及性腺转录组分子差异分析

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摘要：红螯螯虾表现性别二态性，在大小规格、生长速度雄性都比雌性速度快。然而，人们对甲壳动物的性别决定和性别分化的分子机制了解有限。为了研究雌雄间性个体与正常个体的差异，本研究统计雌雄间性及 7 种不同类型间性个体的占比，观察组织切片差异。另外，对正常雌雄及雌雄间性的性腺进行转录组测序，并且在基因表达水平和生物学信息进行了分析。结果显示：统计到自然群体中雌雄间性占比为 1.5%，雌雄间性不同类型的占比在 0.5%-22.5%之间；切片观察发现当存在卵巢的雌雄间性个体对比正常卵巢发育停滞在初级卵母细胞阶段；筛选到可能与性腺发育及性别相关的通路，包括卵巢类固醇合成、雌激素信号通路、卵母细胞减数分裂、孕酮介导的卵母细胞成熟等通路；筛选到可能跟性腺发育和性别相关的基因，包括 tra2a、dmrta2、ccnb2、foxl2、smad4 等基因。该研究为红螯螯虾的性别决定和性别控制育种以及单性育种提供了重要的分子基础。

关键词：红螯螯虾；间性个体；转录组分析；性腺发育基因

Phenotypic sorting of individual male and female intersex cherax quadricarinatus and analysis of molecular differences in the gonadal transcriptome

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Abstract：Cherax quadricarinatus exhibit sexual dimorphism, with males outpacing females in terms of size specification and growth rate. However, there is limited understanding of the molecular mechanisms underlying sex determination and sex differentiation in crustaceans. In order to study the differences between intersex individuals and normal individuals, this study counted the proportion of intersex individuals and 7 different types of intersex individuals, and observed the differences in tissue sections. In addition, transcriptome sequencing was performed on normal and intersex gonads, and gene expression levels and biological information were analyzed.The results showed that: the percentage of intersex in the natural population was 1.5%, and the percentage of different types of intersex ranged from 0.5% to 22.5%; the sections revealed that the development of normal ovaries was stagnant at the primary oocyte stage when intersexed individuals with ovaries were present; and the screening of the pathways that might be related to gonadal development and sex included ovarian steroid synthesis, estrogen signalling pathway, oocyte We also screened for possible pathways related to gonadal development and sex, including ovarian steroid synthesis, oestrogen signalling pathway, oocyte meiosis, progesterone-mediated oocyte maturation, etc. We also screened for genes that may be associated with gonadal development and sex, including tra2a, dmrta2, ccnb2, foxl2 and smad4. This study provides an important molecular basis for sex determination and sex-controlled breeding as well as unisex breeding in red crayfish.

Key words: Cherax quadricarinatus; intersex individuals;transcription analysis; Gonadal development gene

2 个纯合体色品系海湾扇贝的形态测量学分析

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摘要：近年来，研究人员培育了许多不同壳色的生长速度快，出肉率高的优良扇贝品种。它们的壳体形态是如何适应环境的仍存在争议。本研究采用几何形态测量学（GM）对海湾扇贝的两种群体选择品系（红壳品系和黑壳品系）和对照组进行了分析。结果表明，不同颜色之间的壳体形状存在显著性差异。黑色品系扇贝有更多的椭圆的壳盘。红壳品系扇贝样本的壳形分布具有多态性，红色品系扇贝的椭圆和圆壳盘的数量是相似的。与两个实验品系相比，对照组表现出更圆的壳盘。红壳品系扇贝的拇指角小于黑壳品系扇贝，但大于对照组。黑壳扇贝显示出较大的拇指角，说明与红壳组相比，定向喷流更好地提高了其游泳能力。左右壳在几何形态测量学分析中均表现出一致的差异，表明它们可以用于分析差异。

关键词：几何形态学；海湾扇贝；壳色；壳多态性；双壳

Morphometric analysis of two homozygous shell color strains of the bay scallop Argopecten irradians

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Abstract：Recently researchers have cultivated many excellent scallop strains of different shell colors with fast growth rates and high dressing percentage.How did their morphorlogy adapt to the environment is still under debate.In this study, geometric morphometrics (GM) was used to analyze two mass-selected strains (red shell line and black shell line) and control group of bay scallops.The results showed that there were significant differences in the shell shape between different colors. The black shell line had more elliptical shell discs.The sample distribution of the red shell line had polymorphism.The number of elliptical and circular shell disks in the red shell line is similar.The control group exhibited a more round shell discs compared to the two experimental lines. The umbonal angle of the red shell line was smaller than that of the black shell line but larger than that of the control group. The black shell line displayed a larger umbonal angle, indicating that the directional jet is better aligned for enhanced swimming ability compared to the red shell group.Both the left and right shells displayed consistent differences in GM analysis, suggesting they can be utilized to analyze disparities.

Key words: geometric morphology; bay scallops; shell color; shell polymorphism; bivalves

ISG58 调控草鱼呼肠孤病毒复制的分子机制

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摘要：ISG58（Interferon-stimulated gene 58）作为干扰素诱导蛋白在宿主抗病毒效应中发挥重要作用。本研究以 ISG58 为研究对象，深入探究其调控草鱼呼肠孤病毒复制的分子机制。结构分析发现草鱼 ISG56 包含 9 个与抗病毒作用相关的 TPR 结构域，系统发育分析表明，草鱼与鲫鱼的 ISG58 同源性最高，体内时空表达分析显示，在草鱼感染 GCRV 后，该基因的 mRNA 水平在鱼体内均呈现上调趋势，再通过过表达和 siRNA 等方法，明确 ISG58 对 GCRV 复制的影响,最后采用 GST-Pull down、外源免疫共沉淀等技术来完善 ISG58 的具体调控网络。本研究为草鱼出血病的预防与治疗以及将来利用分子标记培育草鱼抗病新品种奠定理论基础。

关键词：草鱼；草鱼呼肠孤病毒；干扰素刺激基因 58；抗病毒机制

The molecular mechanism of ISG58 regulating GCRV replication

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Abstract: Interferon-stimulated gene 58, an early discovered IFN-induced protein, plays an important role in anti-virus immune response. This study is focus on the anti-viral mechanism of ISG58 in fish after GCRV infection. Structural analysis revealed that Ctenopharyngodon idella ISG58(CiISG58) contains nine putative TPR motifs associated with antiviral effect. Phylogenetic analysis demonstrated that the CiISG58 clustered together with the highest homologues of Cyprinus carpio. RT-qPCR analysis revealed that the expression level of CiISG58 was significantly up-regulated after GCRV infection in grass carp. And then the effect of ISG58 on GCRV replication was uncovered by overexpression or knockdown of ISG58. Finally, GST-Pull down and exogenous co-immunoprecipitation were applied to discover the important functional proteins interacted with CiISG58 in anti-viral innate immunity. This study provides important theoretical basis for the prevention and treatment of grass carp hemorrhagic disease, and develop potential paths for disease-resistant grass carp molecular breeding.

Key words: Grass carp; GCRV, ISG58; Anti-viral mechanism

鲍低氧耐受能力的测评方法建立和育种应用

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摘要：水产养殖区低氧事件严重损害了海洋生态和社会经济，威胁着水产食品的持续生产。因此，加快水产动物遗传改良、培育耐低氧的品种和品系已成为当务之急，而准确的表型检测是水产动物低氧耐受研究的基础。基于鲍在低氧暴露条件下的存活率、心率以及附着能力的变化，我们建立了三种鲍低氧耐受能力检测方法，分别是半致死溶解氧浓度（LC50）、心率拐点溶解氧浓度（BPDO）和低氧附着时间（HYAD）。这些方法在受试动物大小和数量、准确度、实验周期等方面各有优劣，已综合应用于养殖鲍的选择育种实践和低氧耐受性状的分子机制解析。

关键词：海洋贝类；鲍；低氧耐受能力；半致死浓度；心率；附着

Development of assessment methods for hypoxia tolerance of abalone and its breeding application

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Abstract： Hypoxic events in aquaculture areas have seriously harmed marine ecology and socioeconomics, posing a threat to the sustained production of aquatic food. It is urgent to accelerate genetic improvement in the aquaculture industry and breed hypoxia-tolerant varieties. Accurate phenotype assessments are fundamental to the study of hypoxia tolerance of aquaculture animals. In our studies, three assessment methods for hypoxia tolerance of abalone were developed based on the survival, heart rate, and adhesion capacity changes of abalone under hypoxia exposure, including median lethal concentration (LC50), heart rate breakpoint of dissolved oxygen (BPDO), and hypoxia adhesion duration (HYAD). It was found that those methods have their advantages and disadvantages in the size and number of tested animals, accuracy, and assessment duration. They have been comprehensively used in the selection breeding of aquaculture abalone and the molecular mechanism analysis of hypoxia tolerance in abalone.

Key words: Marine mollusk; Abalone; Hypoxia tolerance; Median lethal concentration; Heart rate; Adhesion

Mn–XRN1 对日本沼虾的卵巢生殖具有抑制作用

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摘要：XRN1 是一种核糖核酸外酶，可沿 5′-3′方向降解细胞质中的 mRNA。先前的研究表明，它可能与日本沼虾的繁殖有关。采用实时定量 PCR 技术检测 Mn-XRN1 的时空表达模式。在组织水平上，Mn-XRN1 在卵巢中显著表达。在发育过程中，Mn-XRN1 在胚胎的 CS 期、孵化后第 10 天和卵巢发育的 O2 期显著表达。原位杂交结果显示 Mn-XRN1 在卵巢中的位置。体内注射 dsMn-XRN1 RNA 后，Mn-VASA 的表达显著增加。这表明 Mn-XRN1 负调控 Mn-VASA 的表达。此外，我们统计了 RNAi 后不同天数卵巢发育不同时期的日本沼虾数量。结果表明，卵巢发育明显加快。总的来说，本研究的结果表明，Mn-XRN1 对日本沼虾的卵巢成熟具有抑制作用。其抑制作用可能是通过对 Mn-VASA 的负调控进行。

关键词：日本沼虾；XRN1；卵巢生殖；VASA；变态发育

Mn-XRN1 Has an Inhibitory Effect on Ovarian Reproduction in Macrobrachium nipponense

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Abstract： XRN1 is an exoribonuclease that degrades mRNA in the cytoplasm along the 5′–3′ direction. A previous study indicated that it may be involved in the reproduction of Macrobrachium nipponense. Quantitative real-time PCR was used to detect the spatiotemporal expression pattern of Mn-XRN1. At the tissue level, Mn-XRN1 was significantly expressed in the ovary. During development, Mn-XRN1 was significantly expressed at the CS stage of the embryo, on the 10th day post-larval and in the O2 stage of ovarian reproduction. The in situ hybridization results showed the location of Mn-XRN1 in the ovary. The expression of Mn-VASA was significantly increased after in vivo injection of Mn-XRN1 dsRNA. This suggests that Mn-XRN1 negatively regulates the expression of Mn-VASA. Furthermore, we counted the number of M. nipponense at various stages of ovarian reproduction on different days after RNAi. The results showed that ovarian development was significantly accelerated. In general, the results of the present study indicate that Mn-XRN1 has an inhibitory effect on the ovarian maturation of M. nipponense. The inhibitory effect might be through negative regulation of Mn-VASA.

Key words: Macrobrachium nipponense; XRN1; ovarian reproduction; VASA; metamorphosis

中华绒螯蟹早期发育胚胎比较

转录组分析合子基因组激活

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摘要：合子基因组激活（ZGA）是早期胚胎发育关键分子事件， ZGA 启始时间和调控机制具有种的特异性。迄今甲壳类 EGA 研究甚少，本研究系统比较分析了中华绒螯蟹胚胎（受精卵到溞状幼体）转录组，首次确定了其 ZGA 启始时间并解析了 ZGA 潜在通路。中华绒螯蟹胚胎在受精后经历了 48 小时长时间的 1 细胞阶段，转录组差异表达基因（DEG）分析表明， 1991 个转录本和新表达带有内含子序列的转录本在单细胞胚胎显著上调，尤其在受精后 8 小时至 16 小时雌雄原核融合前，有 1425 个转录本上调，ZGA 激活的标志基因 TFIID，TFIIF,TFIIH 等也显著上调，表明 ZGA 发生在合子形成之前的原核阶段。16 小时胚胎转录组 GO 分析富集了基因"DNA 包装"、"染色质组装或分解"等参与 ZGA 转录的通路，3 个转录因子 POU4F1、FOXA2 和 NFYB 被预测靶向 8 小时和 16 小时胚胎中 78%以上上调基因的启动子，强烈暗示它们参与了 ZGA。

关键词：中华绒螯蟹；转录组学；合子基因组激活

Transcriptomic analysis of early embryo reveals zygotic genome activation in the Chinese mitten crab, Eriocheir sinensis

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Abstract： Zygotic genome activation (ZGA) is a critical molecular event during early development. The onset time and regulation of EGA are species-specific. However, little is known about the ZGA in crustacean species. Here we for the first time determined the onset time of EGA and examined the potential pathways of the major ZGA by comprehensive transcriptome analysis of embryos from fertilized egg to zoea in the Chinese mitten crab Eriocheir sinensis. The mitten crab embryo took a unique long period of 48 h at one cell stage after fertilization. Differential expression genes (DEGs) analysis revealed a significantly increased expression of transcripts (1991) and numbers of newly expressed transcripts with intron sequences at 1-cell embryos. Intensive study further revealed 1425 genes were upregulated from 8 h to 16 h post fertilization before the fusion of male and female pronuclei. The abundant of TFIID， TFIIF,TFIIH transcripts, a hallmark gene for ZGA, significantly increased between 0 and 8 h post fertilization, indicating that the ZGA occurred in pronuclei at 1-cell stage. Gene ontology (GO) analysis of 16 h-embryos enriched some pathways for ‘DNA packaging’, ‘chromatin assembly or disassembly’ and etc., involved in substantial transcription process for ZGA. Three transcription factors POU4F1, FOXA2 and NFYB were predicted to target the promoters of more than 78% upregulated genes in 8 h and 16 h embryos, strongly suggesting their involvement in regulation of ZGA.

Key words: Eriocheir sinensis; transcriptomics; zygotic genome activation

大鳍鳠精子生物学特性及几种环境因子对其活力的影响

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摘要：为探究大鳍鳠精子生物学特性及环境因子对精子活力的影响，本研究测定了大鳍鳠精液的 pH、渗透压和精浆成分，观察了精子超微结构，分析了 pH、葡萄糖和 NaCl、KCl、CaCl2 对精子活力的影响。结果表明：大鳍鳠成熟精子由头、颈、尾三部分组成，无顶体，有侧鳍。大鳍鳠平均精子密度为 2.50×109 个/mL，精液 pH 为 7.0~7.2，精浆渗透压为(280.00±2.94)mOsm/kg。精浆中离子成分以 Na+含量最高，其次是 K+，之后依次为 Mg2+、Ca2+、Fe3+、Zn2+，未检测出 Cu2+。精浆水解氨基酸总量为 16985.26(umol/100mL)，其中以亮氨酸含量最高，蛋氨酸含量最低。精子最适 pH 为 8.0；NaCl、KCl、CaCl2 浓度为 1g/L、5g/L、6g/L 时，运动率达到峰值；葡萄糖浓度为 7g/L 时精子活力达到最高。本研究结果可为开展大鳍鳠人工催产，提高受精率提供科学参考。

关键词：大鳍鳠；精子活力；CASA；精浆成分

Biological characteristics of sperm and effects of several environmental factors on viability of Mystus macropterus

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Abstract： To investigate the biological characteristics of e spermatozoa and the effects of environmental factors on sperm motility, we measured pH, osmotic pressure and seminal plasma composition of semen, observed the ultrastructure of sperm, and analyzed the effects of pH, glucose, NaCl, KCl and CaCl2 on sperm motility. The results showed that mature sperm was composed of head, neck and tail, without acrosome and with lateral fins. The mean sperm density of Mystus meatus is 2.50×109 /mL, the pH of semen is 7.0-7.2, and the seminal plasma osmolality is (280.00±2.94)mOsm/kg. In seminal plasma, the content of Na+ was the highest, followed by K+, Mg2+, Ca2+, Fe3+, Zn2+, and no Cu2+ was detected. The total amount of hydrolyzed amino acids in seminal plasma was 16985.26(umol/100mL), of which leucine content was the highest and methionine content was the lowest. The optimal pH of sperm was 8.0. When the concentration of NaCl, KCl and CaCl2 is 1g/L, 5g/L and 6g/L, the motion rate reaches the peak. Sperm motility reached the highest level when glucose concentration was 7g/L. The results of this study can provide scientific reference for developing artificial oxytocin and improving the fertilization rate of Mystus macropinus

Key words: Mystus macropterus; sperm motility; CASA; seminal plasma composition

采用几何形态测量学方法对两种牡蛎进行形态学鉴定

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摘要：遗传和环境因素都影响牡蛎的形态。分子鉴定是目前物种鉴定的主要手段，但不方便且成本高。在这项研究中，我们评估了几何形态计量学(GM)方法识别两种牡蛎(长牡蛎和近江牡蛎)的能力。我们使用传统的形态计量学和几何形态计量学方法，包括主成分分析(PCA)、薄板样条分析(TPS)和典型变量分析(CVA)，来识别区分这两个物种的具体特征。我们发现，形状的差异可以用几何形态计量学方法可视化。普鲁克分析表明，长牡蛎和近江牡蛎在壳形态上存在显著差异。主成分分析结果表明两居群形态差异主要集中在这 3 个主成分上。结合薄板样条分析功能图可以看出，近江牡蛎的壳形以细长和纺锤形为主，而长牡蛎的壳形以椭圆形为主。典型变量分析结果表明，这两个种群的分类率达到 100%，说明近江牡蛎和长牡蛎在壳形态上存在明显差异，根据形态特征可以完全分离。研究结果对于全面地了解不同牡蛎种群的形态特征，为牡蛎的分类鉴定提供重要参考。

关键词：传统形态学；几何形态学；长牡蛎

Geometric morphometric methods for identification of oyster species based on morphology

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Abstract： Both genetic and environmental factors affect the morphology of oysters. Molecular identification is currently the primary means of species identification, but it is inconvenient and costly. In this study, we assessed the ability of geometric morphometric (GM) methods to identify two species of oysters (Crassostrea gigas and C. ariakensis). We used traditional morphometric and GM methods, including principal component analysis (PCA), thin-plate spline analysis (TPS), and canonical variable analysis (CVA), to identify specific features that distinguish the two species. We found that differences in shape can be visualized using GM methods. The Procrustes analysis revealed significant differences in shell morphology between C. gigas and C. ariakensis.. PCA results indicated that the main morphological differences are concentrated in these three principal components. Combining the TPS analysis function plots showed that the shell shape of C. ariakensis is mainly elongated and spindle-shaped, whereas the shell shape of C. gigas is more oval. The CVA results showed that the classification rate for the two populations reached 100% which means that C. ariakensis and C. gigas have distinct differences in shell morphology and can be completely separated based on morphological characteristics. The results of this study provide an important reference for the overall understanding of the morphological characteristics of different oyster populations and for the classification and identification of oysters.

Key words: traditional morphometrics; geometric morphometrics; Pacific oyster

microRNA−mRNA 联合分析为中间球海胆性腺着色提供新见解

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摘要：为了探究不同性别中间球海胆性腺着色机制，本研究利用转录组测序技术对不同性别不同颜色中间球海胆性腺进行了 miRNA-mRNA 联动分析。实验结果表明，通过调控与类胡萝卜素吸收、积累、代谢和能量供应密切相关的基因表达是雌性与雄性中间球海胆调节性腺着色的共同机制，雌性与雄性间特异性分子标记的差异表达可能是导致雌雄海胆产生颜色差异的原因。

关键词：中间球海胆；性腺颜色；性别；microRNA-mRNA 联合分析；着色机制

Integrated microRNA-mRNA analysis provides new insights into gonad coloration in the sea urchin Strongylocentrotus intermedius

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Abstract： In order to investigate the mechanism of gonadal coloring in sea urchins of different genders, this study used transcriptome sequencing technology to perform miRNA-mRNA linkage analysis on the gonads of Strongylocentrotus intermedius of different genders and colors. The experimental results indicate that the regulation of gene expression closely related to carotenoid absorption, accumulation, metabolism, and energy supply is a common mechanism for regulating gonadal coloration in female and male Strongylocentrotus intermedius. The differential expression of specific molecular markers between females and males may be the reason for color differences between females and males.

Key words: Strongylocentrotus intermedius, gonad color, sexes, microRNA-mRNA integrated analysis, coloring mechanism

石斑鱼杂交生长优势的分子遗传解析

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摘要：借助遗传连锁分析，RNA-seq 和全基因组 DNA 甲基化，对本团队培育的“云龙石斑鱼”和“金虎杂交斑”新品种的杂交生长优势开展分子遗传解析。首次构建杂交种石斑鱼单碱基遗传图谱，标记间隔 0.16 cM。结合表型数据，共鉴定 39 个生长连锁 QTLs，候选基因参与泛素化修饰，G-蛋白偶联受体，细胞增殖过程。对生长差异明显“金虎杂交斑”和母本棕点石斑鱼的垂体、肝脏、肌肉开展全基因组 DNA 甲基化和 RNA-seq 联合分析。首次构建杂交种石斑鱼单碱基 DNA 甲基化图谱，杂交种总甲基化水平低于纯种石斑鱼，各组织高表达基因呈低甲基化分布。趋势分析、WGCNA、和等位基因特异表达（ASE）综合表明“金虎杂交斑”通过 DNA 甲基化和亚基因组优势共同调节脂质代谢进而形成杂交生长优势。本研究解析了石斑鱼杂交优势形成的分子遗传机理，在鱼类远缘杂交理论积累和应用研究方面具有重要意义。

关键词：石斑鱼新品种；杂交生长优势；遗传连锁分析；全基因组 DNA 甲基化； RNA-seq

Molecular genetic analysis in grouper heterosis formation

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Abstract： Using genetic linkage analysis, RNA-seq, and whole genome DNA methylation, the molecular genetic analysis was conducted on growth heterosis of the new varieties of “Yunlong grouper” and “Jinhu grouper” cultivated by our team. The first single base genetic map was constructed for a hybrid grouper, with a marker interval of 0.16 cM. Based on phenotype data, a total of 39 growth linked QTLs were identified, with candidate genes involved in ubiquitination modification, G-protein coupled receptors, and cell proliferation processes. The somatotropic tissues (pituitarium, liver, and muscle) were characterized by RNA-seq technology and whole-genome bisulfite sequencing (WGBS) in Jinhu grouper compared with maternal E. fuscoguttatus. Integration analyses showed that the heterotic hybrids showed lower genomic DNA methylation levels than the purebred parent, and the up-regulated genes were mostly DNA hypomethylation. Trend analysis, WGCNA, and allelic specific expression (ASE) comprehensively indicate that the growth heterosis of Jinhu grouper was regulated by DNA methylation and subgenomic dominance through lipid metabolism. Our results provide new and valuable clues for understanding paternal-biased growth heterosis in hybrid groupers, taking a significant step towards the accumulation and application of distant hybridization in fish breeding.

Key words: New varieties of grouper; Growth heterosis; Genetic linkage analysis; Whole genome DNA methylation; RNA-seq

细胞周期蛋白依赖性激酶（CDK）是调节香螺早期发育的关键基因：来自比较转录组和蛋白质组分析的证据

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摘要：为了系统掌握香螺（Neptunea arthritica cumingii）早期胚胎发育过程中基因和蛋白的动态表达规律，本研究利用比较转录组和比较蛋白质组技术，分析比较了香螺早期胚胎不同发育时期基因和蛋白的差异表达规律，筛选出 12 个 CDKs 家族基因，与 5 个 CDKs 下游蛋白，随后利用 q-PCR 等技术，首次明确了 CDKs 家族基因在香螺胚胎中的发育调控功能，确定 CDKs 为香螺早期胚胎发育的关键基因簇。本研究中所获结果，将进一步丰富香螺乃至海水贝类的分子发育生物学的相关信息，为阐明香螺早期胚胎发育机制提供了重要线索，为突破香螺（Neptunea arthritica cumingii）的人工养殖技术提供理论指导。

关键词：香螺；CDKs；转录组；蛋白组

Cyclin-dependent kinases (CDKs) are key genes regulating early development of Neptunea arthritica cumingii: Evidence from comparative transcriptome and proteome analyses

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Abstract： In this study, we applied comparative transcriptomics and proteomics techniques to systematically investigate the dynamic expression patterns of genes and proteins at various stages of early embryonic development of the gastropod Neptunea arthritica cumingii. Twelve cyclin-dependent kinase (CDKs) genes and five downstream proteins associated with these CDKs were identified. Through techniques such as q-PCR, our data elucidate for the first time the regulatory functions of CDK family genes and establish CDKs as a pivotal gene cluster in the early embryonic development of N. cumingii. These findings not only enhance the understanding of molecular developmental biology in N. cumingii and marine bivalves in general but also provide significant insights into the mechanisms involved in early embryonic development in N. cumingii. Furthermore, our results provide theoretical guidance for advancing artificial breeding technology for N. cumingii.

Key words: N. cumingii; CDKs; Transcriptome; Proteome

不同养殖月龄胡子鲇形态性状对体质量的相关性及通径分析

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摘要：为了探究胡子鲇形态性状与体质量之间的相互关系，本研究分别随机选取人工养殖 3 月龄和 6 月龄胡子鲇 176 尾和 254 尾，测量了雌、雄个体的体质量、全长、体长等 16 个形态性状，并运用相关分析、回归分析和通径分析阐明形态性状对体质量的影响。在 3 月龄时，胡子鲇雌、雄个体各形态性状之间无显著性差异，而在 6 月龄时，胡子鲇雌、雄个体间出现明显的性别生长二态性，雄性体质量、全长、体长、头长、腹鳍长、尾柄长、尾柄高、臀鳍长等都极显著大于雌性。多元线性回归方程结果显示，3 月龄雌、雄之间无显著性差异，而在 6 月龄中的体高、尾柄高、背鳍长、臀鳍长和腹鳍前长对体质量的直接作用达极显著水平。实验表明，所有个体间总数分别对 3 月龄体质量和 6 月龄体高变异系数直接影响最大。将胡子鲇的 6 月龄雌雄群体的优良表型作为选育依据，并有效利用影响体质量的关键性状指标，有利于其选育工作的开展。本研究可为胡子鲇的良种选育提供具有一定的参考价值。

关键词：胡子鲇；表型性状；体质量；相关分析；通径分析

Correlation and throughput analysis of morphological traits on body mass of Clarias fuscus at different culture months of age

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Abstract：To investigate the interrelationships between morphological traits and body mass of Hong Kong catfish (Clarias fuscus), a total of 176 and 254 individuals were randomly selected from 3-month-old and 6-month-old, respectively, and 16 morphological traits such as body mass, overall length, and body length were measured for both male and female individuals. Correlation, regression, and path analyses were used to elucidate the effects of morphological traits on body mass. The results showed that there was no significant sexual dimorphism in the 3-month-old group, whereas the 6-month-old group exhibited significant differences between males and females in several traits, such as body mass, overall length, head length, and anal fin length. This suggests that males at 6-month-old are enhancing their reproductive success through growth anisotropy. The multiple linear regression equations revealed that body height, caudal peduncle height, dorsal fin length, anal fin length, and anterior ventral fin length had significant effects on body mass at 6-month-old. The total number of inter-individuals had the greatest direct effect on the coefficient of variation of body mass at 3-month-old and body height at 6-month-old, respectively. The excellent phenotypes of 6-month-old male and female populations of C. fuscus were used as a basis for selection and effective use of key trait indicators affecting body mass, which facilitated their selection. This study can provide a reference value for the selection of a better breed of C. fuscus.

Key words: Clarias fuscus; phenotypic trait; body mass; Related Analysis; pathway analysis

基于等位基因特异性表达解析西盘鲍的耐高温杂种优势

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摘要：鲍是我国重要的海水养殖贝类，远缘杂交是鲍性状遗传改良的重要手段。围绕耐高温这一产业瓶颈问题，我们通过远缘杂交培育出的鲍杂交新品种——西盘鲍，具有显著耐高温杂种优势，并已成功推广应用，是研究鲍杂种优势的重要材料。本项目基于前期解析的多个鲍基因组信息，以西盘鲍杂交种及其亲本为研究对象，开展高温同质园实验，结合转录组和生理学实验，揭示西盘鲍亚基因组等位基因的特异性表达模式，并鉴定若干个耐高温杂种优势相关的关键基因和调控变异位点，阐明等位基因特异性表达在西盘鲍耐高温杂种优势形成过程中的重要作用。本研究对鲍耐高温育种和杂交育种具有重要的借鉴意义。

关键词：西盘鲍；杂种优势；耐高温；等位基因特异性表达

Research on the Heterosis for the High-Temperature Tolerance in the “Xi Pan” abalone through Allele-Specific Gene Expression

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Abstract：Abalone is an important marine mollusk for aquaculture in China, and distant hybridization is a crucial method for genetic improvement of abalone traits. To address the industry bottleneck of high-temperature tolerance, we have developed a hybrid abalone variety, the "Xi Pan" abalone, through distant hybridization. This variety has been successfully introduced due to its significant advantages in high-temperature tolerance, and is considered a valuable resource for studying hybrid vigor in abalone.

In this project, we focused on the "Xi Pan" abalone and its parental species, based on the multiple already established abalone genomes. We conducted a common garden experiment in a high-temperature, combined with transcriptome analysis and physiological experiments, to reveal the specific expression patterns of sub-genomic alleles in "Xi Pan" abalon. Finally, we identified several key genes and regulatory variants associated with high-temperature tolerance, elucidating the crucial role of allele-specific gene expression in the formation of the heterosis for the high-temperature tolerance in "Xi Pan" abalone. This research has significant implications for the breeding of high-temperature-tolerant abalones and hybrid breeding.

Key words: “Xi Pan” abalone; heterosis; high-temperature tolerance; allele-specific gene expression

皱纹盘鲍食物转化率性状解析

及基因组选择研究

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摘要：皱纹盘鲍是我国鲍养殖主导种，作为少有典型的投饵型贝类，其饵料成本占养殖总成本的 60%左右。提高食物转化率，减低饵料投喂是降低养殖成本的重要手段。然而迄今为止，针对贝类食物转化率性状改良的研究几乎是空白。本研究首先建立了针对鲍食物转化率性状的精准测评设施和方法，然后针对养殖模式、温度、饵料以年龄等因素对皱纹盘鲍食物转化率的表型特征及遗传特征进行分析，进而结合肠道菌群、代谢生理、全基因组关联、转录组及能量收支等分析深入探讨鲍食物转化率性状的调控机理，并基于全基因组选择方法，构建培育了高食物转化率的皱纹盘鲍选育系新品系。

关键词：鲍；食物转化率；肠道菌群；代谢生理；基因组选择育种

Trait analysis and genomic selection of food conversion rate in Pacific abalone Haliotis discus hannai

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Abstract： The Pacific abalone Haliotis discus hannai is one of the most important aquaculture shellfish, and its genetic improvement has played an important role in promoting the development of abalone farming industry in China. Abalone is a typical artificial feeding shellfish and its feed cost accounts for around 60% of the total farming cost. However, research on the improvement of food conversion traits in abalone is lacking. In this study, the first step was to establish an individual-based method for food conversion measurement in abalone to solve the phenotypic determination problem. Then, the phenotypic and genetic characteristics of the food conversion rate of the abalone were analyzed based on the effects of feeding mode, temperature, feed type, and abalone age. Furthermore, the regulatory mechanisms of the traits were explored through intestinal microbiota, metabolic physiology, genome-wide association study (GWAS), transcriptome, and energy balance analysis. Finally, new strains of Pacific abalone with high food conversion rates were produced through genomic selection (GS) techniques.

Key words: Food conversion rate; Intestinal microbiota; metabolic physiology; Genomic selection breeding

南美白对虾 Chitin binding proteins 的鉴定及其在抵御副溶血弧菌感染中的作用

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摘要：Chitin binding proteins 在真核生物的免疫防御方面发挥着重要的功能，但其在甲壳动物免疫系统中的研究较少。本研究鉴定出 164 个 chitin binding proteins，表达分析显示它们对副溶血弧菌的刺激作出响应。我们选取 6 个 chitin binding proteins 进行 dsRNA 干扰实验。结果显示，proteoglycan 4 和 keratin-associated protein 16 的沉默导致南美白对虾在副溶血弧菌感染后累积死亡率显著降低，NF-κB 通路和抗菌肽基因的表达上升。此外，SNP 检测及关联分析显示在 PRG4 外显子中存在一个与南美白对虾副溶血弧菌耐受性状显著相关的 SNP（$P < 0.05$）。这些结果将有助于全面了解 chitin binding proteins 在无脊椎动物先天免疫中的作用，助推南美白对虾分子标记辅助育种。

关键词：南美白对虾；副溶血弧菌；Chitin binding proteins；免疫

Identification of Chitin binding proteins in Penaeus vannamei and their functionin immune defense against Vibrio parahaemolyticus

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Abstract：Chitin binding proteins have crucial roles in immune defense in eukaryotes. However, the research of chitin binding proteins in the immune system of crustaceans is relatively limited. In this study, 164 chitin binding proteins were systematically identified in Penaeus vannamei. Expression analysis showed that most chitin binding proteins were responded to the stimulation of Vibrio parahaemolyticus. 6 chitin binding proteins were selected for dsRNA interference experiment. Knockdown of proteoglycan 4 and keratin-associated protein 16 decreased the cumulative mortality of P. vannamei after infection with V. parahaemolyticus and increased expression of NF-κB pathway and antimicrobial peptides. These suggested that PRG4 and KAP15 played negative roles in antibacterial response in shrimp by inhibiting NF-κB pathway and the expression of AMPs. In addition, the SNP analysis revealed that one SNP significantly associated with V. parahaemolyticus tolerance traits was found in the exon of PRG4 in P. vannamei ($P < 0.05$). Collectively, the findings of this study will contribute to overall understand the role of chitin binding proteins in innate immunity of invertebrates, as well as the advancement of molecular marker-assisted breeding in P. vannamei.

Key words: Chitin binding proteins; Vibrio parahaemolyticus; Penaeus vannamei; Immunity

赤眼鳟 CypA 负调控干扰素抗病毒免疫反应的功能研究

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摘要：赤眼鳟（Squaliobarbus curriculus）亲环素 A (CypA，由基因 ppia 编码)是一种重要的免疫调节因子。ppia 在健康的赤眼鳟肝组织中表达量最高，其次是肾脏、皮肤。赤眼鳟肾脏细胞系 SCK 攻毒结果显示，ppia 在 Poly(I:C)、SVCV、GCRV 刺激下显著被诱导表达，显示其潜在参与病毒诱导的免疫应答反应。CypA 可显著抑制由 Poly(I:C)、SVCV、GCRV 以及 RLR 通路分子激活的干扰素启动子活性，同时显著抑制了 ifn，mx 等抗病毒基因的表达，进而促进 GCRV 的复制。进一步机制解析证实，赤眼鳟 CypA 通过靶向 IRF3 来调控 RLR 信号通路介导的干扰素抗病毒反应。

关键词：赤眼鳟；ppia；抗病毒反应；干扰素；负向调节

Function of CypA negatively regulating antiviral immune response of interferon in redeye carp

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Abstract： Squaliobarbus curriculus cyclic A (CypA, encoded by the gene ppia) is an important immunomodulator. The expression of ppia was the highest in liver tissue of healthy trout, followed by kidney and skin. The SCK challenge results of the kidney cell line of red trout showed that ppia was significantly induced under the stimulation of Poly(I:C), SVCV and GCRV, indicating its potential participation in virus-induced immune response. CypA can significantly inhibit the activity of interferon promoters activated by Poly(I:C), SVCV, GCRV and RLR pathway molecules, and significantly inhibit the expression of antiviral genes such as ifn and mx, thus promoting the replication of GCRV. Further mechanism analysis confirmed that CypA of red eye trout regulates the interferon antiviral response mediated by RLR signaling pathway by targeting IRF3.

Key words: Redeye trout; ppia, antiviral response; interferon; negative regulation

脂质代谢对缢蛏耐低盐性能的调控作用

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摘要：我国盐碱水资源丰富，开发潜力较大。缢蛏（Sinonovacula constricta）是广盐性和滤食性贝类，适宜盐碱水域的复杂环境。研究其耐低盐性能的调控机制对耐低盐良种的选育意义重大。盐度 20 和盐度 5 胁迫 48 h 后，取缢蛏鳃组织进行转录组测序。结果表明，磷脂酰肌醇通路在调节缢蛏渗透调节中起关键作用；IP3K 是该通路中的关键酶，利用 dsRNA 干扰技术敲降 IP3K 基因，发现下游 IP3 和 Ca2+含量极显著下降（$p<0.01$）；采用 TUNEL 染色技术检测干扰前后细胞凋亡情况，发现干扰 IP3K 后鳃组织的细胞凋亡程度升高，ROS 含量极显著降低（$p<0.01$）。IP3K 基因参与生成 IP3，其作为重要的细胞信号分子，影响细胞内钙离子释放，从而影响细胞内环境的离子浓度和稳态。综上所述，这些结果将为进一步研究缢蛏耐低盐性能的分子调控机制提供新的思路，同时也为选育优良品种提供理论基础。

关键词：缢蛏；耐低盐性能；转录组；磷脂酰肌醇

Regulation of lipid metabolism on low salt tolerance of Sinonovacula constricta

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Abstract： China is rich in saline-alkali water resources and has great potential for development. Sinonovacula constricta is a euryhaline and filter-feeding shellfish, suitable for the complex environment of saline-alkali waters. It is of great significance to study the regulation mechanism of its low salt tolerance for breeding better varieties. After salinity 20 and salinity 5 stress for 48 h, transcriptome sequencing was performed on gill tissues of sinonoclina constricta. The results showed that the phosphatidylinositol pathway played a key role in regulating the osmotic regulation of sinonovacula constricta. IP3K is a key enzyme in this pathway. Using dsRNA interference technology to knock down IP3K gene, it was found that the downstream IP3 and Ca2+ content decreased significantly ($p<0.01$); TUNEL staining technique was used to detect apoptosis before and after IP3K interference, and it was found that the apoptosis degree of gill tissue cells after IP3K interference increased, and ROS content decreased significantly ($p<0.01$). IP3K gene is involved in the generation of IP3, which, as an important cell signaling molecule, affects the release of intracellular calcium ions, thus affecting the ion concentration and homeostasis of the intracellular environment. In summary, these results will provide a new idea for further research on the molecular regulation mechanism of low salt tolerance of Sinonoclula constricta, and also provide a theoretical basis for breeding excellent varieties.

Key words: Sinonovacula constricta; Low salt resistance; Transcriptome; Phosphatidyl inositol

法罗鱼种质资源研究进展

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摘要：法罗鱼指分布在黑龙江流域的三角鲂(Megalobrama terminalis)，是著名的“三花五罗”之一，该鱼个体大、肉质鲜美、经济价值高，在渔民心中地位较高。法罗鱼曾广泛分布于黑龙江、松花江、嫩江、镜泊湖和兴凯湖，但自从 1960 年代以来，其栖息范围伴随着过度捕捞和环境变化逐年缩小，现仅在黑龙江抚远江段可捕捞到少量个体。由于数量少、暂养和运输死亡率高、缺少原种场的保护，对该鱼的研究十分有限。自 2016 年起，我们开展了法罗鱼（黑龙江种群）种质资源调查、收集、保存、鉴定、繁育及资源恢复等工作，揭示了该鱼在我国境内的栖息范围、食性、性腺发育等特点，阐明了该鱼与同种不同种群及属内不同种间的系统发生关系和遗传分化，明确了该鱼需划分独立的保护单元，开发出该鱼与养殖团头鲂及其杂交种精准区分的分子标记，成功实现了该鱼的人工繁殖、全人工繁殖和人工放流。目前，法罗鱼研究已进入到选育及新种质创制阶段。

关键词：法罗鱼；三角鲂；种质资源

Research progress on germplasm resource of Faluo fish

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Abstract：The Faluo fish refers to the black Amur bream (Megalobrama terminalis) that inhabits the Heilongjiang River Basin. It is a famous endemic fish species with several desirable qualities, such as a large body size, delicious taste and high economic value, making it highly valued by fishermen. The fish species had been widely distributed in several water systems, including the Heilong River, Songhua River, Nen River, Jingpo Lake, and Khanka Lake. Since the 1960s, however, overfishing and environmental changes have caused the habitats of Faluo to decrease dramatically. Currently, only few individuals could be captured per year in Fuyuan section (134°28′E, 48°37′N) of Heilongjiang River. Due to the small population size, high mortality during temporary culture and transportation, and lack of protection from the foundation seed farm, research on the fish species is very limited. Since 2016, we have carried out the resource survey, germplasm collection, preservation and identification, breeding and resource restoration for Faluo fish (Heilongjiang River population). Our work has revealed its habitat range within China, feeding habits, and gonadal development characteristics. Furthermore, based on genomic information, the phylogenetic relationship and genetic differentiation between Faluo fish and other populations within the genus Megalobrama were elucidated, indicating independent protection units need to be provided for wild resource. Moreover, molecular markers were developed for precise discrimination among Faluo fish, bluntnose black bream (Megalobrama amblycephala), and their hybrids. Besides, the artificial reproduction, total artificial reproduction, and artificial releasing of Faluo fish have been successfully achieved. At present, research on Faluo fish has entered the stage of selective breeding and the creation of new germplasm resources.

Key words: Faluo fish; black Amur bream; Megalobrama terminalis; germplasm resource

拟穴青蟹不同发育时期胚胎的形态学观察

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摘要：拟穴青蟹是我国重要的经济蟹类之一，对其胚胎发育过程的研究有助于后期苗种繁育及养殖生产。基于此，本实验从胚胎颜色变化、发育时期以及胚胎中细胞分裂与分布三个方面对拟穴青蟹不同发育时期的胚胎进行了详细的观察与描述。发现在胚胎发育过程中，其颜色的渐变过程为，体内新排出的胚胎为浅黄色，随后变为黄色，经过发育逐渐过渡为橙色，从橙色变为橘红色，然后变为棕色，最后变为黑色；胚胎的分裂形式为混合卵裂，包括早期的完全卵裂、中期的螺旋卵裂和晚期的表面卵裂；在原肠胚期的透明区和细胞聚集的位置能够清晰地观察到胚孔的出现。此外，胚孔区细胞的快速分裂导致卵黄被快速消耗，使得透明区进一步变大。无节幼体时期，细胞的快速分裂聚集形成视叶原基、触角原基、颚足原基。该研究对拟穴青蟹胚胎发育过程中透明区出现的原因及一些器官原基形成时细胞聚集动态过程做了详细的描述，为以后拟穴青蟹或其它甲壳类生物胚胎发育相关的研究积累了重要的数据。

关键词：甲壳类；拟穴青蟹；卵裂；胚泡；胚胎发育

Observations on the embryonic development of the mud crab, Scylla paramamosain

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Abstract： To investigate the embryonic development of the mud crab Scylla paramamosain, we analyzed three critical parameters: egg color, embryo morphology through conventional and laser scanning confocal microscopy, and the distribution of cell divisions. During embryonic development, the egg color exhibited a progressive transition, shifting from orange to reddish-orange, then to brown, before ultimately darkening to black. The embryos displayed a spherical shape, measuring approximately 280 μm in diameter, characterized by a smooth surface devoid of any depressions. The embryonic cell division was in the form of mixed oogenesis, comprised of complete division in the early stage, spiral oogenesis in the middle stage and surface division in the late stage. It is noteworthy that the blastopore appeared at the position where the transparent area and cell aggregation just appeared under the microscope, and the blastomere was a characteristic of the embryo entering the gastrulation stage. After entering the gastrulation stage, the cells aggregated towards the blastopore and formed two symmetrical cell clusters, which formed a V-shape with the void of the classic blastopore. When the transparent region occupied approximately 1/5 of the embryo’s volume, the embryo entered the nauplius stage, and the thoracic and abdominal armor, as well as the optic lobe and abdominal limb primordia, could be clearly distinguished. The appearance of the compound eye pigment band indicated the stage of compound eye pigment formation. At this time, the transparent area accounted for 1/4 of the embryo and a large number of ganglia appeared. The change of the compound eye pigment band from red to black was also one of the reasons for the blackening of the egg color of the crabs. The data obtained through this study have potential applications in the determination of embryonic development status and obtaining of high-quality seeds for S. paramamosain culture.

Key words: Crustacean; Scylla paramamosain; cleavage; blastopore; embryonic development

基于 RNAi 敲降技术的日本沼虾转录组分析鉴定 SDHB 基因所调控的雄性性别相关基因

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摘要：日本沼虾是亚洲重要的水产养殖物种。先前的研究表明，琥珀酸脱氢酶复合体铁硫亚基 B（SDHB）基因通过影响 IAG 基因的表达参与了该物种的精巢发育。本研究利用 RNAi 技术敲降日本沼虾的 Mn-SDHB 基因。通过对促雄性腺和精巢的转录组进行分析，以发现 SDHB 调控的雄性性别相关基因，探讨该物种雄性性别发育的机制。通过转录组研究，每个样本中均注释出了超过 16,623 个基因。在促雄性腺中，大多数差异表达基因富集于肥厚性心肌病通路；而在精巢中，它们富集于柠檬酸循环通路。此外，在 Mn-SDHB 被敲降后，研究发现在促雄性腺中与磷酸化碳水化合物合成和糖酵解/糖异生途径转化相关的生物学过程中有 5 个基因被下调。另外，本研究从差异表达基因中共鉴定出 9 个雄性性别相关基因，证实了 Mn-SDHB 在日本沼虾雄虾发育的调节作用，为进一步研究该物种雄性发育机制提供了参考。

关键词：甲壳类；日本沼虾；RNA 干扰；雄性发育；转录组

Identification of Male Sex-Related Genes Regulated by SDHB in Macrobrachium nipponense Based on Transcriptome Analysis after an RNAi Knockdown

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Abstract：The oriental river prawn (Macrobrachium nipponense) is a commercially important species in Asia. A previous study showed that the succinate dehydrogenase complex iron sulfur subunit B (SDHB) gene participates in testes development in this species through its effect on the expression of the insulin-like androgenic gland hormone gene. This study knocked-down the Mn-SDHB genes in M. nipponense using RNAi. A transcriptome analysis of the androgenic gland and testes was then performed to discover the male sex-related genes regulated by SDHB and investigate the mechanism of male sexual development in this species. More than 16,623 unigenes were discovered in each sample generated. In the androgenic gland, most of the differentially expressed genes were enriched in the hypertrophic cardiomyopathy pathway, while in the testes, they were enriched in the citrate cycle pathway. In addition, after Mn-SDHB knockdown, five genes were found to be downregulated in the androgenic gland in a series of biological processes associated with phosphorylated carbohydrate synthesis and transformations in the glycolysis/gluconeogenesis pathway. Moreover, a total of nine male sex-related genes were identified including Pro-resilin, insulin-like androgenic gland hormone, Protein mono-ADP-ribosyltransferase PAPR11, DNAJC2, C-type Lectin-1, Tyrosine-protein kinase Yes, Vigilin, and Sperm motility kinase Y-like, demonstrating the regulatory effects of Mn-SDHB, and providing a reference for the further study of the mechanisms of male development in M. nipponense.

Key words: crustaceans; Macrobrachium nipponense; RNAi; male sexual development; transcriptome analysis

不同季节香螺鳃组织的转录组分析

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摘要：香螺（Neptunea cumingii）是中国黄渤海地区非常重要的海洋经济贝类，然而由于全球气候变暖等环境因素的影响，中国沿海香螺资源正面衰退的现状。为了明确在自然界季节交替状态下香螺鳃中的基因表达规律及机体调控机制，我们分别在獐子岛、烟台两地，在春、夏、秋、冬、四个季节进行香螺样本的采集，取其鳃组织进行转录组分析，并挖掘差异显著基因进行功能验证。结果显示，在冬季和夏季对比组中差异基因最多，这些差异基因参与到免疫，代谢等相关通路中，对香螺氧化应激、机体代谢、蛋白质合成有显著影响。综上，不同季节香螺鳃组织的转录组结果差异显著，高温季节香螺体内免疫调控基因表达能够被促进，低温季节香螺体内免疫调控相关基因受到抑制，研究结果为进一步了解香螺适应气候变化的分子防御机制提供了依据。

关键词：免疫功能；香螺；温度；转录组

Transcriptome analysis of gill tissues from Neptunea cumingii in different seasons

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Abstract：Neptunea cumingii is an economically important marine shellfish found in the Yellow Sea and Bohai Sea areas of China. However, due to environmental factors, such as global warming, Neptunea cumingii resources are in decline along the coast of China. In this study, samples of Neptunea cumingii were collected in Zhangzidao and Yantai during spring, summer, autumn, and winter to clarify the gene expression patterns and regulatory mechanisms in the gills in different seasons. Transcriptome analysis was conducted using Neptunea cumingii gill tissues and genes with significantly different expression levels were extracted for functional verification. The most genes with differences in expression（DEGs） were found in comparisons of the winter and summer samples. Gene enrichment analysis based on Gene Ontology and Kyoto Encyclopedia of Genes and Genomes terms showed that these DEGs were mainly involved in immune and metabolic pathways, and they had significant effects on oxidative stress, body metabolism, and protein synthesis in Neptunea cumingii. Further screening of DEGs identified 34 genes related to temperature regulation comprising 13 genes with roles in innate immunity in shellfish, 12 genes related to oxidative stress, and nine genes related to protein synthesis and energy metabolism. Eleven DEGs were randomly selected for qPCR verification and the results were consistent with the transcriptome analysis results. In summary, the transcriptome results differed significantly between seasons in the gill tissues of Neptunea cumingii. The expression levels of immune regulatory genes could be promoted in Neptunea cumingii during the high temperature season, whereas the expression of these genes may be inhibited in the low temperature season. The results obtained in this study provide insights into the molecular defense mechanisms that might allow Neptunea cumingii to adapt to climate change.

Key words: immune function; Neptunea cumingii; temperature; transcriptome

组织学观察、抗氧化酶活性和转录组分析揭示了不同品系海湾扇贝(Argopecten irradians)

温度适应机制

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摘要：为探讨海湾扇贝在急性高低温胁迫下的耐受性和调控机制，以两种不同壳色家系为研究对象，分析了“黑壳”(HB)和“红壳”(HR)海湾扇贝在急性温度 36h 胁迫下的组织学、抗氧化酶活性和基因转录水平的差异。

结果表明，海湾扇贝鳃丝宽度随温度的升高呈先增大后减小的趋势(HB > HR)，同一温度下不同壳色间鳃丝宽度差异不显著;急性温度应激下，HB 中 SOD、CAT 逐渐降低，T-AOC 变化不显著($P < 0.05$)。HR 中 SOD、CAT、T-AOC 均呈升高和降低的总体趋势，治疗组与对照组比较差异均有统计学意义($P < 0.05$)。我们发现，在低温胁迫下，HB 的肝脏免疫酶活性高于 HR，初步说明 HB 的耐寒性高于 HR。

转录研究表明，与 22℃(对照)相比，在急性温度胁迫下，HB 有 3180(低温)和 3732(高温)个差异表达基因(DEGs)，HR 有 14261(低温)和 2680(高温)个

关键词：海湾扇贝；温度胁迫；组织学观察；抗氧化酶；转录表达

Histological observation, antioxidant enzyme activity and transcriptome analysis revealed the temperature related adaptation mechanism of bay scallops (Argopecten irradians) from different families

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Abstract：In order to investigate the tolerance and regulatory mechanisms of bay scallops under acute high and low temperature stress, the histology of "black shell" (HB) and "red shell" (HR) bay scallops was analysed under acute temperature stress for 36h, using two different shell-coloured families, antioxidant enzyme activities and gene transcription levels in "black shell" (HB) and "red shell" (HR) bay scallops under acute 36h stress.

The results showed that the gill filament width of bay scallops increased and then decreased with the increase of temperature (HB > HR), and the difference of gill filament width between different shell colours at the same temperature was not significant; under acute temperature stress, SOD and CAT gradually decreased in HB, and the change of T-AOC was significant ($P < 0.05$); the overall trend of increasing and decreasing of SOD, CAT, and T-AOC was observed in HR, and the difference of treatment group and control group was statistically significant ($P < 0.05$). The overall trend of SOD, CAT and T-AOC in HR was higher and lower, and the differences between the treatment group and the control group were all statistically significant ($P < 0.05$). We found that the activities of hepatic immunoenzymes were higher in HB than in HR under low-temperature stress, which preliminarily indicated that the cold tolerance of HB was higher than that of HR.

Transcriptional studies showed that there were 3180 (low temperature) and 3732 (high temperature) differentially expressed genes (DEGs) in HB and 14,261 (low temperature) and 2680 (high temperature) differentially expressed genes (DEGs) in HR under acute temperature stress, compared with those in 22°C (control).GO analysis showed that DEGs were mainly involved in cellular processes, metabolic processes, catalytic activity and membrane binding. Meanwhile, KEGG enrichment analysis indicated that the regulation of temperature acclimation in scallop mainly involved signal transduction, metabolism, genetic information and protein processing. The GO and KEGG enrichment analysis of DEGs screened 12 genes that might be related to temperature stress, and identified nupr1 and hmgb1 as potential key genes in bay scallop in response to temperature stress, in which the expression of apoptosis inhibitor and nupr1 gene under high-temperature stress, whose main function is to inhibit cell necrosis and apoptosis, speculated that bay scallop up-regulates the expression of apoptosis inhibitor and nupr1 gene through nupr1 It is speculated that the bay scallop responds to high temperature by up-regulating the expression of nupr1, which inhibits abnormal apoptosis, and the hmgb1 gene, which plays a role in several cellular processes including inflammation, cell differentiation and tumour cell migration, and responds to the low-temperature environment by regulating the immune response of the bay scallop. Eight DEGs were selected for further validation by real-time fluorescence quantitative PCR, and the results were consistent with the RNA-seq data. The results of this study provide preliminary data for future in-depth research on the regulatory mechanism of temperature tolerance in bay scallops.

Key words: Argopecten irradians; Temperature stress; Histological observation; Antioxidant enzymes; Transcriptional expression

CYP302A1 在调节日本沼虾卵巢成熟和蜕皮中的双重作用

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摘要：CYP302A1 在甲壳动物和昆虫中对 20E 的合成起着重要的调节作用。在本研究中，我们发现该序列包含 CYP450 保守结构域。同时它与甲壳动物和昆虫的亲缘关系较近。q-PCR 分析表明它在卵巢中高表达，并在卵巢成熟前达到顶峰。第 16 天，对照组和实验组的性腺指数差异显著，对照组为 11.72%，实验组为 3.21%。第 9 天，对照组的蜕皮激素含量为 8.91nmol/L，实验组为 6.11nmol/L。第 16 天，对照组和实验组的蜕皮比例出现显著差异。统计结果表明，对照组的平均蜕皮周期为 14.5 天，实验组为 16.5 天。因此，本研究结果表明 Mn-CYP302A1 可以促进雌性日本沼虾的卵巢成熟和蜕皮。

关键词：日本沼虾；CYP302A1；卵巢成熟；蜕皮

Dual roles of CYP302A1 in regulating ovarian maturation and molting in Macrobrachium nipponense

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Abstract：CYP302A1 is a member of the Halloween genes in the cytochrome P450 supergene family, which play an important regulatory role in the synthesis of 20-hydroxyecdysone (20E) in crustaceans and insects. In this study, we found that the Mn-CYP302A1sequence included typical CYP450 conserved domains. Phylogenic showed that it is closely related to crustaceans and insects. q-PCR analysis indicated that Mn-CYP302A1 was highly expressed in the ovaries and peaked before ovarian maturation. Mn-CYP302A1 expression was higher at the post-larval stage of day 15 than at other stages of embryogenesis. In situ hybridization indicated that Mn-CYP302A1 was mainly distributed in the nucleus, yolk granules, cell membrane and cytoplasm To further establish the function of CYP302A1, a 21-day RNA interference experiment was conducted. On day 16, the Gonad Somatic Index of the control group and the experimental group showed significant differences, with GSI of 11.72% in the control group and 3.21% in the experimental group. The cumulative proportion of the second entry into stage O-III was 100% in the control group, while it was 41.67% in the experimental group on day 21. The ecdysone content was 8.91nmol/L in the control group and 6.11nmol/L in the experimental group on day 9. A significant difference in the molting proportion between the control group and the experimental group was also observed (49% in the control group and 34% in the experimental group) on day 16. Statistical results showed that the average molting cycle of the control group was 14.5 days, while that of the experimental group was 16.5 days. However, the morphological structure of ovarian tissue did not abnormal change. Therefore, the results of this study suggest that Mn-CYP302A1 can promote ovarian maturation and molting in female M. nipponense.

Key words: Macrobrachium nipponense ; CYP302A1 ; Ovarian maturation ; Molting

基于单细胞转录组测序技术构建鳜卵巢细胞图谱

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摘要：解析鳜(Siniperca chuatsi)卵巢细胞组成及增殖与分化调控机制对于鳜的生物育种具有重要意义。本研究以 1 龄鳜为研究对象，利用 10XGenomics 单细胞转录组测序技术构建鳜卵巢细胞图谱。结果显示，鳜卵巢主要包含 5 种细胞，分别是生殖细胞、卵泡细胞、基质细胞、自然杀伤细胞和巨噬细胞，各占比为 58.5%、2.4%、1.9%、0.3%和 36.9%。在斑马鱼等模式动物中，ddx4 和 piwil1 等是经典的生殖细胞分子标记，但在鳜生殖细胞中的表达并不特异。类似地，nanos2 标记的生殖干细胞在斑马鱼等物种卵巢中显著富集，然而在鳜卵巢中的表达却极低。这表明鳜在卵巢发育及生殖调控方面与以往研究物种存在明显区别。此外，有数据显示，巨噬细胞在斑马鱼卵巢中仅占 1.6%，但在鳜卵巢中的占比却是前者的 23 倍，提示巨噬细胞在鳜卵巢的发育及生殖中可能扮演重要角色。本研究结果将为鳜的繁育优化打下坚实基础。

关键词：鳜(Siniperca chuatsi)；卵巢；细胞图谱；单细胞转录组测序

Single-cell transcriptome constructs the atlas of ovarian cells in mandarin fish (Siniperca chuatsi)

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Abstract： The investigation of ovarian cell composition and regulatory mechanisms has significant implications for mandarin fish (Siniperca chuatsi) breeding. We used 10XGenomics single-cell transcriptome sequencing to construct an atlas of ovarian cells in 1-year-old fish. Results showed that the ovary consisted of five distinct cell types: germ cells, follicle cells, stromal cells, NK_cells, and macrophages, accounting for 58.5%, 2.4%, 1.9%, 0.3%, and 36.9% respectively. However, ddx4 and piwil1 markers expression for germ cells lacked specificity in mandarin fish. Similarly, nanos2-labeled ovary germline stem cells were significantly less than zebrafish and other species. These disparities suggest that mandarin fish may has special style in ovarian reproductive regulation. Furthermore, data showed that macrophages constituted a much higher proportion (23 times) compared to zebrafish a mere 1.6%. This indicates a potentially crucial role of macrophages specific to the ovary development processes in mandarin fish. The findings provide a foundation for improving mandarin fish breeding.

Key words: Siniperca chuatsi; ovary; atlas of ovarian cells; single-cell transcriptome

基于代谢组学的中间球海胆脂肪酸代谢对高温胁迫的响应研究

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摘要：为探讨温度对中间球海胆性腺中脂肪酸含量的影响，将海胆置于不同温度梯度（15℃、20℃、25℃）不同胁迫周期（30 d、7d）后，使用 LC-MS/MS 技术对其性腺进行代谢物分析。结果显示，胁迫 7d 后，20℃vs15℃组和 25℃vs15℃组分别检测到 33、16 种脂肪酸差异代谢物，ω-3 和ω-6 PUFA 在这两个对比组中均上调，代谢物共注释到 62 条代谢通路。胁迫 30d 后，20℃vs 15℃共检测到 4 种脂肪酸差异代谢物，ω-6 PUFA 下调，其他 PUFA 上调；24℃ vs 15℃共检测到 10 种脂肪酸差异代谢物，ω-3 和ω-6 PUFA 下调，长链 SFA 上调，代谢物共注释到 5 条代谢通路。综上，中间球海胆可能通过调控脂肪酸代谢以减少能量消耗，其中ω-3 和ω-6 PUFA 可能被优先用于氧化供能。随着胁迫周期的增加，海胆不能合成更多的ω-3 PUFA 以应对炎症，脂肪酸组成的变化也可用作敏感预警生物指标。

关键词：中间球海胆；高温胁迫；LC-MS/MS；脂肪酸

Metabolomics of Strongylocentrotus intermedius fatty acid metabolism under high-temperature stress conditions.

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Abstract：To investigate the effect of temperature on the fatty acid content in the Strongylocentrotus intermedius, placing sea urchins in different temperature gradients (15 ° C, 20 ° C, 25 ° C) at different temperature gradients (30d, 7d), their gonads were metabolized using LC-MS/MS technology. The results showed that 33 and 16 different metabolites of fatty acids were detected after high temperature stress7d, 20 ° Cvs15 ° C, and 25 ° Cvs15 ° C respectively. ω-3 and ω-6 PUFA are up in both contrast groups. Metabolites are annotated to 62 metabolic pathways. After high-temperature stress 30d, 20 ° C vs 15 ° C detected 4 different metabolites of fatty acids, ω-6 PUFA downregulated, other PUFA upregulated; 24 ° C vs 15 ° C detected 10 different metabolites of fatty acids, ω-3 and ω-6 PUFA downgrade, long chain SFA upward revision, Metabolites are annotated to 5 metabolic pathways. In conclusion, intermediate bulb urchins may reduce energy consumption by regulating fatty acid metabolism, where ω-3 and ω-6 PUFA may be prioritized for oxidative energy supply. As the stress cycle increases, sea urchins cannot synthesize more ω-3 PUFA to deal with inflammation, and changes in fatty acid composition can also be used as sensitive early warning biometric indicators.

Key words: Strongylocentrotus intermedius; high temperature stress; LC-MS/MS; metabolomics; fatty acids

circARHGEF15 通过 miR–214/hepcidin/NF–κB 信号轴增强团头鲂对嗜水气单胞菌的抗菌免疫应答

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摘要：环状 RNA(circRNA)可通过竞争内源性 RNA (ceRNA)作为人类多种疾病的生物标志物和治疗靶点。本实验室前期研究表明，circRNA 可作为 ceRNA 吸附 miRNA，调控嗜水气单胞菌(Aeromonas hydrophila）感染后团(Megalobrama amblycephala)的固有免疫应答，但具体调控机制尚不明确。在本研究中，我们发现了一个 circRNA，命名为 circARHGEF15，其在嗜水气单胞菌感染后表达上调。进一步数据表明，circARHGEF15 在可以作为 miR-214 的 ceRNA，降低 miR-214 对铁调素的抑制作用，激活 NF-κB 信号通路，促进下游炎症因子的表达。circARHGEF15 在调控对嗜水气单胞菌感染的抗菌免疫中发挥着至关重要的作用，并从 circRNA 的角度为未来有效控制病原体感染和遗传改良鱼类抗性奠定基础。

关键词：环状 RNA；miRNA；铁调素；先天免疫

circARHGEF15 enhances antibacterial immunity against Aeromonas hydrophila infection via miR-214/hepcidin/NF-κB signaling axis in Megalobrama amblycephala

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Abstract： Circular RNAs (circRNAs) can be used as biomarkers and therapeutic targets for various human diseases through competitive endogenous RNA (ceRNA). Previous studies in our laboratory have shown that circRNAs can act as ceRNA to sponge microRNAs (miRNAs) and regulate the innate immune response of blunt snout bream (Megalobrama amblycephala) after Aeromonas hydrophila infection, but the specific regulatory mechanism is still unclear. In this study, by means of overexpression/RNAi silencing, qPCR, and luciferase assay etc., we discovered a circRNA termed circARHGEF15, which was upregulated after A. hydrophila infection and played a positive regulatory role in host antibacterial immunity. Moreover, we found that miR-214 can restore the activation of the NF-κB signaling pathway due to circARHGEF15 overexpression. Further, our data indicated that circARHGEF15 can act as a ceRNA of miR-214 in the immune response induced by A. hydrophila, reduce the inhibitory effect of miR-214 on hepcidin, activate the NF-κB signaling pathway, and promote the expression of downstream inflammatory factors such as il-1β, il-6, il-8, tnf-α, and ifn-γ. The overall results of this study suggested that M. amblycephala circARHGEF15 plays a crucial role in regulating the antibacterial immunity against A. hydrophila infection, and lays the foundation for effective control of pathogen infection and genetic improvement of fish resistance from the perspective of circRNA in the future.

Key words: circRNAs; miR-214; Hepcidin; ceRNA; Innate immunity

黄条鰤种质遗传特性研究进展

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摘要：黄条鰤(Seriola aureovittata)，是一种深远海适养经济鱼类。我国 2017 年突破苗种繁育技术，2019 年实现大规格苗种培育，为黄条鰤养殖产业的发展提供了优质种苗保障。为了推动养殖产业的健康持续发展，围绕种质资源评价与可持续利用，本团队近年来建立了黄条鰤的形态度量与种质模型，构建了三种鰤属鱼类的数量形态学鉴别技术。查明了黄条鰤染色体核型和带型。揭示了黄条鰤线粒体基因组结构特征，开发了 6 种 DNA 条形码，可对三种鰤属鱼类进行有效的物种鉴别。通过群体遗传学分析，发现中国野生、养殖群体和日本野生群体在遗传上来源于同一种群，与澳大利亚野生、养殖群体有极显著的遗传分化。通过全基因组关联分析，筛选出与生长性状相关的 SNP 位点。在染色体水平解析了黄条鰤的基因组结构特征，探索了其快速生长和环境适应的组学机制。研究结果可为我国黄条鰤种质资源科学保护及鉴定，开展良种选育等提供理论和技术依据。

关键词：黄条鰤；种质资源；染色体组型；群体遗传；基因组

Advances for germplasm and genetic characteristics in seriola aureovittata

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Abstract： The yellowtail kingfish (Seriola aureovittata) is Offshore mariculture of significant economic value. In order to promote the healthy and sustainable development of the aquaculture industry, our team has focused on the evaluation and sustainable utilization of genetic resources. In recent years, we have established morphometric measurements and genetic models for yellowtail kingfish and developed quantitative morphological identification techniques for three species of seriola. We have elucidated the karyotype and banding patterns of yellowtail kingfish chromosomes. Unveiling the structural features of the mitochondrial genome in this species. Through population genetics analysis, we discovered that both Chinese wild and farm populations, as well as Japanese wild populations, share genetic origins from a common ancestral population. In contrast, they were genetic divergence from Australian wild and farm populations. Through GWAS, we have pinpointed SNP loci linked to growth traits. Furthermore, at the chromosomal level, we conducted an in-depth analysis of the genomic structure characteristics of yellowtail kingfish, delving into the genomics mechanisms governing its rapid growth and environmental adaptability. These research hold the potential to offer both theoretical and technical support for the scientific preservation and identification of genetic resources of yellowtail kingfish in China, as well as for the selective breeding of superior strains.

Key words: Seriola aureovittata；genetic resources；karyotype；population genetics；genome

基于 MethylRAD—Seq 技术对不同年龄刺参 DNA 甲基化的研究

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摘要：为探讨不同年龄刺参 DNA 甲基化水平之间的差异，本研究采用 4 月龄、1 龄、2 龄、3 龄的刺参，对 4 个年龄的刺参体壁组织进行 MethylRAD—Seq 分析，筛选与刺参年龄有关的差异表达基因。结果显示，在 CCGG 位点共筛选到差异表达基因 1441 个，在 CCWGG 位点共筛选到差异表达基因 966 个。甲基化差异基因 GO 分析显示差异基因多分布在蛋白质定位、有丝分裂细胞分裂等通路。KEGG 分析差异基因大多分布在丙氨酸，天冬氨酸和谷氨酸代谢、坏死性凋亡、轴突引导等通路。通过组间对比筛选，我们推测天冬氨酸氨基转移酶、琥珀酸-半醛脱氢酶、异柠檬酸脱氢酶、H2AX、Hsp90、Pepn、CDC6、Rasgap、slit1、ILK、Mtor、Pka、atg3 等甲基化差异表达的基因可能与刺参年龄相关，并通过上述通路参与刺参生长及衰老的过程，在刺参年龄鉴定中有关键作用。本研究为鉴定刺参年龄和刺参的种质资源保存提供数据。

关键词：MethylRAD—Seq；刺参；体壁；年龄鉴定

MethylRAD-Seq technology reveals DNA methylation characteristics of Apostichopus japonicus of different ages

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Abstract：To explore the differences between DNA methylation levels of A. japonicus of different ages, this study used 4-month-old, 1-year-old, 2-year-old, and 3-year-old A. japonicus to perform MethylRAD-Seq analysis on the body wall tissue of 4-year-old A. japonicus to screen for differentially expressed genes related to the age of A. japonicus. The results showed that a total of 1441 differentially expressed genes were screened at the CCGG check point, and 966 differentially expressed genes were screened at the CCWGG check point. Methylated differential gene GO analysis showed that the differential genes were mostly distributed in pathways such as protein localization and mitotic cell division. KEGG analysis of differential genes was mostly distributed in pathways such as alanine, aspartate and glutamic acid metabolism, necrotizing apoptosis, and axon guidance. As-partate aminotransferase, succinate semialdehyde dehydrogenase, isocitrate dehydrogenase, H2AX, Hsp90, Pepn, CDC6, Rasgap, slit 1, ILK, Mtor, Pka, and atg3 these genes may play key roles in the growth and aging process of A. japonicus. This study provided data for identifying the age of A. japonicus and preserving its germplasm resources.

Key words: MethylRAD-Seq; A. japonicus; body wall; age identification

加州鲈仔稚鱼肠道微生物物种多样性和相对丰度变化研究

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摘要：为了解加州鲈仔稚鱼类的肠道微生物随食性转化演替变化,采集了 14、19、24 和 46 日龄的加州鲈肠道内容物,采用 16S rRNA 扩增子测序,探究了肠道微生物的物种多样性和相对丰度差异。结果表明,样品 Goods _coverage 均为 100%,测序深度合理。转食期(CP1、CP2)肠道微生物种类变化显著,结构单一。摄食活饵期（LP）、饲料时期(FP)微生物均匀度分布较高，其中 FP 微生物物种最丰富、结构最复杂,属水平相对丰度高于 1%的菌群平均达 16 种;LP 期平均仅 8 种,而 CP1、CP2 两时期均不超过 2 种。CP1、CP2 两时期假单胞菌属(Pseudomonas)平均相对丰度分别为 93.27%、97.33%，显著升高。不同时期优势菌相对丰度差异显著，转食对肠道相关功能微生物产生了显著影响,这可能是加州鲈肠道对成分复杂的饵料吸收利用的响应。本研究为鱼类驯化转食的研究提供基础资料。

关键词：加州鲈；仔稚鱼；转食；肠道微生物；多样性分析

Changes in the species diversity and relative abundance of gut microorganisms in juvenile Micropterus salmoides

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Abstract： In order to understand the changes of intestinal microbiota with the transition of food performance, the intestinal contents of 14d, 19d, 24d and 46d Micropterus salmoides were collected and sequencing using 16S rRNA amplicon sequencing to explore the species diversity and relative abundance of intestinal microorganisms. The results showed that the samples were all 100% Goods _coverage, and the sequencing depth was reasonable. During thetransition feeding period (CP1 and CP2), the intestinal microbial species changed significantly and the structure was single. The uniformity distribution of microorganisms in the live bait period (LP) and feed period (FP) was high, among which the FP microbial species were the most abundant and the structure was the most complex, and the average number of microbial groups with a relative abundance of more than 1% at the genus level was 16. There were only 8 species in the LP period, while there were no more than 2 species in the CP1 and CP2 periods. The average relative abundance of Pseudomonas in CP1 and CP2 was 93.27% and 97.33%, respectively, which were significantly increased. The relative abundance of dominant bacteria was significantly different in different periods, and the transfer of food had a significant effect on the intestinal related functional microorganisms, which may be the response of the intestinal tract of Micropterus salmoides to the absorption and utilization of complex bait. This study provides basic data for the study of fish domestication and food switching.

Key words: Micropterus salmoides;juveniles;feeding transformation; gut microorganism； diversity analysis

转录组分析高温胁迫下菲律宾蛤仔 miRNA 的表达规律

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摘要：为了探究菲律宾蛤仔应对极端高温环境的内在分子调控机制，促进蛤仔养殖产业的可持续发展。本研究以菲律宾蛤仔鳃组织作为研究对象，构建了高温下 miRNA 的差异表达谱分析了差异表达 miRNA 的靶基因功能。研究表明：高温组中共发掘了 3 个差异表达 miRNA,其中 1 个上调，2 个下调。高温胁迫下差异表达的 miRNA 为：novel_7、novel_14、novel_59。以二代全长转录组为参考文库，利用 miRanda 软件对差异表达 miRNA 的靶基因进行预测，靶标基因 KEGG 富集分析显示，高温组中共显著富集到 29 条通路。其中氨酰基 tRNA 生物合成、脂肪酸代谢、TGF-β信号通路、Wnt 信号通路等在高温组有显著富集。研究结果表明，miRNA 在菲律宾蛤仔响应高温胁迫中参与了一系列调控来应对环境的变化。

关键词：菲律宾蛤仔；高温；miRNA；靶基因

Transcriptome analysis of miRNA expression patterns in Ruditapes philippinarum under heat stress

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Abstract： In order to explore the inherent molecular regulatory mechanisms of Ruditapes philippinarum in response to extreme high temperature environments and promote the sustainable development of clam farming industry. This study used the gill tissue of Ruditapes philippinarum as the research object, constructed a differential expression profile of miRNA under high temperature, and analyzed the target gene function of differentially expressed miRNA. Research has shown that a total of three differentially expressed miRNAs were discovered in the high-temperature group, with one upregulated and two downregulated. The differentially expressed miRNA under high temperature stress is: novel_ 7. novel_ 14. novel_ 59. Using the second-generation full-length transcriptome as the reference library, miRanda software was used to predict the target genes for differentially expressed miRNA. The KEGG enrichment analysis of the target genes showed that a total of 29 pathways were significantly enriched in the high-temperature group. Aminoacyl tRNA biosynthesis, Fatty acid metabolism, TGF beta signaling pathway and Wnt signaling pathway are significantly enriched in the high-temperature group. The research results indicate that miRNAs are involved in a series of regulatory responses to environmental changes in response to heat stress in Ruditapes philippinarum.

Key words: Ruditapes philippinarum; heat stress; miRNA; target gene

基于转录组与代谢组学联合分析揭示

中间球海胆性腺着色遗传机制

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摘要：性腺颜色是评判性腺品质的重要指标之一，中间球海胆是中国重要的水产经济物种，具有生殖腺色泽及品质好、出肉率高等优点。目前对中间球海胆性腺着色相关的特定物质和相关代谢途径的研究还很少。

为了解析中间球海胆性腺着色遗传机制，本研究将性腺颜色分为 4 种：浅黄色(C1)、黄色(C2)、橙黄色(C3)、和深橙色(C4)。应用 RNA 测序分析方法与 LC-MS/MS 代谢组学方法联合对中间球海胆四种颜色性腺组织的基因表达水平与代谢产物水平进行了研究。本研究对 mRNA 表达谱进行了分析，在 C1&C2、C1&C3、C1&C4 三组间鉴定出 131 个、239 个和 1453 个差异表达基因。与性腺着色相关的差异基因主要在维生素的消化与吸收与嗅觉传导通路中富集，并从中筛选获得了 5 个可能参与β-胡萝卜素与海胆酮积累的差异表达基因。此外，代谢组学分析显示，以 C1 为对照组，与 C2、C3、C4 组各鉴别出 276 种、295 种、427 种差异代谢

关键词：中间球海胆；性腺着色；多组学联合分析

Gonad colour formation mechanisms in Strongylocentrotus intermedius elucidated by integrated metabolite and transcriptome analyses

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Abstract : Gonad colour is one of the most important indicators of gonad quality, and Strongylocentrotus intermedius is an important aquatic and economic species in China, which has the advantages of good gonad colour and quality, high meat yield and so on. Currently, little research has been done on the specific substances and metabolic pathways related to gonad colouration in the Strongylocentrotus intermedius.

In order to analyse the genetic mechanism of gonad colouring in Strongylocentrotus intermedius, the gonad colours were classified into four categories in this study: light yellow (C1), yellow (C2), orange (C3), and dark orange (C4). RNA sequencing analysis methods were applied in conjunction with LC-MS/MS metabolomics methods to investigate the gene expression levels and metabolite levels of the four coloured gonadal tissues of Strongylocentrotus intermedius. In this study, mRNA expression profiles were analysed and 131, 239 and 1453 differentially expressed genes were identified between the C1&C2, C1&C3 and C1&C4 groups. Differential genes related to gonadal colouring were mainly enriched in vitamin digestion and absorption and olfactory transduction pathways, and five differentially expressed genes that might be involved in the accumulation of β-carotene and sea urchin ketone were screened and obtained. In addition, metabolomics analyses showed that 276, 295, and 427 differential metabolites were identified in C1 as the control group, and in each of the C2, C3, and C4 groups. l-Threonine, l-Asparagine, S-Adenosylhomocysteine, Creatine, and alpha-ketoadipic The expression of common differential metabolites such as acid changed significantly with deeper gonad colour. The main pathways affecting gonad metabolism are amino acid biosynthesis, aminoacyl tRNA biosynthesis, ABC transporter, and glycine, serine and threonine metabolic pathways. The results of this study suggest that the gonad colour differentiation of Strongylocentrotus intermedius may be controlled by a series of complex biological processes. As the gonad colour deepens, the biosynthetic and metabolic signalling pathways respond positively, with the down-regulation of the expression of S-Adenosylhomocysteine in amino acid biosynthesis and metabolism affecting cystathionine and methionine metabolism, leading to a significant change in L-Threonine metabolism. This in turn led to the downregulation of L-Threonine expression affecting glycine, serine and threonine metabolic pathway metabolism. At the same time, genes such as PNLIPRP2, NCKX, ST6GALNACI, TUBA1A, and egg petide speract receptor are involved in the regulation of carotenoid deposition in response to the regulation of metabolite levels.The integrated analysis of metabolome and transcriptome will help to understand the biological process of gonadal pigmentation, and provide genetic information and related potential metabolic pathways for the subsequent in-depth understanding of sea urchin gonadal pigmentation mechanism.

Key words: Strongylocentrotus intermedius; Gonadal coloration; Multi-omics joint analysis

番红砗磲性腺发育规律及分子基础研究

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摘要：番红砗磲是一类极具生态价值的热带海洋贝类，具有雌雄同体、雄性先熟的特征，是贝类繁殖生物学研究的良好材料。目前对番红砗磲性腺发育的内在规律和分子基础知之甚少。本研究根据生殖细胞的类型及成熟过程，将番红砗磲性腺分为三种：未分化、雄性和雌雄同体性腺；其中前者为处于休止期的性腺；雄性性腺包括雄性生殖细胞增殖期和成熟期两个阶段；雌雄同体性腺中以雌性生殖细胞发育为主，其发育过程可分为卵原细胞增殖期、卵母细胞生长期、卵母细胞成熟 I 期、卵母细胞成熟 II 期和卵母细胞消退期。同时通过连续的组织学观察，确定了番红砗磲幼贝在 12 月龄时可达到雄性成熟，24 月龄达到雌性成熟。

关键词：砗磲；性腺发育规律；贝类；雌雄同体

Studies of gonadal development and molecular bases in Tridacna crocea

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Abstract： The Tridacna crocea is a highly ecologically valuable tropical marine mollusk with the characteristics of hermaphroditism and male precocity, making it a good material for the study of mollusk reproductive biology. At present, little is known about the internal laws and molecular basis of the gonadal development of the red giant clam. Based on the type and maturation process of germ cells, this study divided the gonads of the Tridacna crocea into three types: undifferentiated, male, and hermaphroditic gonads; The former is a gonad in its resting period; The male gonads include two stages: the proliferative stage and the mature stage of male germ cells; In hermaphroditic gonads, the development of female germ cells is the main process, which can be divided into the stages of oocyte proliferation, oocyte growth, oocyte maturation I, oocyte maturation II, and oocyte regression. Meanwhile, through continuous histological observation, it was determined that the juvenile of the Tridacna crocea can reach male maturity at 12 months old and female maturity at 24 months old.

Key words: Giant clam；Gonadal development ; Bivalves; hermaphroditism

杂交青蟹的形态特征及其遗传基础解析

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摘要：本研究分别以拟穴青蟹和锯缘青蟹为父母进行杂交，获得了不同的杂交青蟹。不同种青蟹卵发育过程在原肠期、五对附肢期存在发育时间的差异。形态数据表明，不同种青蟹仔蟹的形态基本一致；然而，锯缘青蟹为母本的杂交后代的体重和甲宽在仔III期，甲长在仔IV期的增长速度显著快于拟穴青蟹。亲缘关系分析表明，杂交青蟹的线粒体来源于母本；杂交后代可能具有较强的父系亲和性以及与父本拟穴青蟹相似的人工育种潜力。杂交后代的遗传图谱分析表明了杂交后代可能的遗传模式。雄性图谱由 40 个 LGs 组成，其 13 个 LGs 与雌性共享，27 个 LGs 为雄性特有；雌性图谱由 22 个 LGs 组成，9 个 LGs 为雌性特有。LG12 为性别连锁群，且为雌雄共有。

关键词：杂交青蟹；形态特征；转录组；遗传图谱

Morphological characteristics and genetic basis of hybrid Scylla

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Abstract： In this study, S. paramamosain and S. serrata were used as parents for hybridization, and different hybrid crabs were obtained. The results showed that different Scylla species had different developmental time in gastral stage and five pairs of appendages stage. Morphological data showed that the morphology of young mud crabs of different species was basically the same. However, the growth rate of body weight and shell width in maternal S. serrata offspring III stage and shell length in IV stage were significantly faster than S. paramamosain, while the maternal S. serrata offspring had no difference.

Phylogenetic analysis showed that the mitochondria of the hybrid crab were derived from the mother. The difference analysis of population genetic diversity indicates that the hybrid offspring may have strong paternal compatibility and artificial breeding potential similar to that of the paternal. The genetic map analysis shows the possible genetic pattern of the hybrid offspring. The male atlas consisted of 40 LGs, 13 of which were shared with females, and 27 were male-specific. The female atlas consists of 22 LGs, 9 of which are female-specific. LG12 is a sex-linked group, and it is both male and female. In addition, there may be not only diploid but also triploid in the hybrid offspring, and the genetic pattern is only suitable for diploid.

Key words: Hybrid Scylla; Morphological characteristics; transcriptome; genetic map

菲律宾蛤仔 sox 基因在黑色素合成通路中的作用研究

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摘要：本实验通过全转录组分析得出 lgi-miR-216b 分别调控 Rpsox、Rpcreb、Rpmitf 等黑色素合成相关基因，推测通过激活黑色素合成途径参与黑色素形成。通过 qPCR 和 RNA 干扰技术对 Rpsox 等基因进行表达特性分析和功能验证，结果表明，Rpsox 在蛤仔外套膜、足、鳃、消化腺、闭壳肌、水管中均有表达。其中，外套膜中 Rpsox 表达量显著高于其他五种组织。在四种壳色蛤仔中，Rpsox 在黑蛤外套膜中表达量最高，白蛤中表达量最低($P < 0.05$)。注射 siRNA-Rpsox 后，结果显示：与对照组相比，实验组 Rpsox 相关基因表达量显著降低($P < 0.05$)，对照组没有显著变化，表明干扰链成功抑制 Rpsox 等靶基因的表达。双荧光素酶报告基因显示 lgi-miR-216b 显著降低 Rpsox 荧光素酶活性，进一步证明 lgi-miR-216b 可以靶向调控 Rpsox，抑制其表达，从而影响贝壳色素生成。

关键词：菲律宾蛤仔；壳色；黑色素合成通路；microRNAs；mRNA

Role of the SOX gene in the melanin synthesis pathway in Manila clam (Ruditapes philippinarum)

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Abstract：In this study, full transcriptome analysis was used to study the molecular mechanism of shell color formation and regulation, and miRNA libraries were constructed from the mantle tissues of four species of shell colored clams. The results showed that lgi-miR-216b regulates genes related to melanin synthesis, such as Rpsox, Rptyr, Rpcreb, and Rpmitf, respectively, and may participate in the formation of melanin by activating the melanin synthesis pathway. The expression characteristics of lgi-miR-216b target gene Rpsox were analyzed by fluorescence q-PCR, and its function was verified by RNA interference technology. The results showed that Rpsox were expressed in the mantle, foot, gill, digestive gland, adductor muscle and pipe of clam. Among them, the relative expression of Rpsox in the mantle was significantly higher than that in other 6 tissues ($P < 0.05$). Among the four shell colored clams, the expression of Rpsox was the highest in the mantle of the black clams and the lowest in the white clams ($P < 0.05$). After injection of interfering strand siRNA-Rpsox of clam Rpsox, the results showed: Compared with the blank control group, the expression levels of melanin-related genes such as Rpsox and Rpcreb in the positive experimental group were significantly decreased ($P < 0.05$), while the expression levels of related genes in the negative control group were not significantly changed, indicating that the interference chain successfully inhibited the expression of target genes such as Rpsox.This experiment further proved that lgi-miR-216b has a targeted regulatory relationship with Rpsox through double luciferase reporter gene detection.

Key words: Ruditapes philippinarum; shell color; Melanin synthesis pathway; microRNAs; mRNA

厚壳贻贝足丝附着强度的表型性状分析

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摘要：厚壳贻贝是我国重要的海产养殖贝类，通过足丝牢固地黏附于水下固体表面。本研究利用电感耦合等离子体质谱(ICP-MS)、共聚焦显微拉曼光谱(Raman microspectroscopy)、X-射线光电子能谱(XPS)和傅里叶红外变换红外光谱(FTIR)分析足丝微观结构。结果表明，经 DTT 处理后足丝中二硫键的相对强度信号低于对照组,且强韧性显著低于对照组($P<0.05$)，表明 DTT 通过降低足丝中二硫键含量导致了强韧性下降。使用 EDTA 处理足丝并通过 XPS、FTIR 和足丝强韧性分析显示,处理后足丝中 Ca 原子结合能下降， 蛋白二级结构发生改变, 足丝强韧性低于对照组($P>0.05$)，EDTA 通过螯合足丝中金属元素改变蛋白二级导致强韧性下降。综上，二硫键在维持足丝强韧性方面发挥重要作用,本研究揭示了贻贝足丝的材料结构及力学性能,并提供了一种足丝强韧性的分析方法，为筛选高附着强度贻贝群体提供帮助。

关键词：厚壳贻贝；足丝；附着；强韧性

Phenotypic analysis of byssus attachment strength in Mytilus coruscus

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Phenotypic analysis of byssus attachment strength in Mytilus coruscus

Abstract： Mytilus coruscus is an important marine aquaculture shellfish in China, which firmly adheres to underwater solid surfaces through byssal threads. In this study, the microstructure of the byssus was analyzed using ICP-MS, Raman microspectroscopy, XPS, and FTIR. The results indicated that the intensity signal of disulfide bonds in the byssus was lower in the DTT-treated group compared to the control group. Furthermore, the breaking force of the byssus was significantly reduced in the DTT-treated group ($P < 0.05$), suggesting that DTT decreased the content of disulfide bonds, leading to decreased breaking force. By analyzing the byssus treated with EDTA using XPS, FTIR and breaking force, it was observed that the binding energy of Ca decreased, the secondary structure of proteins changed, and the breaking force was lower than that in the control group ($P > 0.05$). This suggests that EDTA altered the secondary structure of byssal proteins by chelating metal ions in the byssus, resulting in decreased toughness. Overall, this study highlights the importance of disulfide bonds in maintaining the toughness of the byssus. It provides insights into the material structure and mechanical properties of mussel byssus and presents an analytical method for assessing its toughness, offering technical support for the identification of high-adhesion mussels.

Key words: Mytilus coruscus; byssal threads; adhesion; strength and toughness

黑斑原鮡性别决定基因

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摘要：黑斑原鮡隶属于鲇形目鮡科原鮡属，主要分布于我国西藏地区雅鲁藏布江中上游。黑斑原鮡表现出的雌性两态性显示同阶段雄性有着体长体重优势。说明掌握黑斑原鮡性别决定和分化相关机制对于人工繁育黑斑原鮡具有指导意义。

本研究中，取成体黑斑原鮡雌雄各三条取其精巢和卵巢组织进行转录组测序分析。在 6 个测序样本中筛选出 9647 个差异基因，包含上调基因 5490 个，下调基因 4157 个。其中发现了许多与配子体发生相关的基因，以及一些先前报道的对性腺分化和发育至关重要的基因，CYP19A、amh、sox9、DMRT1 等均在雄鱼中高度表达；KEGG 注释显示在蛋白质信号和细胞过程以及基因信息处理上参与。目前暂认为是黑斑原鮡的性别决定和分化相关基因。

本研究结果为后续研究黑斑原鮡性别决定基因的筛选、功能研究和全雄新品系创制提供了重要的理论基础和数据支撑。

关键词：黑斑原鮡；转录组；性别决定；性别决定基因

Glyptosternum maculatum sex-determining gene

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Abstract： Glyptosternum maculatum belongs to the genus Protoglyptoides of the Silurus family，It is mainly distributed in the middle and upper reaches of the Yarlung Zangbo River in Tibet。Female dimorphism in Graecoglanis melanoglanis showed that males of the same stage had an advantage in body length and weight. It is suggested that understanding the mechanisms related to sex determination and differentiation is of guiding significance for the artificial breeding of Glyptosternum maculatum.

In this study, taking adult shading Glyptosternum maculatum all three take its testis and ovary organization for the transcriptome sequencing analysis. 9647 differential genes were screened in 6 sequencing samples, including 5490 up-regulated genes and 4157 down-regulated genes.CYP19A, amh, sox9 and DMRT1 are highly expressed in male fish. KEGG annotations have been shown to be involved in protein signaling and cellular processes as well as gene information processing. At present, it is temporarily considered to be a gene related to sex determination and differentiation of Protoglyptoglyptoglyptogramma.

The results of this study provided an important theoretical basis and data support for subsequent research on sex-determining gene screening, functional studies and the creation of a new all-male strain of Pareuglis melanoglanis.

Key words: Glyptosternum maculatum；transcriptome；sex determination；sex-determining gene

通过转录组学和代谢组学分析研究槲皮素对对虾抗副溶血弧菌(Vibrio parahaemolyticus)抗性性状的影响

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摘要：对虾是全球主要的水产养殖品种之一。副溶血性弧菌（VP）是凡纳滨对虾的机会性病原体之一，可引起急性肝胰腺坏死病（AHPND）等疾病，给对虾养殖业造成重大损失。本研究旨在利用对转录组和代谢组数据的综合分析，探讨导致凡纳滨对虾不同种群对 VP 的抗菌性状变化的因素。分析结果表明，类黄酮化合物（尤其是槲皮素）在影响 Mx 和 TH04 的抗菌性状变化中起着关键作用。在饲料中添加适量的槲皮素有可能增加 TLR 和 AP1 等 NF-κB 通路中关键基因的表达，以及抗菌肽的表达，从而降低死亡率。结果表明，适量的槲皮素可增强对虾对 VP 的免疫反应，从而降低 AHPND 的发病率。

关键词：凡纳滨对虾；槲皮素；副溶血性弧菌；转录组学；代谢组学

Investigating the Impact of Quercetin on the Antimicrobial Resistance Traits of Shrimp against Vibrio parahaemolyticus by Transcriptomic and Metabolomic Analysis

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Abstract： Shrimp is one of the primary aquaculture species worldwide. The Vibrio parahaemolyticus (VP) is one of the opportunistic pathogens of Litopenaeus vannamei and can cause diseases such as Acute Hepatopancreatic Necrotic Disease (AHPND), resulting in significant losses to the shrimp farming industry. This study aims to explore the factors contributing to the variations in antimicrobial resistance traits among diverse populations of Litopenaeus vannamei in response to VP, utilizing a comprehensive analysis of both transcriptome and metabolome data. The analysis findings demonstrate that flavonoid compounds, especially quercetin, play a pivotal role in influencing the variations in antimicrobial resistance traits of Mx and TH04. Supplementing the feed with an appropriate quantity of quercetin has the potential to increase the expression of crucial genes in the NF-κB pathways, including TLR and AP1, along with the expression of the antibacterial peptide Crustin, resulting in a decreased mortality rate. The results indicated an appropriate amount of quercetin can strengthen the immune response of shrimp to VP, thereby reducing the incidence of AHPND.

Key words: Litopenaeus vannamei; quercetin; Vibrio parahaemolyticus; transcriptomic; metabolomic

不同性别刺参生长差异解析

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摘要：刺参 (Apostichopus japonicus) 隶属于棘皮动物门，刺参纲、楯手目、刺参科、刺参属，是中国重要的海水养殖品种。性二态性现象在水产养殖动物中广泛存在，培育单性养殖新品种是实现水产养殖行业增产增效的重要手段。本研究首先建立了基于环介导等温扩增、适用于养殖场的刺参鉴定遗传性别的方法。随后，对不同性别的刺参进行生长数据监测，揭示了 1-2 龄性腺未分化的刺参雄性和雌性之间没有显著的生长差异。性腺分化的 2-3 龄刺参中，雄性刺参的体重增量和特定生长率分别比雌性高 1.76 倍和 1.52 倍，此外，刺参体壁组织中生长相关 hgfr1 和 c-myc 的表达量在 1-2 龄不同性别刺参间无显著差异，在 2-3 龄刺参中，其基因的表达水平在雄性中显著高于雌性，且 cyp1a1 和 cyp17a 在分化卵巢中的表达水平显著高于分化精巢。本研究揭示了雌雄刺参之间的生长速度差异，指出刺参全雄养殖具有巨大经济价值。

关键词：刺参；环介导等温扩增；性别；生长差异

Sex differences in the growth of sea cucumber (Apostichopus japonicus)

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Abstract： Sea cucumber (Apostichopus japonicus), a commercially important mariculture species in China. Sexual dimorphism is widely observed in aquaculture animals, and sex control biotechnologies have created typical cases of genetic breeding in several aquaculture species. Clarifying the sex differences in important economic traits and developing a rapid genetic sex identification method are the most critical step for establishing a monosex aquaculture population. In the present study, we first established the loop-mediated isothermal amplification (LAMP) based method to identify the genetic sex of sea cucumber in the field without complex equipment. Subsequently, we investigated the growth difference in terms of weight gain between males and females, and revealed that there was no significant growth difference between male and female 1–2-year-old juvenile sea cucumbers with undifferentiated gonads. However, among 2–3-year-old adult sea cucumbers with differentiated gonads, males exhibited greater growth advantages compared to females. Considering that the weight increment and specific growth rate (SGR) of male sea cucumbers were 1.76 and 1.52 times greater than those of females, respectively, there is tremendous value in producing all-male populations of A. japonicus. Furthermore, the expression levels of growth trait candidate genes (hgfr1 and c-myc) in body wall tissues showed no significant differences between males and females of 1–2-year-old A. japonicus. However, in 2-3-year-old A. japonicus, the expression levels of these genes were significantly higher in males than in females. Conversely, cyp1a1 and cyp17a genes were more highly expressed in differentiated ovaries than in differentiated testes. This study provides a solid basis for achieving sex control breeding in sea cucumbers.

Key words: sea cucumber; LAMP; genetic sex identification; growth differences

低盐胁迫对厚壳贻贝足丝附着和足腺体的影响

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摘要：厚壳贻贝是海洋经济贝类，浙江嵊泗北部贻贝养殖区海水盐度曾数天低于 10‰，贻贝产量受影响。为研究低盐对贻贝足丝附着影响，将贻贝附于养殖绳上暴露于 30、25、20、15、10 和 5‰海水中 7d，观察其掉落和死亡。结果表明各盐度下贻贝脱落无差异，5 和 10‰影响贻贝存活。研究各盐度对贻贝足丝分泌、黏附力和破断力等影响，并通过天狼星红和 HE 染色分析低盐对贻贝足腺体的影响。结果表明贻贝在 5 和 10‰中不分泌足丝；在 15‰中 48h 后开始分泌，分泌量低于 20-30 ‰($p<0.05$)。盐度对足丝直径无影响；足丝黏附力和破断力在 15-25‰间无差异($p>0.05$)，但均低于 30‰($p<0.05$)。经 HE 染色后 5-20‰暴露下贻贝足腺体面积低于 30‰($p<0.05$)；经天狼星红染色后 5-15‰暴露下足组织胶原腺体面积低于 30‰($p<0.05$)。研究表明低盐不影响贻贝脱落，但会缩小贻贝足腺体进而影响足丝分泌和附着。

关键词：厚壳贻贝；低盐；足丝；附着；足腺体

Effect of hyposalinity stress on byssus adhesion and foot glands of Mytilus coruscus

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Abstract： Mytilus coruscus is an important marine economic shellfish in China. The salinity of seawater in the mussel aquaculture area in the northern part of Shengsi, Zhejiang Province, was below 10 psu for several days, and the mussel production was affected. In order to explore the effect of low salinity on mussel byssus adhesion, mussels attached to culture ropes were exposed to 30, 25, 20, 15, 10 and 5 psu of seawater for 7 day, and were observed to fall off and die. The results showed that there was no significant difference in mussel shedding between salinities, while 5 and 10 psu significantly affected mussel survival. The effects of each salinity on the secretion, adhesion and breaking force of mussel byssus were also investigated, and the effects of low salinity on the foot glands of mussels were analysed by Sirius red and HE staining. The results showed that mussels did not produce byssus in 5 and 10 psu; they started to produce byssus after 48 h in 15 psu, and the amount of production was significantly lower than that in 20-30 psu ($p<0.05$). Changes in salinity had no effect on the diameter of the byssus; the adhesion and breaking force of the byssus were not significantly different between 15-25 psu ($p>0.05$), but both were significantly lower than that of 30 psu ($p<0.05$). HE staining showed that the foot gland area of the mussel foot tissue was significantly lower than that of 30 psu ($p<0.05$) under exposure to 5-20 psu; Sirius red staining showed that the collagen gland area of mussel foot tissue was significantly lower than 30 psu at the 5-15 psu exposure ($p<0.05$). The study suggests that low salinity does not affect mussel shedding, but shrinks mussel foot glands and affects byssus secretion and attachment.

Key words: Mytilus coruscus; hyposalinity stress; byssus； adhesion; foot glands

刺参 sdf 基因表达及功能研究

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摘要：刺参隶属于棘皮动物门，海参纲、盾手目、刺参科、仿刺参属，是我国重要的海水经济养殖品种之一。研究表明，雄性刺参的增长速度优于雌性，实现全雄化养殖必将实现刺参养殖产业增产增效。实验室前期研究中，基于雌雄差异简化基因组测序和全基因组关联分析，在刺参中鉴定了 1 段 313bp 的雄性特异 DNA 片段。本研究在此性别特异片段的基础上利用染色体步移扩增得到一段长度约为 7Kb 的雄性特异片段，并在该 DNA 片段中注释出一个 sdf 基因。随后，利用 Race-PCR 技术，克隆得到刺参 sdf 基因全长，阐明了其分子特征和进化关系，并通过组织及性腺定量分析和原位杂交技术解析了其动态表达情况。此外，本研究首次建立了基于胚胎浸泡的刺参 vivo-morpholino 干扰技术，胚胎时期敲降 sdf 基因会影响 cAMP、FoxO、GnRH 信号通路和类固醇激素合成通路及性腺发育相关基因的表达。研究结果为解析刺参性别决定基因奠定基础。

关键词：刺参；性别特异；vivo-morpholino；转录组预测

Expression and Functional Analysis of the Sdf Gene in the Sea Cucumber, Apostichopus japonicus

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Abstract： Sea cucumber (Apostichopus japonicus) is a member of the class of Holothuroid, which belong to Echinodermata. A. japonicus is one of the most important marine aquaculture species in China. Research has revealed that male sea cucumbers exhibit a faster growth rate compared to females, highlighting the potential benefits of establishing an all-male cultivation approach in the sea cucumber aquaculture industry. In our earlier research, we identified a 313bp male-specific DNA fragment in sea cucumbers using the 2b-RAD-seq method. Herein, an approximately 7Kb male-specific fragment was obtained using genome walking, and a sdf gene was annotated within this sequence. Subsequently, the full-length cDNA sequence of the sdf gene was cloned using RACE-PCR, and its molecular characteristics as well as evolutionary relationships were elucidated. Moreover, the dynamic expression patterns of sdf were analyzed by RT-PCR and in situ hybridization. Importantly, this study firstly established gene knockdown technology by soaking with in vivo morpholino during early embryonic development in sea cucumber. Knocking down the sdf gene affected the expression of genes in the cAMP signaling pathways, FoxO signaling pathways, GnRH signaling pathways, steroid hormone synthesis, and sex-related genes. The research findings provide a foundation for deciphering the sea cucumber sex determination genes.

Key words: Apostichopus japonicus; sex-specific; vivo-morpholino; transcriptome prediction

葡萄牙牡蛎四倍体的连续选育：生长、存活、育性和倍性组成的比较分析

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摘要：葡萄牙牡蛎三倍体具有生长快、育性差、品质显著提高的优点，但由于三倍体育性差，很难直接进行遗传改良。四倍体雄性与二倍体雌性进行倍性间杂交已被证明是商业生产三倍体的最佳方法，因此四倍体的遗传改良会直接影响三倍体后代的表型性状。然而，目前对四倍体牡蛎进行遗传改良的研究还很少。本文以诱导的葡萄牙牡蛎四倍体群体为基础群体，进行了连续3代的生长选育研究，系统比较了选育组和对照组的生长、存活率、倍性组成和性别比例。结果表明，选育组的增量存活率没有获得显著提高。但与对照组相比，选择组的生长获得显著提高。两组四倍体中的部分四倍体在第270天前发生了染色体丢失并转化为二倍体或三倍体。而且，随着世代的增加，选育组发生染色体丢失的个体数逐渐减少，其倍性组成比对照组更加稳定。综上所述，本研究成功选育了一种葡萄牙牡蛎四倍体快速生长选育系，可用于快速生长三倍体的商业化生产，也为四倍体牡蛎的遗传改良提供了依据和参考。

关键词：葡萄牙牡蛎；四倍体；连续选育；生长性状；倍性组成

Successive selection responses of tetraploid Crassostrea angulata: comparison of growth, survival, sex ratio and ploidy composition between selected and unselected groups

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Abstract: Triploid C. angulata has the advantages of fast growth, poor fertility and high quality, but it is difficult to directly genetic improvement because of the poor fertility. Mating between tetraploid male and diploid female has been shown to be the best method for commercial triploid production, so genetic improvement of the tetraploid will directly affect the phenotypic traits of the triploid offspring. However, few studies have investigated the genetic improvement of tetraploid oysters so far. In this paper, we carried out 3 successive generations of growth selective breeding research based on the induced tetraploid C. angulata population, and systematically compared the growth, survival, ploidy composition and sex ratio between the selected group and the control group. The results showed that the incremental survival rate of the selected group was not significantly improved, and there was no significant difference between the survival rate of the two group from planktonic larvae to adult. However, the growth of the selected group was significantly improved compared with the control group, that was, the shell height and whole weight of S3 were significantly higher than those of C3, and the selection advantage of shell height increased from 7.80% in S1 to 34.68% in S3. The ploidy compositions of the two tetraploid groups were relatively stable before 90 days, but some tetraploids underwent chromosome loss and conversion to diploid or triploid on the 270th day, which may be related to gametogenesis of tetraploids. Moreover, with the increase of generation, the number of individuals with chromosome loss in the selected group gradually decreased, and its ploidy became more stable than control group. In addition, both groups were fertility, and the sex ratio showed that more males than females, and a certain proportion of hermaphrodite individuals existed. In conclusion, this study successfully selected a fast growth line of tetraploid C. angulata, which can be commercial used in the production of fast growth triploid C. angulata, and provided a basis and reference for genetic improvement of tetraploid oysters.

Key words: Crassostrea angulata; tetraploid; selective breeding; growth trait; ploidy composition

鲫 MC4R 基因克隆和功能研究

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摘要：摄食和能量代谢是影响动物生长发育的两个重要因素，黑素皮质素受体-4（MC4R）在动物食物摄入和能量消耗调节中发挥着重要作用。为此，本研究对鲫 MC4R 基因进行了克隆和功能研究。结果发现，鲫 MC4R 存在 caMC4R 和 caMC4RL 两种同源类似物，二者在结构，与配体发生作用的氨基酸位置和方式存在差异,其中 caMC4RL 的组成活性和对内源性配体的响应均高于 caMC4R，且对 ERK1/2 磷酸化水平高于 caMC4R，但对 AMPK 磷酸化水平低于 caMC4R；对比分析 6 种源自野生鲫群体的突变体发现，内源性配体 ACTH（1-24）和外源合成型配体 NDP-MSH 均能有效激活突变体 P25L、A87S、R302T 和 R302K，但均不能有效激活突变体 E57K、P296S。以上研究结果表明，鲫 MC4RL 可能发挥更重要的生理功能，其 E57K、P296S 突变体可作为鲫分子育种的潜在标记。

关键词：黑素皮质素受体-4（MC4R）；鲫鱼；突变体；信号通路；组成活性

Cloning and Functional Study of MC4R in Crucian Carp (Carassius auratus)

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Abstract： Food intake and energy metabolism are important factors that affect animal growth and development. Melanocortin receptor-4 (MC4R) plays an important role in regulating animal food intake and energy consumption. Therefore, this study cloned and functionally studied the MC4R gene of crucian carp (Carassius auratus). The results showed that there are two homologous isoforms of MC4R, caMC4R and caMC4RL, in crucian carp. The two differ in terms of structure, and interaction with ligands. The constitutive activity and response to endogenous ligands of caMC4RL are higher than those of caMC4R. Moreover, the phosphorylation level of ERK1/2 in HEK293T cells overexpressing caMC4RL was higher than that of caMC4R, but the phosphorylation level of AMPK was lower than that of caMC4R. The study of six mutants derived from wild crucian carp populations found that both the endogenous ligand ACTH (1-24) and the exogenous synthetic ligand NDP-MSH can effectively activate the mutants P25L, A87S, R302T, and R302K. However, neither of them can effectively activate the mutants E57K and P296S. In summary, the crucian carp MC4RL may play a more important physiological role, and its E57K and P296S mutants can be used as potential markers for molecular breeding of crucian carp.

Key words: melanocortin receptor-4 (MC4R); crucian carp (Carassius auratus); mutants; signal pathway; constitutive activity

海胆性腺发育过程中代谢变化及分子机制研究

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摘要：光棘球海胆（Mesocentrotus nudus）隶属于棘皮动物门，海胆纲，拱齿目，球海胆科。性腺是海胆唯一可食用也是最具经济价值的部分，人工控制海胆性成熟、延长有效生产期逐渐成为海胆研究领域的热点之一。本研究以光棘球海胆为研究对象，对分化卵巢（DO）、分化精巢(DT)、未分化卵巢(UO)和未分化精巢(UT)进行转录和代谢组测序，通过转录和代谢联合分析筛选了 HSD17B8、GATA4、SOXE、CYP17A1 和 FST 等在未分化及已分化性腺中的共有差异基因；鉴定了包括葡糖苷酸雌酮和皮质醇在内的重要性别差异代谢物；并系统分析了性腺中芳香化酶基因家族的表达情况，提出了 CYP17A1 和 CYP1A1 可能在性类固醇激素合成中发挥重要作用。本研究为解析海胆性腺发育机制奠定基础。

关键词：光棘球海胆；转录组；代谢组；性腺；CYP

Metabolic changes and molecular mechanisms during the gonadal development in the sea urchin, Mesocentrotus nudus

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Abstract： Mesocentrotus nudus belongs to the phylum Echinodermata, class Echinoidea, family Toxoplasma, genus Echinococidae. Gonads are the only edible and economically valuable part for human. Hence, artificial control of sexual maturation and the extension of the effective production period have gradually become a hot topic in sea urchin research. In this study, we explored the sex differential genes and metabolites, and the sex differentiation regulatory networks by integrated application of transcriptomics and metabolomics of differentiated ovary (DO), differentiated testis (DT), undifferentiated ovary (UO), and undifferentiated testis (UT). Several genes including HSD17B8, GATA4, SOXE, CYP17A1, and FST were identified as differentially expressed genes in undifferentiated and differentiated gonads. Glucuronic acid estradiol and cortisol were also identified as significant gender-specific metabolites. In addition, the expression patterns of aromatase family genes were detected in gonads and revealed that CYP17A1 and CYP1A1 might play important roles in the synthesis of steroid hormones. This study lays the foundation for studying the gonadal developmental mechanism in sea urchins.

Key words: Mesocentrotus nudus; Transcriptomics; Metabolomics; Gonad; CYP

BMP 家族基因在军曹鱼早期发育阶段及骨骼畸形组织中的表达分析

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摘要：骨形态发生蛋白(BMPs)基因在调控鱼类骨骼发育过程中具有重要作用。本研究利用生物信息学方法，从军曹鱼全基因组中鉴定出 19 个 BMP 家族基因，研究了上述基因的染色体分布、外显子/内含子结构及保守基序分析；随后，利用实时荧光定量 PCR 技术检测了上述基因在军曹鱼成鱼中的组织表达分布情况，并进一步分析了 BMP 基因在军曹鱼早期发育阶段及骨骼畸形个体中的表达情况。结果表明：（1）13 个 BMP 基因在米克尔氏软骨中表达水平最高;(2）除 BMP8a 基因的表达水平在 15 日龄后持续显著升高之外，其他 BMP 基因在在仔、稚、幼鱼各时期均未表现出明确的表达量变化趋势；（3）除 BMP1、BMP5 和 BMP7b 之外，米克尔氏软骨畸形个体的 BMP 基因表达均显著下调，而椎骨畸形个体中多数 BMP 基因的表达均显著上调。

关键词：骨形态发生蛋白；军曹鱼；组织表达；早期发育；骨骼畸形

Genome-wide identification, phylogeny and expression analysis of the bmp gene family associated with development and skeleton deformity in cobia (Rachycentron canadum)

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Abstract：Bone morphogenetic proteins (BMPs) are critical for controlling the skeletal development of fish, which has a sigificant influence on external morphology, functional exercise, and even survival rate in aquaculture breeding. In this study, a total of 19 bmp genes were identified in cobia (Rachycentron canadum) and these genes were divided into six sub-families according to phylogenetic analysis, including bmp1, bmp3/11/15, bmp2/4/16, bmp9/10, bmp13/14 and bmp5/6/7/8 subfamily. The identified cobia BMPs, except for BMP1, all possessed a similar TGF_beta domain. Phylogenetic analysis revealed that the cobia bmp genes were most closely related to those of the golden pompano (Trachinotus ovatus). The tissue distribution of these bmps in adult cobia revealed that the highest expression of most bmp genes was found in the Meckel’s cartilage; the highest expression of bmp4 was identified in the vertebrae; five other bmps were highly expressed in non-skeleton tissues including liver, heart and gill. The expression of bmp genes was also identified during the larvae and juvenile stages (1–30 dph), and most bmps revealed no certain expression pattern excepting for bmp8a, which showed a significantly lower mRNA level before 15 dph and then increased to a significant higher level. Due to the high incidence of deformity during the larvae and juvenile stages of cobia, the difference of bmp mRNA levels between deformed and normal skeletons (the Meckel’s cartilage and vertebrae) were also investigated to understand the involvement of bmp genes in skeletal deformity. The results showed that most of the bmp genes were significantly inhibited in the deformed Meckel’s cartilage excepting for bmp1, bmp5, and bmp7b; In contrast, in the deformed vertebrae, expression of most bmps were significantly increased excepting for five genes (bmp1, bmp4, bmp5, bmp7b, and bmp13b).

Key words: BMP; Rachycentron canadum; Tissue distribution; Early developmental stages; Skeleton deformity

三倍体皱纹盘鲍（Haliotis discus hannai）的配子发生及性腺发育

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摘要：在一个完整生殖周期内观测二、三倍体皱纹盘鲍（Haliotis discus hannai）的性腺发育、性激素水平和足肌-软体部系数（FMSI）。结果显示，二倍体具有正常配子发生过程，三倍体雌性可形成成熟卵母细胞，而三倍体精子发生滞育在精母细胞阶段。基于组织细胞学特征制定了适用于三倍体皱纹盘鲍的性腺发育划分标准，发现三倍体卵巢发育中存在滤泡内为大量卵原细胞所占据的时期，而发育中的精巢内出现具有凋亡和自噬特征的细胞。三倍体滞育阶段性腺内雌二醇和睾酮含量显著低于二倍体的相应阶段或成熟阶段，类固醇激素水平的差异可能与三倍体性腺的异常发育有关。以性腺指数（GBIn）为依据证实成熟季节三倍体的性腺饱满度显著下降。GBIn、FMSI 和性别三者之间的关系反映出性腺发育对出肉率存在负面影响，三倍体雌性性腺饱满度显著降低且出肉率（FMSI）显著增加。结果佐证了前期三倍体生长优势来源于性腺不育的能量转移假说。

关键词：皱纹盘鲍，三倍体，配子发生，性腺发育，类固醇激素，性腺指数

Reproductive cycle and gametogenesis in the triploid Haliotis discus hannai

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Abstract： To further investigate the reproduction physiology of triploid Haliotis discus hannai, the gonadal development, sexual hormones parameters and foot muscle-soft tissue index (FMSI) were studied in diploid and triploid abalones during a complete reproductive cycle. Diploid males and females exhibited normal gametogenesis, whereas triploid females retained the ability to produce mature oocytes and triploid males stalled spermatogenesis at the spermatocyte stage. A new classification scheme applied to the description of gonadal development in triploid abalones was established. The stages dominated by mass oogonia in the follicle were observed during the triploid ovarian development, while cells characterized by apoptosis and autophagy were presented in the developing triploid testis. Estradiol and testosterone levels in triploid gonads at the diapause stages were significantly lower than those of diploids in the corresponding or maturation stages ($P < 0.05$), and variations in steroid hormone levels might be related to the abnormal gonadal development in triploids. The gonadal fullness of abalone was evaluated by the quantitative approach depending on the gonad bulk index (GBIn). A significant decrease in gonadal fullness was found in triploids during the maturation season ($P < 0.05$). The relationship among GBIn, FMSI and gender reflected that gonad development had a negative impact on FMSI. Triploid females had decreased markedly gonadal fullness accompanied by a significant increase in FMSI ($P < 0.05$). These results provided further evidence for the hypothesis of energy relocation that the triploid advantage in growth may be attributed to energy redistribution after sterility. Our study clarified the sterility characteristics, hormone variations and the relevance between meat yield and gonadal development in triploid H. discus hannai, providing references for the implementation of subsequent breeding strategies of triploid abalone.

Key words: Haliotis discus hannai; Triploid; Gametogenesis; Gonadal development; Steroid hormones; Gonad bulk index

快速生长和缓慢生长的倒刺鲃

（脑和肝脏的转录组分析）

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摘要：生长速率是水产养殖中受多种因素影响的一种商业性状，其中遗传组成对物种的生长速率起着重要作用。倒刺鲃是一种分布于中国南方的淡水鱼。虽然在中国南方饲养，但该物种生长速率的分子机制尚不清楚。在这里，作者对快速生长（FG）和慢生长（SG）在孵化后 90、150 和 300 天的脑和肝脏组织进行了转录组分析，以阐明其生长机制。

关键词：快速生长；分子机制；脑与肝脏转录组分析；通路分析；华南地区

Transcriptome analysis of the brain and liver of fast- and slow-growing phoenix barb (Spinibarbus denticulatus denticulatus)

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Abstract： Growth rate is a commercial trait in aquaculture that is influenced by multiple factors, among which genetic composition plays a fundamental role in the growth rate of species. The phoenix barb (Spinibarbus denticulatus denticulatus) is a widely distributed freshwater fish species in South China. Although S. d. denticulatus is reared in South China, the molecular mechanisms underlying the growth rate of the species remain unclear. Here, the authors performed transcriptome analysis of muscle tissues from fast-growing (FG) and slow-growing (SG) S. d. denticulatus at 90, 150, and 300 days after hatch (DAH) to elucidate its growth mechanism.Growth rate is a commercial trait in aquaculture that is influenced by multiple factors, among which genetic composition plays a fundamental role in the growth rate of species. The phoenix barb (Spinibarbus denticulatus denticulatus) is a widely distributed freshwater fish species in South China. Although S. d. denticulatus is reared in South China, the molecular mechanisms underlying the growth rate of the species remain unclear. Here, the authors performed transcriptome analysis of brain and liver tissues from fast-growing (FG) and slow-growing (SG) S. d. denticulatus at 90, 150, and 300 days after hatch (DAH) to elucidate its growth mechanism.

Key words: fast-growing; molecular mechanism; brain and liver transcriptome analysis; pathway analysis; South China; Spinibarbus denticulatus denticulatus

WGBS 对菲律宾蛤仔抗鳗弧菌免疫机制的初步分析

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摘要：菲律宾蛤仔（Ruditapes philippinarum）具有先天免疫系统，全基因组亚硫酸氢盐测序（WGBS）为蛤仔甘露糖受体基因（MR）抗鳗弧菌的免疫应答机制进行初步分析。使用 107 CFU/mL 鳗弧菌侵染蛤仔（含对照组），7 天后根据存活情况将蛤仔分为抗性组和易感组，取肝胰腺组织测序，分析 DMR，用 qRT-PCR 验证结果并对差异基因富集分析。结果发现 CG 型是主要的 DNA 甲基化修饰类型，多发于基因外显子和内含子区。抗性组 MR 表达与 DNA 甲基化水平呈负相关，KEGG 分析发现磷脂酰肌醇信号通路具有 DMR 相关基因，如 PI3Ks 基因，参与细胞凋亡等过程。基因启动子区域的甘氨酸、丝氨酸和苏氨酸代谢通路参与转录过程中基因的调控。本研究中，CpG 高甲基化的减少和内含子区域低甲基化的增加可能导致免疫功能下降，低甲基化可促进 MR 表达，提高蛤仔对鳗弧菌的抵抗能力。

关键词：菲律宾蛤仔；DNA 甲基化；鳗弧菌；全基因组亚硫酸氢盐测序

Preliminary analysis of the immune mechanism of Ruditapes philippinarum against V. anguelarensis by WGBS

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Abstract：Manila clam (Ruditapes philippinarum) has an innate immune system, and whole genome bisulfite sequencing (WGBS) is the immune response mechanism of Mannose receptors gene (MR) against Vibrio anguillarum. The clams (including control group) were infected with 107 CFU / mL. After 7 days, the clams were divided into resistant and susceptible groups according to survival. Hepatic and pancreatic tissues were sequenced, DMR was analyzed, and the results were verified by qRT-PCR and differential gene enrichment analysis. The results found that the CG type is the main DNA methylation modification type, mostly in the exonic and intronic regions of the gene. Resistance group MR expression was inversely correlated with DNA methylation levels, and KEGG analysis revealed that the phosphatidylinositol signaling pathway has DMR-related genes, such as PI3 Ks genes, which are involved in apoptosis and other processes. Glycine, serine, and threonine metabolism pathways in the gene promoter region are involved in the regulation of genes during transcription. In this study, decreased CpG hypermethylation and increased hypomethylation in intronic regions may lead to decreased immune function, and hypomethylation could promote MR expression and improve the resistance of clams to V. anguillarum.

Key words: Ruditapes philippinarum; DNA methylation; Vibrio anguillarum; Whole Genome Bisulfite-Seq

不同生境礁膜的分类鉴定：无性与有性生活史比较

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摘要：礁膜是一种高经济价值的单层细胞绿藻（MGA），生活史通常作为其分类标准之一。多数学者认为礁膜生活史为有性或无性的异型世代交替。然而，目前尚不清楚其无性单世代生活史。本研究以 tufA 和 18SrDNA 为分子标记，对两种不同生境的 MGAs 进行分类鉴定和形态学研究。tufA 和 18SrDNA 序列结果显示，阳江和湛江的所有样本均聚于同一支（M.nitidum clade）并得到 Bootstrap 的高度支持，遗传距离分别为 0.000、0.005。形态学观察结果表明，两种生境的植株在外部形态具有极显著差异，两者在早期发育均遵循丝状-叶状的个体发生形式。湛江植株的生活史为典型的异型世代交替，阳江植株只产生负趋光性的双鞭毛无性配子，配子不经过孢子体世代，直接发育形成新的配子体。因此，阳江植株被鉴定为无性单世代礁膜。本研究提供了礁膜无性单世代生活史类型的证据，以期为 MGAs 的分类和物种的进化关系提供理论支撑。

关键词：礁膜；分子分析；生活史；分类学；进化

Classification and Identification of Monostroma nitidum in Different Habitats: A Comparative Analysis of Asexual and Sexual Life Histories

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Abstract： M. nitidum, a monostromatic green algae (MGA) with high economic value. Life history can often be used as one of the standards for its classification in taxonomy. Most scholars consider the life history of the M. nitidum to be a sexual or parthenogenetic heterotypic alternation of generations. However, there remains unclear about its asexual non-alternating generations life history. In this study, tufA and 18S rDNA sequence were used as molecular markers combining with morphology to classify and identify MGAs in two different habitats, Yangjiang (YJ) and Zhanjiang (ZJ). The results of tufA and 18S rDNA sequence analysis showed that all samples from YJ and ZJ were clustered in the same branch (M. nitidum clade), which was highly supported by Bootstrap with genetic distances of less than 0.000 and 0.005, respectively. In addition, the morphological observation results showed that there were significant differences of external morphology in the plants between YJ and ZJ, and both of them followed a filament-blade form in early development. The life history of plants in ZJ is typical dimorphic alternation of generations, and the plants in YJ can only produce asexual gametes with negative phototaxis biflagellated, which can directly develop into new gametophytes without going through the sporophyte stage. Therefore, the collected plants in YJ were identified as asexual M. nitidum with non-alternation generations. In this study, we supplied the evidences of non-alternation generations life history type of asexual M. nitidum, which can provide a new theoretical support for the classification of MGAs and the evolutionary relationship of species in different habitats.

Key words: Monostroma nitidum; molecular analysis; life history; taxonomy; evolution

红耳彩龟体色变异分子机理研究

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摘要：为阐明红耳彩龟发生多种体色变异现象及相关机理，本研究基于非靶向代谢组学对白化型、黄化型、黑化型及野生型进行差异代谢物检测；对皮肤、眼球组织进行石蜡切片观察及酪氨酸酶活性、通路相关基因进行检测。结果显示 4 种表型在色素相关代谢途径中存在共通性，差异代谢物富集于苯丙氨酸、酪氨酸、半胱氨酸和蛋氨酸代谢通路等；组织切片表明 4 种表型在皮肤、眼球组织中黑色素含量及分布存在显著差异，以黑化型黑色素含量最多、白化型最少，黄化型在眼球组织表现特异性，黑色素表达在脉络膜和色素细胞层中出现差异，表明黑色素在皮肤中存在生成且表达或维持功能出现障碍。酶活性结果显示，黑化型酶活性显著上升，与其他组存在显著差异。通过 qPCR 对色素表达相关基因进行检测，发现 3 种突变体表型共同在小眼畸形转录因子（MITF）上与对照组存在显著差异，说明 MITF 在红耳彩龟体色变异上可能存在作用。

关键词：红耳彩龟；体色变异；黑色素；皮肤；非靶向代谢组学

Color Mutations Development Mechanism in the Red-Eared Slider Turtle (Trachemys scripta elegans)

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Abstract： In order to elucidate the occurrence of multiple body color mutations and related mechanisms of red-eared slider turtles, non-targeted metabolomics was used to detect differential metabolites of albino, yellowing, melanistic and wild-type types,observation of paraffin sections through skin and eye tissue, detection of tyrosinase activity and pathway-related genes. The results showed that the four phenotypes had commonality in pigment-related metabolic pathways, the differential metabolites were enriched in phenylalanine, tyrosine, cysteine and methionine metabolic pathways. Tissue sections showed that there were significant differences in the content and distribution of melanin in skin and eye tissues among the four phenotypes, with the melanistic type having the highest melanin content and the albino type having the least. The yellowing type is specific in the eyeball tissue, the expression of melanin is different in the choroid and pigment cell layers, indicating that melanin is produced in the skin and its expression or maintenance function is impaired. The results of enzyme activity showed that the activity of melanized enzyme increased significantly, which was significantly different from that of other groups. The chromin-expression-related genes were detected by qPCR, and it was found that the phenotypes of the three mutants were significantly different from those of the control group in microphthalmia transcription factor (MITF), indicating that MITF may have a role in the body color variation of the red-eared slider turtle.

Key words: Red-eared sliders; Color mutations; Melanin; skin; Non-targeted metabolomics

性别决定和分化相关基因在军曹鱼性腺发育不同时期的表达水平分析

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摘要：为探索性别决定和分化相关基因在军曹鱼性腺发育过程中的作用，本研究从军曹鱼全基因组中鉴定出 9 个候选基因，并利用实时荧光定量 PCR 技术检测了各基因在成鱼中的组织表达分布及 III～V 期性腺组织中的表达情况。结果显示，Amh 和 Dmrt1 在精巢中特异表达，Gdf6a 和 Gdf6b 在精巢和皮肤中高表达，Hsd17b1 在心脏和卵巢高表达，其他 4 个基因均具有较为广泛的组织表达分布。III～V 精巢中，Cyp19a2、Amh、Sox9a、Sox9b、Gdf6a、Gdf6b 及 Dmrt1 的表达量均极显著高于各期卵巢；III～V 期卵巢中 Sox3 表达量均极显著高于各期精巢。基于上述结果可推测，军曹鱼 Amh 及 Dmrt1 可能为雄性特异基因，Gdf6a、Gdf6b 和 Hsd17b1 可能分别为雄性和雌性偏向基因，这 5 个基因在军曹鱼精巢、卵巢发育过程中可能发挥了重要作用。

关键词：军曹鱼；性别决定基因；性别分化基因；基因表达

Analysis of the expression levels of sex determination and differentiation-related genes at different periods of gonadal development in the military crocodile, Rachycentron canadum

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Abstract： In order to explore the roles of sex determination and differentiation-related genes in the gonadal development of Rachycentron canadum, nine candidate genes were identified from the whole genome of Rachycentron canadum, and the distribution of tissue expression of each gene in adult fish and the expression in gonadal tissues of stages III-V were examined by real-time fluorescence quantitative PCR. The results showed that Amh and Dmrt1 were specifically expressed in the spermathecae, Gdf6a and Gdf6b were highly expressed in the spermathecae and skin, and Hsd17b1 was highly expressed in the heart and ovary, while the other four genes had a broader distribution of tissue expression. The expression of Cyp19a2, Amh, Sox9a, Sox9b, Gdf6a, Gdf6b, and Dmrt1 was highly significantly higher in stage III-V spermathecae than in all stages of the ovaries; the expression of Sox3 was highly significantly higher in stage III-V ovaries than in all stages of the spermathecae. Based on the above results, it can be hypothesized that Amh and Dmrt1 may be male-specific genes, and Gdf6a, Gdf6b and Hsd17b1 may be male- and female-biased genes, respectively, and that these five genes may play important roles in the development of spermatheca and ovary in Rachycentron canadum.

Key words: Rachycentron canadum; Sex-determining genes; Sex-differentiating genes; Gene expression

综合分析菲律宾蛤仔壳色调控的差异表达的 mRNA、lncRNA 和 miRNA 及其 ceRNA 网络

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摘要：在本研究中，我们对不同壳色的蛤仔外套膜进行转录组测序，其中筛选卟啉途径和黑色素途径的 7 个 mRNAs、8 个 lncRNAs 和 4 个 miRNAs 用于竞争性内源 RNA (ceRNA)网络构建。结果表明，以 efu-miR-101、mle - banam -3p、egr-miR-9-5p 和 sma-miR-75p 为中心的由 mRNA 和 lncRNA 组成的 ceRNA 网络可能在贝壳颜色沉着中发挥重要的调节作用。对以 TCONS_00025035，efu-miR-101 和 UROS 构成的 ceRNA 网络进行研究分析，双荧光素酶试验和拮抗剂实验发现 efu-miR-101 负调控 TCONS_00025035 和 UROS;UROS 功能验证表明其参与卟啉色素合成。以上结果表明 TCONS_00025035，efu-miR-101 和 UROS 构成的 ceRN 网络参与蛤仔贝壳色素的沉着。

关键词：菲律宾蛤仔；壳色；ceRNA 网络；色素沉着

Comprehensive analysis of differentially expressed mRNA, lncRNA and miRNA, and their ceRNA networks in the regulation of shell color in the Manila clam (Ruditapes philippinarum)

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Abstract： The regulatory mechanism of ceRNA network plays an important role in molecular function and biological processes, however, the molecular mechanism in the shell color of Ruditapes philippinarum has not yet been reported. In this study, we performed transcriptome sequencing on the mantle of R. philippinarum with different shell colors, and screened for mRNA, miRNA, and lncRNA. A total of 61 mRNAs, 3725 lncRNAs and 90 miRNAs were obtained from all the shell color comparison groups (all mRNAs, lncRNAs and miRNAs $P < 0.05$), and 7 mRNAs, 8 lncRNAs, and 4 miRNAs of the porphyrin pathway and melanin pathway were screened for competitive endogenous RNA (ceRNA) network construction. The results indicate that the ceRNA network composed of mRNA and lncRNA, centered around efu-miR-101, mle-bantam-3p, egr-miR-9-5p, and sma-miR-75p, may play a crucial regulatory role in shell color formation. The ceRNA network composed of TCONS_00025035, efu-miR-101 and UROS is studied and analyzed, and it is found that efu-miR-101 negatively regulates TCONS_00025035 and UROS, indicating that TCONS_00025035, The ceRNA network composed of efu-miR-101 and UROS participated in the formation of porphyrin pigments in clam shells, which also proved that the construction of ceRNA network might participate in the pigmentation of clam shells. This study reveals for the first time the mechanism of ceRNA regulatory networks in the shell color of R. philippinarum and providing important reference data for molecular breeding of shell color in R. philippinarum.

Key words: Ruditapes philippinarum; Shell color; ceRNA network; Pigmentation

不同生长速率斑点叉尾鮰脑-肝脏-肌肉组织的比较转录组分析

罗微微 1，迟爽 1，王俊如 2,4，俞小牧 2，童金苟 2,3
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摘要：生长是水生动物的重要经济性状。养殖斑点叉尾鮰在中国的受欢迎度日益增加，促使研究者对其生长和发育的遗传调控进行研究，以便选育快速生长品系。以生长速率慢的组为对照组，本研究采用 RNA-Seq 技术对不同生长速率的斑点叉尾鮰进行脑、肝脏和肌肉组织的比较转录组分析，分别在脑、肝脏和肌肉组织中获得 63、110 和 83 个差异表达基因。KEGG 通路注释揭示了调控鮰鱼差异生长的 97 条信号通路，如 PI3K-Akt 信号通路、NF-kappa B 信号通路、脂肪酸代谢等。在此转录组数据的基础上，进一步鉴定出 27 个主要参与生长发育、代谢和免疫功能的重要差异表达基因，包括生长激素受体 b (ghrb)、成纤维细胞生长因子受体 4 (fgfr4)、骨形态发生蛋白 1a (bmp1a)、胰岛素样生长因子 2a (igf2a)、胶原蛋白 I 型、α 1a (col1a1a)、酰基辅酶 a 合成酶长链家族成员 2 (acsl2)等。本研究为斑点叉

关键词：斑点叉尾鮰，生长，转录组，脑-肝脏-肌肉组织，差异表达基因

Comparative transcriptomic analyses of brain-liver-muscle in channel catfish (Ictalurus punctatus) with differential growth rate

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Abstract： Growth is an important economically trait for aquatic animals. The popularity of farmed channel catfish (Ictalurus punctatus) in China has recently surged, prompting a need for research into the genetic mechanisms that drive growth and development to expedite the selection of fast-growing variants. In this study, the brain, liver and muscle transcriptomes of channel catfish between fast-growing and slow-growing groups were analyzed using RNA-Seq. Totally, 63, 110 and 86 differentially expressed genes (DEGs) were from brain, liver and muscle tissues. DEGs are primarily involved in growth, development, metabolism and immunity, which are related to the growth regulation of channel catfish, such as growth hormone receptor b (ghrb), fibroblast growth factor receptor 4 (fgfr4), bone morphogenetic protein 1a (bmp1a), insulin-like growth factor 2a (igf2a), collagen, type I, alpha 1a (col1a1a), acyl-CoA synthetase long chain family member 2 (acsl2) and caveolin 1 (cav1). This study advances our knowledge of the genetic mechanisms accounting for differences in growth rate and offers crucial gene resources for future growth-related molecular breeding programs in channel catfish.

Key words: Ictalurus punctatus; growth; transcriptome; brain-liver-muscle tissues; differentially expressed genes

5 个方正银鲫养殖群体肌肉品质评价

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摘要：为了评价不同地区方正银鲫的肌肉品质，对 5 个方正银鲫养殖群体的生长性状、一般营养成分、氨基酸和脂肪酸组成等进行了分析。方正银鲫蛋白含量高于其他淡水鱼类，营养价值高且属于中低脂鱼类，脂肪酸组成符合中国淡水鱼的脂肪组成特征。方正银鲫 5 个群体的体长、体重、一般营养成分、氨基酸、脂肪酸均存在着差异(P<0.05)。其中中国水产科学研究院黑龙江水产研究所宽甸试验场的方正银鲫多数营养成分含量高于其他 4 个群体中，可作为繁殖群体进行重点保护与资源利用。

关键词：方正银鲫；氨基酸；脂肪酸；评价

Evaluation of muscle quality of 5 cultured Carassius auratus carassius

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Abstract： In order to evaluate the muscle quality of Carassius carassius in different regions, the growth traits, general nutrients, amino acid and fatty acid composition of 5 Carassius carassius cultured populations were analyzed. The protein content of Carassius cruciatus is higher than that of other freshwater fish, and it is a medium and low fat fish with high nutritional value, and the fatty acid composition accords with the fat composition characteristics of Chinese freshwater fish. There were differences in body length, body weight, general nutrients, amino acids and fatty acids among 5 groups (P<0.05). Among them, the nutrient content of Crucian Carassius crucian in Kuandian Test Field of Heilongjiang Fisheries Research Institute of Chinese Academy of Fishery Sciences is higher than that of the other four populations, so it can be used as a breeding population for key protection and resource utilization.

Key words: Carassius gibelio; Amino acids; Fatty acids; evaluate

碱度对淇河鲫生长性能、生理特征及肌肉品质的影响

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摘要：本研究对不同碱度条件下淇河鲫的生长性能、生理特性和肌肉品质进行了分析。实验分为对照组（0 mmol/L）、中碱组（20 mmol/L）和高碱组（40 mmol/L），每个组 60 尾鱼，养殖实验持续 60 d。结果显示：各碱度组的成活率均为 100%；末体长、末体重、增重率、特定生长率和摄食率随碱度升高逐渐降低。中、高碱组的血清钠离子含量显著高于对照组，中碱组的血清钾离子含量显著低于高碱组；各组血清钙、镁、氯离子含量无显著差异。中、高碱组肾组织中钠钾和钙镁 ATP 酶活性均显著低于对照组，高碱组鳃组织钠钾 ATP 酶活性显著升高，但各组鳃组织钙镁 ATP 酶活性无显著差异。高碱组灰分含量显著高于但蛋白含量却显著低于对照组，各组粗脂肪含量无显著差异；与对照组相比，高碱组肌肉的硬度、弹性、胶黏性和咀嚼性均显著降低。随着碱度的升高，肌肉中必需氨基酸比例、总量、呈味氨基酸含量及必需氨基酸指数均呈逐渐降低的趋势。

关键词：淇河鲫；碱度；生长；生理；肌肉品质

Effects of alkalinity on growth performance, physiological characteristics and muscle quality of Qihe crucian carp Carassius auratus

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Abstract： Improving and utilizing of saline-alkali land scientifically is an important way to promote ecological protection and high-quality development in saline-alkali areas. Qihe crucian carp Carassius auratus is a special local species in Henan Province, which is a potential target for saline-alkali aquaculture because of its advantages of fast growth, strong stress resistance and high economic value. In this study, the growth performance, physiological characteristics and muscle quality of Qihe crucian carp under different alkalinity conditions were analyzed. The experiment was designed with control group (CG, 0 mmol/L), medium alkalinity group (MAG, 20 mmol/L) and high alkalinity group (HAG, 40 mmol/L), with 60 fish in each group, and the experiment lasted for 60 d. Results showed that the survival rate in each group was 100%. The final body length, final body weight, weight gain, specific growth rate and feeding rate gradually decreased with the increase of alkalinity. Compared with CG, the serum Na+ contents of MAG and HAG were significantly higher, and the serum K+ content of MAG was significantly lower than that of HAG. There were no significant differences in serum Ca2+, Mg2+ and Cl- contents among groups. Compared with CG, the activities of Na+/K+-ATPase and Ca2+/Mg2+-ATPase in kidney of MAG and HAG were significantly decreased, and the activity of Na+/K+-ATPase in gill of HAG was significantly higher, but there were no significant differences in the Ca2+/Mg2+-ATPase activities in gill among groups. The ash content of HAG was significantly higher but the protein content was significantly lower than that of CG, and there were no significant differences in fat contents among all groups. Compared with CG, the hardness, springiness, gumminess and chewiness of muscle in HAG were significantly lower. With the increase of alkalinity, the percentage and content of essential fatty acids, the content of delicious amino acids and the essential amino acid index in muscle gradually decreased. These results indicated that the alkalinity stress significantly decreased the growth performance, changed the ability of osmotic pressure regulation, and affected the muscle quality of Qihe crucian carp. The results of this study provide reference information for salt-alkali aquaculture and breeding of Qihe crucian carp.

Key words: Qihe crucian carp Carassius auratus; alkalinity; Growth; Physiology; Muscle quality

基于 GWAS 和比较转录组分析挖掘长吻性别、生长性状相关分子标记及候选基因

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摘要：长吻鮠 (Leiocassis longirostris)，又名江团，是我国特色经济鱼类。其因肉质鲜美、口感爽滑，深受广大消费者的喜爱。但关于长吻鮠生长及性别决定等相关的调控机制未见报道。为此，我们构建了首个长吻鮠高质量的染色体水平参考基因组。基因组大小为 703.19Mb，利用高通量染色体构象捕获(Hi-C)数据，将 685.53Mb 的基因组序列锚定到 26 条染色体上，并从中鉴定出 23708 个蛋白质编码基因。我们还对不同性别、不同生长速率长吻鮠个体进行了基因组重测序，通过生长相关性状的 GWAS 分析筛选出 50 余个与生长性状显著关联的 SNP；性别相关 GWAS 分析筛选出 3 个高效的雄性特异分子标记，其中一个位于 acap1 基因序列中，推测该基因可能参与长吻鮠的性别决定或分化。另外，对不同生长速率的长吻鮠肌肉、肝脏和脑组织进行转录组测序和比较分析，结果显示，两种不同生长速率长吻鮠肌肉、肝脏和脑组织转录组比较分别筛选出 580、511 和 518 个差异表达基因，从中筛选出 gnrh、trh、sst、gipr、leptin 等与生长相关的候选基因。我们的研究为后续基因组比较和进化研究奠定基础，也为长吻鮠经济性状的遗传改良提供遗传背景知识、辅助育种的分子标记和遗传操作的目标基因。

关键词：长吻鮠；基因组；转录组；全基因组关联分析；基因组重测序

GWAS and Comparative Transcriptome Analysis to Identify the Sex and Growth-related Markers and Candidate Genes of the Chinese longsnout catfish Leiocassis longirostris

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Abstract: The Chinese longsnout catfish (Leiocassis longirostris), an important economic fish species in China, has been famous in the Chinese table for many years because of its tasty flavour and smooth mouthfeel. However, the key bioinformation related to its growth and sex determination has not been reported, as well as its related molecular regulatory mechanisms. Here, we constructed the first high-quality chromosome-level reference genome for L. longirostris. The genome size was 703.19 Mb. Using high-throughput chromosome conformation capture (Hi-C) data analysis, we anchored 685.53 Mb of genome sequence to 26 chromosomes, from which 23,708 protein-coding genes were identified. We also resequenced the genomes of different sexes and growth rates individuals. Based on that, more than 50 SNPs significantly associated with growth traits through GWAS analysis of growth-related traits were selected. We also screened three highly efficient male-specific molecular markers through GWAS analysis of sex-related traits, one of which was located in the sequence of acap1, which was hypothesized to be involved in the sex determination or differentiation of L. longirostris. In addition, transcriptome sequencing and comparative analysis of muscle, liver and brain tissues of L. longirostris at different growth rates showed that 580, 511 and 518 differentially expressed genes were identified.

We screened out the candidate genes such as gnrh, trh, sst, gipr, lepti, etc. as the candidate genes for the regulation of the L. longirostris growth. This study lays the foundation for subsequent genome comparisons and evolutionary studies and also provides genetic background knowledge, molecular markers to assist breeding, and target genes for genetic manipulation for the molecular improvement of economic traits in L. longirostris.

Key words: Leiocassis longirostris; genome; Transcriptome; Genome-wide association study; Genome resequencing

模式贝—侏儒蛤实验室驯化过程代际遗传结构分析

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摘要：模式生物在现代生命科学研究中具有不可替代的重要地位，而贝类所在的冠轮动物类群一直缺乏合适的模式物种。侏儒蛤(Mulinia lateralis)是一种小型双壳埋栖贝类，因其生长迅速、世代周期短等特点而被认为是双壳类潜在模式物种。近年来，本团队首次将侏儒蛤引入国内，并成功地在实验室完成驯化。研究团队通过对不同世代的310个侏儒蛤进行分型，旨在揭示它们在实验室驯化过程代际遗传结构变化。结果表明，侏儒蛤在驯化过程能够保持较高的遗传多样性和较低的遗传分化水平。通过选择压力分析，在侏儒蛤基因组共检测到316个受选择的区域，其中168个受到正选择。此外，在正选择区鉴定出227个候选基因，这些基因与生长、抗逆和繁殖功能有关。总的来说，我们的研究结果揭示了侏儒蛤在驯化过程的遗传变化及选择特征，有助于了解它们对实验室驯化的适应性，并证明了利用该物种探索双壳类动物的适应性进化的潜力。

关键词：模式生物；侏儒蛤；实验室驯化；遗传结构

Analysis of genetic structure across generations in model bivalve-Mulinia lateralis during laboratory domestication

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Abstract： Model organisms play an important role in the study of modern life science. However, there is a lack of suitable model species in bivalve. Dwarf surf clam, Mulinia lateralis, is considered as a model species for bivalve because of its rapid growth and short generation. Recently, this species has been introduced into China and successfully domesticated in our laboratory. Here, 310 individuals obtained from different generations were genotyped, aiming to uncover the change in genetic structure across generations during laboratory domestication. The results revealed that M. lateralis consistently maintained high genetic diversity in each generation, and there were low levels of genetic differentiation in M. lateralis during domestication. Totally, 316 genomic regions were detected under divergent selection, of which 168 regions were under positive selection. Furthermore, 227 candidate genes were identified in the positive selection regions, which were functionally involved growth, stress resistance and reproduction. Overall, our findings reveal the genetic changes and selection signatures in M. lateralis during laboratory domestication, contribute to the understanding of their adaptation to laboratory domestication, and demonstrate the potential for using this species to explore the adaptive evolution of bivalves.

Key words: model organism; Mulinia lateralis; laboratory domestication; genetic structure

Methoprene−tolerant (Met) acts as methyl farnesoate receptor to regulated larva metamorphosis in mud crab, Scylla paramamosain

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Abstract: The conserved role of Juvenile hormone (JH) signals in preventing larva from precocious metamorphosis has been confirmed in insects. Crustaceans have different metamorphosis type with insects, we previously proved that methyl farnesoate (MF) could prohibited larva metamorphosis in mud crab, but the molecular signal of this process still need to be convinced. In this study, Scylla paramamosain Met was obtained and characterized, which we named as Sp-Met. Sp-Met possessed a 3,360-bp ORF that encoding 1119 amino acids, the predicted protein sequences of Sp-Met contains one HLH, two PAS domains, one PAC domain and long unusual Gln repeats at the C-terminal. AlphaFold2 was used to predict the 3D structure of Sp-Met, further CB-DOCK2 was used to analysis the binding properties between Sp-Met and MF, indicating a putative high affinity between the receptor and ligand. In addition, we found that the expression of Sp-Met was significantly higher in female reproductive tissues than males, but lower in most of other examined tissues. During the larval development, the variation of Sp-Met was consistent with the treatment effect of MF. While the most interesting thing is that knocking down of Sp-Met blocked the prohibited effect of MF on Zoea 5th, and induced some pre-metamorphosis phenotype at the Zoea 4th larva. In conclusion, this study firstly prove that MF prohibited crustacean larva metamorphosis through Met, and MF might have the conserved role in preventing larva from precocious metamorphosis in mud crab.

Keywords: Methyl farnesoate; Met; Metamorphosis; crustacean; Scylla paramamosain

罗氏沼虾 CFSH 基因 cDNA 克隆及 RNAi 介导的基因敲降效应

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摘要：甲壳动物雌性性激素（*crustacean female sex hormone*，*CFSH*）基因最先在蓝蟹被分离鉴定，在雌性个体特异表达，参与雌性第二性征的发育。本研究克隆了罗氏沼虾 *CFSH* 全长 cDNA（918bp），编码 306 个氨基酸，RT-PCR 结果显示其转录本在雌雄个体眼柄和脑特异表达。Western Blot 分析显示 *MrCFSH* 蛋白主要在雌雄脑中表达，但在鳃中也检测到。荧光定量 PCR 结果显示 *MrCFSH* 在仔虾（pl10-pl60）没有性别差异表达。利用 RNAi 干扰 1000 只仔虾（pl30）*MrCFSH* 基因表达，经过为期两个月的基因干扰（每星期注射 1 次双链 RNA），存活 248 只仔虾，随机挑选 100 只仔虾（pl120）利用性别分子标记 PCR 鉴定与表型性别特征观察，未见对性别分化产生影响，但仔虾生长受到显著抑制，实验组的体长和体重远小于对照组的体长和体重，pl120、pl150、pl180 和 pl210 体长差异分别为：25%、35%、28%、26%；体重差异分别为：69%、76%、65%、61%。在第四个月实验组和对照组（pl210）雌性个体体长和体重的差异分别为：26%、60%；雄性个体体长和体重的差异分别为：22%、54%。以上结果说明 *MrCFSH* 对雌雄仔虾生长均有诱导作用，但不影响性别分化。该结果与之前蟹类研究结果不同，与日本对虾 *CFSH* 基因功能相似，说明 *CFSH* 在虾蟹甲壳动物具有不同功能。

关键词：罗氏沼虾；甲壳动物雌性性激素；雌雄生长

cDNA cloning and RNAi mediate gene knock-down effect of CFSH in the giant freshwater prawn, *Macrobrachium rosenbergii*

Abstract: *Crustacean female sex hormone (CFSH)* was first identified in blue crab and was found to be specific expressed in female, involving in the development of female secondary sex characteristics. In this study, We identified a crustacean female sex hormone in the *M. rosenbergii*, and the full-length cDNA was cloned, containing 918 nucleotides that encodes 306 amino acid. The transcript was expressed in the eye stalk and brain of male and female adults. Western Blot showed that *MrCFSH* protein was mainly expressed in the brain, but expressed in the gill among male and female. RT-PCR showed that *MrCFSH* was not differentially expressed in *M. rosenbergii* post-larvae 10-60 between males and females. To further elucidate physiological functions of *MrCFSH*, we conducted gene knockdown analysis using 1000 post-larvae 30 for a period of two months. A total of 100 post-larvae (pl120) were randomly selected, using molecular sex marker and observing sexual characteristics to determine sex. We found did not effect on sex differentiation, but the growth rate of post-larvae was significantly inhibited. It was found that the body length and weight of the experimental group were much smaller than that of the control group, and the difference of body length rate (pl120, pl150, pl180, pl210) was 25%, 35%, 28%, 26%, respectively. The difference of weight rate (pl120, pl150, pl180, pl210) was 69%, 76%, 65% and 61%, respectively. At the fourth month, the growth rate (pl210) between the experimental group and the control group was compared. The difference of the body length and weight was 26% and 60% in female, respectively. The difference of male body length and body weight was 22% and 54%, respectively. As a results, *MrCFSH* induces the growth of male and female juveniles, which did not affect the development. The result is different from the previous results of crabs, and the function of *CFSH* is similar to *Marsupenaeus japonicus*, indicating that *CFSH* has different functions in crustacean.

Key words: *Macrobrachium rosenbergii; Crustacean female sex hormone;* male and female growth rate

第三专题：水产养殖动物营养与饲料

贯叶连翘提取物对锦鲤生长性能、抗氧化能力、免疫性能和肠道菌群的影响

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摘要：本试验评估贯叶连翘提取物（HPLE）对锦鲤生长、抗氧化、免疫和肠道菌群的影响。HPLE 以 0%（对照组）、0.1%、0.3%或 0.5%添加到基础日粮，饲喂 10 周。结果表明，0.5%组 WG、WGR 和 SGR 增加，0.3%组 SI 降低，0.1%组 VSI 降低。HPLE 组降低 FCR 和血清 TP、ACP 和 ALP 的浓度，提高血清 IGF-1、LZM 和 GH 的浓度。0.5%组血清中 DA、5-HT 和 NE 水平升高，tnf-α、il-6 和 il-1β表达下调，而 sod、ghr1a 和 ghr1b 表达上调。Chao 1，observed_otus 指数、主坐标分析坐标分析（PCoA）显示，HPLE 组的肠道菌群更多样化。属水平 LEfSe 分析表明，0.1%组富含 Ralstonla 和 Clostridium_sensu_stricto_1，0.3%组富含气单胞菌，0.5%组富含弧菌和 Dielma。综上，贯叶连翘提取物最佳添加量为 0.5%。

关键词：贯叶连翘提取物；生长性能；抗氧化；肠道菌群；锦鲤

Dietary Hypericum perforatum L. extract improves growth performance, antioxidant capacity, immune performance and intestinal flora of Koi carp (Cyprinus carpio)

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Abstract: This study aimed to evaluate the effects of Hypericum perforatum L. extract (HPLE) on the growth, antioxidant, non-specific immunity, and intestinal flora of Koi carp (Cyprinus carpio). HPLE was added to the basal diet at 0% (control), 0.1%, 0.3%, or 0.5% and fed for 10 weeks. The results showed that WG, WGR and SGR were increased in the 0.5% group, SI was decreased in the 0.3% group, and VSI was decreased in the 0.1% group.The HPLE group decreased FCR and serum TP, ACP, and ALP concentrations, and increased serum IGF-1, LZM, and GH concentrations.The serum levels of DA, 5-HT, and NE were elevated in the 0.5% group, and tnf-α, il-6, and il-1β expression were down-regulated, while sod, ghr1a and ghr1b expression were up-regulated. chao 1, observed_otus index, and principal coordinate analysis coordinate analysis (PCoA) showed that the HPLE group had a more diverse intestinal flora. Genus's level LEfSe analysis showed that the 0.1% group was enriched with Ralstonla and Clostridium_sensu_stricto_1, the 0.3% group was enriched with Aeromonas, and the 0.5% group was enriched with Vibrio and Dielma.In conclusion, the optimal addition of the extract of Hypericum perforatum was 0.5%.

Key words: Hypericum perforatum L. extract, Growth, Antioxidant, Gut microbiota, Cryprinus carpio

工厂化循环水养殖对大口黑鲈肌肉营养成分和挥发性风味物质的影响研究

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摘要：以池塘养殖大口黑鲈（LY1）为对照，测定了 RAS 中大口黑鲈第 10 天（LY2）、第 20 天（LY3）和第 30 天（LY4）肌肉营养成分和挥发性风味物质，建立了挥发性风味指纹图谱。结果显示，肌肉水分含量 LY3 组最低，粗蛋白和粗脂肪含量各组之间无显著性差异；总氨基酸含量 LY4 组最高；AAS 模式下各组第一限制性氨基酸为缬氨酸，CS 评分模式下，各组第一限制性氨基酸为甲硫氨酸+胱氨酸，AAS 和 CS 评分以及必需氨基酸指数均表现为 LY3 组最低；EPA、DHA 及 EPA+DHA 以 LY4 组最高。RAS 养殖对肌肉挥发性气味物质种类及含量影响显著。经 PCA 分析，筛选出 2 个变量的贡献率分别 61%和 26%，且 4 组无重叠区域，可明显区分。肌肉中共检测出 56 种挥发性风味化合物，工厂化循环水养殖提高了大口黑鲈肌肉中 2-庚酮、2-戊酮、2-丁酮、环戊酮、1-辛烯-3-醇、1-己醇等物质含量，具有改善肌肉挥发性气味的潜能。

关键词：工厂化循环水；大口黑鲈；肌肉；营养成分；挥发性风味物质

Effects of factory recirculating aquaculture on muscle nutrient composition and volatile flavor compounds of Micropterus salmoides

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Abstract： Taking the pond cultured Micropterus salmoides (LY1) as a control, the muscle nutrient components and volatile flavor compounds were identified and analyzed on the 10th (LY2), 20th (LY3) and 30th (LY4) days after the traditional pond cultured Micropterus salmoides was put into the factory circulating aquaculture system, and the fingerprints of the volatile flavor compounds of the muscle of four groups Micropterus salmoides were established. The results showed that: the total amino acid content and EPA + DHA content in muscle of Micropterus salmoides were the highest in LY4 group, but the PUFA content was the lowest in LY4 group; The main component analysis (PCA) of volatile flavor compounds in muscle of Micropterus salmoides showed that the contribution rates of two variables were pc1:61% and pc2:26%, the cumulative contribution rate of them was 87%; A total of 56 kinds of volatile flavor compounds were detected in the muscle of Micropterus salmoides. Compared with the traditional pond culture group, the factory circulating aquaculture increased the content of 2-heptanone, 2-pentanone, 2-butanone, cyclopentanone, 1-octene-3-ol, 1-hexanol and other substances in the muscle of Micropterus salmoides, which has the potential to improve the volatile flavor compounds of Micropterus salmoidess muscle.

Key words: RAS; Micropterus salmoides; muscle; nutritional composition; volatile flavor compounds

饲料不同淀粉水平对黄河鲤肌肉营养组成和质构特性的影响

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摘要：为探讨不同淀粉水平日粮对黄河鲤肌肉营养组成和质构特性的影响，本试验设计 15%（LC）、30%（MC）、45%（HC）糖水平的等氮等脂饲料，饲喂黄河鲤（451.20±18.65）g 9 w，每组 3 个重复，每个重复 25 尾鱼。结果表明，随着糖水平升高，肌肉粗脂肪和肌糖原含量显著增加、粗蛋白含量显著降低，肌肉 EPA、DHA、PUFA 显著下调，MUFA 显著上调（P＜0.05），SFA 和胶原蛋白含量在各组间差异不显著，总氨基酸有降低的趋势。肌肉硬度、黏着性和咀嚼性与饲料糖水平成反比，且 HC 组显著低于 LC 组（P＜0.05）。饲料糖水平能够影响肌纤维生长，肌肉 myog、pax7 的 mRNA 表达水平随糖水平的升高而上调（P＜0.05），肌肉 atrogin-1、murf-1 的 mRNA 表达水平相反（P＜0.05）。综上，高糖饲料能够促进黄河鲤肌纤维生长，但造成黄河鲤脂肪沉积、肌肉营养价值和口感。

关键词：黄河鲤；糖水平；肌肉；营养组成；质构特性

Effects of dietary carbohydrate levels on growth, muscle nutrient composition and texture characteristics of Yellow River carp (Cyprinus carpio haematopterus)

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Abstract： In this study, we investigated the effects of different carbohydrate levels on muscle nutritional composition and texture characteristics of Yellow River carp (Cyprinus carpio haematopterus). The diets containing 15% (LC), 30% (MC) and 45% (HC) carbohydrate levels with equal nirtogen and lipid were designed, and fed Yellow River carp (451.20±18.65) g 9 w with 3 replicates per group and 25 fish per replicate. The results showed that the final body weight, weight gain rate and specific growth rate of the three groups showed no difference, but the hepatosomatic index of the Yellow River carp in HC group was up-regulated, and the condition factor was significantly down-regulated (P < 0.05). With the increase of carbohydrate level, the contents of crude lipid and glycogen in muscle were significantly increased, the content of crude protein was significantly decreased, the contents of EPA, DHA and PUFA in muscle were significantly down-regulated, but the contents of MUFA were significantly up-regulated (P < 0.05). The contents of SFA, amino acid and collagen in muscle showed no difference among all groups. The hardness, adhesiveness and chewiness of muscle were inversely proportional to dietary carbohydrate levels, and HC group was significantly lower than LC group (P < 0.05). Muscle fiber density in HC group were significantly higher than those in LC group, and average muscle fiber diameter were lower than those in LC group, but there was no significant difference between HC group and MC group. The mRNA expression levels of myog and pax7 in muscle were up-regulated with the increase of carbohydrate level, and HC group were significantly higher than those in LC group (P < 0.05). The mRNA expression levels of muscle atrogin-1 and murf-1 were down-regulated with the increase of carbohydrate level, and the mRNA expression levels in HC group were significantly lower than those in MC and LC groups ($P < 0.05$). In addition, Yellow River carp has a good carbohydrate adaptation ability, and high- carbohydrate feed can promote the growth of muscle fiber, but high dietary carbohydrate level can cause lipid deposition, muscle nutritional value and taste reduction.

Key words: Yellow River carp; carbohydrate level; Muscle; nutrient composition; texture

桑叶提取物对黑斑侧褶蛙生长、抗氧化能力和血清生化指标的影响

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摘要：本实验研究桑叶提取物(MLE)对黑斑侧褶蛙(Rana nigromaculata)生长、抗氧化能力和生理指标的影响。实验选取黑斑蛙，分别投喂在基础饲料中添加 0(C)、3(M03)、6(M06)、9(M09) g/kg MLE 的实验饲料，饲喂 56 天。结果表明，M03 组 WGR、SGR 显著高于 C 组(P＜0.05)，M09 组显著下降(P＜0.05)。M03、M06 组 FCR、FR 显著低于 C 组(P＜0.05)，肝脏 SOD 显著高于 C 组(P＜0.05)。实验组肠道 MDA 显著低于 C 组(P＜0.05)，T-AOC 显著高于 C 组(P＜0.05)，M03 组 SOD 显著高于 C 组(P＜0.05)，M09 组显著低于 C 组(P＜0.05)。M03 组 TC、LDL 显著低于 C 组(P＜0.05), M06 组 ALT、AST 显著高于 C 组(P＜0.05)。综上所述，在基础饲料中添加适量的 MLE 可促进黑斑蛙生长和健康，提高机体抗氧化能力。

关键词：黑斑侧褶蛙；桑叶提取物；生长性能；抗氧化能力；血清生化

Effects of mulberry leaf extract on growth, antioxidant ability and serum biochemical indices of Rana nigromaculata

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Abstract：The effects of mulberry leaf extract (MLE) on the growth, antioxidant ability and serum biochemical indexes on Rana nigromaculata was researched. The frogs were fed the basal diet supplemented with 0 (C), 3 (M03), 6 (M06) and 9 (M09) g/kg MLE respectively. The experiment lasted for 56 days. The weight gain rate and specific growth rate in M03 group were significantly higher than those in group C(P<0.05), significantly decreased in M09 group(P<0.05). The feeding coefficient and feeding rate in M03 and M06 groups were significantly lower than those in group C (P<0.05). The SOD of liver in M03 and M06 groups showed significantly higher than those in group C(P<0.05). The MDA of intestinal in experimental groups were significantly lower than those of group C(P<0.05). The T-AOC of experimental groups were significantly higher than those of group C(P<0.05). The SOD of M03 group was significantly higher than that of group C(P<0.05), the SOD in M09 group was significantly lower than that of group C(P<0.05). The TC and LDL of M03 group were significantly lower than those of group C(P<0.05). The ALT and AST of M06 group were significantly higher than those in group C(P<0.05). In this experiment, adding an appropriate amount of MLE to the basic feed can promote the growth and body health of R. nigromaculata.

Key words: Rana nigromaculata; Mulberry leaf extract; Growth performance; Antioxidant ability; Serum biochemistry

棕榈油替代鱼油可经 Mfn2 介导的线粒体融合促进黄颡鱼的脂肪酸β-氧化

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摘要：线粒体是脂肪酸β-氧化的主要场所，因此，线粒体的完整性与稳态是脂肪酸β-氧化的基础。而线粒体作为双层膜结构的细胞器，需要不断的融合与分裂来维持其稳态。然而，目前就线粒体如何直接影响脂肪酸β-氧化尚无证据。此外，饲料脂肪酸配比优化缓解鱼类肝脂沉积的机制仍有待深入。因此，本研究以黄颡鱼为研究对象，设定不同棕榈油（PA）/鱼油(FO)比例的饲料，投喂 8 周后取其肝脏分析。本研究取得的主要结论如下：1，适量棕榈油替代鱼油可通过激活脂肪酸β-氧化而缓解黄颡鱼肝脂沉积情况；2，适量棕榈油替代鱼油可经抑制 Mfn-2 泛素化，而激活黄颡鱼肝脏内的线粒体融合机制；3，Mfn-2 可经其自身的 GTPase-domain 与 Cpt-1α产生蛋白互作机制，而互作机制又可以直接促进下游脂肪酸β-氧化。更为重要的是，本研究首次发现 Mfn-2 介导线粒体融合可通过促进脂肪酸进入线粒体的速率而调控线粒体的β-氧化。

关键词：Mfn2；线粒体融合；脂肪酸β-氧化；Cpt1α；脂肪酸配比

Partial Replacement of Fish Oil with Palmitic Acid-Stimulated Mitochondrial Fusion Promotes β-oxidation by Mfn2 Interacting with Cpt1α via Its GTPase-domain

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Abstract：Since mitochondrial matrix is the main site where the fatty acids (FAs) β-oxidation takes place. Meanwhile, maintenance of mitochondrial integrity and homeostasis, which is achieved through continual fusion, is extremely critical for FAs β-oxidation. However, despite this well-accepted fact, no study has yet explored whether and how mitochondrial fusion directly promotes FAs β-oxidation. Moreover, the underlying mechanism of a balanced FAs ratio favors hepatic lipid homeostasis are still largely unclear. To address these gaps, this study was conducted to investigate the mechanism by which proper dietary FAs ratio promotes hepatic FAs β-oxidation, focusing on the role of Mfn2-mediated mitochondrial fusion regulating Cpt1α in this process. To this end, a model animal for lipid metabolism, yellow catfish (Pelteobagrus fulvidraco), were fed six different diets with a range of FAs ratio in vivo for 8 weeks, and in vitro experiments were conducted to intercept Mfn2-mediated mitochondrial fusion in isolated hepatocytes by transfecting them with si-mfn2, also to demonstrate key regions of Cpt1α/Mfn2 interactions by constructing the deletion mutants of Mfn2 and Cpt1α. The key findings of studies are as follows: 1. Proper palmitic acid (PA) replacing fish oil (FO) was profit for alleviating hepatic lipid accumulation, instead of hepatic health risk, mainly via activating mitochondrial FAs β-oxidation. 2. Proper PA substitute stimulated mfn2-mediated mitochondrial fusion by weakening Mfn2 ubiquitination and then contributing to its protein retention. 3. Mfn2-mediated mitochondrial fusion promoted FAs β-oxidation by Mfn2 directly interacting with Cpt1α via its GTPase-domains, which is essential for the maintenance of Cpt1 activity. Importantly, our findings also revealed a previously unidentified mechanism of Mfn2-mediated mitochondrial fusion facilitating FAs β-oxidation by directly enhancing the capability of FA trafficking to mitochondrion (MT), not only by enlarging mitochondrial matrix, which highlighting the critical contribution of mitochondrial fusion in maintaining hepatic lipid homeostasis. Notably, our results confirmed these mechanisms are conservative from fish to mammals.

Key words: Mfn2; Mitochondrial Fusion; β-oxidation; Cpt1α; Fatty Acids Ratio

PXR 在铜暴露诱导的大口黑鲈脂肪代谢和异源物质响应上的作用

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摘要：为探究 PXR 在大口黑鲈铜暴露下脂质代谢紊乱和异源物质代谢响应中的作用，大口黑鲈被随机分为对照组、Cu 暴露组、Cu+RIF 注射组（PXR 激动剂）和 Cu+ KET 注射组（PXR 抑制剂）。研究结果显示，铜暴露刺激血浆 TG 水平、肝脏脂滴和脂肪合成基因的表达。铜暴露导致肝组织结构受损，表现为肝组织空泡化和细胞凋亡的发生。铜暴露显著刺激 PXR 表达表明其对铜暴露产生响应。RIF 注射通过刺激 pparγ和 cd36 的表达显著加剧脂肪肝生成，表明 PXR-PPARγ是潜在的调控铜暴露引起的脂肪蓄积的通路。RIF 注射显著激活自噬并抑制细胞凋亡，而 KET 注射在诱导铜暴露引起的脂肪沉积和肝脏损伤上均表现出相反趋势。综上所述，本研究结果表明 PXR 可通过调控自噬和凋亡发挥铜暴露胁迫下的肝脏保护作用，是潜在的用于异源物质暴露引起的脂代谢紊乱和肝毒性损伤调控靶点。

关键词：PXR；脂代谢；铜暴露；自噬；凋亡

Role of nuclear pregnane X receptor (PXR) in Cu-induced lipid metabolism and xenobiotic responses in largemouth bass (Micropterus salmoides)

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Abstract： The pregnane X receptor (PXR) is a master xenobiotic-sensing receptor in response to toxic byproducts, as well as a key regulator in intermediary lipid metabolism. Therefore, the present study was conducted to investigate the potential role of PXR in mediating the lipid dysregulation and xenobiotic responses under Cu-induced stress in largemouth bass (Micropterus salmoides). Four groups of largemouth bass (52.66 ± 0.03 g) were treated with control, Cu waterborne (9.44 μmol/L, equal to 20% of 48 h LC50), Cu+RIF (Rifampicin, 100 mg/kg, PXR activator), and Cu+KET (Ketoconazole, 20 mg/kg, PXR inhibitor) for 48 h. Results showed that Cu exposure significantly triggered the antioxidant signaling pathways to counteract Cu-induced oxidative stress. Acute Cu exposure caused liver steatosis, as indicated by the significantly higher levels of plasma triglycerides (TG), lipid droplets, and mRNA levels of genes related to lipogenesis in the liver of largemouth bass. Liver injuries were detected, as shown by hepatocyte vacuolization and severe apoptotic signals after Cu exposure. Importantly, Cu exposure significantly stimulated mRNA levels of PXR, suggesting the response of this regulator in the xenobiotic response. The pharmacological intervention of PXR by the agonist and antagonist significantly altered hepatic mRNA levels of PXR, implying that RIF and KET were effective agents of PXR in largemouth bass. Administration of RIF significantly exacerbated the liver steatosis, and such alterations were dependent on the regulations on the mRNA of pparγ and cd36 rather than the srebp1 signaling, which suggested that PXR-PPARγ might be another pathway for Cu-induced lipid deposition in fish. Activation of PXR stimulated autophagy and inhibited apoptosis, leading to lower hepatic vacuolization. Whereas inhibition of PXR showed reverse effects as suggested by the higher apoptotic signals, inhibition of autophagic genes and stimulation of apoptotic genes. Taken together, our data has demonstrated for the first time that PXR played a cytoprotective role in Cu-induced liver hepatotoxicity through regulations on the autophagy and apoptosis pathways, as well as regulating lipid metabolism through PXR-PPARγ signaling, which implying the potential of PXR as a therapy target for xenobiotics-induced lipid dysregulation and hepatotoxicity.

Key words: PXR; Lipid metabolism; Cu exposure; Autophagy; Apoptosis

美洲大蠊渣替代鱼粉对尼罗罗非鱼幼鱼生长、代谢、抗氧化及免疫力的影响

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摘要：为研究美洲大蠊渣替代鱼粉对尼罗罗非鱼幼鱼生长性能、代谢、抗氧化及免疫力的影响，采用美洲大蠊渣分别替代饲料中 0%、25%、50%、75%和 100%的鱼粉，配制五种等氮等脂饲料（命名为 1#~5#饲料），对体重 3g 左右的尼罗罗非鱼进行 10 周的养殖试验。结果表明：（1）各组之间试验鱼的终末体重、增重率和特定生长率均无显著差异，而 4#饲料组的饵料系数最高，蛋白质效率最低；（2）各组鱼体的常规营养成分和氨基酸含量均无显著差异；（3）1#和 2#饲料组肠道中的胰蛋白酶、α-淀粉酶和几丁质酶活性显著高于 3#、4#和 5#饲料组；（4）4#饲料组血清中的尿素氮含量显著高于其他组，而肝脏中的过氧化氢酶、谷胱甘肽过氧化物酶和血清溶菌酶活性均在 2#饲料组较高，血清丙二醛含量在 2#饲料组最低。综上，采用美洲大蠊渣替代鱼粉对尼罗罗非鱼的生长性能无负面影响，可提高抗氧化及免疫力，而鱼粉替代水平超过 75%时会降低饲料利用率。

关键词：美洲大蠊，鱼粉替代，尼罗罗非鱼，生长性能，生理代谢，抗氧化能力

Effects of dietary fish meal replacement by Periplaneta americana residue on the growth, metabolism, antioxidant capacity, and immunity of juvenile Nile tilapia

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Abstract：This study was conducted to investigate the effects of dietary fish meal replacement by P. americana residue on the growth performance, proximate composition, metabolism, antioxidant capacity, and immunity of juvenile Nile tilapia Oreochromis niloticus. Five isonitrogenous and isolipidic experimental diets were formulated to replace 0 %, 25 %, 50 %, 75 %, and 100 % of dietary fish meal with P. americana residue, and defined as Diet 1, Diet 2, Diet 3, Diet 4, and Diet 5, respectively. There were five diet groups, and each group had three replicate tanks (20 fish per tank), and the juvenile O. niloticus with an initial body weight of 3 g was fed with respective diets for 10 weeks. The results showed that there were no significant differences in the final body weight, weight gain rate, and specific growth rate of juvenile O. niloticus among five diet groups, while the highest feed conversion ratio and the lowest protein efficiency ratio were recorded in Diet 4. There were no significant differences in the contents of crude protein, total lipid, ash, and total amino acid in the whole fish body among all groups. The Diet 1 and Diet 2 had higher activities of trypsin, α-amylase, and chitinase in the intestine and α-amylase in the liver. The highest serum urea content was detected in Diet 4, while the lowest liver urea content and the highest serum total protein content were detected in Diet 3. A higher liver catalase, glutathione peroxidase, and serum lysozyme activities were detected in Diet 2, and the lowest serum malondialdehyde content was detected in Diet 2. Dietary fish meal replacement by the P. americana residue had no negative effects on the growth performance and body composition of juvenile O. niloticus, and could significantly improve the antioxidant capacity and immunity, while feed utilization rate was reduced when dietary fish meal replacement levels exceeded 75%.

Key words: Periplaneta americana; Fish meal replacement; Oreochromis niloticus; Growth performance, Metabolism, Antioxidant capacity

桑叶提取物对鳜脾、肾、鳃结构及功能的影响

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摘要：本实验旨在探究饲料中添加不同水平桑叶提取物（MLE）对鳜鱼（Sinipeca cuatsi）脾、肾、鳃结构及功能的影响，以不添加桑叶提取物为对照组(D1)，处理组分别添加 2.5g/kg(D2)、5.0g/kg(D3)、7.5g/kg(D4)和 10.0g/kg(D5)的 MLE，饲喂初始重为(47.82±0.19)g 的鳜 8 周。与 D1 组相比，结果显示：1）脾脏 IgM 显著升高，T-AOC 与 T-SOD 均显著升高，MDA 除 D2 组均显著降低，D4 组白髓细胞明显增多；2）头肾 IgM、T-AOC 与 T-SOD 除 D2 组外均显著升高，MDA 在 D4 和 D5 组显著降低，且 D4 组头肾的淋巴细胞密度明显增加；3）鳃组织 IgM 在 D3 和 D4 组显著升高，T-AOC 与 T-SOD 均显著升高，MDA 显著降低，D4 组鳃丝排列相对更为紧密，鳃小叶长度更长，鳃丝末端杯状细胞数量增多。

关键词：鳜;桑叶提取物；免疫；抗氧化能力

Effects of mulberry leaf extract on Sinipeca cuatsi spleen, kidney, gills structure and function

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Abstract： The purpose of this study was to explore the effects of different levels of mulberry leaf extract (MLE) added to feed on spleen, kidney and gill structure and function of Mandarin fish (Sinipeca cuatsi), with no mulberry leaf extract added as control group (D1). Siniperca siniperca with an initial weight of (47.82±0.19)g was fed with 2.5g/kg(D2), 5.0g/kg(D3), 7.5g/kg(D4) and 10.0g/kg(D5) MLE, respectively, for 8 weeks. Compared with group D1, the results showed as follows: 1) IgM, T-AOC and T-SOD were significantly increased, MDA was significantly decreased except in group D2, and white myeloid cells were significantly increased in group D4; 2) IgM, T-AOC and T-SOD in head kidney were significantly increased except in D2 group, MDA was significantly decreased in D4 and D5 groups, and lymphocyte density in head kidney was significantly increased in D4 group; 3) Branchial IgM, T-AOC and T-SOD were significantly increased in D3 and D4 groups, and MDA was significantly decreased. Branchial filaments were more closely arranged, branchial lobule length was longer, and the number of end-of-filament goblet cells was increased in D4 group.

Key words: Mandarin; Mulberry leaf extract; Immunity; Antioxidant capacity

三叶唇鱼消化系统的组织学观察

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摘要：为了研究三叶唇鱼消化系统组织特征，采用组织切片技术对该鱼的消化系统进行组织学观察。结果发现：三叶唇鱼消化道由口咽腔、食道、小肠和直肠构成。口咽腔内颌齿和咽齿发达，颌齿单行排列，1 对上咽齿呈三角形，下咽齿呈“T”型；肠道短粗，在体腔内形成一个弯曲，比肠长 0.32±0.11；消化腺由肝胰脏和胆囊构成，肝脏分成三片包裹在小肠上，胰脏沿肝血管呈弥散状分布，胆囊呈椭圆型，肝总管在食道后与小肠相连。食道由粘膜层、粘膜下层、肌层和浆膜层组成，基部有“凹”型类似外分泌腺的结构。小肠和直肠均由粘膜层、粘膜下层、肌层和浆膜层组成，粘膜层多为一级和二级指状突起，中间分布有大量粘液细胞，偶见梨状细胞，未见肠腺；粘膜下层含有大量被伊红染成红色的嗜酸性颗粒细胞；肌层由内层环肌和外层纵肌等两层平滑肌组成。本文旨在阐明三叶唇鱼消化系统组织学特征，为开展肉食性无胃鱼类营养学及养殖学研究提供基础数据。

关键词：三叶唇鱼；组织学；消化道；消化腺

Histology of the digestive system in Cheilinus trilobatus

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Abstract： The Tripletail wrasse (Cheilinus trilobatus Lacépède) is a species of the genus Labridae with significant economic value in tropical sea. It is a carnivorous fish and feeds on a variety of small fishes, crustaceans, and mollusks. The digestive system of this fish is well adapted to its feeding habits. The digestive system of an organism is a complex system responsible for the breakdown and absorption of food. The digestive tract of C. trilobatus is no exception, and it is characterized by a unique set of structural features that are well-suited to its feeding habits. In this study, we report the histological observation study of the digestive system of C. trilobatus using tissue sectioning technique. The digestive tract is an essential part of an organism's body system responsible for breaking down and processing food for energy and nutrient absorption. In this paper, the structural characteristics of the digestive tract of C. trilobatus are discussed, as well as the relationship between its organizational characteristics and feeding habits. The digestive tract of C. trilobatus consists of oral-pharyngeal cavity, esophagus, small intestine, and rectum. The oral-pharyngeal cavity is the initial part of the digestive tract and consists of uniseriate jaw teeth and a pharyngeal tooth. These teeth are tough and strong, enabling C. trilobatus to crush the hard shells of crustaceans and mollusks. Moreover, it has one pair of epiglottis teeth, which are triangularly shaped from left to right and symmetrically distributed. In additional, its hypopharyngeal teeth are healed by granular teeth in a "T" shape and gut is short and thick with“ ”shape in body cavity. Based on observation and measurement, we find the gun forms a bend and the average ratio between the length of the intestine and the body length is 0.32±0.11. The digestive gland consists of the hepatopancreas and the gallbladder. The liver with dispersed pancreas is divided into three pieces, large in the middle and small on both sides, which are wrapped around the small intestine. The gallbladder is elliptical in shape and located in the lower ventral lobe of the liver. The common hepatic duct is in the anterior part of the small intestine immediately after the esophagus and connected to the small intestine and the average ratio between the weight of the liver and pancreas 1.43%±0.32%. As the oropharyngeal cavity, it is found that the wall of the cavity is smooth and composed mainly of mucosal layer. The surface layer of the wall contains taste buds and a small number of cup-shaped cells. The mucosal layer is composed of compound flat cells, and the oropharyngeal cavity has a well-developed muscular layer that consists of an outer circular muscle and an inner longitudinal muscle. The longitudinal layer is discontinuous and fasciculated, and the muscle layer is covered with a layer of plasma membrane. The oropharyngeal cavity is not clearly demarcated from the submucosa, and the intermuscular nerve plexus can be seen between the two layers.. The esophagus consists of four layers, including the mucosal layer, the submucosal layer, the muscular layer, and the plasma layer.. Meanwhile, the muscle layer is one of the most prominent features of the digestive tract of C. trilobatus is the well-developed muscular layer. This layer is composed of two smooth muscle layers, the inner ring muscle and the outer longitudinal muscle, separated by a small amount of loose connective tissue. Additionally, the intermuscular nerve plexus can be seen between the two layers, suggesting that this layer plays a crucial role in the digestive process. The muscular layer is particularly well developed, which is indicative of the importance of muscular contractions in the digestion of food.. The mucosal layer is another important component of the digestive tract of C. trilobatus. It is composed of secondary and tertiary finger-like projections, and the base is commonly "concave" like the structure of exocrine glands. The mucosal layer is mostly primary and secondary finger-like protrusions, consisting of a single layer of columnar epithelial cells with a large number of mucous cells distributed in the middle and occasional pear-shaped cells. No intestinal glands were seen, which suggests that the mucosal layer is primarily responsible for the absorption of nutrients rather than the secretion of digestive enzymes.. The submucosal layer is also an essential component of the digestive tract of C. trilobatus. It contained mostly eosinophilic granular cells whose cytoplasm is stained red by eosin. This layer likely plays a role in the production of mucus, which helps to lubricate the digestive tract and aid in the movement of food through the system.. The outermost layer of the digestive tract is composed of a plasma layer. While less prominent than the other layers, the plasma layer likely serves a protective function, helping to prevent damage to the underlying layers. The structural features of the digestive tract, including the well-developed muscular layer, the mucosal layer, the submucosal layer, and the plasma layer, all play crucial roles in the digestive process of C. trilobatus. By understanding the relationship between the organizational characteristics of the digestive system and the feeding habits of C. trilobatus, we also can gain insights into the broader principles governing the evolution of digestive systems in herbivorous organisms.

Key words: Cheilinus trilobatus Lacépède; Histology; Digestive tract; Digestive gland

饲料中添加锌对刺参生长消化、抗氧化酶活性及免疫应答的影响

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摘要：锌是生物体内调节多种生命活动所必需的微量元素。本研究旨在评估不同锌水平的饲料对刺参生长性能、消化酶活性、抗氧化水平及免疫应答的影响。本实验在刺参基础饲料中分别添加了不同水平的甘氨酸锌进行了为期两个月的养殖实验，锌的添加量依次为 0、 20,、40、60 and 80 mg/kg, 0mg/kg 为对照组。结果表明，刺参的生长性能、淀粉酶活性和蛋白酶活性随着饲料中锌的添加显著升高，且在锌添加量为 40mg/kg 时表现最佳。饲料中添加锌显著提高了刺参体腔液中 SOD、CAT、ASA 和 IHR 活性，且明显降低了 MDA 含量。另外，免疫相关基因（hsp90、p105、rel、lsz）的表达量在较高的锌水平下显著上调表明高剂量的锌引起了氧化应激。以增重率为标准，折线回归分析表明，刺参对锌的最适需求量约为 66.95 mg/kg。

关键词：刺参、甘胺酸锌、生长性能、抗氧化能力、免疫应答

Effects of dietary zinc on growth performance, digestive enzyme activities, antioxidant status and immune responses of sea cucumber Apostichopus japonicus.

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Abstract：Zinc is an essential micronutrient for organisms involved in regulating various biological processes. This study evaluated the effects of dietary zinc on growth performance, digestive enzyme activities, antioxidant status and immune responses of sea cucumber Apostichopus japonicus. Five experimental diets were formulated with graded levels of zinc (0, 20, 40, 60, and 80 mg/kg, respectively), and the actual dietary zinc values were 31.4, 51.0, 68.2, 91.9, and 110.8 mg/kg diet, respectively. Sea cucumbers were fed with diets for 2 months. The results showed the growth performance, amylase and trypsin activities of sea cucumber increased significantly with zinc supplementation, and the best growth performance and enzyme activities were observed at 40 mg/kg zinc diet. Zinc supplementation significantly increased activities of superoxide dismutase, catalase, anti-superoxide anion and inhibiting hydroxyl radical, while significantly reduced the malondialdehyde content. Furthermore, the higher zinc supplementation levels resulted in significantly upregulated immune-related genes of hsp90、p105、rel、lsz, suggesting that excessive zinc caused oxidative stress. The broken-line regression analysis of specific growth rate indicated dietary zinc requirement in juvenile sea cucumber was ~66.3 mg/kg diet. Overall, dietary zinc contributes to the growth and immune resistance of juvenile sea cucumber, and our study will provide insights into the rational use of dietary zinc in aquaculture.

Key words: Apostichopus japonicus; zinc glycine; growth performance; antioxidant status; immune response

五倍子单宁酸对大口黑鲈生长性能和肠道健康的影响

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摘要：本试验旨在研究五倍子单宁酸对大口黑鲈生长性能和肠道健康的影响。选取 450 尾体重为（10.23±0.05）g 的大口黑鲈，随机分成 5 个组，每组 3 个重复，每个重复 30 尾。各组分别饲喂在基础饲料的基础上添加 0（F0 组）、0.05%（F1 组）、0.10%（F2 组）、0.15%（F3 组）、0.20%（F4 组）五倍子单宁酸的试验饲料，进行为期 90 d 的养殖试验。结果表明：1）与 F0 组相比，F2 和 F3 组的增重率和特定生长率显著升高，饲料系数显著降低。各组之间肝体比、摄食率和存活率无显著差异；2）与 F0 组相比，其他各组肠道绒毛增多，排列紧密；在前肠组织中，F1 组和 F2 组的隐窝深度显著低于 F0 组；3）与 F0 组相比，其他各组肠道变形菌门相对丰度均有所下降，肠道菌群稳态指数均有所升高，且 F3 组肠道菌群稳态指数显著高于 F0 组。综上所述，饲料中添加五倍子单宁酸可以提高大口黑鲈的生长性能，改善肠道组织结构，优化肠道菌群。

关键词：大口黑鲈；五倍子单宁酸；生长；肠道健康；

Effect of gallnut tannic acid on growth performance and gut health of largemouth bass

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Abstract： The purpose of this trial was to investigate the effects of gallic tannic acid on the growth performance and gut health of largemouth bass. A total of 450 largemouth bass weighing (10.23±0.05) g were randomly divided into 5 groups, with 3 replicates in each group and 30 repeats in each replicate. Each group was fed with 0 (F0 group), 0.05% (F1 group), 0.10% (F2 group), 0.15% (F3 group) and 0.20% (F4 group) gallnut tannic acid on the basis of basic feed, and the breeding experiment was carried out for 90 days. The results showed that: 1) Compared with the F0 group, the weight gain rate and specific growth rate of the F2 and F3 groups were significantly increased, and the feed coefficient was significantly reduced. There were no significant differences in liver-to-body ratio, feeding rate and survival rate between the groups. 2) Compared with the F0 group, the intestinal villi in the other groups increased and were closely arranged. In the foregut tissue, the crypt depth of the F1 and F2 groups was significantly lower than that of the F0 group. 3) Compared with the F0 group, the relative abundance of intestinal proteobacteria in the other groups decreased, and the homeostasis index of intestinal microbiota increased in the other groups, and the homeostasis index of intestinal microbiota in the F3 group was significantly higher than that in the F0 group. In summary, the addition of gallic tannic acid to the feed can improve the growth performance of largemouth bass, improve the structure of intestinal tissue, and optimize the intestinal flora；

Key words: gallnut tannin acid; largemouth bass; growth performance; intestinal health

营养强化卤虫对开口期鳜仔鱼生长存活和消化机能的影响

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摘要：鳜（Siniperca chuatsi）开口期以活鱼为食的独特习性限制了鳜产业的发展。为探索替代开口活饵并了解其对鳜消化机能的影响，本实验以 3 dph 的鳜仔鱼为对象，一组饲喂鲢仔鱼至 9 dph，另一组用裂壶藻强化的卤虫饲喂 4-6 dph 后再改喂鲢仔鱼至 9 dph。结果显示：饲喂卤虫会降低鳜仔鱼的体重、全长、特定生长率和存活率，改变肠绒毛长度和肠壁厚度，消化酶活性与其所摄食活饵的营养成分含量呈正相关；转录组和 qPCR 结果表明，饲喂卤虫使炎症反应和凋亡反应相关的差异基因表达量显著升高。综上，裂壶藻强化卤虫能在初次摄食后短期内替代活鱼作为鳜仔鱼的开口饵料，但其身体构造和营养成分与鳜早期发育阶段的固有活饵鱼存在差异，一定程度上导致鳜仔鱼肠道产生损伤，应激、免疫等相关基因表达上调，降低鳜仔鱼的生长和存活。

关键词：鳜仔鱼；卤虫；生长；消化酶；肠道损伤

Effects of nutritionally enhanced Artemia on growth, survival and digestive function of mandarin fish (Siniperca chuatsi) during the first feeding

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Abstract： The unique feeding habit of live larvae during mandarin fish's (Siniperca chuats) first feeding period limits its farming development. This study used the 3dph larvae, focusing on the effects of feeding Artemia supplemented with algae (Schizochitrium) compared to feeding silver carp (Hypophthalmichthys molitrix).The results indicated that feeding with Artemia reduced growth and survival rates, and altered intestinal villus length and intestinal epithelial thickness.Furthermore, there is a positive correlation between digestive enzyme activity and the nutritional composition of their respective food sources. Transcriptome and qPCR analysis revealed significant up-regulating DEGs related to inflammatory and apoptotic responses in Artemia-fed larvae. In conclusion, Artemia is a feasible alternative initial food source for mandarin fish in the short term after first feeding, but its body structural and nutritional differences from live fish may impair the larvae's intestines, trigger stress and immune-related gene expressions, and decrease growth and survival.

Key words: Siniperca chuatsi; Artemia; growth; digestive enzyme; intestine impair

饥饿再投喂促进鳜组织能量储备的调动

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摘要：为解明饥饿对鳜幼鱼的影响，采用饥饿再投喂的方法，将初始体重为 7.18 ± 0.15 g 的鳜进行持续饱食（对照组）、饥饿 3-25 天，研究饥饿后 20 d 补偿性生长条件下鳜体内能量物质的利用情况。根据体重和特殊生长率（SGR）的结果，饥饿 3、7d 组在 20 d 恢复投喂下能实现完全补偿生长，而饥饿 16、25d 组表现为部分补偿生长。肝体比（HSI）、肝糖原、甘油三酯含量在饥饿阶段显著降低，肌糖原含量仅在饥饿 25 d 时有所下降，而肝脂质呈上升趋势。肝脏、肌肉中与调控能量代谢相关 ampk ??1、ampk ??2 基因表达显著上升。恢复投喂结束后，各饥饿组能量储备都能恢复到对照组水平。结果说明，能量代谢 AMPK 在饥饿胁迫下被激活，促进鳜的能量物质调动，并依次利用肝糖原、脂质和肌糖原储备作为饥饿期的能量来源维持机体能量供应稳态。本研究为深入研究 AMPK 通路对鳜补偿生长的调控机制和能量储备调动提供了基础数据。

关键词：鳜；补偿生长；能量储备；AMPK 信号通路；饥饿再投喂

Fasting and refeeding of mandarin fish (Siniperca chuatsi) promotes the mobilization of body reserves

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Abstract: To elucidate the effect of fasting and refeeding on body energy reserves (BER) in juvenile mandarin fish (Siniperca chuatsi), fish body weight 7.18 ± 0.15 g were fed continuously (control) and fasted for 3-25 days, followed by refeeding for 20 days. 3d and 7d groups could achieve fully compensated growth (CG) after 20 d of refeeding, while 16d and 25d groups showed partial CG. There was a decrease in the hepatosomatic index, liver glycogen, muscle glycogen and triglyceride levels for fasted fish, while an increase in liver lipid levels. In addition, the genes expressions of ampk ??1 and ampk ??2 in energy metabolism AMPK pathway were significantly increased in liver and muscle. After refeeding, the BER of fasted fish could recover to the level of control group. These results indicate that under fasting, AMPK pathway was activated which promotes sequentially utilizing liver glycogen, lipid, and muscle glycogen as energy sources to maintain the energy homeostasis. This study provides basic data for further study of compensatory growth and energy reserves mobilization in mandarin fish.

Key words: Siniperca chuatsi; compensatory growth; energy reserves; AMPK signaling pathway; fasting and refeeding

环境因子对卤虫 HUFA 含量的影响及低温促进 HUFA 积累的转录组分析

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摘要：卤虫是海水鱼虾幼苗培育重要的开口饵料。但与桡足类相比，卤虫 HUFA 含量普遍较低，且不同产地卤虫 HUFA（尤其 EPA）含量差异显著。本研究针对 HUFA 含量最高的西藏拉果错卤虫 A. tibetiana 和 HUFA 含量较低的美国大盐湖卤虫 A. franciscana，探究温度、盐度和饵料 HUFA 水平等因素对两种卤虫 HUFA 积累的影响。研究表明，卤虫 HUFA 含量与饵料 HUFA 水平密切相关，且低温和低盐可显著提高卤虫 C18:3 n-3、ARA、EPA 和 DHA 含量。PCA 分析显示，饵料脂肪酸的组成和含量对卤虫 HUFA 含量的贡献程度最高，其次是温度和盐度，受品系影响较小。RNA-Seq 研究发现，低温环境调控卤虫脂肪酸合成、跨膜运输和脂类代谢等过程，Elovl4 延长酶和 Fad 去饱和酶基因表达显著提高。研究结果有助于解释西藏卤虫高 HUFA 含量的成因和分子机制，并为通过养殖调控环境因子提高卤虫 HUFA 含量提供参

关键词：环境因子；卤虫；高不饱和脂肪酸；调控

Effect of Environmental Factors on HUFA content of Artemia and Transcriptomic analysis on HUFA accumulation at low temperature

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Abstract： Artemia is an important live food for marine fish and crustacean larviculture. The highly unsaturated fatty acids (HUFA) are essential nutrients for marine aquatic animals. However, compared to copepods, the HUFA content of Artemia is generally lower, and the HUFA (especially EPA) content of different Artemia strains are various. This study investigated the impact of temperature, salinity, and feed composition on the HUFA accumulation in two Artemia strains, of which Artemia tibetiana originated from Lakgor Co, Tibet, China, containing the highest HUFA, and Artemia franciscana of the Great Salt Lake in the United States containing relatively low HUFA. The results showed that HUFA content of Artemia closely related to the HUFA profile in feed, and low temperature and low salinity significantly increased the content of C18:3n-3, ARA, EPA, and DHA of Artemia. PCA analysis showed that the composition and content of fatty acids in feed contributed the most to the HUFA content of Artemia, and the temperature and salinity were also critical factors. The HUFA content of Artemia was less affected by strains. RNA Seq revealed that low temperature regulated the synthesis of fatty acids, transmembrane transport and lipid metabolism processes in Artemia, with significantly increased expression of long chain fatty acid extender (Elovl4) and fatty acid desaturase (Fad) genes. The findings are helpful to explain the cause and molecular mechanism of rich HUFA content in Tibet Artemia, and provide reference for improving the HUFA content of Artemia through regulating the culture conditions.

Key words: Environmental factor; Artemia; HUFA; Regulation

饲料中添加辅酶 Q10 对花鲈生长性能和抗亚硝酸盐胁迫的影响

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摘要：摘要：本试验以花鲈作为研究对象，配制两种辅酶 Q10 水平（0mg/kg、20mg/kg）的颗粒饲料，分别投喂花鲈幼鱼（4.2±0.2g）60 天，养殖结束后进行 120h 的亚硝酸盐（27mg/L）急性胁迫试验。结果表明，饲料中添加 20mg/kg 的辅酶 Q10 可显著提高花鲈的增重率（P＜0.5），并提高花鲈在急性亚硝酸盐胁迫中的存活率，显著降低花鲈血清谷草转氨酶（GOT）、谷丙转氨酶（GPT）活性。

关键词：关键词：辅酶 Q10；亚硝酸盐；花鲈

The influence of dietary coenzyme Q10 on the growth rate and the resistance against nitrite stress of spotted seabass (Lateolabrax maculatus)

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Abstract： Abstract: This experiment used spotted seabass as the research object and prepared two types of pellet feed with coenzyme Q10 levels (0mg/kg, 20mg/kg). The juvenile spotted seabass (4.2 ± 0.2g) were reared for 60 days, then, a 120 hour acute nitrite stress test (27mg/L)was conducted after the breeding experiment was completed. The results showed that adding 20mg/kg of coenzyme Q10 to the diet could significantly increase the weight gain rate of spotted seabass (P<0.5), improve the survival rate of spotted seabass under acute nitrite stress, and significantly reduce the activities of serum glutamic oxaloacetic transaminase (GOT) and glutamic pyruvic transaminase (GPT) in spotted seabass.

Key words: Coenzyme Q10; Nitrite; Lateolabrax maculatus

大口黑鲈雌雄摄食、生长与代谢差异的比较研究

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摘要：本试验在比较研究大口黑鲈(Micropterus salmoides)雌雄幼鱼(均重 11.02±0.07 g)生长代谢差异的基础上，进一步探讨高淀粉胁迫下雌雄鱼的代谢调控差异。60 天的生长实验结果表明，雄鱼生长速度显著高于雌鱼，同时雄鱼肝脏超氧化物歧化酶(SOD)、谷胱甘肽过氧化物酶(GSH-Px)活性及其 sod、gpx1a 的 mRNA 相对表达量显著上调，而丙二醛（MDA）含量显著低于雌鱼。雄鱼肝脏促炎因子(IL-1β)、脂肪合成基因（fas、acaca）的 mRNA 相对表达量显著下调。肝脏转录组（RNA-seq）分析，共检测到 28158 个基因，筛选出 469 个差异基因，其中上调 328 个、下调 161 个。GO 分析发现差异表达基因富集到细胞进程、代谢过程等 20 个生物学过程，细胞组分、信号转导活性等 11 个生物学功能，同时筛选出 5 个关键基因（elovl6、acsbg2、degs2、gpat4、vtg1）

关键词：大口黑鲈；性别；摄食；生长；代谢

A comparative study on the differences in feeding, growth and metabolism between male and female largemouth bass

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Abstract： In this study, we initially investigated the differences in the regulation of nutrient metabolism between male and female largemouth bass (Micropterus salmoides), providing information for single-sex selection in cultured fish. Based on the comparative study of the differences in growth and metabolism of male and female juvenile largemouth bass (weighing 11.02 ± 0.07 g), we further explored the differences in metabolic regulation of male and female juvenile largemouth bass under high starch stress. The results of the 60-day growth trial showed that the growth rate of male fish was significantly higher than that of female fish. Meanwhile, the liver superoxide dismutase (SOD) and glutathione peroxidase (GSH-Px) activities and their mRNA (sod and gpxla) expression of male fish were significantly up-regulated, while malondialdehyde (MDA) content was significantly lower in male than that in female fish ($p < 0.05$). The mRNA expression of liver pro-inflammatory factor (il-1β) and lipid synthesis genes (fas, acaca) were significantly down-regulated in male fish ($p < 0.05$). According to the transcriptome (RNA-seq) analysis of liver, totally 28,158 genes were detected and 469 differential genes were screened, of which 328 genes were up-regulated and 161 genes were down-regulated. GO analysis identified that differentially expressed genes were enriched to 20 biological processes such as cellular processes, single organism processes and metabolic processes, as well as 11 biological functions such as cellular components, catalytic activities, cell junctions, transport activities, signal transduction activities, etc. In addition, 5 key genes (elovl6, acsbg2, degs2, gpat4, vtg1) were discovered based on the GO analysis.

Key words: Micropterus salmoides; sex; feed intake; growth; metabolism

EGCG 缓解草鱼高糖摄食易感 GCRV 的机理初探

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摘要：为探究 EGCG 缓解草鱼高糖摄食易感 GCRV 的机理，本实验以三组不同饲料（高糖组、高糖+EGCG 组、对照组）饲喂草鱼 8 周，通过检测草鱼生长性能、血清免疫指标的变化以及对未感染（对照）和感染 GCRV 72 h 三组饲料饲喂草鱼的脾脏样品进行转录组和 WGCNA 的联合分析发现：高糖+EGCG 组饲料饲喂草鱼 8 周后的增重率显著高于其它两组；检测血清免疫指标发现高糖饲料中添加 EGCG 饲喂草鱼血清中的 C3 含量在未感染（对照）和感染 GCRV 72 h 后都显著高于对照组和高糖组；通过转录组 WGCNA 关联 C3 含量分析得到 EGCG 缓解草鱼高糖摄食易感 GCRV 的关键基因为 UBE2D2，以上结果为下一步探索 EGCG 缓解草鱼高糖摄食易感 GCRV 的机理奠定基础。

关键词：草鱼；EGCG；GCRV；转录组

A preliminary study on the mechanism of EGCG in alleviating the susceptibility to GCRV in Ctenopharyngodon idellus with high sugar intake.

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Abstract： In order to investigate the mechanism of EGCG in alleviating the susceptibility of Ctenopharyngodon idellus to GCRV by high sugar intake, this experiment was conducted by feeding grass carp with three different groups of feeds (high sugar, high sugar + EGCG, and control) for 8 weeks, and by detecting the changes in the growth performance of the Ctenopharyngodon idellus, the changes in serum immunity indexes, as well as by conducting a combined transcriptome and WGCNA analysis on the spleen samples of Ctenopharyngodon idellus fed with the three groups of feeds for 72 h without infection (control) and with GCRV. The analysis showed that the weight gain rate of the high glucose+EGCG group was significantly higher than that of the other two groups after 8 weeks of feed feeding; the serum immunity indexes showed that the C3 content in the serum of the high glucose feed-fed Ctenopharyngodon idellus was significantly higher than that of the control and high glucose groups in both the uninfected (control) and the GCRV-infected groups after 72 h of feed feeding; and the analysis of the WGCNA-associated C3 content of the transcriptomes showed that the EGCG alleviated the susceptibility to GCRV of high glucose feeding of Ctenopharyngodon idellus by the transcriptomes. By analyzing the WGCNA-associated C3 content of the transcriptome, it was found that the key gene of EGCG in alleviating the susceptibility of Ctenopharyngodon idellus to high glucose intake to GCRV was UBE2D2.

Key words: Ctenopharyngodon idellus; EGCG; GCRV; transcriptome

发芽蚕豆饲料对尼罗罗非鱼肠道健康和肠道微生物菌群的影响

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摘要：尼罗罗非鱼过量食用蚕豆饲料可引起肠道炎症由于其内源性抗营养因子(ANFs)。发芽是降低蚕豆 ANFs 的有效方法。发芽蚕豆中 ANFs 对罗非鱼的影响机制尚不清楚。我们设计在饲料中添加干蚕豆(FB0)，发芽蚕豆(FB5)，基础饲粮(对照组)饲喂尼罗罗非鱼 75 天后，测定尼罗罗非鱼肌肉质构和肠道消化酶活性，肠道组织切片，免疫相关基因表达，肠道菌群组成。结果显示，FB5 组肌肉硬度最高。FB0 组胰蛋白酶活性显著升高，FB5 组胰蛋白酶活性降低。与对照组相比，FB0 组和 FB5 组中 TNF-α，IL-1β，CCL3 基因水平均显著升高；IFN-γ和 Hsp70 基因表达 FB0 组上调，FB5 下调。肠道微生物多样性分析显示，组内多样性排序为对照组> FB5 > FB0。在其中，在门水平，对照组中丰度最高的是变形菌门，FB0、FB5 组中丰度最高的为梭杆菌。总之,以发芽蚕豆为饲料的尼罗罗非鱼具有较高的肌肉硬度，减少肠道损伤。

关键词：罗非鱼；蚕豆；发芽；免疫；肠道菌群

Effects of diet containing germinated faba bean (Vicia faba L.) on the intestinal 1 health and gut microbial communities of Nile tilapia (Oreochromis niloticus)

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Abstract: Nile tilapia (Oreochromis niloticus) is a commercially farmed fish species worldwide.We reported previously that Nile tilapia fed with diet supplemented with faba bean(Vicia Faba L.) might change the structure of muscle and were popular in market.However, the overconsumption of faba bean could induce intestinal inflammation in Nile tilapia due to its endogenous anti-nutritional factors (ANFs). It is believed that germination is an effective method for reducing ANFs in faba beans. However, the effects of ANFs in germinated faba beans on the tilapia remains enigmatic. In this report, Nile tilapia fed with diet supplemented with dry faba beans (FB0), or germinated faba beans (FB5), or basal diet only (control group) for 75 days. Thereafter, the textural quality and digestive enzyme activity, histology of the inner intestinal wall, expression of related genes, and composition of intestinal microbes were measured. The hardest fillets were obtained from the FB5 group (406.17 ± 42.51 gf), followed by the FB0 (301.17 ± 24.70 gf) and control (117.50 ± 8.19 gf) ($P<0.05$) groups. The amylase levels were lower in the FB0 and FB5 groups ($P<0.05$), whereas the trypsin activities were up to 1.9-fold higher than that in the control group ($P<0.05$). The expressions of the immune-related genes interleukin-1 beta (IL-1β), C-C motif chemokine ligand 3 (CCL3), and tumour necrosis factor-alpha (TNF-α) in both the FB0 and FB5 groups were significantly up-regulated, whereas metallothionein (MT) expression was downregulated in the intestine when compared with that in the control group ($P<0.05$).Moreover, Interferon-γ (IFN-γ) and heat shock protein 70 (Hsp70) expression in FB5 were down-regulated, but up-regulated in FB0 compared with that in the control group. Diversity analysis of intestinal microbes revealed lower diversity in both the FB0 and FB5 groups, with the diversity in the groups ranking as control > FB5 > FB0. In particular, the most abundant phylum was Proteobacteria in the control group, while that in the FB0 and FB5 groups was Fusobacteria, accounting for 26.70%, 79.18%, and 55.87% of the microbiota, respectively, indicating that the intestinal microbiota structure and these microbes were affected by changes in the FB diet. In summary, Nile tilapia fed with germinated faba beans showed higher textural quality and decreased intestinal damage, therefore germinated faba beans could be a superior substitute for dry faba beans in tilapia culture.

Key words: Faba beans; Germination; Immunity; Intestinal flora; Oreochromis niloticus

于桥水库 4 种经济鱼类肌肉营养成分分析与评价

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摘要：为全面了解于桥水库鲤、鲢、鲫和鳙的营养成分特征，对 4 种鱼肌肉的水分、灰分、粗脂肪、粗蛋白质、矿物质元素含量、氨基酸及脂肪酸组成进行分析与评价。结果表明，鲢粗蛋白含量最高（16.13%），鲫含量最低（15.00%）；鳙粗脂肪含量最高（3.1%），鲫含量最低（0.7%）。4 种鱼富含矿物质 K、Na、Ca、Mg、P 及 Fe、Zn、Se，为优质的高钾低钠膳食来源。人体必需氨基酸均占氨基酸总量的 37.54%以上，鲜味氨基酸占 40.51%~41.04%，谷氨酸含量均为最高。鲤、鲫、鲢和鳙肌肉中分别检出 11、10、16 和 15 种脂肪酸，饱和脂肪酸、单不饱和脂肪酸和多不饱和脂肪酸相对含量差异较小。4 种鱼蛋白质含量较高，富含 16 种氨基酸，矿物质元素和脂肪酸含量丰富，具有较高的营养价值和食用风味。

关键词：于桥水库；鲤；鲫；鲢；鳙；营养成分

Nutritional Compositions and Evaluations in muscles of Four Species Economic Fishes in Yuqiao Reservoir

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Abstract： In order to comprehensively characterize the nutrient composition of Cyprinus carpio, Hypophthalmichthys molitrix, Carassius auratus and Aristichthys nobilis in Yuqiao Reservoir, Tianjin, the muscles of the four species was analyzed and evaluated in terms of the water content, ash, crude fat, crude protein, mineral element content, amino acid and fatty acid composition. The results showed that the content of crude protein in H. molitrix was the highest (16.13%), while was the lowest in C. auratus (15.00%). The content of crude fat in A. nobilis was 3.10%, which was the highest, while the lowest was 0.70% in C. auratus. Rich in mineral elements in all of these fishes, including K, Na, Ca, Mg, P, Fe, Zn, and Se, which were high-potassium and low-sodium dietary sources. There were more than 37.54% essential amino acids in the muscles of these 4 species. The ratio of Umami amino acids in total amino acids ranged from 40.51% to 41.04%, with the maximal glutamic acid in the muscles of four species. There were 11, 10, 16 and 15 kinds of fatty acids in C. carpio, H. molitrix, C. and A. nobilis respectively. There has low difference between the relative contents of saturated fatty acid, monounsaturated fatty acid, and polyunsaturated fatty acids in these 4 species. Furthermore, all of these fishes have high protein content, including 16 kinds of amino acids, mineral elements and fatty acids, with high nutritional value and edible flavor.

Key words: Yuqiao Reservoir; Cyprinus carpio; Carassius auratus; Hypophthalmichthys molitrix; Aristichthys nobilis; nutritional component

江苏沿海滩涂四角蛤蜊与文蛤组织间营养成分差异分析

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摘要：对取自江苏南部沿海滩涂的四角蛤蜊与文蛤的斧足、闭壳肌、内脏团和外套膜等 4 种组织进行营养成分测定。结果表明，四角蛤蜊与文蛤在不同组织中的水分、粗脂肪、粗蛋白均存在显著性差异(P<0.05)；同种组织中总糖差异不显著，而文蛤各组织中糖原含量均更高；两种蛤均含有 18 种编码氨基酸，其中包含 7 种人体所需的必需氨基酸（色氨酸除外），外套膜中共有 8 种氨基酸存在差异(P<0.05)，而文蛤闭壳肌中苏氨酸、亮氨酸、丝氨酸等显著高于四角蛤蜊(P<0.05)，两种蛤组织中的ΣEAA/ΣTAA 均高于 45%；两种蛤均含有 13 种脂肪酸，外套膜中存在差异的脂肪酸种类最多，而文蛤内脏团中总多不饱和脂肪酸含量显著高于四角蛤蜊(P<0.05)。研究表明，两种蛤均为较理想的蛋白质来源，文蛤营养成分更佳。

关键词：四角蛤蜊；文蛤；营养成分分析；不同组织

Analysis of the difference of nutrient components between the tissues of Mactra veneriformis and Meretrix meretrix in the coastal mudflat of Jiangsu Province

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Abstract：The nutritional composition difference of four kinds of tissues of Mactra veneriformis and Meretrix meretrix were determined including foot, adductor muscle, visceral mass and mantle which were taken from the coastal mudflat of southern Jiangsu Province.The results indicated that there are significant differences in water content, crude fat, and crude protein in different tissues of two kinds of shellfish(P<0.05). There is no significant difference in total sugar in the same tissue. And the glycogen content in all tissues of M.meretrix is higher.There were 18 common amino acids and 7 essential amino acids for human demand in two kinds of shellfish except tryptophan.There are 8 different amino acids in the outer membrane(P<0.05). And the levels of threonine, leucine and serine in the adductor muscle of M.meretrix are significantly higher than M.veneriformis(P<0.05). The ratio of essential amino acids to total amino acids are all higher than 45%. There were 13 fatty acids in two kinds of shellfish. There were most diverse types of fatty acids exist in the mantle.The content of total polyunsaturated fatty acids in the visceral mass of M.meretrix is significantly higher than M.veneriformis(P<0.05). Therefore, two kinds of shellfish are ideal sources of protein, and M.meretrix is batter.

Key words:：Mactra veneriformis, Meretrix meretrix, nutrient composition analysis, different tissues

饲料中胰酶添加水平对大口黑鲈（Micropterus salmoides）幼鱼生长性能、生化指标和肝肠组织结构的影响

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摘要：为研究饲料中添加胰酶对大口黑鲈幼鱼生长性能、生化指标与肝肠组织结构的影响，试验设计 6 个处理组，对照组投喂基础饲料，在其基础上添加 5 种不同浓度的胰酶，配制成 5 种等氮等脂的试验饲料，开展 70d 大口黑鲈养殖试验.结果显示：1）添加浓度为 750mg/kg 时，FBW、WGR 及 SGR 达到峰值，FCR 达到最低值。2）。添加浓度为 500mg/kg 及 750mg/kg 时，血清甘油三酯（TG）与总胆固醇（TC）与含量显著降低（P＜0.05）。血清中碱性磷酸酶（AKP）活性随着胰酶添加量的增加，呈先上升后下降的趋势。3）添加浓度为 500mg/kg 及 750mg/kg 时，肝脂空泡化面积相较于对照组显著降低（P＜0.05）；添加浓度为 500mg/kg 时，绒毛数量相较于对照组显著提高（P<0.05）。综上：综合分析及以增重率为指标，建议大口黑鲈饲粮中胰酶适宜添加量为：679mg/kg。

关键词：大口黑鲈；胰酶；生长性能；肝肠组织结构

Effects of dietary pancreatin level on growth performance, biochemical indices and enterohepatic structure of juvenile largemouth bass

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Abstract：To evaluate the effects of dietary pancreatin on growth performance, biochemical indexes and enterohepatic structure of juvenile largemouth bass (Micropterus salmoides), 70-day breeding experiment was carried out in 6 treatment groups （Each group has 35 fishes with 3 duplicates.）. Among them, the control group was fed with basal diet. On the basis of that, five different concentrations of pancreatin were added to prepare five isonitrogenous experimental diets. The results showed as follows: 1) Different concentrations of pancreatic have a significant impact on the final body weight (FBW), weight gain rate (WGR), specific growth rate (SGR), and feed coefficient (FCR). Note particularly, when the concentration was 750mg/kg, FBW, WGR, and SGR reach their peak, while FCR reaches its lowest value. 2) The content of serum total protein (TP) and albumin (ALB) increased. Of which the content of ALB decreased first and then increased with the increase of pancreatin addition, peaked at 750 mg/kg. The content of serum triglyceride (TG) and total cholesterol (TC) decreased significantly ($P < 0.05$) when the concentration were 500 mg/kg and 750 mg/kg. The activities of aspartate aminotransferase (AST) and alanine aminotransferase (ALT) in serum decreased first and then increased with the increase of trypsin addition，the activity of alkaline phosphatase (AKP) showing the opposite law.) When the concentration were 500 mg/kg and 750 mg/kg, the area of liver fat vacuolization was significantly lower than that of the control group ($P < 0.05$). The villus width was significantly increased compared with the control group ($P < 0.05$). the number of villi was significantly higher than that of the control group ($P < 0.05$)， especially when the concentration was 500mg / kg,. In conclusion, dietary pancreatin could significantly improve the growth performance, biochemical indexes, liver antioxidant and enterohepatic structure of largemouth bass, and there was a dose effect of pancreatin. Based on the comprehensive analysis and the index of weight gain rate, it is suggested that the appropriate amount of pancreatin in the diet of largemouth bass is 679 mg/kg.

Key words: Largemouth bass; Pancreatin; Performance of growth; Enterohepatic structure

饲料磷水平对牛蛙的生长性能、血清和肝脏生化及骨骼矿化的影响

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摘要：本实验以牛蛙（46.71 ± 0.04g）为研究对象，探究不同饲料磷水平对牛蛙的生长性能、血清和肝脏生化、骨骼矿化的影响，进而确定牛蛙对饲料磷元素适宜的需求量。分别配制磷水平为 0.46%(对照组)、0.73%、0.96%、1.15%、1.46%和 1.70%的六种饲料，每天投喂两次，投喂 56 天。实验结果表明：饲料磷含量为 0.96%、1.15%和 1.44%的牛蛙增重率和饲料效率显著高于磷含量为 0.46%、0.73%和 1.70%的牛蛙($P < 0.05$)。与对照组相比，当饲料中磷含量为 1.15%时，牛蛙全体的粗蛋白质含量显著增加($P < 0.05$)。与饲料磷含量为 0.46%和 0.73%的牛蛙相比，磷含量为 0.96%、1.15%、1.46%和 1.70%的牛蛙全身粗脂肪含量显著降低($P < 0.05$)。此外，与对照组相比，饲料磷含量为 0.96%、1.15%、1.44%和 1.70%的牛蛙肝脏总胆固醇和血清甘油三酯含量显著降低($P < 0.05$)；饲料磷含量为 0.96%、1.15%、1.44%和 1.70%的牛蛙全体的磷和钙含量显著增加($P < 0.05$)。综上所述，饲料中添加 1.15%的磷能促进牛蛙的生长，降低肝脏中的总胆固醇和血清中甘油三酯的含量，增加全体和脊椎中磷和钙的沉积量。

关键词：牛蛙；饲料；生长性能；磷；沉积率

Effects of dietary phosphorus levels on growth performance, biochemistry of the liver and serum, and bone mineralization of bullfrog (Lithobates catesbeianus)

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Abstract： This study was conducted to investigate the effects of different dietary phosphorus (P) levels on growth performance, biochemistry of the liver and serum, and bone mineralization of bullfrog (46.71 ± 0.04g). Six diets with P levels of 0.46% (the control group), 0.73%, 0.96%, 1.15%, 1.46% and 1.70% were prepared and fed bullfrogs twice a day for 56 days. The body weight gain rate and feed efficiency of bullfrogs fed diets with 0.96%, 1.15% and 1.44% P were significantly higher than those fed diets with 0.46%, 0.73% and 1.70% P ($P < 0.05$). Compared with the control group, dietary P content of 1.15% significantly increased the protein content in whole body of bullfrogs ($P < 0.05$). The fat content of bullfrogs fed diets with 0.96%, 1.15%, 1.46% and 1.70% P was significantly lower than that of bullfrogs fed with 0.46% and 0.73% P ($P < 0.05$). Furthermore, compared with the control group, total cholesterol and triglyceride contents in the liver and serum of bullfrogs fed diets with 0.96%, 1.15%, 1.44% and 1.70% P were significantly decreased ($P < 0.05$). Compared with the control group, the contents of total phosphorus and calcium in bullfrogs fed diets with 0.96%, 1.15%, 1.44% and 1.70% P were significantly increased ($P < 0.05$). In conclusion, adding 1.15% P to the diet can promote the growth, reduce the content of total cholesterol in the liver and triglyceride in the serum, and increase the deposition content of phosphorus and calcium in the whole body and spine.

Key words: Lithobates catesbeianus; Feed; Growth performance; Phosphorus; Rate of deposition

不同温度下花鲈对饲料磷需要量的研究

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摘要：本研究以花鲈（3.53±0.34g）为研究对象，探究饲料磷水平对适温（27℃）和高温（33℃）饲养下花鲈的生长性能、磷周转代谢、脂代谢、抗氧化状态和肠道微生物群的影响。分别配制了五种有效磷水平为0.35%、0.55%、0.71%、0.82%和0.92%的饲料，实验期间每天投喂两次，持续10周。与27℃相比，33℃的水温显著降低了花鲈的生长、饲料利用率、全体磷沉积率和血清钙磷含量，但显著提高了血清碱性磷酸酶和肠道磷转运相关蛋白的基因表达水平，并且造成花鲈氧化应激和腹腔脂肪异常沉积。同时，高温增加了花鲈对磷的摄入量和抗氧化酶的活性，并改变花鲈肠道微生物组成（如增加Bacillus的丰度）。在饲料中添加0.55%-0.82%的磷可以缓解因磷摄入不足引起的脂质过度沉积和脂质代谢紊乱。以增重率为评价指标，二次回归模型分析表明，花鲈在27℃和33℃条件下的最适饲料磷水平分别为0.72%和0.78%。

关键词：花鲈；磷；温度；生长；肠道菌群

Dietary phosphorus requirement of spotted seabass (Lateolabrax maculatus) reared at different temperatures

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Abstract：This study was conducted to investigate the effects of dietary phosphorus levels on growth performance, phosphorus turnover metabolism, antioxidant status and intestinal microflora of spotted seabass (3.53±0.34g) reared at moderate (27°C) and high (33°C) temperatures. Five diets were formulated with effective phosphorus levels of 0.35%, 0.55%, 0.71%, 0.82% and 0.92%, respectively, and fed fish twice daily for 10 weeks during the experimental period. Water temperature of 33°C significantly reduced growth performance, feed utilization, the total phosphorus deposition rate and serum calcium and phosphorus content, which caused oxidative stress and abnormal abdominal fat deposition in spotted seabass compared with 27°C. However, the activity of serum alkaline phosphatase and gene expression levels of intestinal phosphorus transport-related proteins in fish reared at 33°C were significantly increased compared with fish reared at 27°C. Meanwhile, compared with 27°C, 33°C increased the phosphorus uptake, antioxidant enzyme activity, and changed the intestinal microflora composition (e.g., increased abundance of Bacillus) of spotted seabass. The addition of 0.55%-0.82% phosphorus to the diet alleviated the excessive lipid deposition and lipid metabolism disorders caused by insufficient phosphorus intake. Using weight gain rate as an evaluation indicator, quadratic regression model analysis showed that the optimum feed phosphorus levels for spotted seabass reared at 27°C and 33°C were 0.72% and 0.78%, respectively.

Key words: Lateolabrax maculatus; phosphorus; temperature; growth; intestinal microflora

泥螺软体部营养成分差异分析

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摘要：泥螺(Bullacta exarata)属软体动物门、腹足纲、后鳃亚纲、头楯目、阿地螺科、泥螺属，是一种重要的经济贝类。本研究将泥螺软体部分为头盘、腹足等可食用部分和内脏团等非食用部分，分别对其营养成分进行测定分析。结果显示，泥螺的整体含水率在86%左右，可食部中粗蛋白含量显著高于非食用部分（P＜0.05)；共检测出18种氨基酸，包括了7种人体必需氨基酸和2种半必需氨基酸，其中可食部的谷氨酸及天冬氨酸含量最高（P＞0.05）；两部分的必需氨基酸与总氨基酸比值差异明显（P＜0.05)，可食部高于FAO/WHO的理想蛋白质模型；呈味氨基酸与总氨基酸比值分别为50.96%和51.36%，两部分间差异不显著（P＞0.05）；37种脂肪酸中共检测出脂肪酸13种，两部分相较而言，非食用部分中饱和脂肪酸比例最高，而可食部中的EPA和DHA总量最高。

关键词：泥螺(Bullacta exarata)；可食用部分；非食用部分；营养成分

Analysis of Nutritional Differences in the soft tissue of Bullacta exarata

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Abstract： Bullacta exarata is an important economic mollusk belonging to the phylum Mollusca, gastropoda, suborder Postbranchia, order Cephaloptera, family Aralidae, and genus Bullacta. In this study, the soft tissue of the B. exarata were divided into edible parts such as the head plate, gastropod, and non edible parts such as visceral masses, and their nutritional components were determined and analyzed separately.The results showed that the overall moisture content of B. exarata was around 86%, and the crude protein content in the edible part was significantly higher than that in the non edible part (P<0.05); A total of 18 amino acids were detected, including 7 essential amino acids and 2 semi essential amino acids, with the highest levels of glutamic acid and aspartic acid in the edible part (P>0.05); There is a significant difference in the ratio of essential amino acids to total amino acids between the two parts (P<0.05), and the edible part is higher than the ideal protein model of FAO/WHO; The ratio of flavor amino acids to total amino acids was 50.96% and 51.36%, respectively, with no significant difference between the two parts (P>0.05); A total of 13 out of 37 fatty acids were detected, compared to the two parts, the non edible part had the highest proportion of saturated fatty acids, while the edible part had the highest total amount of EPA and DHA.

Key words: Bullacta exarata; Edible parts; Non edible parts; Nutrient composition

硫辛酸对花鲈生长、血清生化及脂肪沉积的影响

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摘要：本研究旨在探究在饲料中添加硫辛酸对花鲈生长、血清生化及脂肪沉积的影响。配制11％和 17％两种脂肪水平的饲料，其中 17％脂肪水平饲料分别添加 0.02％、0.04％和 0.06％水平硫辛酸，进行为期 57d 养殖实验。结果表明，添加 0.04％硫辛酸显著提高了花鲈的增重率、特定生长率和蛋白质效率（p＜0.05），显著降低了饲料系数（p＜0.05）；随着添加水平的提高，花鲈血清和肝脏的 T-CHO、TG 和 NEFA 含量显著降低（p＜0.05），其中 0.04％硫辛酸还显著降低了花鲈血清中 ALT、AST 活性（p＜0.05），这表明硫辛酸可能是通过保护肝脏，调节脂肪代谢，从而缓解脂肪的过度沉积。

关键词：花鲈，硫辛酸，生长性能，血清生化，脂肪沉积

Effect of lipoic acid on the growth, serum biochemistry and fat deposition of Lateolabrax maculatus

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Abstract：The aim of this study was to investigate the effects of the addition of lipoic acid to feed on the growth, serum biochemistry and fat deposition of Lateolabrax maculatus. Two types of feeds with 11% and 17% fat levels were prepared, in which the 17% fat level feeds were supplemented with 0.02%, 0.04% and 0.06% lipoic acid, respectively, and the culture experiment lasted for 57 d. The results showed that the addition of 0.04% lipoic acid significantly increased the weight gain and fat deposition of Lateolabrax maculatus. The results showed that the addition of 0.04% lipoic acid significantly increased the weight gain rate, specific growth rate and protein efficiency ratio of Lateolabrax maculatus ($p<0.05$), and significantly reduced the feed conversion rate ($p<0.05$). Meanwhile, T-CHO, TG and NEFA levels in serum and liver of Lateolabrax maculatus were significantly reduced with increasing levels of additions ($p<0.05$), in which the 0.04% lipoic acid significantly reduced the activity of ALT, AST in the serum of Lateolabrax maculatus ($p<0.05$), this suggests that lipoic acid may mitigate excessive fat deposition by protecting the liver and regulating fat metabolism.

Key words: Lateolabrax maculatus; Lipoic acid; Growth performance; Serum biochemistry; Fat deposition

成纤维生长因子 1（FGF1）

对虹鳟糖脂代谢的调控机制研究

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摘要：肉食性冷水鱼对糖的利用能力较低，而成纤维细胞生长因子 1（FGF1）具有调节脊椎动物生长发育和能量代谢的能力。本研究通过给试验虹鳟注射重组蛋白（rFGF1），研究了其对高脂饮食虹鳟糖脂代谢调控的作用。结果显示，外源补充 rFGF1 能显著上调脂质分解相关基因的表达，明显降低 HFD 虹鳟的全身和肝脏脂质、血清 TG 含量（$P < 0.05$），并显著提高 AKT 和 GSK3β磷酸化水平，促进葡萄糖摄取并增加肝糖原含量。同时 rFGF1 还可能通过激活自噬和 AMPK 信号，显著下调炎症因子的表达和降低机体炎症水平。血清非靶代谢组学分析表明，rFGF1 可通过上调嘧啶合成途径中的关键酶和下调尿苷磷酸化酶的表达，从而显著提高血清尿苷水平，并可能进一步通过内分泌循环改善全身糖脂代谢紊乱以弥补 FGF1 的自/旁分泌缺陷。以上研究结果表明，虹鳟 FGF1 可有效调节高脂饮食造成的虹鳟糖脂代谢紊乱。

关键词：虹鳟；成纤维生长因子；高脂饮食；糖脂代谢；炎症反应

Fibroblast growth factor 1 (FGF1) ameliorates disorders of glycolipid metabolism in rainbow trout (Oncorhynchus mykiss) fed a high-fat diet

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Abstract： In this study, the coding region of rainbow trout fgf1 was cloned and sequenced to synthesize recombinant protein (rFGF1) and investigate its potential role in improving glycolipid metabolism. Acute injection of rFGF1 into rainbow trout revealed that it was effective in lowering serum glucose levels. To investigate the effect of rFGF1 on high fat diet (HFD)-induced metabolic disorders in rainbow trout, a 6 weeks feeding experiment was conducted. At the end of the third week, the fish were injected with either PBS or rFGF1. The results revealed a significant increase in the final body weight (FBW) of rainbow trout ($P < 0.05$), but there were potential risks, including disturbances in glycolipid metabolism and increased inflammatory responses. However, these effects were altered by rFGF1 treatment. The rFGF1 significantly reduced the crude fat content of the liver, serum TG, GOT, and GPT content caused by HFD ($P < 0.05$). The upregulation in atgl, hsl, and acc2 mRNAs implied the promotion of TG catabolism. Moreover, rFGF1 decreased serum glucose levels by promoting glucose uptake and stimulating glycogen content in the liver via increasing AKT and GSK3β phosphorylation levels. Notably, rFGF1 did not exacerbate the inflammatory response but down-regulated the expression of inflammatory factors. Interestingly, the activation of autophagy and the AMPK signaling pathway may contribute to the positive effect of rFGF1. Lastly, rFGF1 injection significantly increased the levels of LC3I/II protein and phosphorylated AMPKα ($P < 0.05$). In addition, serum untargeted metabolomics analysis showed that pyrimidine metabolism was the pathway significantly altered among groups. Serum uridine levels were significantly lower in the HFD group compared to the control group, whereas serum uridine levels were elevated after rFGF1 supplementation. Further analyses indicated that rFGF1 administration up-regulated key enzymes during the pyrimidine synthesis pathway and down-regulated the expression of uridine phosphorylase to regulate uridine metabolism, which further may improve systemic glycolipid metabolism through the endocrine cycle.

Key words: Rainbow trout; Recombinant fibroblast growth factor 1; Glycolipid metabolism; Inflammation

花鲈摄食脱脂黄粉虫粉饲料后不同生长速率个体免疫和肠道健康的差异分析

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摘要：本试验探究摄食脱脂黄粉虫(Tenebrio molitor)粉饲料后，不同生长速率的花鲈个体(Lateolabrax maculatus)免疫能力和肠道健康的差异比较。选取 54 尾初重 4.3±0.02 g 的花鲈，投喂 15%水平脱脂黄粉虫粉的试验饲料，经过 8 周的养殖，共选取 15 尾体重最大和 15 尾最小的个体分别作为快速生长组(FG)和缓慢生长组(SG)。结果发现，FG 的增重率和特定生长率显著高于 SG（P＜0.05）。与 SG 相比，FG 的血清溶菌酶和补体 4 活力显著升高（P＜0.05）。此外，FG 的肠道绒毛数、绒毛高度、肌层厚度和杯状细胞数均显著高于 SG（P＜0.05）。综上，FG 花鲈的免疫能力和肠道健康优于 SG 花鲈，这可能是导致花鲈个体生长速率差异的原因之一。

关键词：脱脂黄粉虫粉；花鲈；生长速率；免疫能力；肠道健康

Difference analysis of immunity and intestinal health of individuals with different growth rates after taking defatted Tenebrio molitor meal diet

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Abstract： This experiment explores the differences in immune capacity and intestinal health of individuals with different growth rates of spotted seabass (Lateolabrax maculatus) after consuming defatted Tenebrio molitor meal feed. 54 spotted seabass with an initial weight of 4.3 ± 0.02 g were selected and fed with 15% level of defatted Tenebrio molitor meal as experimental feed. After 8 weeks of breeding, a total of 15 individuals with the largest body weight and 15 individuals with the smallest body weight were selected as the fast growth group (FG) and slow growth group (SG), respectively. The results showed that the weight gain rate and specific growth rate of FG were significantly higher than those of SG (P<0.05). Compared with SG, the serum lysozyme and complement 4 activities of FG were significantly increased (P<0.05). In addition, the number of intestinal villi, villus height, muscle layer thickness, and goblet cell count in FG were significantly higher than those in SG (P<0.05). In summary, the immune capacity and intestinal health of FG spotted seabass were better than those of SG spotted seabass, which may be one of the reasons for the differences in individual growth rates of spotted seabass.

Key words: Defatted Tenebrio molitor meal; Lateolabrax maculatus; Growth rate; Immunity capacity; Intestinal health

美洲大蠊粉替代鱼粉对罗氏沼虾生长性能、体组成、氨基酸及酶活的影响

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摘要：旨在探究用美洲大蠊粉替代鱼粉对罗氏沼虾生长性能、体组成、氨基酸、消化和免疫酶活的影响。选取健康、初始体重为（8.65±0.004）g 罗氏沼虾 420 尾，随机分成 4 组，每组 3 个重复，每个重复 35 尾虾。对照组（FM 组）饲喂添加 14%鱼粉的基础饲料，试验组分别饲喂用美洲大蠊粉替代 36％（T36 组）、64％（T64 组）和 100%（T100 组）鱼粉的试验饲料。试验期 60d。结果表明：1）各组之间罗氏沼虾生长性能均无显著差异。2）T64 组粗脂肪和粗蛋白含量显著低于 FM 组（P＜0.05）。3）各试验组虾体氨基酸含量显著高于 FM 组（P＜0.05）。4）各试验组脂肪酶活性显著低于 FM 组（P＜0.05）。5）显著降低罗氏沼虾丙二醛和过氧化氢酶活性（P＜0.05）。本研究条件下，不同替代比例不影响罗氏沼虾生长性能且能提高虾体氨基酸含量，以 36%替代水平最佳。64%替代水平下能改善罗氏沼虾免疫力，但会降低抗氧化能力。

关键词：美洲大蠊粉；生长性能；体组成；氨基酸；酶活

Effects of replacement of fish meal by Periplaneta americana meal on growth performance, body composition, amino acid and enzyme activity of Macrobrachium rosenbergii

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Abstract: Objective To investigate the effects of replacing fish meal with Periplaneta americana meal on growth performance, body composition, amino acid, digestion and immunoenzyme activity of Macrobrachium rosenbergii. A total of 420 healthy macrobrachium rosenbergii shrimps with an initial body weight of (8.65±0.004) g were randomly divided into 4 groups with 3 replicates per group and 35 shrimps per replicate. The control group (FM group) was fed a basal diet supplemented with 14% fish meal, and the experimental groups were fed experimental diets in which 36% (T36 group), 64% (T64 group) and 100% (T100 group) fish meal were replaced by Periplaneta americana meal, respectively. The experiment lasted for 60 days. The results showed as follows: 1) There were no significant differences in the growth performance of Macrobrachium rosenbergii among all groups. 2) The contents of crude fat and crude protein in T64 group were significantly lower than those in FM group ($P < 0.05$). 3) The amino acid content of shrimp in experimental groups was significantly higher than that in FM group ($P < 0.05$). 4) The lipase activity of experimental groups was significantly lower than that of FM group ($P < 0.05$). 5) The malondialdehyde and catalase activities of Macrobrachium rosenbergii were significantly decreased ($P < 0.05$). Under the conditions of this study, the different substitution ratio did not affect the growth performance of Macrobrachium rosenbergii and could increase the amino acid content of shrimp body, and the best substitution level was 36%. At 64% substitution level, the immunity of macrobrachium rosenbergii was improved, but the antioxidant capacity was decreased.

Key words: Periplaneta americana meal; Growth performance; Body composition; Amino acids; Enzyme activity

n–3 多不饱和脂肪酸对驯养异齿裂腹鱼繁殖的影响

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摘要：异齿裂腹鱼是西藏重要本土鱼类之一，在人工养殖条件下表现出了繁殖功能障碍，为探究 n-3 多不饱和脂肪酸对驯养异齿裂腹鱼繁殖的影响，本试验对 VI 期雌性驯养和野生异齿裂腹鱼血清中性激素含量、性腺发育、组织切片及组织中脂肪酸进行了比较分析。结果显示：驯养雌激素（E）含量极显著低于野生（P＜0.01），孕酮含量显著高于野生（P＜0.05），睾酮含量显著低于野生（P＜0.05）。野生和驯养在肝脏中均检测出 14 中脂肪酸，在卵母细胞中，野生检测到 14 种氨基酸，驯养检测到 17 种脂肪酸。驯养α-亚麻酸（ALA）在肝脏中显著高于野生(P＜0.05），在卵母细胞中极显著高于野生（P＜0.01），在两种组织中，驯养二十碳五烯酸（EPA）极显著高于野生(P＜0.01），二十碳三烯酸（EET）和二十二碳六烯酸（DHA）差异不显著（P＞0.05）。综上表明，驯养异齿裂腹鱼繁殖功能障碍与 n-3PUFAs 存在着一定联系。

关键词：异齿裂腹鱼；性激素；n-3 多不饱和脂肪酸；繁殖

n-3 Polynsaturated Fatty Acids: Effects on breed of domestic of Schizothorax oconnori

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Abstract： Schizothorax oconnori is one of the important native fishes of Xizang, which shows reproductive dysfunction under artificial culture conditions. To explore the effect of n-3 polyunsaturated fatty acids on the reproduction of domesticated Heterodonts, the serum sex hormone content, gonadal development, tissue sections, and fatty acids in domesticated and wild Heterodont fishes at the VI stage were compared and analyzed. The results showed that the content of estrogen (E) in domestication was significantly lower than that in the wild ($P < 0.01$), the content of progesterone was significantly higher than that in the wild ($P < 0.05$), and the range of testosterone was significantly lower than that in wild ($P < 0.05$). 14 fatty acids were detected in both wild and domesticated livers, 14 amino acids in wild oocytes, and 17 fatty acids in domesticated oocytes. The content of domesticated α-linolenic acid (ALA) in liver was significantly higher than that in wild ($P < 0.\ 05$), and that in oocytes was significantly higher than that in wild ($P < 0.\ 01$). In the two tissues, domesticated eicosapentaenoic acid (EPA) was significantly higher than that in wild ($P < 0.\ 01$). Still, there was no significant difference in eicosapentaenoic acid (EET) and 22 carbon hexaenoic acid (DHA). To sum up, it is suggested that there is a specific relationship between reproductive dysfunction and n-3PUFAs in domesticated Heterodonts.

Key words: Schizothorax oconnori; sex hormone; n-3PUFA; breed

高比例豆粕日粮中添加胆汁酸改善黄鳝肝脏胆汁酸代谢和肠道健康

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摘要：本试验以黄鳝为养殖对象，分别投喂全鱼粉日粮(FM)、全鱼粉+胆汁酸盐日粮(FB)、50%豆粕日粮(SM)和 50%豆粕+胆汁酸盐日粮(SB)，以探究外源胆汁酸缓解高豆粕日粮诱发鱼类胆汁酸代谢异常的作用机制。黄鳝生长性能并未受实验处理的显著影响。高豆粕日粮肝脏局部出现脂滴蓄积的现象，添加胆汁酸后肝脏油滴蓄积现象减缓。外源胆汁酸显著降低了鱼粉组肠道菌群生物多样性，但能恢复豆粕组的菌群生物多样性。高豆粕组添加胆汁酸可显著降低肠道邻单胞菌细菌的丰度，并大幅提高乳杆菌的含量。FM 组肠道内胆汁酸含量显著高于 SM 组。SB 组肠道内胆汁酸含量明显增加。鱼粉组添加胆汁酸促进了肝脏脂肪的合成进程，同时也显著加强了脂肪的分解代谢；SM 组肝脏的脂肪合成和转运代谢均比 FM 组和 SB 组活跃，但是 FM 组和 SB 组的脂肪分解代谢显著加强。高比例豆粕日粮则显著降低了黄鳝肠道屏障相关基因的表达量，但显著增加了肠道炎症因子表达。

关键词：黄鳝；豆粕；胆汁酸；肠道菌群；炎症

Adding bile acids to a high proportion of soybean meal diet to improve hepatic bile acid metabolism and intestinal health in monopterus albus

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Abstract：This experiment used eel as the breeding object and fed them with a whole fish meal diet (FM), a whole fish meal+bile acid salt diet (FB), a 50% soybean meal diet (SM), and a 50% soybean meal+bile acid salt diet (SB) to explore the mechanism of exogenous bile acids alleviating the abnormal bile acid metabolism induced by high soybean meal diet in fish. The growth performance of eel was not significantly affected by experimental treatment. There is a phenomenon of lipid droplet accumulation in the liver of high soybean meal diet, and the accumulation of liver oil droplets slows down after adding bile acids. Exogenous bile acids significantly reduced the gut microbiota biodiversity of the fish meal group, but restored the microbiota biodiversity of the soybean meal group. Adding bile acid to the high soybean meal group can significantly reduce the abundance of intestinal Pseudomonas bacteria and significantly increase the content of lactobacilli. The content of bile acids in the intestine of the FM group was significantly higher than that of the SM group. The content of bile acids in the intestine of the SB group significantly increased. The addition of bile acids to the fish meal group promoted the synthesis process of liver fat, while also significantly enhancing the decomposition and metabolism of fat; The liver fat synthesis and transport metabolism in the SM group were more active than those in the FM and SB groups, but the fat catabolism in the FM and SB groups was significantly enhanced. A high proportion of soybean meal diet significantly reduced the expression of intestinal barrier related genes in monopterus albus, but significantly increased the expression of intestinal inflammatory factor related genes.

Key words: Monopterus albus; Soybean meal; Bile acid; intestinal microbiota; inflammation

第四专题：水产病害防治与水产品质量安全

特异性识别大口黑鲈虹彩病毒（LMBV）核酸适配体的筛选与应用

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摘要：大口黑鲈虹彩病毒（Largemouth bass virus，LMBV）是从患病大口黑鲈中分离得到的病毒性病原，致死率高。然而，目前尚未有治疗 LMBV 感染的有效药物，急需开发新型的快速检测和治疗技术。核酸适配体（aptamer）是一种单链的寡核苷酸链，通过二级或三级结构折叠而特异性地与靶标结合。本研究以 LMBV 为靶标，运用 SELEX 技术筛选出 3 条特异性识别 LMBV 的核酸适配体。二级结构和最小自由能（ΔG）分析表明，核酸适配体具有稳定的茎环结构。经验证，这些核酸适配体均可特异性结合 LMBV，且亲和力达到纳摩尔级别。3 条核酸适配体均未显示出明显的毒性作用，可抑制 LMBV 感染。将核酸适配体截短优化并建立应用于 LMBV 快速诊断的酶联适配体免疫吸附测定技术(enzyme-linked apta-sorbent assay，ELASA)。ELASA 的病毒检出率略低于 qR

关键词：大口黑鲈；核酸适配体；LMBV；快速检测

Selection and Application of novel DNA aptamers specificly recognized Largemouth bass virus (LMBV)

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Abstract：Largemouth bass virus (LMBV) causes high mortality in largemouth bass, and results in serious economic loses in the aquaculture industry. However, there is no effective treatment to control LMBV infection. Aptamers are single-stranded oligonucleotides with high specificity and affinity to various targets, including viruses, viral components, and virus-infected cells. In this study, three novel DNA aptamers (LA38, LB49, and LA13), which specifically targeted LMBV, were identified by selective evolution of ligands by exponential enrichment. All aptamers formed stable stem-loop structures identified by secondary structures and minimum free energy pre-dictions. Moreover, dissociation constant (Kd) measurements and flow cytometry analyses showed that these aptamers specifically bound to LMBV with high affinity at the nanomolar level. Furthermore, these aptamers were nontoxic, and significantly inhibited LMBV infection in vitro and in vivo. Accurate and early detection of LMBV is crucial for diagnosis and prevention. Therefore, we developed an aptamer-based sandwich enzyme-linked apta-sorbent assay (ELASA) for the rapid detection of LMBV. The detection limit of the ELASA was as low as 1.25 × 102 LMBV-infected cells, and the incubation time of the lysate and biotin labeled aptamer was as short as 10 min. For the fish samples collected from the field, the sensitivity of ELASA was 13.3% less than PCR, but the ELASA was much more convenient and less time consuming. The procedure of ELASA mainly requires washing and incubation, with completion in approximately 4 h. Meanwhile, we also developed aptamer-based lateral flow biosensor

(LFB) to detect LMBV. It only needed shorter time for detection, with the complete process needing no more than 90 min. This biosensor detected LMBV infection in a number-dependent manner in LMBV-infected cells as low as 4 × 105 /mL. The LFB method did not need sophisticated manipulation and equipment, when compared to conventional PCR. What’s more, the LFB designed by aptamers, which effectively reduces false positives in the detection process and has the potential to become a tool for rapid field detection of LMBV.

Key words: Micropterus salmoides; Aptamer; LMBV; Rapid detection

鱼类 MARCH7/MARCH8 负调控干扰素抗病毒免疫反应的分子机制

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摘要：泛素化、磷酸化等翻译后修饰（PTM）在干扰素（interferon，IFN）抗病毒免疫反应中发挥重要调控作用。作为一种介导泛素化修饰的E3泛素连接酶，MARCH家族成员近年来获得了越来越多的关注，然而鱼类MARCH蛋白的相关功能机制研究却少有报道。鱼类MARCH7和MARCH8蛋白在结构方面虽然存在差异，代表MARCH家族成员的两种不同形式，但研究发现它们都是RLR通路介导的IFN反应的负调控因子。MARCH8、MARCH7分别靶向STING和TBK1蛋白，使其以K48-连接的泛素化依赖的方式降解，进而阻断免疫级联反应向下游传导，抑制IFN、ISG等抗病毒分子上调表达；同时MARCH7也靶向TBK1直接影响了TBK1-IRF3的信号转导过程，使TBK1介导的IRF3磷酸化水平显著降低，抑制下游IFN抗病毒免疫反应。研究结果揭示了鱼类MARCH蛋白参与负调控IFN抗病毒免疫反应的分子机制。

关键词：干扰素反应，MARCH，E3连接酶，泛素化修饰，调控机制

Molecular mechanism of fish MARCH7/MARCH8 negatively regulating interferon-mediated antiviral immune response

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Abstract：Post-translational modifications (PTM) such as ubiquitination and phosphorylation play an important role in the regulation of antiviral immune response of interferon (IFN). As an E3 ubiquitin ligase that mediates ubiquitination modification, MARCH family members have received increasing attention in recent years, but the related functional mechanisms of MARCH proteins in fish have been rarely reported. Although fish MARCH7 and MARCH8 proteins differ in structure and represent two different forms of MARCH family members, they were found to be negative regulators of IFN response mediated by RLR pathway. MARCH8 and MARCH7 target STING and TBK1 proteins for degradation, respectively, in a K48-linked ubiquitination dependent manner, thus blocking the downstream conduction of the immune cascade and inhibiting the expression of antiviral molecules such as IFN and ISG. Besides, MARCH7 also directly attenuates the signal transduction of TBK1-IRF3, significantly reducing the level of TBK1-mediated IRF3 phosphorylation and inhibiting the downstream IFN antiviral immune response. The results reveal the molecular mechanism of fish MARCH protein involved in negative regulation of IFN antiviral immune response.

Key words: IFN response; MARCH; E3 ubiquitin ligase; ubiquitination modification; regulatory mechanism

黄鳍棘鲷鳃细胞系构建及其作为眼点淀粉卵涡鞭虫体外感染载体的应用

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摘要：眼点淀粉卵涡鞭虫是一种常见的寄生鞭毛虫，对海水鱼产业造成巨大的经济损失。然而，淀粉卵涡鞭虫病的发病机理尚不清楚，这一现状严重阻碍了抗寄生虫药物的开发。因此，本研究拟建立眼点淀粉卵涡鞭虫体外感染体系，并从细胞和分子水平探究淀粉卵涡鞭虫病的致病机理。从黄鳍棘鲷鳃组织中分离并建立了一株新的细胞系，命名为 ALG，该细胞系在添加了 15%胎牛血清的 DMEM 培养基中具有稳定、良好的培养效果，并稳定继代培养至第 30 代。根据 Cyt b 基因序列扩增和比对结果可确定所建立的鳃细胞系来源于黄鳍棘鲷。将 ALG 接种于细胞小室，并应用于眼点淀粉卵涡鞭虫体外感染，眼点淀粉卵涡鞭虫体外感染时感染率为 37.23 ± 5.75%。此外，扫描电子显微镜进一步确认滋养体可通过假根寄生于细胞单层表面。眼点淀粉卵涡鞭虫体内及体外感染时均可上调宿主 Casp 3、IL-1、IL-10、TNF-α等凋亡和炎症相关基因的表达，表明体外感染体系可成功复制出鱼体感染眼点淀粉卵涡鞭虫后的病理反应。因此，本研究建立的体外感染体系有望成为研究寄生虫与宿主相互作用的重要工具。

关键词：眼点淀粉卵涡鞭虫；黄鳍棘鲷；细胞系；体外感染

Establishment of a gill cell line from yellowfin seabream (Acanthopagrus latus) for in vitro infection of Amyloodinium ocellatum

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Abstract： Amyloodinium ocellatum is among the most devastating protozoan parasites, causing huge economic losses in the mariculture industry. However, the pathogenesis of amyloodiniosis remains unknown, hindering the development of targeted anti-parasitic drugs. The A. ocellatum in vitro model is an indispensable tool for investigating the pathogenic mechanism of amyloodiniosis at the cellular and molecular levels. The present work developed a new cell line, ALG, from the gill of yellowfin seabream (Acanthopagrus latus). The cell line was routinely cultured at 28 °C in Dulbecco's modified Eagle medium (DMEM) supplemented with 15% fetal bovine serum (FBS). ALG cells were adherent and exhibited an epithelioid morphology; the cells were stably passed over 30 generations and successfully cryopreserved. The cell line derived from A. latus was identified based on partial sequence amplification and sequencing of cytochrome B (Cyt b). The ALG was seeded onto transwell inserts and found to be a platform for in vitro infection of A. ocellatum, with a 37.23 ± 5.75% infection rate. Furthermore, scanning electron microscopy (SEM) revealed that A. ocellatum parasitizes cell monolayers via rhizoids. A. ocellatum infection increased the expression of apoptosis and inflammation-related genes, including caspase 3 (Casp 3), interleukin 1 (IL-1), interleukin 10 (IL-10), tumor necrosis factor-alpha (TNF-α), in vivo or in vitro. These results demonstrated that the in vitro gill cell monolayer successfully recapitulated in vivo A. latus host responses to A. ocellatum infection. The ALG cell line holds great promise as a valuable tool for investigating parasite-host interactions in vitro.

Key words: Amyloodinium ocellatum; Acanthopagrus latus; cell line; in vitro infection

虹鳟疫病防控技术研究

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摘要：虹鳟是我国重大国家战略“深远海养殖”首选品种之一，被列为水产“种业翻身仗”必须攻克的难题，对于践行“大食物观”具有重要意义。可该产业一直遭受传染性造血器官坏死病（IHN）和传染性胰脏坏死病（IPN）的致命打击，苗种存活率不到30%，产业发展停滞不前。团队针对该问题，开展了疫病防控技术研发工作，在疫苗研制与产业化及抗病药物筛选方面取得了显著效果。创制了保护率高达90%以上的IHN核酸疫苗，免疫后四天即可提供完全的免疫保护作用，获批了我国首个水产核酸疫苗转基因生物安全证书；研发了IHN/IPN二联灭活疫苗，通过添加佐剂成功将灭活疫苗保护期延长至9个月以上；通过筛选3000多种药物，获得效果良好的预防及治疗IHN和IPN的药物，最高可提高患病虹鳟存活率50%以上。该系列抗病毒产品的产业化将极大的解决我国虹鳟产业卡脖子病害难题。

关键词：虹鳟；核酸疫苗；灭活疫苗；抗病毒；药物筛选

Research on prevention and control technologies for infectious diseases of rainbow trout

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Abstract： Rainbow trout is one of the best species for the national key strategy “profound Marine aquaculture”, and is listed as a problem that must be overcome in aquaculture "Seed Industry Recovery", which is of great significance for practicing "Big Food Concept". However, the industry has been suffering from infectious hematopoietic organ necrosis disease (IHN), the survival rate of fish fry is less than 30%, and the development of the industry has stagnated. To solve this problem, our team carried out research and development of disease prevention and control technologies, remarkable results have been achieved in the development and industrialization of vaccines and the screening of antiviral drugs. We created an IHN nucleic acid vaccine with a protection rate of more than 90%, which can provide complete immune protection four days after immunization which was approved China's first aquatic nucleic acid vaccine GMO safety certificate. IHN/IPN vaccine was developed, and the protection period of the inactivated vaccine was extended to more than 9 months by adding an adjuvant. Through screening more than 3,000 drugs, we obtained candidate drugs those could provide effective prevention and treatment of IHN and IPN, and the survival rate of infected rainbow trout could be improved more than 50% by treatment with those drugs. The industrialization of this series of antiviral products will greatly solve the disease problem of China's rainbow trout industry.

Key words: Rainbow trout; DNA vaccine, Attenuated vaccine, Antiviral Research, Drug Screening

浸泡灭活疫苗对新加坡石斑鱼虹彩毒的免疫应答和保护作用的评价

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摘要：新加坡石斑鱼虹彩毒(Singapore grouper iridovirus, SGIV)在水产养殖业的石斑鱼幼虫和幼鱼阶段具有很高的死亡率。迄今为止，使用腹腔注射的灭活病毒和重组 DNA 疫苗已被证明可提供对 SGIV 的保护，但这种疫苗递送模式限制了它们在现场试验中的应用。本文研究了含 Montanide IMS 1312 佐剂(IMS 1312)的浸泡病毒灭活疫苗对 SGIV 感染的保护作用。与 PBS 对照组相比，IMS 1312 灭活疫苗(IMS- v 组)浸泡的鱼对 SGIV 具有显著的保护作用，相对存活率(RPS)为 57.69%。此外，IMS-V 组的病毒核心基因转录减少，SGIV 引起的病理严重程度在多个组织中相对较轻。浸泡疫苗激活了 AKP 和 ACP 的活性，提高了免疫相关基因的 mRNA 水平，包括干扰素刺激基因 56 (ISG56)、白细胞介素(IL)-1β、CD8α、黏液病毒抗性基因(MXI)、肿瘤坏死因子(TNF) α和 toll 样受体(TLR)21。此外，通过 RNA-Seq 转录组分析研究了浸液疫苗诱导脾和肾的免疫应答。与 PBS 对照组相比，IMS-V 组脾脏和肾脏中分别有 106 个和 22 个基因上调或下调。KEGG 分析显示，这两种受调控的差异基因均富集于免疫信号通路，包括 MAPK 信号通路、PI3K-Akt 信号通路、细胞因子-细胞因子受体相互作用通路和 JAK-STAT 信号通路。同样，脾脏和肾脏中受疫苗免疫调节的差异基因在干扰素免疫和炎症相关的 KEGG 通路中显著富集。此外，随机选择的 8 个基因 MKNK、DUSP1-A、CACNB1、FASLG、SGK1、MCL1、IL2RB 和 CCR9A 的转录变化与转录组数据一致。总之，我们的研究结果提供了证据，证明含有 IMS 1312 的灭活 SGIV 浸泡疫苗可诱导石斑鱼对 SGIV 产生保护性免疫反应。

关键词：新加坡石斑鱼虹彩病毒、灭活疫苗、浸泡、保护作用、免疫反应

Evaluation of immune response and protection against Singapore grouper iridovirus induced by immersion inactivated vaccine

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Abstract：Singapore grouper iridovirus (SGIV) always causes high mortality rates in the larval and juvenile stages of grouper in aquaculture industry. To date, inactive virus and recombinant DNA vaccines using intraperitoneal injection have been demonstrated to provide protection against SGIV, but this mode of vaccine delivery limited their applications in field test. Here, we investigated the protection efficacy against SGIV infection by immersion virus-inactivated vaccine containing Montanide IMS 1312 adjuvant (IMS 1312). Compared to PBS control group, fish immersed with inactivated virus vaccine containing IMS 1312 (IMS-V group) were significantly protected against SGIV, with a relative percent survival (RPS) of 57.69%. Furthermore, the transcripts of viral core genes were reduced, and the pathological severity evoked by SGIV were relative mild in multiple tissues of IMS-V group. The immersion vaccine activated AKP and ACP activities and increased the mRNA levels of immune-associated genes, including interferon stimulated gene 56 (ISG56), interleukin (IL)-1β, CD8α, myxovirus resistance gene (MXI), tumor necrosis factor (TNF) α and toll-like receptor (TLR)21. Moreover, the immune response in spleen and kidney induced by the immersion vaccine was studied by RNA-Seq transcriptome analysis. A total of 106 and 22 genes were both upregulated or downregulated in spleen and kidney of IMS-V group compared to PBS control group. KEGG analysis showed that these both regulated DEGs were enriched in the pathways related to immune signaling, including MAPK signaling, PI3K-Akt signaling, cytokine-cytokine receptor interaction and JAK-STAT signaling pathways. Similarly, the DEGs regulated upon vaccine immunization in spleen and kidney specially were significantly enriched in interferon immune and inflammation related KEGG pathways. Furthermore, the transcriptional changes of 8 randomly selected genes, such as MKNK, DUSP1-A, CACNB1, FASLG, SGK1, MCL1, IL2RB and CCR9A from quantitative PCR were consistent with transcriptome data. Together, our results provided evidence that immersion vaccine of inactivated SGIV with IMS 1312 induced protective immune response of grouper against SGIV.

Key words: Singapore grouper iridovirus; Inactivated vaccine; Immersion; Protection; Immune response

五氯酚钠胁迫对泥蚶 SOD、Na+-K+-ATP 酶活力及基因表达和血细胞功能的影响

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摘要：为探讨五氯酚钠长期胁迫对泥蚶(Tegillarca granosa)的毒性效应，本文研究了不同浓度五氯酚钠胁迫对泥蚶生理代谢相关酶活力、酶活相关基因表达和血细胞功能的影响。实验设置 3 组：低浓度组（五氯酚钠质量浓度 10 μg/L）、高浓度组（五氯酚钠质量浓度 100 μg/L）和对照组，实验持续 14 d，分别在第 1 d、7 d、14 d，检测生理代谢相关酶活力、酶活基因表达量及血细胞功能指标。结果显示，随着胁迫时间的延长和 PCP-Na 浓度的增加，泥蚶 SOD 和 Na+-K+-ATP 酶活力均发生显著变化，PCP-Na 胁迫后 SOD 和 Na+-K+-ATP 酶活力均呈现下降趋势，且均低于对照组。PCP-Na 胁迫对泥蚶转录水平造成了一定影响，不同组织中 SOD 和 ATP 合酶基因表达量变化趋势不同。肝胰腺中 SOD 和 ATP 合酶基因表达量随浓度的增加呈现先增加后降低趋势，鳃中则呈现先降低后增加趋势。PCP-Na 胁迫抑制

关键词：五氯酚钠；泥蚶；酶活性；基因表达；血细胞

Effects of sodium pentachlorophenol stress on SOD, Na+-K+-ATPase activity, gene expression and blood cell function of Tegillarca granosa

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Abstract： To explore the toxic effects of sodium pentachlorophenol on Tegillarca granosa under long-term stress, the effects of sodium pentachlorophenol stress on the activities of enzymes related to physiological metabolism, expression of genes related to enzyme activity and blood cell function of Tegillarca granosa were studied in this paper. Three concentration gradients were set up in the experiment: low concentration group (mass concentration of sodium pentachlorophenol 10 μg/L), high concentration group (mass concentration of sodium pentachlorophenol 100 μg/L) and the control group. The experiment lasted for 14 days, physiological metabolism related enzyme activity, enzyme activity gene expression, and blood cell function indicators were measured on the 1st, 7th, and 14th day. The results showed that with the prolongation of stress time and the increase of PCP-Na concentration, the SOD and Na+- K+- ATPase activities of Tegillarca granosa were significantly changed. After PCP-Na stress, the SOD and Na+-K+-ATPase activities showed a downward trend, and were lower than the control group. PCP-Na stress had a certain impact on the transcription level of Tegillarca granosa. Besides The changes of SOD and ATP synthase gene expression were different in different tissues. The expression levels of SOD and ATP synthase genes in the liver and pancreas showed a trend of first increasing and then decreasing with increasing concentration, while in the gills, they showed a trend of first decreasing and then increasing.PCP-Na stress inhibited the cellular immunity of Tegillarca granosa. Under PCP-Na stress, the total number of blood cells, cell viability, hemoglobin count, and phagocytic rate of the mud clam showed a decreasing trend, and the total number of blood cells, cell viability, and phagocytic rate were lower than those of the control group. The above results indicated that sodium pentachlorophenol stress had an impact on the physiological metabolism, gene expression and blood cell function of Tegillarca granosa. Sodium pentachlorophenol stress could lead to oxidative stress, which also induced changes in gene transcription levels, and affected immune defense parameters. This study could provide reference for the study of the toxic effects of new pollutants on marine organisms, and provide scientific basis for ecological risk assessment.

Key words: Sodium pentachlorophenol; Tegillarca granosa; enzyme activity; gene expression; blood cells

白介素 8 参与尼罗罗非鱼抗细菌感染

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摘要：白细胞介素 8（IL8）对促进炎症至关重要，是各种生理病理过程中的重要介质，同时影响免疫功能。IL8 对尼罗罗非鱼（Oreochromis niloticus）急性细菌感染免疫反应的影响尚不清楚。这项研究发现了尼罗罗非鱼的 IL8 基因（On-IL8）。它包括一个 285 bp 的开放阅读框，编码 94 个氨基酸。On-IL8 的转录水平在头肾组织中最高，并能被无乳链球菌和嗜水气单胞菌急剧诱导。此外，体外实验显示，On-IL8 可调控多种免疫过程，如上调 IL-1β 和 TNFα，下调 IL-10 和 TGFβ，抑制 P38 和 P65，促进 MyD88 和 STAT3，促进炎症反应。此外，On-IL8 还能抑制 NF-κB 信号通路，这与体外实验结果一致。这些重要发现为进一步研究 IL8 如何保护硬骨鱼免受细菌感染奠定了基础。

关键词：白介素 8；尼罗罗非鱼；细菌感染；急性炎症

Interleukin-8 involved in Nile Tilapia (Oreochromis niloticus) against bacterial infection

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Abstract: Interleukin 8 (IL8) is vital in promoting inflammation and is a crucial mediator in various physiopathological processes while influencing immunological function. The effect of IL8 on the immunological response to acute bacterial infections in Nile tilapia (Oreochromis niloticus) remains unknown. This work found an IL8 gene from Nile tilapia (On-IL8). It includes a 285 bp open reading frame and codes for 94 amino acids. The transcript levels of On-IL8 were highest in the head-kidney tissue and sharply induced by Streptococcus agalactiae and Aeromonas hydrophila. Besides, in vitro experiments revealed that On-IL8 regulated a variety of immunological processes, such as up-regulating IL-1β and TNFα, down-regulating IL-10 and TGFβ, inhibiting P38 and P65, promoting MyD88 and STAT3, and promoting inflammatory responses. Moreover, On-IL8 suppressed the NF-κB signaling pathway, consistent with in vitro results. These significant findings serve as the basis for further investigation into how IL8 confers protection to bony fish in opposition to bacterial infections.

Key words: interleukin 8; Nile tilapia; bacterial infection; acute inflammation

金属铜锌对鱼类多子小瓜虫病和刺激隐核虫病的防控效果研究

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摘要：为了测试金属铜锌能否预防海水鱼刺激隐核虫病和淡水鱼多子小瓜虫病，我们将金属铜、锌及其合金材料铺设于鱼缸底部，并向鱼缸中转入经刺激隐核虫或多子小瓜虫感染的病鱼。结果表明，铜、锌及其合金薄板或者筛网可在数日内有效阻断刺激隐核虫和多子小瓜虫的生活史，大大减少了病虫的数量，从而降低了染虫鱼的死亡率。体外实验结果显示，虫细胞质膜在与上述金属表面接触仅数分钟后就发生破裂，细胞质溢出。而上述寄生虫的包囊期细胞在与铜合金片直接接触一小时左右后，虽然没有出现破损，但它们却完全丧失了增殖能力并最终死亡。推测认为通过接触，虫细胞从金属表面摄入了过量的铜或者锌，其最终含量为对照组的数十甚至上百倍。但在整个实验中，上述金属材料未导致养殖鱼类或养殖用水中的重金属含量超标。

关键词：刺激隐核虫；多子小瓜虫；金属铜锌；大黄鱼；虹鳟鱼

Stationary metal sheets (copper and/or zinc) in fish tanks prevent Cryptocaryon irritans and Ichthyophthirius multifiliis infection of large yellow croaker and rainbow trout: In vivo and in vitro effects

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Abstract：-

Key words: Cryptocaryon irritans, Ichthyophthirius multifiliis, metal sheets (copper and/or zinc), large yellow croaker, rainbow trout

17 种精油对褶皱臂尾轮虫的杀灭效果试验

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摘要：为了解 17 种植物精油对褶皱臂尾轮虫的杀灭效果，对褶皱臂尾轮虫的杀灭活性进行初筛，初筛后对轮虫进行急性毒性试验，研究这几种精油对褶皱臂尾轮虫的杀灭效果（24 h 内）和对轮虫种群增长的抑制作用（7 d 内）。结果表明，在 17 种植物精油的初筛中，丁香酚、薄荷醇、柠檬烯、香芹酚、肉桂醛、大蒜素显示出了对褶皱臂尾轮虫高毒性；在急性毒性试验中，测得这 6 种精油在 24 h 时的半致死浓度分别为 0.462、0.548、0.600、0.680、0.720 和 0.841 mg/L；在 24 h 杀灭试验中，几种精油对轮虫的杀灭率随时间的增加而上升，其中丁香酚、薄荷醇可在 6 h 内杀灭所有供试轮虫，显著优于同时间其他处理组（P＜0.05）。在抑制轮虫群体增长试验中，精油组的轮虫数量增长均小于对照组，其中丁香酚、薄荷醇组的轮虫数量增长缓慢。指出，薄荷醇、丁香酚的杀灭效果优于辛硫磷，可作为水产养殖中具有潜力的植物源轮虫防控药物。

关键词：植物精油；褶皱臂尾轮虫；杀灭活性；轮虫防治

Study on Killing Effect of 17 Essential Oils on Brachionus plicatilis

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Abstract： In order to understand the killing effect of 17 plant essential oils on the Brachionus plicatilis, and the best killing oil was selected for acute toxicity tests on the Brachionus plicatilis. The killing effect of these essential oils on the Brachionus plicatilis (within 24 hours) and the inhibitory effect on the population growth of the Brachionus plicatilis (within 7 days) were studied. The results showed that in the initial screening of 17 plant essential oils, eugenol, menthol, limonene, carvacrol, cinnamaldehyde, and allicin showed high toxicity to the Brachionus plicatilis; In the acute toxicity test, the half lethal concentrations of these six essential oils at 24 hours were measured to be 0.462, 0.548, 0.600, 0.680, 0.720, and 0.841 mg/L, respectively; In the 24-hour killing experiment, several essential oils at absolute lethal concentrations showed an increase in the killing rate of Brachionus plicatilis over time. Among them, eugenol and menthol essential oils were able to kill all the tested Brachionus plicatilis within 6 hours, significantly better than other treatment groups at the same time (P<0.05).In the experiment of inhibiting the growth of Brachionus plicatilis population, the growth of rotifer numbers in the essential oil group was smaller than that in the control group. Among them, the growth of rotifer numbers in the eugenol and menthol groups was slow, respectively. It is pointed out that the killing effect of menthol and eugenol are superior to phoxim. They can be used as potential plant-based rotifer control drugs in aquaculture.

Key words: Plant essential oil; Brachionus plicatilis; Killing activity; Rotifer control

Low–temperature augmentation of Acinetobacter johnsonii pathogenicity in American bullfrog

(Rana catesbeiana)

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Abstract：Acinetobacter johnsonii is a denitrifying bacterium commonly used as an environmental probiotic in aquaculture and industrial wastewater treatment. However, the research on its potential pathogenicity to animals is limited. Recently, 23 isolates were obtained from diseased American bullfrogs on several bullfrog farms in Guangdong Province, China, during low-temperature seasons. Three representativ

Key words: Acinetobacter johnsonii; American bullfrog; Probiotics; Low-Temperature; Systemic infection

Low-temperature augmentation of Acinetobacter johnsonii pathogenicity in American bullfrog (Rana catesbeiana)

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Abstract：Acinetobacter johnsonii is a denitrifying bacterium commonly used as an environmental probiotic in aquaculture and industrial wastewater treatment. However, the research on its potential pathogenicity to animals is limited. Recently, 23 isolates were obtained from diseased American bullfrogs on several bullfrog farms in Guangdong Province, China, during low-temperature seasons. Three representative isolates were selected for virulence testing, which revealed high virulence toward bullfrogs. The artificial infection demonstrated that the strain was more virulent at 15°C than at 28°C, and no lesion or death was observed in mice after 14 days of intraperitoneal injection with the strain at a concentration of 3.27 × 106 Colony-Forming Units (CFU)/g. Additionally, the expression levels of at least 11 virulence genes in these strains were found to be significantly higher at 15°C than at 28°C. Bullfrog immune genetic and pathological examinations revealed a rapid and distinctive immune response after infection with A. johnsonii. Our findings uncovered the novel phenomenon of the pathogenicity of A. johnsonii in bullfrogs under low-temperature conditions, warning of the risks of probiotic use in aquaculture, and the potential threat of A. johnsonii to amphibian populations.

Key words: Acinetobacter johnsonii; American bullfrog; Probiotics; Low-Temperature; Systemic infection

台湾泥鳅一种细菌性病原的分离鉴定

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摘要：为研究台湾泥鳅腐皮病的病原，对其腐皮等病变部位进行细菌分离纯化，获得一株优势菌株，命名为P1，利用革兰氏染色观察其形态特征，利用PCR扩增技术、16S rRNA基因测序，得到病原菌的序列，用MEGA软件构建系统进化树，再结合生理生化分析结果鉴定菌种名称。结果发现：革兰氏染色阴性，弧形，两端钝圆；菌体长1-1.5μm，宽度1-1.2μm，有菌丝和鞭毛；16S rRNA基因1395bp；建立系统进化树后发现P1与霍乱弧菌处于同一分支；生理生化实验结果与霍乱弧菌一致。最终鉴定出该菌株为霍乱弧菌(Vibrio.cholerae)。药敏实验结果表明该分离菌株对头孢哌酮、卡那霉菌、万古霉素等9种抗生素高度敏感；对四环素中度敏感；对呋喃唑酮、复方新诺明、克林霉素等18种抗生素耐药。实验结果为台湾泥鳅腐皮病的病原鉴定和药物防治提供实验研究价值。

关键词：台湾泥鳅；腐皮病；霍乱弧菌；分离；鉴定

Isolation and Identification of a Bacterial Pathogen from Paramisgurnus dabryanus ssp.

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Abstract： In order to study the pathogen of P. dabryanus ssp., a dominant strain named P1 was obtained by bacterial isolation and purification of the diseased parts such as the rotting skin . The morphological characteristics of the strain were observed by Gram staining, and the sequence of the pathogen was obtained by PCR amplification and 16SrRNA gene sequencing. The phylogenetic tree was constructed by MEGA software.Then through physiological and biochemical analysis identification.The results showed that Gram staining was negative, curved, and blunt round at both ends. 1-1.5μm long and 1-1.2μm wide, with mycelium and flagella.16SrRNA gene 1395bp;After phylogenetic tree was established, P1 and Vibrio cholerae were found to be in the same clade.The physiological and biochemical results were consistent with V. cholerae.The strain was eventually identified as V. cholerae.The results of drug sensitivity test showed that the isolated strain was highly sensitive to nine kinds of antibiotics, such as cefoperazone, canomyces and vancomycin.Moderate sensitivity to tetracycline;It is resistant to 18 kinds of antibiotics such as furazolidone, cotrimoxazole and clindamycin.The results provided reference value for pathogen identification and drug control of P. dabryanus ssp..

Key words: Paramisgurnus dabryanus ssp.; rotting skin disease; Vibrio cholerae; isolation; identification

鱼类干扰素强大的抗病功能

及其在替抗制剂和育种中的应用

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摘要：干扰素具有抗病毒、抗肿瘤、免疫调节等功能，是现代医学研究热点之一。近年来研究发现：鱼类干扰素不仅在抗病毒免疫中发挥着强大的调控功能，而且在抗细菌免疫中也发挥着直接杀菌和调控抗菌的功能。本文首先介绍了鱼类干扰素的特征。然后，以草鱼干扰素 1 为代表，重点阐述了原核重组表达干扰素在抗草鱼出血病中功效及机制、原核重组表达干扰素体内外直接杀菌及调控抗菌功能及机制。接着，基于草鱼干扰素 1 蛋白结构，设计了 20 个氨基酸的小肽，利用酵母表达系统实现真核发酵表达，制备成纳米肽，拌饲投喂，对多种水产动物表现出抗病毒病、抗细菌病、促进生长、改善品质等功效，形成理想“替抗”制剂。最后，介绍了利用基因编辑技术敲除鱼类干扰素几个负调控基因，显著增强了抗病毒能力和人工感染存活率，显示出抗病育种潜能。本文综述了近年来我国水产科技工作者在鱼类干扰素领域突出贡献，进一步推动具有强大抗病毒抗细菌免疫调节功能的鱼类干扰素研究和应用。

关键词：干扰素；抗病毒活性；抗细菌活性；纳米制剂；抗病育种

The powerful disease resistance function of fish interferon and its application in substitute resistance preparations and breeding

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Abstract： Interferons possess antiviral, anti-tumor, immunomodulatory functions, and is one of the hot spots in modern medical research. In recent years, it has been found that fish interferons not only play a powerful regulatory function in antiviral immunity, but also play a direct bactericidal and regulatory antibacterial function in anti-bacterial immunity. This paper first introduces the characteristics of fish interferons. Then, taking grass carp interferon 1 as the representative, the effects and mechanisms of prokaryotic recombinant expression of interferon in the fight against grass carp hemorrhagic disease, the direct bactericidal function and the regulation of antibacterial function and mechanism of prokaryotic recombinant expression interferon in vivo and in vitro were addressed. Further, based on the protein structure of grass carp interferon 1, a small peptide of 20 amino acids was designed, which was expressed by eukaryotic fermentation using yeast expression system, and prepared into nanopeptides, which were mixed and fed to a variety of aquatic animals and showed antiviral diseases, antibacterial diseases, growth promotion, quality improvement and other effects, forming an ideal "instead of antibiotics" preparation. In addition, gene editing technology was used to knock out several negative regulatory genes of interferon in fishes, which significantly enhance their antiviral ability and improve survival rate of artificial infection, showing the breeding potential for disease resistance. This paper reviews the outstanding contributions of Chinese aquatic scientists in the field of fish interferons in recent years, and further promotes the researches and applications of fish interferons, which exhibit strong anti-viral and anti-bacterial immune regulation functions.

Key words: Interferon; antiviral activity; antibacterial activity; nanopeptide; anti-disease breeding

海鲈肠道分离的乳酸乳球菌作为海鲈益生菌的表征研究

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摘要：使用益生菌是一种有效的预防鱼类传染病的方法。本研究旨在评估一株从海鲈肠道内分离的乳酸乳球菌作为海鲈益生菌的特征。我们的结果表明，分离到的乳酸乳球菌菌株不具备运动性和溶血性，但能形成生物膜，对低 pH、高渗透压和胆盐的环境具有良好的耐受性。乳酸乳球菌对哈维氏弧菌和嗜水气单胞菌等多种细菌性病原具有抑制作用。体外细胞实验表明，乳酸乳球菌对海鲈细胞系（SPF）具有较高的黏附性。乳酸乳球菌与海鲈虹彩病毒（SPIV）共孵育能够降低 SPIV 在海鲈细胞系（SPF）的增殖，调节 SPF 细胞多种细胞因子的表达。动物实验结果表明，长时间饲喂乳酸乳球菌对海鲈的生长发育不会产生任何不利影响。同时，乳酸乳球菌能够降低 SPIV 感染对海鲈造成的损伤，降低 SPIV 感染海鲈的死亡率。总之，新分离的乳酸乳球菌菌株在海鲈抗病毒、抗病原菌方面以及免疫调节功能方面具有良好的应用前景。

关键词：益生菌；海鲈；抗病毒；免疫调节

Characterization of Lactococcus lactis isolated from sea perch (Lateolabrax japonicus) gut as probiotics in sea perch

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Abstract：The use of probiotics is an effective method to prevent infectious diseases in fish. The aim of this study was to assess the characteristics of a Lactococcus lactis strain isolated from the gut of sea perch (Lateolabrax japonicus) as a probiotic for sea perch. Our results showed that the isolated Lactococcus lactis strains were not motile and hemolytic, were able to form biofilm forces, and were well tolerated in low pH, high osmolality, and bile salt environments. Lactococcus lactis has an inhibitory effect on various bacterial pathogens such as Vibrio harveyi and Aeromonas hydrophila. In vitro cell experiments showed that Lactococcus lactis had high adhesion to sea perch cell lines (SPF). Lactococcus lactis co-incubation with sea perch iridovirus (SPIV) was able to reduce the proliferation of SPIV in SPF cells and regulate the expression of multiple cytokines in SPF cells. The results of animal experiments showed that prolonged feeding of Lactococcus lactis did not have any adverse effects on the growth and development of sea perch. At the same time, Lactococcus lactis can reduce the damage caused by SPIV infection to sea perch and reduce the mortality of SPIV infected sea perch. In conclusion, the newly isolated Lactococcus lactis strains have good application prospects in antiviral, anti-pathogen and immunoregulatory functions of sea perch.

Key words: Probiotics; sea perch; antiviral; immunomodulatory

罗非鱼源无乳链球菌附属分泌系统及相关蛋白功能鉴定

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摘要：除了经典分泌系统外，许多革兰阳性菌还具有附属分泌系统，负责输出包括毒力因子在内的胞外分泌。本研究发现鱼无乳链球菌 THN0901 菌株 SecY2A2 辅助分泌系统的缺失导致缺失株ΔaccSec 的生长能力酸耐受能力减弱；缺失株ΔaccSec 的细胞黏附能力、巨噬细胞内存活能力减弱，在罗非鱼全血中生长能力减弱；毒力方面辅助分泌系统的缺失降低了该菌株在尼罗罗非鱼中的毒力。采用 label Free 定量蛋白质组学方法比较ΔaccSec 和野生型菌株胞外差异表达蛋白，结果表明ΔaccSec 相较于野生型胞外分泌蛋白 33 个下调 512 个上调，其中依赖辅助 Sec 的 lpxtg 锚定黏附蛋白、具有 PDZ 结构域的长链样蛋白酶、ESAT-6 样蛋白质依赖于 SecY2A2 辅助分泌系统进行分泌；另一方面，细胞伸长因子、甘油醛-3-磷酸脱氢酶、磷酸甘油酸激酶等等蛋白在缺失突变株ΔaccSec 分泌显著上调。

关键词：无乳链球菌；附属分泌系统；蛋白质组分析

Characterization of the accessory secretion system and related proteins of Streptococcus agalactiae of tilapia origin

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Abstract： In addition to canonical Sec system, several Gram-positive bacteria also possess a accessory Sec system, which is a specialized translocation system， responsible for the export of a subset of secretory proteins, including virulence factors. In this study, we found that inactivation of the SecY2A2 accessory Sec system resulted in reduced growth capacity and acid tolerance in Streptococcus lactis-free strain THN0901. Compared with the wild strain, ΔaccSec had diminished cell adhesion capacity, intracellular survival in macrophages, and diminished growth capacity in tilapia whole blood. The absence of the auxiliary secretion system of SecY2A2 in terms of virulence reduced the virulence of the strain in Nile tilapia. To better understand the SecY2A2 accessory Sec system on biological functions, label Free quantitative proteomics was used to compare the extracellular differentially expressed proteins of ΔaccSec and the wild-type strain, and the results showed that 33 down-regulated and 512 up-regulated extracellular secretory proteins were present in ΔaccSec compared to the wild-type. The accessory Sec-dependent LPXTG-anchored adhesin protein, Lon-like protease with PDZ domain, and ESAT-6-like proteins were secreted in dependence on the accessory Sec system.The elongation factor, glyceraldehyde-3-phosphate dehydrogenase, and phosphoglycerate kinase were significantly up-regulated in the secretion of ΔaccSec mutant strain.

Key words: Streptococcus agalactiae; Accessory secretory system; Proteomic analysis

血管活性肠肽(VIP)帮助尼罗罗非鱼(Oreochromis niloticus)抵抗无乳链球菌感染

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摘要：血管活性肠肽(VIP)是胰高血糖素家族成员之一，参与肠道蠕动、免疫反应等多种生物学活动。本研究从尼罗罗非鱼(Oreochromis niloticus)中鉴定了 VIP 前体(On-VIP)及其受体 VIPR1 (On-VIPR1)，并探究了其在尼罗罗非鱼抗细菌感染中的免疫调节功能。On-VIP 和 On-VIPR1 均高表达于肠道且能被无乳链球菌显著诱导表达。同时，免疫组化结果表明 On-VIP 和 On-VIPR1 分别定位于肠道纵肌层和肠道黏膜上皮。此外，体外和体内试验证明 On-VIP 具有多种免疫调节功能，包括降低 P65, P38, MyD88, STAT3 和 AP1，上调 CREB 和 CBP，以及抑制炎症反应。体内实验还表明 On-VIP 可以帮助尼罗罗非鱼抵抗细菌侵染，并促进细胞凋亡和细胞焦亡。这些数据为进一步了解 VIP 保护硬骨鱼抵抗细菌感染的机制奠定了理论基础。

关键词：尼罗罗非鱼，无乳链球菌，血管活性肠肽，血管活性肠肽受体，免疫应答

Vasoactive intestinal peptide (VIP) protects Nile tilapia (Oreochromis niloticus) against Streptococcus agalatiae infection

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Abstract： Vasoactive intestinal peptide (VIP), a member of secretin/glucagon family, is involved in a variety of biological activities such as gut motility, immune responses, and carcinogenesis. In this study, the VIP precursor gene (On-VIP) and its receptor gene VIPR1 (On-VIPR1) were identified from Nile tilapia (Oreochromis niloticus), and the functions of On-VIP in the immuno-modulation of Nile tilapia against bacterial infection were investigated and characterized. On-VIP and On-VIPR1 contain a 450 bp and a 1326 bp open reading frame encoding deduced protein of 149 and 441 amino acids, respectively. Simultaneously, the transcript of both On-VIP and On-VIPR1 were highly expressed in the intestine and sharply induced by Streptococcus agalactiae. Moreover, the positive signals of On-VIP and On-VIPR1 were detected in the longitudinal muscle layer and mucosal epithelium of intestine, respectively. Furthermore, both in vitro and in vivo experiments indicated several immune functions of On-VIP, including reduction of P65, P38, MyD88, STAT3, and AP1, up-regulation of CREB and CBP, and suppression of inflammation. Additionally, in vivo experiments proved that On-VIP could protects Nile tilapia from bacterial infection, and promote apoptosis and pyroptosis. These data lay a theoretical basis for further understanding of the mechanism of VIP guarding bony fish against bacterial infection

Key words: Nile tilapia; Streptococcus agalatiae; Vasoactive intestinal peptide (VIP); Vasoactive intestinal polypeptide receptor 1(VIPR1); immune response

红鳍东方鲀干扰素调节因子家族的结构特征及表达分析

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摘要：干扰素调节因子（IRF）家族是启动宿主天然免疫应答抵抗病原体入侵的关键调节因子。IRFs 通过单独或共同调控干扰素基因（IFN）的转录表达进而诱导免疫基因的表达，实现机体的免疫应答。本研究在红鳍东方鲀基因组中共鉴定得到 12 个 TrIRF 基因，分布在 11 条染色体上；系统进化分析显示红鳍东方鲀 IRFs 分为 4 个亚家族，分别为 IRF1 亚家族、IRF3 亚家族、IRF4 亚家族和 IRF5 亚家族；结构域预测结果显示 IRF1 亚家族只具有 IRF 结构域，其他亚家族还具有 IRF3 结构域。12 个 TrIRF 基因在红鳍东方鲀健康组织中具有不同表达模式，大部分基因在造血器官和淋巴器官等重要的免疫器官中有较高的表达。哈维氏弧菌感染红鳍东方鲀后肠道、脾脏和肝脏中 TrIRF 基因表达量均有显著的差异变化，且总体随时间变化呈现先上调后下调的趋势。本研究结果可为探究鱼类 IRF 功能提供参考数据，也为揭示硬骨鱼类先天免疫机制提供依据。

关键词：干扰素调节因子；红鳍东方鲀；哈维氏弧菌；表达分析

Molecular characterization and expression analysis of Interferon regulatory factor gene family in Japanese pufferfish(Takifugu rubripes)

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Abstract： The interferon regulatory factor (IRF) are key regulatory factors that initiates the host's natural immune response to resist pathogen invasion. IRFs induce the expression of immune genes by individually or collectively regulating the transcription and expression of interferon genes (IFN). In this study, a total of 12 TrIRF genes were identified in the genome of the Japanese pufferfish, distributed in 11 chromosomes. Phylogenetic analysis showed that TrIRFs were divided into four subfamilies, including IRF1 subfamily, IRF3 subfamily, IRF4 subfamily, and IRF5 subfamily. Structural analysis showed that the IRF1 subfamily contain only one IRF domain, while the other subfamilies also contain IRF3 domain. The 12 TrIRF genes have different expression patterns in healthy tissues of the Japanese pufferfish. Most of the genes are highly expressed in important immune organs such as hematopoietic organs and lymphoid organs. In addition, the expression of TrIRF genes in the intestine, spleen and liver after Vibrio harveyi infection showed significant differences, and displayed a trend of upregulation followed by downregulation over time. Our results provided supporting data for exploring the roles of IRFs in fish, as well as evidences for revealing the innate immune mechanism of teleost fish.

Key words: Interferon regulatory factor; Japanese pufferfish; Vibrio harveyi; Expression analysis

高效液相色谱-三重四极杆复合线性离子阱质谱法检测水产品中农、兽药多残留

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摘要：为了满足水产品中农药和兽医残留检测的要求，本研究制备了三维壳聚糖微球，并将其用作可生物降解的 QuEChERS 纯化吸附剂。结合 HPLC-QTRAP-MS/MS，成功地建立了一种改进的涡流振荡净化法测定农药和兽药残留。结果表明，三维壳聚糖微球能有效吸附和去除水产品样品乙腈提取物中的干扰物质。95 种农药和兽药的回收率在 64.0%至 114.3%之间，相对标准偏差为 0.47 至 20.02%。研究结果表明，3D 壳聚糖微球作为 QuEChERS 纯化材料具有良好的性能。20 份药物阳性的真实样本中有 18 份检测到氢化可的松，最高检测浓度为 444.69μg·kg-1，因此相关风险监测值得关注。

关键词：农药和兽药；QuEChERS 吸附剂；壳聚糖微球；检测；水产品

Three-dimensional chitosan microsphere as biodegradable QuEChERS sorbent for the rapid purification and determination of pesticides and veterinary drug multi-residues in aquatic products combined with HPLC-QTRAP-MS/MS

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Abstract：To meet the requirements for pesticide and veterinary residues’ determination in aquatic products, the three-dimensional (3D) chitosan microspheres were easily prepared and used as biodegradable QuEChERS purification sorbents in this study. Combined with HPLC-QTRAP-MS/MS, an improved vortex oscillating clean-up method was successfully developed for the determination of pesticide and veterinary drug residues. The results showed that the 3D chitosan microspheres could effectively adsorb and remove the interfering substances in acetonitrile extract of aquatic product samples. The recoveries of 95 pesticides and veterinary drugs were ranging from 64.0% to 114.3% with the relative standard deviations (RSDs) of 0.47–20.02%. The research results show that 3D chitosan microspheres have excellent performance as QuEChERS purification materials. Hydrocortisone were detected in 18 of 20 drug-positive real samples with highest detected concentration of 444.69 μg·kg-1, so relevant risk monitoring work should also be carried out in future for hydrocortisone in aquatic products.

Key words: Pesticides and veterinary drugs; QuEChERS sorbent; Chitosan microsphere; Determination; Aquatic products

基于多组学联合分析揭示亚麻酸在新加坡石斑鱼虹彩病毒 SGIV 感染中的作用

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摘要：本研究对新加坡石斑鱼虹彩病毒（Singapore grouper iridovirus，SGIV）后的肝脏组织结构、理化指标及转录、蛋白和代谢组学进行分析，并分析关键代谢物在 SGIV 感染中发挥的作用。SGIV 感染石斑鱼可导致肝脏嗜碱性物质增多、坏死及脂质含量下降。组学分别鉴定出 232 个 DEMs，12830 个 DEGs 和 357 个 DEPs。SGIV 感染后许多氨基酸代谢物上调，而脂质代谢物显著下调。转录和蛋白组学结果显示，DEGs 和 DEPs 主要参与胆固醇代谢、吞噬体、PPAR 等途径。联合分析结果显示，亚麻酸、亚油酸、谷氨酸与 CPTIA、JUN、IL6、SCD 相互关联。体外实验结果显示亚麻酸处理 GS 细胞可激活 Nrf2，抑制 NFκB，从而抑制 SGIV 的复制，降低病毒滴度。综上，本研究解析了 SGIV 感染石斑鱼肝脏基因、蛋白至代谢物的调控关系，验证了亚麻酸的体外抗病毒作用，为寻找抗病毒策略提供了参考。

关键词：SGIV；转录组学；蛋白质组学；代谢组学；亚麻酸

The role of linolenic acid in Singapore grouper iridovirus SGIV infection was revealed based on multi-omics analysis

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Abstract： In this study, the liver structure, physical and chemical indexes, transcriptome and proteome and metabolome of grouper (Epinephelus spp.) after Singapore grouper iridovirus (SGIV) infection were analyzed, and the role of key metabolites in SGIV infection was analyzed. SGIV infection of grouper resulted in increased basophil, necrosis, and decreased lipid content in liver. Omics identified 232 DEMs, 12,830 DEGs, and 357 DEPs, respectively. Many amino acid metabolites were up-regulated after SGIV infection, while lipid metabolites were significantly down-regulated. Transcriptional and proteomic results showed that DEGs and DEPs were mainly involved in cholesterol metabolism, phagosome, PPAR and other pathways. The results of joint analysis showed that linolenic acid, linoleic acid, and glutamic acid were correlated with CPTIA, JUN, IL6 and SCD. In vitro experiment results showed that GS cells treated with linolenic acid could activate Nrf2, inhibit NFκB, thus inhibit SGIV replication, and reduce virus titer. In conclusion, this study analyzed the regulatory relationship between genes, proteins, and metabolites in the liver of SGIV-infected groupers, verified the antiviral effect of linolenic acid in vitro, and provided a reference for searching for antiviral strategies.

Key words: SGIV; Transcriptomics; Proteomics; Metabolomics; Linolenic acid

鬼手海兔胚胎发育观察及初步研究

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摘要：为研究鬼手海兔早期胚胎发育阶段的形态特征和发育速度，将其放在水温 23~27℃，水体盐度 32‰，pH 值 8.1~8.4 条件下完成整个胚胎发育观察。结果表明，鬼手海兔的胚胎发育过程主要包括受精卵、2 细胞期、4 细胞期、8 细胞期、16 细胞期、囊胚期、担轮幼虫期、面盘幼虫期、幼苗九个阶段。受精卵在离开母体 20min 左右开始卵裂，转入较低温度培养，10h 后进入囊胚期（100±25μm），3d 后进入面盘幼虫期（400±50μm），6d 后脱离外壳及卵袋，形成幼苗（600±50μm）。研究表明，鬼手海兔更适合在 23~27℃条件下生长，温度降低至 25℃以下会延长其发育时间，低于 23℃则会降低成活率。通过后期对鬼手海兔的研究可探究其生物价值及繁育方式，在未来研究中鬼手海兔将在改善水质及垃圾葵生物防治中起到重要作用，力求对水族环境进行无污染治理，并在水族观赏方面进行探究，对其发育过程及人工繁育提供理论研究基础。

关键词：鬼手海兔；胚胎；形态特征；幼苗发育；人工繁育；生物防治

Observe Ghost Sea Hare Embryonic Development And Pilot Study

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Abstract：To study Ghost Sea Hare embryo development, conditions of 23~27°C water temperature, 32‰ salinity, and pH 8.1~8.4 were used. The development was observed in 9 stages, from fertilized eggs to juveniles. Lowering the temperature below 25°C extended development, and going below 23°C reduced survival rates. Future research can explore their biological value, breeding methods, improve water quality, control nuisance algae, maintain pollution-free aquatic environments, and promote aquatic observation. This provides a theoretical foundation for Ghost Sea Hare juvenile development and artificial breeding.

Key words: Sea Hare; Embryo; Morphological characteristics; Seedling development; Artificial breeding; Biological control

中间球海胆 TNFSF14 基因克隆及其与 miRn−38 相互作用调节病原体诱导的先天免疫机制的研究

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摘要：为了明确中间球海胆中 TNFSF14 基因（SiTNFSF14）的序列信息并探究其在响应致病菌感染过程中的作用模式及规律，本研究运用实时荧光定量 PCR（qRT-PCR）和蛋白免疫印迹（Western Blotting）等技术，探究不同组织中 SiTNFSF14 基因在“黑嘴病”致病菌刺激下的表达模式和生物功能，并进一步探讨 SiTNFSF14 基因与 miRNA novel-38 (miRn-38)的相互作用关系及其在“黑嘴病”致病菌感染过程中的防御作用机制。本研究结果可丰富海胆等无脊椎动物的 TNFSF14 基因生物功能的分子资料，同时为阐明中间球海胆免疫防御分子机制以及养殖病害防控提供基础数据。

关键词：中间球海胆；TNFSF14；miRn-38；基因克隆；致病菌感染；表达模式

Cloning of a novel TNFSF14 gene in the sea urchin Strongylocentrotus intermedius and its pathogen-induced innate immune regulatory function via interacting with miR-novel-38

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Abstract：In order to clarify the sequence information of tumour necrosis factor superfamily member 14 (TNFSF14) gene and explore its response expression pattern after pathogen infection in Strongylocentrotus intermedius. The present study was conducted to investigate the expression pattern and biological function of TNFSF14 in different tissues after pathogen infection of “Black mouth disease”, and to further explore the interaction between TNFSF14 and miRNA novel-38 (miRn-38) and its defense mechanism, by using molecular biological techniques such as quantitative Real-Time PCR (qRT-PCR) and Western blotting. The results of this study can enrich the molecular information on the biological function of TNFSF14 in sea urchin and other invertebrates, and also provide basic data for the molecular mechanism of immune defense and the control of aquatic disease in Strongylocentrotus intermedius.

Key words: Strongylocentrotus intermedius; TNFSF14; miRn-38; gene cloning; pathogen infection; expression pattern

虾夷扇贝应答香螺捕食的行为特征

及生理生态响应

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摘要：为探究虾夷扇贝在底播养殖中，敌害生物香螺的捕食对虾夷扇贝存活、行为特征和相关生理生态指标的影响。本研究选用大（119.85±3.23 mm）、中（89.24±3.77 mm）、小（60.10±3.23 mm）三种规格虾夷扇贝应对敌害生物持续刺激后的行为特征，鳃、闭壳肌和外套膜的超氧化物歧化酶(SOD)、过氧化氢酶(CAT)、精氨酸激酶(AK)和章鱼碱脱氢酶(ODH)活力变化，并选取以上差异显著的组织进行转录组测序。结果显示：（1）扇贝主要通过多次、快速开闭双壳来逃避香螺捕食，规格越小其肌肉力量较小，被香螺包裹后较难逃脱，随着规格的增大扇贝开闭双壳的能力也逐渐增强，逃避方式逐渐转变为延长闭壳时间，较难被香螺包裹或捕捉。（2）通过比较未受刺激和香螺刺激后的虾夷扇贝各组织酶活（SOD、CA、ODH、AK）变化发现均有差异，中规格扇贝闭壳肌酶活均差异显著，且 ODH 活力差异极显著。（3）对中规格闭壳肌进行转录组测序，共识别到 405 个差异基因调节，其中上调 172 个，下调 233 个，对各组间差异表达基因进行 KEGG 通路聚类分析，发现 Wnt 信号通路富集差异表达的基因最多，包括 RYK、APC、BAMBI、WNT16、CACYBP 和 RUVBL1 等，这些通路和基因在虾夷扇贝受到惊吓等外部刺激时能起到调节作用。综上，虾夷扇贝在受到敌害生物刺激时，其行为特征和相关生理生态指标会发生显著变化，本研究结果对于虾夷扇贝在底播养殖过程中投苗规格提供了科学参考。

关键词：虾夷扇贝；香螺；闭壳行为；酶活；转录组；

Behavioral characteristics and physiological ecological responses of Mizuhopecten yessoensis in response to Neptunea arthritica cumingii predation

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Abstract： To investigate the effects of predation of the paddle Neptunea arthritica cumingii on the culture and survival of scallops (Mizuhopecten yessoensis) during bottom culture, we investigated the behavioral characteristics of three sizes (small, medium, and large) of scallops in response to exposure to N. cumingii We also measured the activities of superoxide dismutase, catalase, arginine kinase, and octopine dehydrogenase in the gill, adductor muscle, and mantle of scallops before and after exposure to predation.Tissues that showed significant differences between control and test specimens were selected for deep sequencing of the transcriptome to identify and validate the key genes that were sensitive to predation. We found that scallops escaped from N. cumingii predation by continuous shell closure or movement.We found that scallops escaped from N. cumingii predation by continuous shell closure or movement. Shell closure force increased with scallop size, and scallops of the same size that were stimulated by the presence of crabs closed their shell more frequently than control scallops.The shell closure ability of scallops of all sizes decreased with increasing duration of the experiment. The enzyme activities of the three scallop tissues changed significantly after continuous stimulation, and the trend was particularly obvious in the enzyme activities of the adductor muscles of the medium-sized scallops.Transcriptome analysis of the adductor muscles of medium-sized scallops revealed 405 differentially expressed genes (172 up-regulated and 233 down-regulated), and expression levels of RYK、APC、BAMBI、WNT16、CACYBP and RUVBL1 changed after stimulation by N. cumingii.Their sequencing results were verified by quantitative real-time PCR. We hypothesize that these genes may be related to muscle movement and regulation in M. yessoensis after stimulation. In conclusion, when M. yessoensis is stimulated by the presence of predators, its behavioral characteristics and related physiological and ecological indexes undergo significant changes.The results are relevant for developing specifications for M. yessoensis seedling casting during bottom culture.

Key words: Mizuhopecten yessoensis; Neptunea arthritica cumingii;dynamometer method; behavioral traits;enzyme activity;transcriptome.

卵形鲳鲹 NCCRP1 的分子特征及其功能分析

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摘要：非特异性细胞毒细胞（NCCs）在硬骨鱼先天免疫系统中在免疫防御中起着至关重要的作用。非特异性细胞毒性细胞受体蛋白 1 (NCCRP1)负责识别靶细胞并激活 NCCs。在本次研究中，我们从卵形鲳鲹中鉴定出 NCCRP1 (ToNCCRP1)。ToNCCRP1 的开放阅读框长度为 702 bp，编码 233 个氨基酸的蛋白，与其他鱼类的 NCCRP1 相似度超过 61%。qPCR 分析显示 ToNCCRP1 的 mRNA 在各组织中普遍表达，且在肝脏中表达水平最高。此外，ToNCCRP1 的表达在病原菌刺激后表达水平显著上调。体外实验表明，重组 ToNCCRP1 蛋白具有细菌凝集和结合能力，暗示其具有抗菌功能。此外，ToNCCRP1 对前肾白细胞（HKLs）的炎症反应和信号通路也具有调控作用。这些结果表明，NCCRP1 参与了硬骨病原菌时感染的免疫防御，为硬骨鱼的免疫机制提供了新的思路。

关键词：卵形鲳鲹；NCCRP1；免疫应答；NCCs

Molecular characteristics and expression functional analysis of non-specific cytotoxic cell receptor (NCCRP1) in golden pompano (Trachinotus ovatus)

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Abstract: Non-specific cytotoxic cells (NCCs) are cytotoxic cell population found in innate immune system of teleost, playing crucial role in immune defense. Non-specific cytotoxic cell receptor protein 1 (NCCRP1) is responsible for recognizing target cells and activating NCCs. That said, since the studies regarding NCCs' role in fish during pathogen infection are few, it is necessary to conduct more comprehensive studies. In this study, we identified NCCRP1 from Trachinotus ovatus (ToNCCRP1). The open reading frame of ToNCCRP1 was found to be 702 bp, encoding a protein of 233 amino acids. Additionally, ToNCCRP1 contained a conserved F-box-associated domain and exhibited more than 61% similarity to NCCRP1 in other fish species. Quantitative real-time PCR analysis showed that ToNCCRP1 mRNA was generally expressed in all tissues, with the highest level expressed in the liver. Furthermore, the expression of ToNCCRP1 was significantly upregulated following infection with Streptococcus iniae. In vitro experiments demonstrated that recombinant ToNCCRP1 possessed bacterial agglutination and binding capabilities, suggesting its antibacterial function. Additionally, we investigated the immune response of head kidney Leukocytes (HKLs) to ToNCCRP1. The challenge experiments revealed that ToNCCRP1 played a role in the immune response by influencing the inflammatory response and regulating signaling pathways in HKLs. These findings suggest that NCCRP1 is involved in the immune defense against pathogenic infections in golden pompano, providing insights into the immune mechanisms of teleost.

Key words: Trachinotus ovatus; Non-specific cytotoxic cell receptor protein 1(NCCRP1); Immune response; NCCs

miR-2013-3p/HIF-1α轴通过靶向 GDH 调节中间球海胆中病原体诱导的能量产生变化

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摘要：为明确中间球海胆缺氧诱导因子-1α（HIF-1α）的生物学功能，本研究运用实时荧光定量 PCR（qRT-PCR）、蛋白免疫印迹（Western Blotting）、基因体内干扰（RNAi）、双荧光素酶和 miRNA 体内转染等技术，克隆并鉴定了中间球海胆中 HIF-1α（SiHIF-1α）的全长 cDNA，并探讨了 SiHIF-1α及其调控因子（miR-2013-3p）在病原体诱导的中间球海胆代谢反应中的功能。为阐明常氧条件下 HIF-1α调控功能的分子机制提供了基础数据，加深我们对重要的经济棘皮动物物种病原体防御反应的认识，同时本研究在分子角度为海胆养殖疾病防治策略的制定提供了新的线索。

关键词：缺氧诱导因子；miR-2013-3p；中间球海胆；病原菌感染；能量产生

HIF-1α interacting with miR-2013-3p regulates pathogen-induced energy production changes via targeting glutamate dehydrogenase in the sea urchin Strongylocentrotus intermedius

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Abstract: To investigate the functions of hypoxia inducible factor-1α (HIF-1α) homologs, we cloned and characterized the full-length cDNA of a novel HIF-1α homolog (SiHIF-1α) from the sea urchin Strongylocentrotus intermedius and explored the functions of SiHIF-1α and its regulatory factor (miR-2013-3p) in the pathogen-induced metabolic response of S. intermedius, by using molecular biological techniques such as quantitative Real-Time PCR (qRT-PCR), Western blotting, specific small interfering RNAs, luciferase reporter assay, and miRNA transfection in vivo. Generally speaking, the findings in this study will not only clarified the molecular mechanism of the regulatory functions of HIF-1α homologs under normoxic conditions but also deepened our understanding of the pathogen defense response of economically important species of echinoderms. The observations from this study will also provide new clues for developing disease control strategies for sea urchins aquaculture from the molecular aspect.

Key words: Hypoxia inducible factor-1α; MiR-2013-3p; Strongylocentrotus intermedius; Pathogen infection; Energy production

头足类动物中的寄生虫研究进展

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摘要：头足类（Cephalopod）分布于太平洋、大西洋和印度洋等各大海域，其生物量极为丰富，且生命周期短、生长速度快，是海洋中最具潜力的蛋白质资源之一。以头足类为中间宿主或终末宿主的寄生虫，广泛存在于海洋食物链的不同营养级之中，是海洋生物多样性的重要组成部分。本文主要从寄生于头足类的寄生虫种类、生活史过程、感染状况等方面对头足类动物中的寄生虫研究进行总结。结果显示，感染头足类的寄生虫类群主要有二胚虫（Dicyemida）、绦虫（Cestoda）和线虫（Nematoda）等。二胚虫是头足类所特有的寄生虫，其成熟与繁殖都在头足类肾脏中进行，头足类是二胚虫的终末宿主。而头足类作为中间宿主，容易被绦虫和线虫的幼体所感染，且感染率相对较高，感染部位主要是胃壁和体腔。基于上面所提到的，未来头足类动物中寄生虫的研究方向将主要围绕分类鉴定、生物标记以及开放信息数据库等方面展开。

关键词：头足类；寄生虫；二胚虫；绦虫；线虫

Progress of the Studies on Parasites in Cephalopods

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Abstract：Cephalopods are distributed in the Pacific Ocean, the Atlantic Ocean and the Indian Ocean. Its biomass is extremely abundant, and its life cycle is short, growth rate is fast, it is one of the most potential protein resources in the ocean. Parasites with cephalopods as intermediate or terminal hosts are widely present in different trophic levels of the Marine food chain and are an important part of Marine biodiversity. This article mainly summarizes the research on parasitesin cephalopods' from the aspects of species, life history process and infection status. The results showed that the main parasites infected with cephalopods were dicyemids, Cestodas and nematodes. Dicyemids are unique parasites of cephalopods, and their maturation and reproduction are carried out in the kidneys of cephalopods, which are the final hosts of dicyemids. Cephalopods, as intermediate hosts, are easily infected by the larval stage of Cestodas and nematodes, and the infection rate is relatively high, mainly in the stomach wall and body cavity. Based on the above mentioned, the future research direction of parasites in cephalopods will mainly focus on taxonomic identification, biomarkers and open information database.

Key words: Cephalopod; Parasites; Dicyemids; Cestodas; Nematodes

罗非鱼源无乳链球菌 S8 家族蛋白酶 SFPB 的功能探究

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摘要：无乳链球菌（Streptococcus agalactiae）是危害罗非鱼养殖业的主要病原菌。细菌有能力发展出多种策略来入侵宿主免疫系统，而蛋白酶是其中之一。在本研究中，我们鉴定了鱼源无乳链球菌 THN0901 的一种 S8 家族丝氨酸蛋白酶(SFPB)并确定了其在入侵中的作用。利用同源重组构建了该蛋白酶的突变株(ΔsfpB)和回补株(CΔsfpB)。与野生株 THN0901 相比，突变株的生长未受影响，但对盐度和高 pH 的敏感性存在差异。此外，ΔsfpB 对溴化乙锭染料的通透性改变，表明与野生株和 CΔsfpB 相比，细胞膜的通透性发生了变化。研究结果显示，在对罗非鱼腹腔注射攻毒后，突变株造成的死亡率降低。同样，突变株的巨噬细胞存活和组织定植能力均显著低于野生株。此外，与野生株相比，ΔsfpB 中毒力因子(cpsG、fbsB、bibA、sip 等)的 mRNA 表达水平显著下调。综上所述，我们的研究表明该丝氨酸蛋白

关键词：罗非鱼；无乳链球菌；SFPB；免疫逃避

Functional Exploration of the S8 Family Protease SFPB in Streptococcus agalactiae from NileTilapia

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Abstract： Streptococcus agalactiae is the primary pathogen in tilapia cultivation. Bacteria possess the capacity to employ varied methods to invade the host immune system, including proteases. In this study, we examined a serine protease (SFPB) belonging to the S8 family that originated from S. agalactiae THN0901. We characterised its role in invasion and constructed a mutant strain (ΔsfpB) and a complement strain (CΔsfpB) via homologous recombination. The growth of the mutant strain was not impacted compared to the wild strain THN0901, however, differences were observed in sensitivity to salinity and high pH. Moreover, a change in cell membrane permeability was indicated by the altered ethidium bromide dye permeability of ΔsfpB, when compared to the wild strain and CΔsfpB. After intraperitoneal injection challenges, the results exhibited decreased mortality caused by the mutant strain. Both macrophage survival and tissue colonization were significantly lower in the mutant strain compared to the wild strain. Additionally, the mRNA expression levels of ΔsfpB virulence genes (including cpsG, fbsB, bibA, and sip) were significantly down-regulated in the mutant strain compared to the wild strain. These findings suggest that this serine protease enzyme plays a crucial function in enhancing the cell membrane stability and immune evasion of S. agalactiae. Therefore, these enzymes have the potential to become valuable antimicrobial agents and play a significant role in preventing and controlling diseases.

Key words:： NileTilapia；Streptococcus agalactiae；Immune evasion

健康杉虎斑与烂体杉虎斑肠道菌群结构差异分析

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摘要：为研究健康杉虎斑和烂体杉虎斑肠道微生物的多样性，采用 PacBio 三代高通量测序技术对其肠道 16S rDNA 基因的 v1～v9 区进行测序，比较不同生理状态下杉虎斑的肠道微生物菌群结构的种类差异和丰度变化。试验结果显示，在不同生理状态下杉虎斑肠道菌群的组成及丰度出现显著变化：杉虎斑肠道主要优势菌群为变形菌门、梭杆菌门、厚壁菌门和拟杆菌门，烂体杉虎斑的菌群多样性高于健康杉虎斑。在门水平下，梭杆菌门和厚壁菌门在烂体杉虎斑中相对丰度较低，而变形菌门相对丰度较高；在属水平下，弧菌属在烂体组中相对丰度较高，而鲸杆菌属相对丰度较低；在种水平下，河口弧菌在烂体组中相对丰度较高，而美人鱼发光杆菌相对丰度较低。美人鱼发光杆菌作为条件致病菌，在一定条件下与河口弧菌及哈维氏弧菌相互作用导致杉虎斑患皮肤溃疡，因此推测弧菌为致病菌。本研究对比健康与烂体杉虎斑肠道菌群结构差异，望能够为杉虎斑疾病防治及科学养殖提供理论支持。

关键词：杉虎斑；肠道内容物；高通量测序；菌群多样性

Analysis of differences in intestinal flora structure between healthy hybrid grouper and rotten hybrid grouper

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Abstract： In order to study the intestinal microbial diversity of healthy hybrid grouper and rotten hybrid grouper, the v1-v9 region of 16 S rDNA gene was sequenced by PacBio three-generation high-throughput sequencing technology, and the species differences and abundance changes of intestinal microbial flora structure of hybrid grouper under different physiological conditions were compared. The results showed that the composition and abundance of intestinal flora of hybrid grouper changed significantly under different physiological conditions. The main dominant bacteria in the intestine of hybrid grouper were Proteobacteria, Fusobacteria, Firmicutes and Bacteroidetes. The diversity of intestinal flora of rotten hybrid grouper was higher than that of healthy grouper. At the phylum level, the relative abundance of Fusobacteria and Firmicutes in the rotten hybrid grouper was lower, while the relative abundance of Proteobacteria was higher. At the genus level, the relative abundance of Vibrio was higher in the rotten body group, while the relative abundance of Cetobacterium was lower. At the species level, the relative abundance of Vibrio estuarineis was higher in the rotting group, while the relative abundance of Photobacterium mermaid was lower. As a conditional pathogenic bacterium, Photobacterium damselae interacts with Vibrio estuaries and Vibrio harveyi under certain conditions, resulting in skin ulcers in hybrid groupers. Therefore, it is speculated that Vibrio is a pathogenic bacterium.This study compared the differences in the intestinal flora structure of healthy and rotten hybrid groupers, hoping to provide theoretical support for the prevention and control of hybrid grouper diseases and scientific breeding.

Key words: Hybrid grouper; intestinal contents; high-throughput sequencing; bacterial diversity

石斑鱼 TRAF3 的分子克隆及功能分析

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摘 要：近年来，赤点石斑鱼神经坏死病毒（Red-spotted grouper nervous necrosis virus, RGNNV）在水产养殖过程中频繁暴发，严重制约了石斑鱼养殖业的发展，造成了重大的经济损失。TRAF3 是已知的巨噬细胞、pDC 以及成纤维细胞中 TLR 连接和病毒感染后产生 I 型干扰素需要的唯一分子，在生物学生理和病理过程中扮演着非常重要的角色。本文克隆和表达了斜带石斑鱼 TRAF3，并进行了亚细胞定位和功能的初步分析。EcTRAF3 抑制 RGNNV 在 GS 细胞中的复制，与 RGNNV 的 CP 蛋白可能发生相互作用，在 EcSTING 介导的 IFN 信号通路中可能发挥增强子作用。该研究结果表明，EcTRAF3 参与细胞抗病毒反应，并在鱼类免疫应答系统中发挥重要作用。

关键词：石斑鱼；TRAF3；神经坏死病毒；免疫应答

Molecular Cloning and Functional Analysis of TRAF3 in Grouper

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Abstract： In recent years, Red-spotted grouper nervous necrosis virus (RGNNV) breaks out frequently in the process of aquaculture, which seriously restricts the development of grouper aquaculture industry and causes significant economic losses. TRAF3 is the only known molecule required for TLR ligation and the production of type I interferon after viral infection in macrophages, pDCs, and fibroblasts and plays a very important role in biological physiology and pathology. In this paper, TRAF3 was cloned and expressed in grouper, and subcellular localization and function were preliminarily analyzed. EcTRAF3 inhibits replication of RGNNV in GS cells and may interact with the CP protein of RGNNV and may play an enhancer role in EcSTING mediated IFN signaling pathway. The results of this study suggest that EcTRAF3 is involved in cellular antiviral responses and plays an important role in the fish immune response system.

Key words: Grouper; TRAF3; RGNNV; Immune response

红鳍东方鲀 g 型溶菌酶的分子结构特征及功能研究

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摘要：溶菌酶能够水解细菌细胞壁的肽聚糖层，在先天性免疫反应中起到至关重要的作用。本研究对红鳍东方鲀（Takifugu rubripes）中的 g 型溶菌酶（TrLysG）基因进行了分子特征及物理化学性质检测、表达分析和抑菌活性研究。该基因由一个 573bp 的开放阅读框构成，编码 190 个氨基酸，其肽链分子量为 20.87 kDa，理论等电点（pI）为 5.96。TrLysG 具有一个细菌可溶性溶菌酶（SLT）结构域，包含三个催化残基和一个高度保守的 GLMQ 基序。qRT-PCR 结果显示，TrLysG 在哈氏弧菌感染后的肠道、鳃和肝脏中均显著上调。重组 TrLysG 蛋白（rTrLysG）在 55℃以及 pH 为 6 时具有最适活性，并且 rTrLysG 对三种革兰氏阳性菌以及五种革兰氏阴性菌均有一定的抑菌活性，可见 TrLysG 在抵御外来入侵病原体的免疫过程中起到重要作用，有助于预防水产养殖中的疾病。

关键词：红鳍东方鲀；g 型溶菌酶；抑菌活性；先天免疫

Molecular characterization and functional analysis of goose-type lysozyme from Japanese pufferfish (Takifugu rubripes)

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Abstract : Lysozyme plays a crucial role in the innate immune response against bacterial phagocytosis by hydrolyzing the peptidoglycan layer of the bacterial cell wall. In this study, we analyzed the molecular properties, physical and chemical properties, phylogenetic analysis, expression analysis and antibacterial activity of goose-type lysozyme gene (TrLysG) in Japanese pufferfish. The TrLysG consists of an open reading frame composed of 573 bp, which encodes a polypeptide consisting of 190 amino acids. The predicted molecular mass of the polypeptide is 20.87 kDa, while its theoretical isoelectric point (pI) is 5.96. It has been found that TrLysG protein include a characteristic bacterial soluble lytic transglycosylase (SLT) domain, which contains three catalytic residues (Glu71, Asp84 and Asp95) and a highly conserved GLMQ motif (Gly90, Leu91, Met92 and Gln93). Phylogenetic analyses showed that the TrLysG is clustered together with its counterparts from other teleost fishes. Furthermore, expression analyses were performed in healthy tissues of Japanese pufferfish and after infection with Vibrio harveyi in the intestine, gill and liver. The results showed that TrLysG was highly expressed in healthy mucosal tissues (intestine and gill) and significantly up-regulated in response to bacterial treatment in all three tissues. The purified recombinant TrLysG (rTrLysG) has optimal activity at 55 ℃ and pH 6. It also displayed antimicrobial activity against three Gram-positive bacteria (Streptococcus parauberis, Staphylococcus pasteuri and Staphylococcus epidermidis) as well as five Gram-negative bacteria (Shewanella, Aeromonas hydrophila, Escherichia coli, Vibrio parahaemolyticus and V. harveyi). Our results highlighted the significant role of TrLysG in immune defense against invading pathogens, thereby contributing to the prevention and alleviation of disease spread in aquaculture.

Key words: Japanese pufferfish; Goose-type lysozyme; Antibacterial activity; Innate immunity

一例感染不动杆菌的中华鲟病例的诊断分析

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摘要：中华鲟是国家一级保护动物，具有难以估量的生态、社会、经济价值。现有一尾人工养殖的中华鲟突然死亡，为明确死亡原因，对该例中华鲟进行体表观察、病理解剖、组织病理学观察、细菌分离鉴定和分子生物学检测综合分析。该例中华鲟体表表现出肛门红肿且有血样腹水流出。剖检见大量血样腹腔液，内脏整体呈现黑红色，肝脏发绀充血，质脆易碎，胆囊发白，脾脏和胰脏肿大。组织病理结果表明，肝脏、肾脏、肠道和胃的细胞间有大量的炎性细胞和红细胞浸润。肝细胞肿大且结构紊乱，包浆内有大量的空泡和脂褐素沉积。脾脏组织结构松散，肾小球结构紊乱。瓣肠绒毛脱坏死脱落，黏膜层伴有出血、瘀血现象。对腹腔液中细菌进行分离鉴定，得到 3 株优势菌株，经分子生物学检测，鉴定均为不动杆菌。由此初步判定该例中华鲟是不动杆菌感染导致死亡。

关键词：中华鲟；组织病理；分子生物学检测；不动杆菌

The diagnostic analysis of Acinetobacter infection in Chinese sturgeon Acipenser sinensis

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Abstract：The Chinese sturgeon Acipenser sinensis is a national first-level protected animal and has inestimable ecological, social and economic value. An artificially bred Chinese sturgeon Acipenser sinensis died suddenly. In order to clarify the cause of its death, comprehensive analyzes including surface observation, pathological anatomy, histopathological observation, bacterial isolation and identification, and molecular biology testing were conducted on the Chinese sturgeon Acipenser sinensis. In this case, the body surface of the Chinese sturgeon Acipenser sinensis showed redness and swelling in the anus, and blood-like ascites flowed out. The autopsy showed a large amount of blood samples in the peritoneal fluid, the internal organs were overall black and red, the liver was cyanotic and congested, brittle and brittle, the gallbladder was white, and the spleen and pancreas were enlarged. Histopathological results showed that there were a large number of inflammatory cells and red blood cells infiltrating among the cells of the liver, kidney, intestine and stomach. The liver cells were enlarged and structurally disordered, and there were a large number of vacuoles and lipofuscin deposition in the slurry. The spleen tissue structure is loose and the glomerular structure is disordered. The villi of the intestinal valve are denecrotic and fall off, and the mucosal layer is accompanied by bleeding and blood stasis. The bacteria in the peritoneal fluid were isolated and identified, and 3 dominant strains were obtained, which were identified as Acinetobacter by molecular biology testing. It was initially determined that the death of this Chinese sturgeon Acipenser sinensis was caused by Acinetobacter infection.

Key words: Chinese sturgeon Acipenser sinensis; Histopathology; Molecular biology testing; Acinetobacter

单次给药下恩诺沙星及其代谢产物在石斑鱼体内的残留消除研究

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摘要：本研究按 150 mg/kg·bw 恩诺沙星剂量对小瞪石斑鱼进行单次灌胃给药实验，采用高效液相色谱-串联质谱法测定石斑鱼血浆、肝脏和肌肉中恩诺沙星及其代谢产物环丙沙星的含量水平。结果显示，恩诺沙星在血浆、肝脏和肌肉中较快的达到最大值，达到峰值的时间分别是给药后 60、40 和 60 min，浓度分别为 9.85 mg/kg、4.93 mg/kg 和 3.57 mg/kg，随后出现明显的下降趋势。恩诺沙星的代谢产物环丙沙星在给药后 60 min 在血浆、肝脏和肌肉中都达到峰值，峰值浓度为 0.122 mg/kg、0.574 mg/kg 和 0.032 mg/kg。研究表明仅有少量的恩诺沙星代谢为环丙沙星。在本实验条件下，建议休药期不少于 23 d。本研究掌握了恩诺沙星及其代谢产物环丙沙星在小瞪石斑鱼体内的残留消除规律，为石斑鱼养殖业提供合理的休药期和给药方案。

关键词：恩诺沙星；环丙沙星；石斑鱼；药物残留; 休药期

Metabolic study of enrofloxacin in grouper at single dosage

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Abstract： The current study investigated the residue elimination of enrofloxacin and its metabolite ciprofloxacin in grouper at single dosage to provide a reasonable dosing plan and withdrawal period for the aquaculture industry of grouper.The concentration of enrofloxacin and its metabolite ciprofloxacin in the plasma,liver and muscle of grouper after single dose of 150 mg/kg body weight were detected by high performance liquid chromatography tandem mass spectrometry method.The results showed that the peak concentration of enrofloxacin in grouper was fast reached after dosage,while the peak time of enrofloxacin in plasma,liver and muscle were 60min,40min and 60min,respectively.The peak concentration of enrofloxacin in plasma,liver and muscle were 9.85mg/k,4.93mg/kg and 3.57mg/kg,respectively. The peak time of ciprofloxacin in plasma,liver and muscle were 60min,60min and 60min,respectively,and the peak concentration of ciprofloxacin were 0.122mg/kg,0.574mg/kg and 0.032mg/kg.Enrofloxacin metabolized less ciprofloxacin in grouper.The withdrawal time of enrofloxacin in grouper should not be less than 23 days under this experimental condition.

Key words: enrofloxacin; ciprofloxacin; grouper; drug residue; withdrawal time

基于不同免疫策略的壳寡糖包被无乳链球菌疫苗对尼罗罗非鱼的免疫应答和保护效果

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摘要：在过去的十年中，无乳链球菌的爆发给罗非鱼养殖业造成了重大的经济损失。疫苗免疫方法和策略逐渐从单一模式向多模式整体防控策略发展。本研究采用腹腔注射(Ip)、浸泡联合腹腔注射(Im+Ip)、浸泡联合口服(Im+Or)和口服(Or)等不同给药方式构建了无乳链球菌壳寡糖佐剂灭活疫苗。安全性分析表明，该疫苗对罗非鱼无副作用。通过浴浸+口服或口服免疫能显著促进鱼类的生长发育。疫苗可诱导强烈而持久的体液或细胞免疫应答(血清抗体产生、免疫相关参数和免疫相关基因表达)。此外，浴浸+腹腔注射组的相对存活率最高。最后，本研究鼓励进一步研究其他种类疫苗在其他水生经济动物中的多渠道免疫策略，以提高其抗病能力。

关键词：尼罗罗非鱼；无乳链球菌；壳寡糖；灭活疫苗；免疫策略

Immune response and protective efficacy of Streptococcus agalactiae vaccine coated with chitosan oligosaccharide for different immunization strategy in Nile tilapia (Oreochromis niloticus)

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Abstract： In the past decade, the outbreak of Streptococcus agalactiae has caused significant economic losses in tilapia farming. Vaccine immunization methods and strategies have gradually evolved from single-mode to multi-mode overall prevention and control strategies. In this study, an inactivated vaccine of S. agalactiae with a chitosan oligosaccharide (COS) adjuvant was constructed using different administration methods: intraperitoneal injection (Ip), immersion combined with intraperitoneal injection (Im+Ip), immersion combined with oral administration (Im+Or), and oral administration (Or). Safety analysis showed that the vaccine had no side effects on tilapia. Im+Or group and Or group can significantly promote the growth and development of fish. Vaccine can induce a strong and lasting humoral or cellular immune response (serum antibody production, immune-related parameters and immune-related gene expression). In addition, the relative survival rate of the Im+Ip group was the highest. Finally, this study encourages further research on multi-channel immunization strategies of other kinds of vaccines in other aquatic economic animals to improve their disease resistance.

Key words: Nile tilapia; S.agalactiae; Chitosan oligosaccharide; Inactivated vaccine; immunization strategy

大口黑鲈虹彩病毒（LMBV）亚单位疫苗的制备及效果评价

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摘要：大口黑鲈（Micropterus salmoides）因其肉质优良等优点，已成为重要淡水养殖品种之一。大口黑鲈虹彩病毒（Largemouth bass virus，LMBV）是在大口黑鲈养殖过程中爆发病毒性病害的重要病原，具有高传染性和高致病性等特点，且无特效药治疗。疫苗是预防鱼类病害有效的方法之一，但目前市面上并无预防 LMBV 的疫苗可用。本文开展大口黑鲈虹彩病毒（LMBV）亚单位疫苗的制备及效果评价的研究，取得以下创新研究结果。

构建 pET-21a-MCP-BL21 原核表达菌株，表达并纯化蛋白。将纯化蛋白与佐剂混合乳化后免疫大口黑鲈，攻毒后统计结果表明，加佐剂组疫苗相对保护率达 100%，纯抗原组疫苗为 83.3%。进一步分析发现，脾脏、肾脏和头肾组织中 MHC II-α、CD4-1、CD8-α、IL-6、IgM、TNF-α免疫基因转录水平呈现不同程度的上调。其血清中的 MCP 特异性抗体在第 7 天

关键词：大口黑鲈；虹彩病毒；LMBV；亚单位疫苗

Preparation and immune protection evaluation of a subunit vaccine against Largemouth bass virus (LMBV) in Micropterus salmoides

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Abstract：Largemouth bass (Micropterus salmoides) has become one of the important freshwater cultured species due to its excellent meat quality and other advantages. Largemouth bass iridovirus (LMBV) is an important pathogen causing the outbreak of viral diseases in the cultivation process of largemouth bass. It is highly infectious and pathogenic, and has no specific treatment. Vaccines are one of the effective methods to prevent fish diseases, but there is currently no vaccine available to prevent LMBV. In this thesis, the preparation and effect evaluation of two novel vaccines against largemouth bass iridovirus (LMBV) were studied, and the following innovative research results were achieved.

A prokaryotic expression strain of pET-21a-MCP-BL21 was constructed, and the protein was expressed and purified. The purified protein was mixed with adjuvant for emulsification, and the largemouth bass was immunized. The statistical results after inoculation showed that the relative protection rate of the vaccine in the adjuvant group was 100%, and that of the pure antigen group was 83.3%. Further analysis showed that the transcription levels of MHC II-α, CD4-1, CD8-α, IL-6, IgM, and TNF-α immune genes in the spleen, kidney and head kidney tissues were increased to different degrees. Serum MCP-specific antibodies were also detected at high levels on Day 7, suggesting that the LMBV subunit vaccine may protect against the virus LMBV by up-regulating host immune gene expression and producing specific antibodies.

The results showed that the subunit vaccine immunization of largemouth bass obtained good immune protection effect, and the research results laid an important theoretical basis for the prevention and treatment of iridovirus disease of largemouth bass.

Key words: Micropterus salmoides; LMBV; Subunit vaccine

Nrf2 在血红蛋白诱导下的细胞损伤中的机制研究

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摘要：溶血性病原的感染，导致体内溶血，释放大量的血红蛋白并产生 ROS，对组织细胞造成氧化损伤甚至细胞死亡。Nrf2 是维持调节细胞氧化应激稳态的重要因子。然而，目前对 Nrf2 在草鱼溶血诱导的氧化损伤中的调控机制尚不清楚。因此，本研究利用 PHZ 诱导的草鱼溶血模型，系统的探究 Nrf2 在溶血情况下的损伤调控机制。实时定量 PCR、WB、免疫荧光/组化检测结果表明，PHZ 诱导的溶血导致组织中 Hb 的沉积，上调了 AMPK/Nrf2 通路和抗氧化相关基因的表达水平，并增加了组织中 ROS 含量。转录组分析结果进一步显示，PHZ 诱导的溶血显著激活了 Nrf2 通路的转录水平。此外，体外实验结果发现，过表达或者加入 Nrf2 激活剂可以拯救血红素诱导的细胞损伤，Nrf2 抑制剂的加入进一步加剧血红素诱导的细胞损伤。总之，本研究的数据表明，Nrf2 参与由血红蛋白诱导的细胞损伤作用。

关键词：Nrf2；血红蛋白；氧化损伤

Study on the mechanism of Nrf2 in hemoglobin-induced cell damage

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Abstract：Infection with hemolytic pathogens causes hemolysis in the body, releases a large amount of hemoglobin and produces ROS, causing oxidative damage to tissue cells and even cell death. Nrf2 is an important factor in maintaining and regulating cellular oxidative stress homeostasis. However, the regulatory mechanism of Nrf2 in hemolysis-induced oxidative damage in grass carp is currently unclear. Therefore, this study used the PHZ-induced grass carp hemolysis model to systematically explore the damage regulation mechanism of Nrf2 in hemolysis. The results of real-time quantitative PCR, WB, and immunofluorescence/histochemistry showed that PHZ-induced hemolysis led to the deposition of Hb in tissues, up-regulated the expression levels of AMPK/Nrf2 pathway and antioxidant-related genes, and increased the ROS content in tissues. Transcriptome analysis results further showed that PHZ-induced hemolysis significantly activated the transcription level of the Nrf2 pathway. In addition, in vitro experimental results found that overexpression or the addition of Nrf2 activators can rescue heme-induced cell damage, and the addition of Nrf2 inhibitors further exacerbates heme-induced cell damage. Taken together, the data from this study indicate that Nrf2 is involved in cell damage induced by hemoglobin.

Key words: NRF2；HB；Oxidative damage

天津地区水产养殖源气单胞菌耐药性及耐药基因分布特征

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摘要：摘要：文章采用生化鉴定与16SrRNA相结合的方法对从天津地区水产养殖源分离出的77株气单胞菌进行分类，用K-B琼脂扩散法和微量肉汤稀释法检测77株气单胞菌的耐药性，并用PCR方法对耐药菌株进行耐药基因携带情况的检测。结果显示：我市77株气单胞菌对14种抗菌药物的耐药率从0%-98.7%，对阿莫西林耐药率最高，其次是红霉素、链霉素、和磺胺异噁唑。多重耐药性气单胞菌的比例高达66.23％，对5类及以上的药物具有抗性的菌株比例已超过30％；通过对77株气单胞菌对11种抗菌药物感受性测定，盐酸环丙沙星是防治我市水生动物由气单胞菌引起疾病的最佳药物，其次是恩诺沙星和盐酸多西环素。本研究通过PCR方法对25种特定耐药基因进行检测，大环内酯类、氯霉素类、β-内酰胺类、抗叶酸类耐药基因在我市水产养殖源气单胞菌种占据优势。

关键词：气单胞菌；耐药性；耐药基因

Drug resistance and drug resistance gene distribution of aquaculture-derived Aeromonas in Tianjin area

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Abstract： In this paper, 77 strains of aeromonas isolated from aquaculture sources in Tianjin were classified by biochemical identification combined with 16SrRNA. The drug resistance of 77 strains of aeromonas was detected by K-B AGAR diffusion method and microbroth dilution method, and the drug resistance gene carrying was detected by PCR method. The results showed that the resistance rate of 77 strains of Aeromonas in our city to 14 kinds of antibiotics ranged from 0% to 98.7%, and the resistance rate of amoxicillin was the highest, followed by erythromycin, streptomycin, and sulfamisoxazole. The proportion of multi-drug resistant aeromonas was as high as 66.23%, and the proportion of resistant strains to 5 or more drugs was more than 30%. The susceptibility of 77 strains of aeromonas to 11 kinds of antibiotics was determined. Ciprofloxacin hydrochloride was the best drug to prevent and treat the disease caused by aeromonas in aquatic animals in our city, followed by enrofloxacin and doxycycline hydrochloride. In this study, 25 specific drug resistance genes were detected by PCR method. Macrolides, chloramphenicol, β-lactam and anti-folic acid resistance genes were dominant in aquaculically-derived aeromonas strains in our city.

Key words: Aeromonas Drug resistance Drug resistance gene

拟六青蟹的层粘连蛋白受体基因的鉴定及功能研究

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摘要：模式识别受体在先天免疫系统中发挥重要作用，负责识别外来微生物的存在。在本研究中，我们克隆了层粘连蛋白受体基因(SpLR)，并对其进行了结构特征、组织分布、MCDV-1 刺激后表达变化分析,以及干扰后对病毒感染做出反应等研究。SpLR 全长 1075bp,含有 1 个 66bp 的 5 非编码区和 1 个 49bp 的 3 非编码区，以及一个 960bp 的开放阅读框，编码 319 个氨基酸。预测的蛋白质包含两个核糖体 s2 结构域和一个 40S-SA-C 结构域。SpLR 基因在鳃中高表达，其次是肝胰腺和黏膜。感染青蟹双顺反子病毒后，SpLR 在肝胰腺和鳃组织中表达上调。体内 RNA 干扰敲低 SpLR 显著增加了 MCDV-1 感染后 toll 样受体和和钙调蛋白(CAM)的表达。体内沉默 SpLR 可提高青蟹的存活率，降低 MCDV-1 感染后的复制。以上结果表明，SpLR 在拟六青蟹的抗病毒感染中可能起重要作用。

关键词：拟穴青蟹；层粘连蛋白受体；青蟹双顺反子病毒；RNA 干扰

Identification and functional characterization of Laminin receptor in the mud crab, Scylla paramamosain, in response to MCDV-1 challenge

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Abstract：Pattern recognition receptors (PRRs), which are responsible for recognizing the presence or absence of foreign microorganisms, play an important role in the innate immune system. In the present study, a laminin receptor gene (SpLR) was cloned and characterized from the mud crab, Scylla paramamosain. The full length of SpLR contained a 5’ untranslated region (UTR) of 66 bp, a 3’ UTR of 49 bp, and an open reading frame (ORF) of 960 bp encoding 319 amino acids. The predicted protein contains two Ribosomal-S2 domains and a 40S-SA-C domain. The mRNA of SpLR was highly expressed in the gill, followed by the hepatopancreas and mucosa. The expression of SpLR was up-regulated in hepatopancreas and gill after infection with mud crab dicistrovirus-1(MCDV-1). Knocking down SpLR in vivo by RNA interference significantly increased the expression of Toll-like receptors (TLRs) and the expression of calmodulin (CAM) after MCDV-1 infection. Silencing of SpLR in vivo increased the survival rate of mud crabs and decreased the MCDV-1 replication after MCDV-1 infection. All these results suggested that SpLR could play an important role in pathogen infection in mud crab.

Key words: Scylla paramamosain; Laminin receptor; MCDV-1; RNA interference

高温胁迫下虾夷扇贝 PyLKB1/ PyAMPKα 信号通路的激活及其对糖代谢的调节

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摘要：虾夷扇贝是我国北方重要的冷水型贝类。高温胁迫导致虾夷扇贝糖代谢紊乱，但具体的调节机制仍未阐明。本研究在扇贝中鉴定了 AMPK 通路的关键分子——LKB1 和 AMPK 的同源分子（PyLKB1 和 PyAMPKα），分析了两者的组织表达模式。免疫荧光分析结果显示，PyLKB1 定位在血淋巴细胞中的细胞质和细胞核中，PyAMPKα主要定位在细胞质中。在高温胁迫下，肝胰腺中 PyLKB1 和 PyAMPKα的 mRNA 水平显著升高，PyAMPKα的磷酸化水平显著升高,PyGLUT1 和 PyPFK 的 mRNA 水平显著升高；肝胰腺、血淋巴细胞和血清中的葡萄糖含量显著升高。敲降 PyLKB1 后，肝胰腺中 PyAMPKα的磷酸化水平降低，PyGLUT1 的 mRNA 水平显著下浆，血清和肝胰腺中的葡萄糖含量显著降低，血淋巴细胞中的葡萄糖含量未见显著变化。以上结果表明，在高温胁迫下虾夷扇贝通过激活 PyLKB1/PyAMPKα通路调节糖代谢。

关键词：肝激酶；腺苷酸激活蛋白激酶；虾夷扇贝；糖代谢；高温胁迫

Activation of PyLKB1/PyAMPKα signaling pathway and its regulation of glucose metabolism in Yesso scallop Patinopecten yessoensis under high temperature stress

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Abstract: There is increasing evidence that high temperature stress can lead to the energy disorder in Yesso scallop Patinopecten yessoensis, an important aquaculture species in North China. However, the regulation mechanism of energy metabolism in scallops remains unelucidated. Herein, two key molecules in the AMPK signaling pathway, Liver kinase B1 (LKB1) and AMP-activated protein kinase (AMPK) homologous molecules (PyLKB1and PyAMPKα) were identified from Yesso scallop. Both PyLKB1 and PyAMPKα contained serine/threonine kinase domains, which were highly evolutionarily conserved. PyLKB1 and PyAMPKα were expressed in haemocytes, gills, mantle, gonad, hepatopancreas, adductor muscle, and both were highly expressed in hepatopancreas. The immunofluorescence assays showed that PyLKB1 was localized in the cytoplasm and nucleus of haemocytes, while PyAMPKα was mainly located on the cytoplasm. Under high temperature stress (25 °C), the mRNA levels of PyLKB1 and PyAMPKα were significantly increased ($p < 0.05$), the phosphorylation levels of PyAMPKα ($p < 0.05$), and the mRNA levels of PyGLUT1 and PyPFK were significantly increased ($p < 0.05$). Glucose levels in hepatopancreas, haemocytes, and serum were significantly elevated ($p < 0.05$). When PyLKB1 was knockdown by RNAi, there was a significant decrease of PyGLUT1 mRNA level in hepatopancreas ($p < 0.05$). The glucose content also significantly decreased in both serum and hepatopancreas ($p < 0.05$), but not in haemocytes. These results showed that scallop regulated carbohydrate metabolism through activating the PyLKB1/PyAMPKα signaling pathway under high temperature stress.

Key words: LKB1; AMPKα; Patinopecten yessoensis; glucose transport; high temperature stress

一种新型 perlucin 样蛋白(PLP)保护凡纳滨对虾免受哈维氏弧菌感染

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摘要： c 型凝集素(CTLs)作为模式识别受体(PRRs)在凡纳滨对虾的先天免疫中起重要作用。本研究从凡纳滨对虾中鉴定出一种新的 CTL，命名为泛荧光素样蛋白 (PLP)，与凡纳滨对虾 PLP 同源。来自凡纳滨对虾的 PLP 是在肝胰腺、眼球、肌肉和脑中表达，感染哈维氏弧菌后可在组织(肝胰腺、肌肉、鳃和肠)中激活。细菌(溶藻弧菌、副溶血性弧菌、哈维氏弧菌、无乳链球菌和枯草芽孢杆菌)可以被 PLP 重组蛋白以 Ca2+依赖的方式结合和凝集。此外，PLP 还能稳定细胞的表达免疫相关基因(ALF、SOD、HSP70、Toll4 和 IMD)和凋亡基因(Caspase2)。PLP 的 RNAi 可显著影响抗氧化基因、抗菌肽基因、其他 CTLs、凋亡基因、Toll 信号通路和 IMD 信号通路的表达。这些结果表明，PLP 通过识别细菌病原体和激活免疫相关基因和凋亡基因的表达，参与了抗哈维氏弧菌感染的先天免疫应答。

关键词： 凡纳滨对虾；C 型凝集素；哈维氏弧菌；免疫相关基因

A novel perlucin-like protein (PLP) protects Litopenaeus vannamei against Vibrio harveyi infection

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Abstract： C-type lectins (CTLs), as pattern recognition receptors (PRRs), play an important role in the innate immunity of Litopenaeus vannamei. In this study, a novel CTL, named perlucin-like protein (PLP), was identified from L. vannamei, which shared homology sequences of PLP from Penaeus monodon. PLP from L. vannamei was expressed in the hepatopancreas, eyestalk, muscle and brain and could be activated in the tissues (hepatopancreas, muscle, gill and intestine) after infection with the pathogen Vibrio harveyi. Bacteria (Vibrio alginolyticus,

V. parahaemolyticus, V. harveyi, Streptococcus agalactiae and Bacillus subtilis) could be bound and agglutinated by the PLP recombinant protein in a Ca2+-dependent manner. Moreover, PLP could stabilise the expression of the immune-related genes (ALF, SOD, HSP70, Toll4 and IMD) and apoptosis gene (Caspase2). The RNAi of PLP could

remarkably affect the expression of antioxidant gene, antimicrobial peptide genes, other CTLs, apoptosis genes, Toll signaling pathways, and IMD signaling pathways. Moreover, PLP reduced the bacterial load in the hepatopancreas. These results suggested that PLP was involved in the innate immune response against V. harveyi infection by recognising bacterial pathogens and activating the expression of immune-related and apoptosis genes.

Key words: Litopenaeus vannamei; C-type lectins; Vibrio harveyi; Immune-related genes

菲律宾蛤仔在副溶血弧菌刺激下自噬作用机制初步研究

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摘要：菲律宾蛤仔（Ruditapes philippinarum）是目前重要海产经济贝类，由于致病副溶血弧菌的存在，近年来蛤仔养殖业面临着巨大的挑战。本研究中，用高通量测序分析在副溶血弧菌感染后抗性个体和易感个体的蛤仔肝胰腺组织的转录组。持续 10 天将蛤仔浸泡在 2×10-7CFU/mL 浓度的副溶血弧菌海水中，检测 ATG16L1、mTOR、CTSL 和 NFkB 等基因在不同时间内显著升高，证明副溶血弧菌的刺激诱导蛤仔发生自噬反应。检测 ATG16L1 基因在蛤仔组织中表达分布，结果显示该基因在血细胞中显著表达，其次是肝胰腺。在蛤仔注射 ATG16L1 基因的 siRNA 后血细胞中该基因的表达显著下调，通路下游基因基因也显著下调，透射电镜观察血细胞显示干扰组自噬受到抑制，对照组自噬显著。研究综上表明，蛤仔在副溶血弧菌刺激后，ATG16L1 基因对自噬作用起到的关键的调节作用，为研究菲律宾蛤仔自噬作用机制提供新见解。

关键词：菲律宾蛤仔，副溶血弧菌，自噬通路，基因干扰

Preliminary study on autophagy mechanism of Ruditapes philippinarum stimulated by Vibrio parahaemolyticus

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Abstract： Ruditapes philippinarum is one of the most commercially important bivalve shellfish. However, the clam aquaculture industry has faced a great challenge due to Vibrio parahaemolyticus in recent years. In this study, we performed RNA-seq to profile the transcriptome of hepatopancreas tissue in the R. philippinarum with resistant individuals (survival group, VpS) and susceptible individuals (moribund group, VpM) after V. parahaemolyticus infection. The KEGG analysis reveal that immune related functional genes were significantly enriched in AMPK, mTOR signaling pathway, Autophagy and Lysosome, and phagosome in the hepatopancreas of Manila clams under V. parahaemolyticus challenge. In addition, histological observation of hepatopancreas from Manila clam after V. parahemolyticus challenge was conducted and inflammatory response in tissues were appeared from the pathological morphology.

Subsequently, we conducted an experiment on chronic stimulation of Philippine clams by V.parahaemolyticus. The clams were immersed in 2×10-7 CFU/mL of seawater for 10 days. The ATG16L1 、 mTOR 、 CTSL and NFkB genes were detected, and the genes were significantly increased at different time. We hypothesized that the stimulation of V. parahaemolyticus induced the autophagy of the clam. The expression of ATG16L1 gene in blood cells was significantly down-regulated after injection of siRNA of ATG16L1 gene, as well as the downstream genes LC3, ATG3 and ATG7 genes of autophagy pathway. Tem observation of blood cells showed that autophagy was inhibited in the interference group and significantly in the control group. The results obtained in this study provide valuable insights into the immune function of R. philippinarum under V. parahaemolyticus challenge.

Key words: Ruditapes philippinarum; Vibrio parahaemolyticus; autophagy pathway; gene interference

血红素加氧酶-1 参与萝卜硫素修复凡纳滨对虾氧化鱼油引起的氧化损伤

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摘要：血红素加氧酶-1（HO-1）在氧化应激刺激下高度诱导，具有减轻氧化应激造成的损伤的作用，萝卜硫素（SFN）是一种抗氧化剂。本研究旨在探讨 HO-1 是否参与萝卜硫素（SFN）修复凡纳滨对虾氧化鱼油（OFO）引起的氧化损伤。通过饲喂 OFO 饲料（OFO 占 6%）建立南美白对虾氧化应激模型，将其分为以下四组：对照组（注射 dsRNA-EGFP 并饲喂普通饲料）、dsRNA-HO 组-1 组（dsRNA-HO-1，普通饲料），dsRNA-HO-1 + SFN 组（dsRNA-HO-1，补充 50 mg kg−1 SFN 饲料），和 SFN 组（dsRNA-EGFP，补充 50 mg kg−1 SFN 饲料）。结果显示，与 dsRNA-HO-1 组相比，dsRNA-HO-1+SFN 组 HO-1 的表达水平显着升高（$p < 0.05$）。dsRNA-HO-1 组肌肉中 SOD、肝胰腺中 GPX 以及血清中的 GPX 活性均显着低于对照组，且 dsR

关键词：凡纳滨对虾；萝卜硫素； HO-1;氧化损伤；细胞凋亡；自噬

血红素加氧酶-1 参与萝卜硫素修复凡纳滨对虾氧化鱼油引起的氧化损伤

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Abstract： Heme oxygenase-1 (HO-1), which could be highly induced under the stimulation of oxidative stress, functions in reducing the damage caused by oxidative stress, and sulforaphane (SFN) is an antioxidant. This study aims to investigate whether HO-1 is involved in the repair of oxidative damage induced by oxidized fish oil (OFO) in Litopenaeus vannamei by sulforaphane (SFN). The oxidative stress model of L. vannamei was established by feeding OFO feed (OFO accounts for 6%), and they were divided into the following four groups: control group (injected with dsRNA-EGFP and fed with common feed), dsRNA-HO-1 group (dsRNA-HO-1, common feed), dsRNA-HO-1 + SFN group (dsRNA-HO-1, supplement 50 mg kg−1 SFN feed), and SFN group (dsRNA-EGFP, sup- plement 50 mg kg−1 SFN feed). The results showed that the expression level of HO-1 in the dsRNA-HO-1 + SFN group was significantly increased compared with the dsRNA-HO-1 group ($p < 0.05$). The activities of SOD in muscle and GPX in hepatopancreas and serum of the dsRNA-HO-1 group were significantly lower than those of the control group, and MDA content in the dsRNA-HO-1 group was the highest among the four groups. However, SFN treatment increased the activities of GPX and SOD in hepatopancreas, muscle, and serum and significantly reduced the content of MDA ($p < 0.05$). SFN activated HO-1, upregulated the expression of antioxidant-related genes (CAT, SOD, GST, GPX, Trx, HIF-1α, Nrf2, prx 2, Hsp 70), and autophagy genes (ATG 3, ATG 5), and stabilized the expression of apoptosis genes (caspase 2, caspase 3) in the hepatopancreas ($p < 0.05$). In addition, knocking down HO-1 aggravated the vacuolation of hepatopancreas and increased the apoptosis of hepatopancreas, while the supplement of SFN could repair the vacuolation of hepatopancreas and reduce the apoptosis signal. In summary, HO-1 is involved in the repair of the oxidative damage induced by OFO in L. vannamei by SFN.

Key words: Litopenaeus vannamei; sulforaphane; HO-1; oxidative damage; apoptosis; autophagy

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摘要：载脂蛋白 A-I（ApoA-I）是一种涉及各种生理学和病理学的脂蛋白。然而，ApoA-I 在鱼类免疫调节功能中的作用尚未得到很好的阐明。在这项研究中，从尼罗罗非鱼（Oreochromis niloticus）中发现了 ApoA-I，并研究了其在细菌感染中的作用。On-ApoA-I（Oreochromis niloticus-ApoA-I）有一个 792 bp 的开放阅读框架，编码含有 263 个氨基酸的蛋白质。On-ApoA-I 与其他硬骨鱼有 60%以上的相似性，与哺乳动物有 20%以上的相似性。肝脏的 On-ApoA-I 表达水平最高，On-ApoA-I 在链球菌感染期间被显著诱导。此外，体内研究表明，On-ApoA-I 的重组蛋白可以抑制炎症、凋亡，并提高细菌感染存活的概率。这项研究为进一步研究 ApoA-I 在鱼类免疫学中的作用提供了理论基础。

关键词：ApoA-I；尼罗河罗非鱼；炎症；无乳球菌链球菌；免疫反应

Apolipoprotein A-I (ApoA-I) protects Nile Tilapia (Oreochromis niloticus) against Bacterial Infection

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Abstract： Apolipoprotein A-I (ApoA-I) is a lipoprotein that involves in various physiology and pathology. However, the role of ApoA-I in immunomodulatory functions in fish are not well elucidated. In this study, the ApoA-I was identified from Nile tilapia (Oreochromis niloticus) and its function in bacterial infection was investigated. On-ApoA-I (Oreochromis niloticus-ApoA-I) has an open reading frame of 792 bp which codes for a protein with 263 amino acids. On-ApoA-I shared over 60% similarity with other teleost fish and more than 20% similarity with mammal. The liver has the highest level of On-ApoA-I expression and On-ApoA-I could be significant inducted during Streptococcus agalatiae infection. Moreover, in vivo studies revealed the recombinant protein of On-ApoA-I could suppress the inflammation, apoptosis and improve the probability of surviving a bacterial infection. This study offers a theoretical basis for further investigation of ApoA-I role in fish immunology.

Key words: ApoA-I; Nile tilapia; inflammation; Streptococcus agalatiae; immune response

牛磺酸对氨暴露下大鳞副泥鳅免疫指标的影响

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摘要：牛磺酸作为水产饲料的重要添加剂之一，对水产动物的生长健康起着重要作用。本实验我们探究牛磺酸对氨暴露下大鳞副泥鳅免疫指标的影响。实验设置牛磺酸组（暴露于 30 mmol/L NH4Cl 环境并注射牛磺酸）、氨暴露组（暴露于 30 mmol/L NH4Cl 并注射等量生理盐水）、对照组（暴露于清水并注射等量生理盐水），在实验开始 12、24、48、96 h 后检测大鳞副泥鳅肝胰腺与肾脏免疫指标（蛋白浓度，SOD、IgM、TNF-α、IL-1β、补体 C3、tlr5、lyz、hsp70、myd88）的变化情况。结果表明，氨暴露引起大鳞副泥鳅组织蛋白浓度、超氧化物歧化酶活力及相关免疫因子浓度增加，同时会上调 tlr5 和 myd88 基因以激活 NF-κB 信号通路。外源性牛磺酸添加可减轻大鳞副泥鳅氨中毒的不良反应，加速机体氨代谢相关指标恢复至正常水平。这一结果为牛磺酸应用于养殖鱼类氨氮解毒代谢提供了理论依据。

关键词：牛磺酸；大鳞副泥鳅；免疫指标；氨毒性

The effect of taurine on immune indicators of Paramisgurnus dabryanus under ammonia exposure

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Abstract： As one of the important additives in aquatic feed, taurine is of great significance to the growth and health of aquatic animals. This experiment explored the effect of taurine on immune indicators of Paramisgurnus dabryanus under ammonia exposure. Experiment included three groups: Taurine group (exposed to 30 mmol/L NH4Cl and injected with 100 ng/g fish body weight taurine), amonia exposure group (exposed to 30 mmol/L NH4Cl and injected with the same amount of physiological saline), control group (cultured in freshwater and injected with an equal amount of normal saline). After 12-, 24-, 48-, and 96-hours, the liver and kidney were used to measure the changes of immune factors (protein concentration,SOD,IgM,TNF-α,IL-1β,C3) and immune-related genes (tlr5, lyz,hsp70,myd88). The results show that exposure caused an increase in tissue protein concentration, SOD and other enzyme activities, meanwhile an up-regulation of tlr5 and myd88 genes indicated the activation of NF-κB signaling pathway. In summary, the addition of exogenous taurine can alleviate the adverse reactions of ammonia poisoning in loach, and it can accelerate the recovery of immune-related indicators under ammonia exposure. This result provides a theoretical basis for the application of taurine in ammonia detoxification of fish farming.

Key words: taurine; Paramisgurnus dabryanus; immunological indexes; ammonia toxicity

肝肠胞虫（EHP）未萌发和萌发孢子的转录组比较分析

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摘要：虾肝肠胞虫(EHP)是一种专性细胞内寄生虫，被分类为微孢子虫，是一种新兴的病原体，对全球虾类养殖业产生了重大影响。了解微孢子虫如何萌发是探索其感染过程的关键因素。然而，EHP 的萌发过程鲜有报道。为了深入了解萌发过程，我们对经过体外萌发处理的纯化 EHP 孢子进行了高通量测序分析。结果显示 137 个差异表达基因，其中上调 84 个，下调 53 个。虽然部分基因的功能尚不清楚，但本研究提供了 EHP 萌发前后转录组学变化的重要数据，有助于进一步研究 EHP 感染机制。

关键词：肝肠胞虫，萌发，转录组

Comparative transcriptome analysis of non-germinated and germinated spores of Ecytonucleospora hepatopenaei (EHP) in vitro

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Abstract： Ecytonucleospora hepatopenaei (EHP), an obligate intracellular parasite classified as microsporidia, is an emerging pathogen with a significant impact on the global shrimp aquaculture industry. The understanding of how microsporidia germinate has been a key factor in exploring its infection process. However, the germination process of EHP was rarely reported. To gain insight into the germination process, we conducted a high-throughput sequencing analysis of purified EHP spores that had undergone in vitro germination treatment. This analysis revealed 137 differentially expressed genes, with 84 up-regulated and 53 down-regulated genes. While the functions of some of the genes remain unknown, this study provides important data on the transcriptomic changes before and after EHP germination, which can aid in further studies on the EHP infection mechanism.

Key words: Ecytonucleospora hepatopenaei; Germination; Transcriptome

线粒体呼吸链在血红蛋白诱导的铁死亡中的机制研究

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摘要：溶血是鱼体多种疾病的常见症状之一，鱼体出血释放的血红蛋白（Hb）快速发生自氧化，造成组织细胞死亡。研究表明 Hb 诱导的细胞死亡方式主要是铁死亡，并导致线粒体呼吸链障碍，但是草鱼 Hb 诱导线粒体呼吸链功能障碍机制及其在铁死亡中的调控作用还不清楚。本研究以苯肼建立草鱼溶血模型，深入探究线粒体电子传递链在 Hb 诱导的铁死亡中的机制研究。普鲁士蓝染色发现，苯肼诱导的鱼体出血导致肝脏组织中大量的铁沉积。氧化损伤相关检测结果显示，溶血会导致肝脏中 4-HNE、MDA、ROS 等氧化损伤指标增加，激活了肝脏中铁代谢和铁死亡相关基因的表达水平。透射电镜观察发现，溶血导致肝脏细胞中线粒体超微结构改变。进一步的转录组分析结果显示，苯肼诱导的溶血激活了线粒体呼吸链通路。体外实验结果表明，血红素诱导肝细胞氧化损伤和膜电位下降，调控了线粒体呼吸链复合物的活性。综上所述，本研究结果表明线粒体呼吸链参与了 Hb 诱导的铁死亡。

关键词：血红蛋白；铁死亡；呼吸链

The Mechanism of Mitochondrial Respiratory Chain in Hemoglobin Induced Ferroptosis

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Abstract： Hemolysis is one of the common symptoms of various diseases in fish, and the hemoglobin (Hb) released from fish bleeding rapidly undergoes self oxidation, causing tissue cell death. Research has shown that the main mode of cell death induced by Hb is ferroptosis, which leads to mitochondrial respiratory chain disorders. However, the mechanism of mitochondrial respiratory chain dysfunction induced by Hb in grass carp and its regulatory role in ferroptosis are still unclear. This study used phenylhydrazine to establish a grass carp hemolytic model and delved into the mechanism of mitochondrial electron transfer chains in Hb induced iron death. Prussian blue staining revealed that phenylhydrazine induced fish body bleeding resulted in a large amount of iron deposition in liver tissue. The results of oxidative damage related tests showed that hemolysis can lead to an increase in oxidative damage indicators such as 4-HNE, MDA, and ROS in the liver, activating the expression levels of iron metabolism and iron death related genes in the liver. Transmission electron microscopy observation revealed that hemolysis caused changes in the mitochondrial ultrastructure of liver cells. Further transcriptome analysis showed that phenylhydrazine induced hemolysis activated the mitochondrial respiratory chain pathway. In vitro experimental results showed that heme induced oxidative damage and decreased membrane potential in liver cells, regulating the activity of mitochondrial respiratory chain complexes. In summary, the results of this study indicate that the mitochondrial respiratory chain is involved in Hb induced ferroptosis.

Key words: Hemoglobin; Ferroptosis; Respiratory Chain

血红素加氧酶 1(HO-1)在苯肼诱导的草鱼溶血中的损伤调控机制

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摘要：出血释放的血红蛋白(Hb)具有氧化活性，会对细胞造成损伤。血红素氧合酶 1(HO-1)主要催化血红素分解，在抗氧化中有重要作用。但是，目前 HO-1 在草鱼溶血中损伤的调控机制尚不清楚。本研究以苯肼(PHZ)构建草鱼溶血模型，探究 HO-1 在溶血中的损伤调控机制。H&E 和普鲁士蓝结果显示，苯肼诱导的溶血明显增加了组织中 Hb 和铁的沉积，伴随炎性浸润和组织空泡化。qRT-PCR 和 WB 检测显示，苯肼处理激活了组织中铁代谢和炎症相关基因的表达水平。此外，PHZ 诱导的溶血显著增加了组织中的 MDA、4-HNE 和 ROS 含量，并促进了组织细胞发生凋亡。体外结果显示，L8824 和 CIK 过表达 HO-1 后，显著降低了血红素(Heme)诱导的氧化损伤和炎症相关基因的表达水平。相反，敲降和抑制 HO-1 后，显著加剧了 heme 诱导的细胞损伤。综上所述，HO-1 可以缓解由 Hb 诱导的细胞损伤。

关键词：血红素氧合酶 1；草鱼；溶血；损伤

Damage regulation mechanism of heme oxygenase 1(HO-1) in hemolysis induced by phenylhydrazine in grass carp

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Abstract： Haemoglobin (Hb) released by bleeding has oxidative activity and can cause damage to cells. Heme oxygenase 1(HO-1) mainly catalyzes the decomposition of heme and plays an important role in antioxidant. However, the regulatory mechanism of HO-1 damage in hemolysis of grass carp remains unclear. In this study, the hemolysis model of grass carp was constructed with phenylhydrazine (PHZ) to explore the damage regulation mechanism of HO-1 in hemolysis. H&E and Prussian blue results showed that phenylhydrazine-induced hemolysis significantly increased the deposition of Hb and iron in tissues, accompanied by inflammatory infiltration and tissue vacuolation. qRT-PCR and WB tests showed that phenylhydrazine treatment activated the expression levels of genes related to iron metabolism and inflammation in the tissues. In addition, PHZ-induced hemolysis significantly increased the content of MDA, 4-HNE and ROS in tissues, and promoted the apoptosis of tissue cells. In vitro results showed that overexpression of HO-1 in L8824 and CIK significantly decreased the expression levels of heme-induced oxidative damage and inflammation-related genes. In contrast, knockdown and inhibition of HO-1 significantly aggravated Heme-induced cell damage. In summary, HO-1 can alleviate cell damage induced by Hb.

Key words: Heme oxygenase 1；Grass carp；Hemolysis；Damage

3 株抗弧菌解淀粉芽孢杆菌的筛选和鉴定以及生物学特性研究

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摘要：从三疣梭子蟹养殖池塘的底泥中分离出三株潜在益生菌 ZJOU-B01、ZJOU-B02 和 ZJOU-B03。根据 16S rRNA 基因序列分析,与解淀粉芽孢杆菌 MT585518.1 株的同源性为 99.79%,结果得出 ZJOU-B01、ZJOU-B02 和 ZJOU-B03 都是解淀粉芽孢杆菌。3 株解淀粉芽孢杆菌均对溶藻弧菌和副溶血弧菌致病菌均有抑制效果，且可以在盐度 1%~5%液体培养基中生长，且对溶藻弧菌的抑菌能力更强。采用 K-B 纸片法药敏试验证明 ZJOU-B01 对哌拉西林等 20 种抗菌药物敏感，ZJOU-B02 对哌拉西林等 12 种抗菌药物敏感，而 ZJOU-B03 菌株对卡那霉素等 12 种抗菌药物具有较强的耐药性。本研究成功分离出筛选出的三株解淀粉芽孢杆菌 ZJOU-B01、ZJOU-B02 和 ZJOU-B03 均对斑马鱼无毒,综合比较，ZJOU-B01 可做三疣梭子蟹微生态制剂的候选菌株。

关键词：解淀粉芽孢杆菌；抑菌作用；生物学特性；药敏试验

Screening and characterization of three strains of Vibrio vulnificus-resistant Bacillus amyloliquefaciens and their biological properties

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Abstract: In order to screen strains with potential probiotics for Portunus trituberculatus, three strains of potential probiotics, ZJOU-B01, ZJOU-B02 and ZJOU-B03, were isolated from the substrate of Portunus trituberculatus aquaculture ponds, and three strains of the bacteria were identified using morphological observation and molecular characterization, which were mainly verified in terms of bactericidal properties and tolerance. Morphological observation showed that strains ZJOU-B01, ZJOU-B02 and ZJOU-B03 were Gram-positive bacteria with round or oval spores. According to the 16S rRNA gene sequence analysis and morphological observation, ZJOU-B01, ZJOU-B02 and ZJOU-B03 were all Bacillus amyloliquefaciens, with 99.79% homology to Bacillus amyloliquefaciens strain MT585518.1. All three strains were sensitive to Aeromonas hydrophila, Aeromonas lysimachiae, Aeromonas sp. All three strains had inhibitory effects on Aeromonas hydrophila, Vibrio alginolyticus and Vibrio parahaemolyticus, and they could also grow in liquid medium with salinity of 1%~5%, among which ZJOU-B01 grew more stably and had stronger inhibitory ability on Vibrio alginolyticus. The drug sensitivity test using the K-B paper slide method proved that ZJOU-B01 and ZJOU-B02 were sensitive to 20 antimicrobial drugs such as piperacillin, while ZJOU-B03 strain had strong resistance to 12 antimicrobial drugs such as kanamycin. The three strains of Bacillus amyloliquefaciens ZJOU-B01, ZJOU-B02 and ZJOU-B03 successfully isolated and screened in this study were all antagonistic to Aeromonas hydrophila, Vibrio alginolyticus and Vibrio parahaemolyticus pathogens, and they had no toxicity to zebrafish, of which strain ZJOU-B03 was more resistant to antibiotics, and to summarize ZJOU-B01, ZJOU-B02, ZJOU-B03 can all be used as candidate strains of probiotics for the healthy culture of Portunus trituberculatus crab and as a source of microecological preparations for research and development.

Key words: Bacillus amyloliquefaciens; Bacteriostatic effect; Biological properties; Drug sensitivity test

虾夷扇贝（Mizuhopecten yessoensis）应答多棘海盘车（Asterias amurensis）捕食行为特征及相关生理生态指标的变化研究

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摘要：海星是虾夷扇贝（Mizuhopecten yessoensis）底播养殖过程中重要的敌害生物，为弄清敌害生物（多棘海盘车（Asterias amurensis））捕食行为对扇贝养殖和存活的影响，本文以虾夷扇贝和多棘海盘车作为研究对象，观察并量化了不同规格虾夷扇贝应对多棘海盘车刺激时运动行为及闭壳能力，研究了当多棘海盘车持续刺激后虾夷扇贝鳃、闭壳肌和外套膜的超氧化物歧化酶（superoxide dismutase SOD），过氧化氢酶（catalase, CAT），精氨酸激酶（arginine kinase AK）和章鱼碱脱氢酶（octopine dehydrogenase, ODH）活力变化，并根据酶活结果对差异显著的扇贝组织进行转录组深度测序，挖掘关键基因，进行功能验证。

关键词：虾夷扇贝；多棘海盘车；闭壳行为；转录组

Behavioral responses of the Yesso scallop Mizuhopecten yessoensis to predation by the northern Pacific seastar Asterias amurensis and their related physiological and ecological indicators

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Abstract：Starfish are important predators in bottom-culture farming systems for the Yesso scallop (Mizuhopecten yessoensis). We studied M. yessoensis and its predator the northern Pacific seastar (Asterias amurensis) in order to understand the impact of A. amurensis predation on M. yessoensis farming and survival. We observed and quantified the movement behavior and shell closure ability of different sized M. yessoensis when exposed to stimulation from A. amurensis. Furthermore, we investigated changes in the activities of the enzymes superoxide dismutase (SOD), catalase (CAT), arginine kinase (AK), and octopine dehydrogenase (ODH) in the gills, adductor muscles, and mantle tissues of M. yessoensis after continuous stimulation by A. amurensis. Based on enzyme activity results, we performed transcriptome deep sequencing on the differentially expressed enzymes in the various scallop tissues to identify the key genes for further functional validation. The results showed that: (1) small scallops exhibited frequent shell closure behavior within the first 30 seconds after stimulation, significantly different to the reaction times of medium and large scallops ($P < 0.05$), which showed no significant difference in reaction time. With increasing time after stimulation, the frequency and force of shell closure decreased in all sizes of scallop, until there were no further significant change in their response behavior. Small scallops escaped predation by A. amurensis through rapid and frequent shell closure, while medium and large scallops avoided predation by tightly closing their shells; (2) there were significant differences in enzyme activity among the different tissues, with significant differences observed in four enzymes in the adductor muscle of medium sized scallops (P <

0.05). The activities of SOD, CAT, and AK were significantly reduced, while ODH activity increased significantly; (3) transcriptome analysis of the adductor muscle tissue from medium scallops revealed differential expression of 514 genes, of which 243 were upregulated and 271 were downregulated. Among them, eight genes involved in phenylalanine metabolism, tyrosine metabolism, and amino acid biosynthesis, such as ALDHS, RAD17, CSADC, HSL, TRXL, TLR2, and C1QL4, showed significant differences. PCR based quantitative expression validation gave results consistent with the transcriptome analysis findings. In conclusion, the behavioral responses and related physiological ecological indicators of M. yessoensis underwent significant changes when stimulated by A. amurensis. The results of this study provided partial data support and theoretical references for strategies to control predatory organisms targeting scallops and pointed the way to means to improve bottom-seeding techniques in M. yessoensis aquaculture.

Key words: Yesso Scallop; Mizuhopecten yessoensis; northern Pacific seastar; Asterias amurensis; shell clap behavior; transcriptome analysis

CgLITAF 通过调节 CgTNF 介导的细胞凋亡参与长牡蛎的免疫反应

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摘要：LPS 诱导的 TNF-α因子（LPS induced TNF-α factor, LITAF）是一种能诱导肿瘤坏死因子（Tumor necrosis factor, TNF）和其他细胞因子表达的转录因子。本研究从长牡蛎（Crassostrea gigas）中鉴定到一个具有保守锌指结构域的 CgLITAF，发现其在长牡蛎各组织中均有表达。LPS 处理后，血淋巴细胞中 CgLITAF mRNA 表达量的变化不显著，但 CgLITAF 蛋白发生明显的从细胞质向细胞核转位。注射 CgLITAF 的 siRNA 后，抑制了 CgLITAF 的表达，使血淋巴细胞的总凋亡率显著下降。同时使 CgTNF 及细胞凋亡相关分子的表达量显著降低。此外，CgTNF 还可以和受体 CgTNFR 的蛋白相互结合。这些结果表明，CgLITAF 可能通过介导 CgTNF 表达，进而与相应受体结合影响细胞凋亡相关因子的表达，在长牡蛎免疫应答过程中发挥着重要作用。

关键词：长牡蛎；LITAF；血淋巴细胞；凋亡

An LPS-induced TNF-α factor involved in immune response of oyster Crassostrea gigas by regulating CgTNF mediated apoptosis

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Abstract： LPS induced TNF-α factor (LITAF) is a transcription factor involved in activation of Tumor necrosis factor (TNF) and other cytokines in the inflammatory response. In the present study, a homologue of LITAF with the conserved zinc bind domain was identified from the Pacific oyster Crassostrea gigas. The transcripts of CgLITAF were detected in all examined tissues. An obvious nucleus translocation of CgLITAF protein was observed in haemocytes after LPS stimulation. While the mRNA level of CgLITAF changed slightly after LPS stimulation. The siRNA of CgLITAF was injected to inhibit its expression and the total apoptosis rate of haemocytes decreased observably after LPS stimulation. The expression of CgTNF and other apoptosis-related molecules was also significantly suppressed in CgLITAF-RNAi oysters. In addition, the CgTNF can bind to CgTNFR. These results indicated that CgLITAF regulated the expression of CgTNF, thereby binding with the corresponding receptor to affect the expression of apoptosis related factors and playing an important role in the immune response of oysters.

Key words: Crassostrea gigas; LITAF; haemocytes; apoptosis

高温胁迫下长牡蛎 RIPK 通过泛素化修饰调控细胞凋亡

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摘要：受体相互作用蛋白激酶（RIPK）是细胞凋亡的关键调节因子，存在多种多聚泛素化修饰，且多聚泛素化修饰种类和水平的变化能决定细胞的命运-炎症、凋亡或坏死。本研究发现28℃胁迫后，长牡蛎血淋巴细胞凋亡率与对照组（15℃）相比显著升高。抗凋亡相关基因的mRNA 表达量在胁迫前 12 小时逐渐上升，在 12 小时达到最高，之后逐渐下降。凋亡相关基因的 mRNA 表达量在胁迫 12 小时后开始升高,泛素酶 C-IAP1 在胁迫后逐渐升高，在 6 小时达到最高，12 小时后逐渐降低。去泛素化酶 CYLD 及 A20 在胁迫 12 小时后显著升高。CgRIPK 泛素化水平在胁迫后先升高后降低，其蛋白水平逐渐升高，CgRIPK 与 CgFADD-like 结合程度逐渐增加。结果表明，在高温胁迫 12 小时内，CgRIPK 被泛素化修饰，启动抗凋亡途径；胁迫 12 小时后，CgRIPK 去泛素化，开启凋亡途径，CgRIPK 可能通过不同程度泛素化修饰调节细胞存活和凋亡。

关键词：RIPK；泛素化；细胞凋亡；长牡蛎；高温胁迫

The involvement of CgRIPK ubiquitination in regulating haemocyte apoptosis after high temperature stress in Pacific oyster Crassostrea gigas

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Abstract： The receptor interacting protein kinases (RIPK) is a key regulatory factor for apoptosis with various polyubiquitination modifications. The changes in the type and level of RIPK ubiquitination can determine the cell fate, including inflammation, apoptosis or necroptosis. In the present study, after acute high temperature stress, the apoptosis rate of haemocytes increased gradually. The expression levels of anti-apoptosis related genes were upregulated significantly, and reached the peak level at 12h, then decreased gradually. The expression of apoptosis related genes began to increase after 12 hours of high temperature stress. Meanwhile, the expression of ubiquitinase C- IAP1 gradually increased after stimulation, reached the highest point at 6h, and then descend gradually after 12h. The deubiquitinating enzymes CYLD and A20 were significantly increased after 12 hours of high temperature stress. The ubiquitination modification of CgRIPK showed a trend of first increasing and then decreasing, and the protein expression of CgRIPK increased gradually, the degree of integration between CgRIPK and apoptosis regulator CgFADD increased gradually. The results indicated that CgRIPK was ubiquitinated within 12 hours of high temperature stress to initiate the anti-apoptotic pathway and deubiquitinated after 12 hours of stress to activate the apoptotic pathway. CgRIPK might regulate cell survival and apoptosis via varying degrees of ubiquitination modification after acute high temperature stress.

Key words: RIPK; Ubiquitination; Apoptosis; Crassostrea gigas; High temperature stress

基于转录组和微生物组对米尔伊丽莎白菌感染黑斑蛙的机制研究

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摘要：本研究首次采用转录组学和微生物组学分析揭示了米尔伊丽莎白菌对黑斑蛙的影响。肝脏和肾脏转录组学分析显示，与未感染组相比，在感染黑斑蛙肝脏中分别发现了 1469 和 4737 个差异表达基因（DEGs），这些 DEGs 主要参与免疫和代谢，揭示了米尔伊丽莎白菌感染严重影响了黑斑蛙的免疫和代谢功能。在肝脏和肾脏的 DEGs 中分别筛选出了 10 个免疫相关 DEGs，其中大多出现显著下调，推测米尔伊丽莎白菌感染能够抑制宿主的免疫应答。肠道菌群分析显示，一些机会性病原菌的丰度在受感染黑斑蛙体内升高。在本研究中，还将筛选出的免疫相关基因与肠道微生物组进行了关联分析，发现大多免疫相关基因都与机会性致病菌的丰度有关。总体而言，我们的结果表明，米尔伊丽莎白菌感染导致肝脏和肾脏免疫功能受到抑制，代谢紊乱以及肠道菌群中致病菌丰度增加。本研究结果为了解米尔伊丽莎白菌感染黑斑蛙的致病机制提供了提供了初步依据。

关键词：黑斑蛙；肝脏；肾脏；转录组；微生物组；

Transcriptome, microbiome perspectives on the mechanism of infection of the black spotted frog by Elizabethkingia miricola

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Abstract： In this study, we first artificially infected black spotted frogs with E. miricola. Transcriptomic and microbiomic analyses were conducted to ascertain the effects of this organism on the frogs. The liver transcriptomic analysis indicated that the livers of infected frogs had 1469 differentially expressed genes (DEGs) when compared to the uninfected group. These DEGs are mainly involved in immunity and metabolism, including neutrophil extracellular trap formation, NOD-like receptor signalling pathway, leukocyte transendothelial migration, chemokine signalling pathway, Fc gamma R-mediated phagocytosis, and "metabolism" related pathways such as the pentose phosphate pathway, carbon metabolism, glycerophospholipid metabolism, and glycerolipid metabolism. Similarly, 4737 differentially expressed genes (DEGs) were found in the kidney of infected frogs. These DEGs are mainly involved in immunity and include: neutrophil extracellular trap formation, NOD-like receptor signalling pathway, B cell receptor signalling pathway, C-type lectin receptor signalling pathway, complement and coagulation cascade and Toll-like receptor signalling pathway. Ten immune-associated DEGs were screened in liver and kidney DEGs, respectively. And it was hypothesised that E. miricola. infection could suppress the host immune response. Analysis of microbiomic showed no significant difference in abundance and diversity between infected and uninfected groups. However, some opportunistic pathogens such as Citrobacter, Shigella and Providencia were significantly elevated ($P < 0.05$) in the infected frogs. Additionally, functional prediction confirmed that most of the microbiota in infected frogs were linked to metabolism-related KEGG pathways. In this study, the screened genes linked to immunity showed an association with the gut microbiome. The majority of these genes were found to be linked with the abundance of opportunistic pathogens.The outcomes indicate that E. miricola. infection leads to suppressed liver and kidney immune function, metabolic disturbances and increased abundance of pathogenic bacteria in the gut flora. The findings of this investigation offer a preliminary foundation for comprehending the pathogenic processes of E. miricola. infection in black spotted frogs.

Key words: Black spotted frog; Elizabethkingia miricola; Liver; Kidney; Transcriptomes; Gut microbiota

草鱼 mst2 在免疫应答中的作用机制

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摘要：为了初步阐明草鱼 mst2 在机体免疫中的作用机制，实验采用 RNA-Seq 技术对干扰 mst2 后经脂多糖(LPS) 应激的草鱼肾细胞系进行了转录组测序与验证分析。测序原始数据经拼接与组装后共获得 22374 个独立功能基因(unigenes)，其中已知功能基因为 21199 个，预测的新基因为 1175 个。表达差异分析表明，对照组与实验组之间共存在 38 个差异基因(DEGs)。利用 RT-qPCR 技术对 38 个 DEGs 结果进行验证，结果证实转录组分析结果可靠。此次分析中筛选得到的 DEGs 参与免疫代谢的途径主要有 MAPK 信号通路、内吞作用途径、自噬途径和细胞因子受体相互作用途径。凋亡相关基因检测结果显示，干扰 mst2 并经 LPS 处理后，促凋亡基因转录水平上调，抗凋亡基因转录水平下调，证明干扰 mst2 后经 LPS 处理会诱发细胞发生凋亡。综上所述，mst2 可通过调控凋亡相关过程参与机体免疫反应。

关键词：草鱼；mst2；CIK 细胞系；RNA-Seq；细胞凋亡

Mechanism of mst2 in grass carp (Ctenopharyngodon idella) during the immune response

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Abstract： In recent years, RNA-seq technology has been used in fish researches. The transcriptome analysis in Ctenopharyngodon idella kidney cell lines (CIK) is focused on virus, and that based on bacteria or lipopolysaccharide (LPS) is rarely reported. In order to elucidate the mechanism of mammalian sterile20-like kinase 2 (mst2) in C. idella during immune response, we analyzed and verified the transcriptome sequence of CIK incubated with LPS after being interfered with mst2 by small interfering RNA technology (siRNA). Firstly, a total of 22 374 unigenes were obtained from the original sequence data by De novo assembly, of which 21 199 genes were known and 1 175 new genes were predicted. Secondly, the analysis of unigenes expression showed that there were 38 differential genes (differentially expressed genes, DEGs) including 16 up-regulated genes and 22 down-regulated genes. Thirdly, 38 DEGs were verified by quantitative real-time PCR (qRT-PCR). The results showed that the qRTPCR analysis was consistent with transcriptome sequencing, indicating that the transcriptome sequencing was reliable. 38 DEGs in CIK cells were mainly involved in immune metabolism pathway, containing MAPK signal pathway, endocytosis pathway, autophagy pathway and cytokine receptor interaction pathway. Moreover, after being interfered with mst2 and treated with LPS, the detection of apoptosis-related genes showed that the transcriptional levels of pro-apoptotic genes (fas, bad1, bad2, caspase-3, caspase-8 and caspase-9) were up-regulated, while the anti-apoptotic genes (bcl2) were down-regulated. Therefore, it was proved that interfering mst2 could induce cell apoptosis after LPS treatment. To sum up, mst2 can participate in the body's immune response by regulating apoptosis-related processes. The present results preliminarily clarified the molecular mechanism of mst2 in grass carp during immune response, and may provide some basic theoretical reference for the prevention and control of grass carp bacterial diseases.

Key words: Ctenopharyngodon idella; mst2; CIK cell lines; RNA-Seq; cell apoptosis

半滑舌鳎 rab5b 的抗菌活性特性及其相关机制研究

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摘要：现今抗生素的滥用造成其他严重的问题，如细菌耐药性和药物残留。因此，寻找抗生素的有效替代品是迫在眉睫和需要探索的方法。rab5 是存在于吞噬小体上的蛋白质，而 rab5b 是 rab5 的一种特殊亚型，在病原体捕获后，rab5b 被招募到吞噬体表面，这种招募对吞噬体成熟的早期阶段非常重要。本研究探究其抗菌活性及作用机制。双倍稀释培养法检测，rab5b 对创伤弧菌、迟缓爱德华氏菌等 8 种细菌具有抑菌活性。荧光显微镜分析显示，rab5b 增强细菌的膜通透性，可推测，rab5b 可能会损害细菌膜。与细菌直接孵育后，WB 和 SEM 检测到 rab5b 在细菌上的明显阳性信号，综上所述，rab5b 通过靶向某些 PAMPs 与细菌表面结合，干扰正常代谢，这可能是其发挥抗菌活性的途径。

关键词：半滑舌鳎；创伤弧菌；rab5b；抑菌机制

Study on Antibacterial Activity and Related Mechanism of Rab5b in Cynoglossus semiliaevis

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Abstract： Nowadays, the abuse of antibiotics causes other serious problems, such as bacterial resistance and drug residues. Therefore, finding effective alternatives to antibiotics is an imminent and need to be explored approach. Rab5 is a protein present on phagosomes, whereas rab5b is a particular isoform of rab5 that is recruited to the phagosome surface following pathogen capture, and this recruitment is important for the early stages of phagosome maturation. This study investigated its antibacterial activity and mechanism of action. Rab5b showed antibacterial activity against 8 bacteria including Vibrio vulnificus and Edwardsiella tarda by double dilution culture. Fluorescence microscopy analysis showed that rab5b enhanced membrane permeability in bacteria, and it can be speculated that rab5b may damage the bacterial membrane. Following direct incubation with bacteria, significant positive signals of rab5b on bacteria were detected by WB and SEM, and in summary, rab5b interferes with normal metabolism by targeting certain PAMPs to bind to the bacterial surface, which may be a pathway for its antibacterial activity.

Key words: Cynoglossus semiliaevis; Vibrio vulnificus; Rab5b; bacteriostatic mechanism

纳米聚苯乙烯和辛硫磷复合暴露对中华绒螯蟹肠道的毒理效应

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摘要：纳米聚苯乙烯(NP)广泛存在于水生系统中，辛硫磷(PHO)作为杀虫剂进入水生系统后对甲壳类动物危害极大。因此，本文研究了环境浓度的 NP 和 PHO 单独或联合暴露对中华绒螯蟹肠道组织结构、抗氧化能力和免疫力的影响。结果表明，NP 和 PHO 单独或联合暴露增加了肠道上皮内淋巴细胞的数量，损伤了肠上皮和间充质细胞。而且根据 SOD、POD 等生理指标以及促炎基因表达变化诱导肠道氧化应激和炎症。转录组分析显示炎症相关通路(TGF - β信号通路、TNF 信号通路、MAPK 信号通路和 NF-κB 信号通路)受到影响。其中，NF-κB 通过上调 p70S6K (NP 暴露效应)和 ATF-2 (PHO 暴露效应)诱导表达，而 p70S6K 和 ATF-2 同时暴露于 NP 和 PHO 时均上调以诱导 NF-κB 表达。复合暴露可能导致肠道产生更多的 ROS，但抑制炎症。这些发现为研究环境相关浓度的 NP 或/和 PHO 暴露对肠道的影响提供了新的见解。

关键词：组织病理学；氧化应激；炎症；免疫力；转录组

Exposure to nanopolystyrene and phoxim causes oxidative stress and inflammation in the intestinal tract of Chinese mitten crab (Eriocheir sinensis)

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Abstract： Nanopolystyrene (NP) is widely present in aquatic systems, and phoxim (PHO) is extremely harmful to crustaceans when it enters aquatic systems as an insecticide. In this study, we investigated the effects of exposure to environmentally relevant concentrations of NP or/and PHO on the organizational structure, antioxidant capacity, inflammatory factors, and immunity of the intestinal tract of Eriocheir sinensis. After a 14-day exposure period, exposure to NP or/and PHO increased the number of intestinal intraepithelial lymphocytes. In addition, exposure to NP damaged intestinal epithelial cells and mesenchymal cells, while exposure to PHO degraded mucous glands. Exposure to NP or/and PHO also caused oxidative stress and inflammation while decreased intestinal immunity. The results of enzyme activity and gene expression assays showed that in comparison to the control group, antioxidant enzyme activity, T-AOC, and immune-related genes were significantly suppressed in the three exposure groups. Whereas the expression of proinflammatory genes (TLR, TLR2, LITNF-α, Myd88, ILF2, and IL-16) was significantly increased in the NP and PHO groups, and it was significantly decreased in the NPP group. Transcriptome analysis showed that inflammation-related pathways (TGF-beta signaling pathway, TNF signaling pathway, MAPK signaling pathway, and NF-κB signaling pathway) were affected. Among them, NF-κB was induced to be expressed by upregulation of p70S6K (effect of NP exposure) and ATF-2 (effect of PHO exposure), and both p70S6K and ATF-2 were upregulated to induced NF-κB expression when simultaneously exposed to NP and PHO. It was hypothesized that exposure to NP and PHO may resulted in greater intestinal production of ROS but inhibited inflammation compared to exposure alone. These findings provide new insights into the intestinal effects of NP or/and PHO exposure at environmentally relevant concentrations and emphasize the relevance of NP/PHO contamination to intestinal health.

Key words: Histopathology; Oxidative stress; Inflammations; Immunity; Transcriptome

警惕克氏原螯虾传播虾肝肠胞虫

（ Ecytonucleospora hepatopenaei)

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摘要：虾肝肠胞虫（Ecytonucleospora hepatopena, EHP）是一种专性细胞内寄生的病原，其感染造成对虾生长迟滞，合并感染细菌易引起白便综合症，在世界对虾养殖国家和地区造成重大经济损失。本研究检测了感染 EHP 的凡纳滨对虾塘中的野生克氏原螯虾。研究发现，采集的克氏原螯虾在实验室培养条件下排出白便, 其肝胰腺偏白且严重萎缩；荧光显微镜检及 EHP ptp2 qPCR 定量检测发现 EHP 存在于克氏原螯虾的肝胰腺、肠道及白便中，载量分别为 103、103、104 copies/50 ng gDNA；HE 染色显示肝胰腺小管间的边界模糊，上皮细胞肿大或脱落，可见成簇 EHP 聚集在细胞核周围；间接免疫荧光实验显示克氏原螯虾肝胰腺中存在增殖期的 EHP。克氏原螯虾和凡纳滨对虾是我国养殖规模最大的虾类，养殖环境有交叉。本研究是对克氏原螯虾养殖的病害预警，也表明了克氏原螯虾在 EHP 传播过程中的潜在作用

关键词：克氏原螯虾；凡纳滨对虾；虾肝肠胞虫；肝胰腺微孢子虫病；传播

Ecytonucleospora hepatopenaei Proliferate in Procambarus clarkii: A Warning for Crayfish and Shrimp Aquaculture

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Abstract：The pacific whiteleg shrimp (Litopenaeus vannamei) and the crayfish (Procambarus clarkii) are the most productive aquatic animals in the world. The prevalence of the microsporidium Ecytonucleospora hepatopenaei (EHP), an intracellular spore-forming unicellular parasite which leading retarded growth of L. vannamei, has caused severe economic losses in most shrimp farming country. In this study, we found that the wild P. clarkii, living in shrimp ponds with EHP outbreak, excreted white faeces after temporary laboratory culture. The hepatopancreas (HP) of symptomatic crayfish exhibited a lighter color and severely atrophied. H&E-stain showed tissue lesions in both hepatopancreas and intestine, and clustered microsporidian spores were filled in the cytoplasm of the cells. PCR using EHPptp2 and two microsporidian-universal primers sets demonstrated the existence of EHP in the hepatopancreas, intestine and the white feces of P. clarkii. The EHP loads of 103-104 copies of EHPptp2/50 ng HPgDNA were detected by qPCR. Developing stages and mature spores of EHP were observed in hepatopancreas of P. clarkii through indirect-immunofluorescence assay (IFA) and transmission electron microscopy (TEM). Considering the large-scale cultivation of L. vannamei and P. clarkii, overlap farming areas between these two species as well as the ability of crayfish to crawl on land and water, our finding indicates the potential role of P. clarkii in the transmission of EHP, and it is an early warning for crayfish and shrimp farming.

Key words: Procambarus clarkii; Litopenaeus vannamei; Ecytonucleospora hepatopenaei; Hepatopancreatic microsporidiosis; Transmission

缺血状态下大鼠骨髓造血机制的研究

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摘要：骨髓是最主要的造血器官，红细胞的生成受骨微环境因子和基因调控网络共同作用影响。本研究以大鼠为研究对象，通过眼眶采血建立缺血模型，探究红细胞生成过程中关键的分子调控机制。首先，利用 10×单细胞转录组测序技术对骨髓细胞类型聚类分析，一共鉴定出 18 类细胞亚群，对红细胞生成进行拟时分析和关键 maker 基因进行验证。差异基因富集分析显示，骨髓缺血显著富集到红细胞生成、炎症、吞噬以及铁死亡相关通路。为探究铁死亡在红细胞生成中的调控作用，本研究设置了对照组、贫血组、贫血组+ Ferrostatin-1（抑制剂）、贫血组+ Rsl3（诱导剂）。外周血血细胞计数和 CD71 骨髓有核细胞数目显示，在应激条件下，如铁死亡诱导剂组减少了红细胞的生成，抑制骨髓造血，反之铁死亡抑制剂制剂组，促进红细胞数目的生成。进一步的 HE 染色、普鲁士蓝染色、CD235a 免疫组化、原位杂交实验等结果均显示铁死亡参与到红细胞的生成过程。

关键词：红细胞；分子调控机制；铁死亡

Mechanisms of bone marrow haemopoiesis in rats under ischaemia

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Abstract： Bone marrow is the most important haematopoietic organ, and erythropoiesis is affected by both bone microenvironmental factors and gene regulatory networks. In this study, we used rats as research subjects and established an ischemia model through orbital blood sampling to investigate the key molecular regulatory mechanisms in the process of erythropoiesis. Firstly, bone marrow cell types were clustered and analysed using 10× single-cell transcriptome sequencing, and a total of 18 cell subpopulations were identified for mimetic analysis of erythropoiesis and validation of key maker genes. Differential gene enrichment analysis revealed that bone marrow ischaemia was significantly enriched for erythropoiesis, inflammation, phagocytosis, and iron death-related pathways. To investigate the regulatory role of iron death in erythropoiesis, a control group, an anaemic group, an anaemic group + Ferrostatin-1 (inhibitor), and an anaemic group + Rsl3 (inducer) were set up in this study. Peripheral blood haematocrit and CD71 bone marrow nucleated cell count showed that under stress conditions such as iron death inducer group reduced erythropoiesis and inhibited bone marrow haematopoiesis and conversely iron death inhibitor preparation group, promoted erythropoiesis number. Further results of HE staining, Prussian blue staining, CD235a immunohistochemistry, and in situ hybridisation experiments showed that iron death was involved in the process of erythropoiesis.

Key words: Erythrocytes; Molecular regulatory mechanisms;Ferroptosis

多纹钱蝶鱼鳗弧菌病原的分离鉴定及药敏试验

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摘要：为探究 2023 年钦州湾渔排养殖区多纹钱蝶鱼 Selenotoca multifasciata 以烂身为主要症状大规模发病的原因。本试验从患病多纹钱蝶鱼的组织中分离纯化出优势菌株，对其进行了形态学观察、生理生化特性鉴定、 16S rRNA 和 dnaJ 基因序列分析、 7 种毒力基因的检测、人工感染实验以及对 28 种抗菌药物做敏感性检测。结果表明：分离出的 3 株优势菌 QZ991 、 QZ992 和 QZ993 均为鳗弧菌 Vibrio anguillarum ，均携带 virA 、 Vah1 、 virC 、 empA 、 angM 、 flaA 和 ompU 等 7 种毒力基因，3 株分离菌株对多纹钱蝶鱼的半致死浓度（LD50）分别为 5.10×105、 4.33×105 、 2.45×106 cfu/mL，均对多粘菌素 B、庆大霉素、四环素类、喹诺酮类和多数头孢烯类等多种抗菌药物敏感

关键词：多纹钱蝶鱼；鳗弧菌；分离鉴定；毒力基因；药敏试验

Isolation, identification and drug sensitivity tests of Vibrio anguillarum in Selenotoca multifasciata

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Abstract： To investigate the causes of the large-scale morbidity of Selenotoca multifasciata with rotting body as the main symptom in the fishing row culture area of Qinzhou Bay in 2023, the dominant strains of the pathogen were isolated from diseased S. multifasciata on the farm, and the isolated strains were subjected to morphological observation, physicochemical and biochemical characteristics, 16S rRNA and dnaJ gene sequence analysis. The results showed that the three dominant strains of QZ991, QZ992, and QZ993 were identified as Vibrio anguillarum. The results of the artificial infection experiment showed that the three strains of V.anguillarum were highly pathogenic to healthy S. multifasciata, which were the causative agents of the disease in S. multifasciata. Histopathological examination found that the three isolates of V.anguillarum caused different degrees of damage to various organs of S. multifasciata, which was mainly manifested as degeneration and inflammatory cell infiltration, etc; PCR analysis detected seven virulence genes (virA, Vah1, virC, empA, angM, flaA, and ompU) in the three isolated strains. The antibiotic susceptibility test showed that the three isolated strains were sensitive to various antimicrobial drugs, such as polymyxin B, gentamicin, tetracyclines, quinolones, and most of the cephalosporins. According to the findings, the disease outbreak affecting S. multifasciata in the Beibu Gulf area was caused by V.anguillarum. This study's results will help establish a scientific foundation for preventing and managing V.anguillarum disease in S. multifasciata in the future.

Key words: Selenotoca multifasciata; Vibrio anguillarum; isolation and identification; virulence gene;drug sensitivity test.

Caspase−8/Caspase−3/GSDME 介导的细胞焦亡参与长牡蛎的炎症和抗菌免疫

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摘要：细胞焦亡是一种程序性细胞死亡形式，它是一种固有免疫机制，促进宿主抵御病原菌入侵。本研究从长牡蛎中鉴定出一种保守的 gasdermin E (命名为 CgGSDME)。CgGSDME 含有四个 Caspase-3 切割位点，产生 4 个 N 端片段(CgGSDME-Ns)。灿烂弧菌刺激后，CgGSDME 蛋白被切割为两个片段，血淋巴细胞发生肿胀以及出现囊泡。CgCaspase-3 可以和 CgGSDME 结合，它们的结合活性在灿烂弧菌刺激后增强。CgCaspase-8、CgCaspase-3 和 CgGSDME 可诱导鳃组织炎症细胞因子的表达和分泌。重组蛋白 CgGSDME-N(rCgGSDME-N)能够结合多种细菌并在细菌表面组装形成孔洞。综上，CgCaspase-3 和 CgCaspase-8 对 CgGSDME 的切割不仅介导了血淋巴细胞焦亡和炎症发生，而且首次证明 GSDME 在双壳类软体动物的免疫应答中出现直接抑菌或杀菌活性。

关键词：细胞焦亡；Caspase-8；Caspase-3；GSDME；长牡蛎

The Caspase-8/Caspase-3/GSDME-mediated pyroptosis contributes to inflammation and antibacterial immunity in oysters

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Abstract： Pyroptosis is a form of lytic programmed cell death mediated by the cleavage of gasdermins, which functions as an innate immune mechanism to facilitate host defense against invasive bacteria. In the present study, a gasdermin E (GSDME) was identified from the Pacific oyster Crassostrea gigas (defined as CgGSDME) with a conserved N-terminal pyroptosis-triggering domain and a C-terminal repressor domain. There were four Caspase-3 cleavage sites in CgGSDME sequence, which generated four N-terminal fragments (CgGSDME-Ns). The obvious cleavage of CgGSDME protein into fragments (CgGSDME-N and CgGSDME-C) in haemocytes and the swollen haemocytes with the presence of many vesicles were observed after V. splendidus stimulation. The binding of CgGSDME/CgCaspase-3 was evident in haemocytes pulled down by either CgCaspase-3 or CgGSDME immunoprecipitation after V. splendidus stimulation. When the activation of CgCaspase-8 and CgCaspase-3 was inhibited, the amount of CgGSDME-N protein in haemocytes was reduced after V. splendidus stimulation. CgCaspase-8, CgCaspase-3 and CgGSDME could induce the expressions and secretions of cytokines, as well as histological damage in gills. The recombinant CgGSDME-N (rCgGSDME-N) was able to bind multiple bacteria and assemble on the bacterial surface to generate pores. It displayed directly bactericidal activity and inhibited the growth of V. splendidus and Staphylococcus aureus. These results indicated that the cleavage of CgGSDME by CgCaspase-3 and CgCaspase-8 not only mediated haemocyte pyroptosis and induced inflammation, and for the first time also showed direct bacteriostatic/bactericidal activity in the immune response of bivalve molluscs.

Key words: Pyroptosis; Caspase-8; Caspase-3; GSDME; Crassostrea gigas

载脂蛋白 Eb (On–ApoEb)保护尼罗罗非鱼免受无乳链球菌感染

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摘要：载脂蛋白 E (ApoE)是一种重要的靶向蛋白，在抗感染和炎症中起着重要的作用。然而，ApoE 对鱼类细菌感染的免疫功能尚未研究。本研究从尼罗罗非鱼 Oreochromis niloticus 中克隆了全长 ApoE 的 cDNA，命名为 On-ApoEb。预测的 cDNA 序列长度为 831bp，编码 276 个氨基酸残基，与其他鱼类 ApoEb 的同源性为 63.87% ~ 98.55%，与哺乳动物 ApoEb 的同源性约为 22%。尼罗罗非鱼的 On-ApoEb 在肝脏中高表达，感染无乳链球菌后可在肝脏、脾脏、脑、肠等组织中被激活。此外，实验结果显示 On-ApoEb 可以降低促炎因子、免疫相关通路和凋亡的表达水平，同时增加抗炎因子的表达水平。此外，On-ApoEb 可以提高存活率，并减少肝脏和脾脏的细菌负荷。这些结果提示 On-ApoEb 参与免疫应答。

关键词：ApoE；尼罗罗非鱼 Oreochromis niloticus；无乳链球菌；炎症；免疫相关途径；细胞凋亡

Apolipoprotein Eb (On-ApoEb) protects Oreochromis niloticus against Streptococcus agalactiae infection

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Abstract： Apolipoprotein E (ApoE), a critical targeting protein, has been found to play an essential role in the protection against infection and inflammation. However, the immune functions of ApoE against bacterial infection in fish have not been investigated. In this study, a full-length cDNA for ApoE, named On-ApoEb was cloned from Oreochromis niloticus. The predicted cDNA sequence was 831bp in length and coded for a protein of 276 amino acid residues, which shared 63.87%-98.55% identity with ApoEb from other fishes, and about 22% identity with ApoEb from mammals. On-ApoEb from O. niloticus was highly expressed in the liver and could be activated in the tissues (liver, spleen, brain, and intestine) after infection with Streptococcus agalactiae. Moreover, the results revealed that On-ApoEb could decrease the expression levels of pro-inflammatory factors, immune-related pathways, and apoptosis, while increasing the expression levels of anti-inflammatory factors. Furthermore, On-ApoEb was noted to improve the survival rate and reduce the bacterial load in the liver and spleen. These results suggested that On-ApoEb was connected with immune response and had anti-inflammation and anti-apoptosis activities.

Key words: ApoE; Oreochromis niloticus; Streptococcus agalactiae; inflammation; immune-related pathways; apoptosis

尼罗罗非鱼（Oreochromis niloticus）C 型凝集素受体（CD302）的分子特征及其功能分析

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摘要：C 型凝集素受体(CLRs)是一组糖类结合蛋白，通过调节多种生理过程发挥作用，包括细胞间的黏附、血清糖蛋白的转运以及先天免疫系统对潜在病原菌的反应。尼罗罗非鱼 CD302 (OnCD302) 由一个 C 型凝集素结构域和跨膜区组成，且 OnCD302 氨基酸序列与其他物种共享高度保守的氨基酸位点。亚细胞定位显示其为细胞膜定位。OnCD302 在所有测定的器官中都表达，尤其在肝脏中高表达。OnCD302 在免疫组织中能被无乳链球菌(Streptococcus agalactiae)和嗜水气单胞菌(Aeromonas hydrophila)感染诱导表达。OnCD302 重组蛋白(rOnCD302)可与多种病原菌结合，对无乳链球菌的生长有抑制作用，但对嗜水气单胞菌无抑制作用。并且未见到 rOnCD302 对嗜水气单胞菌和无乳链球菌的凝集作用。最后，rOnCD302 降低了巨噬细胞吞噬无乳链球菌和嗜水气单胞菌的能力。

关键词：CD302；尼罗罗非鱼；无乳链球菌；嗜水气单胞菌

Molecular characterization of a novel C-type lectin receptors (CD302) in Nile tilapia (Oreochromis niloticus) and its functional analysis in host defense against bacterial infection

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Abstract： C-type lectin receptors (CLRs) are a group of carbohydrate-binding proteins which function by mediating mul-tiple biological events, including adhesion between cells, the turnover of serum glycoproteins, and the innate immune system’s reaction to prospective invaders. However, how CLRs affects bony fish’s innate immunity to bacterial infection is ill-defined. Therefore, CD302, a member of the CLRs family, was found in Nile tilapia (Oreochromis niloticus) (OnCD302) and the functions in the immune activities of tilapia against bacterial infection were examined. The OnCD302 consists of a C-type lectin domain, a transmembrane domain, and a deduced protein encoded by 242 amino acids. Besides, the OnCD302 protein has a series of highly conserved amino acid sites with other CD302 proteins. Subcellular localization showed that OnCD302 is located in the cell membrane.

Transcriptional level investigation showed that OnCD302 was extensively expressed in all selected organs and had high expression in the liver. The transcriptional levels of OnCD302 are induced by Streptococcus agalactiae and Aeromonas hydrophila in the liver, spleen, head kidney, brain, and intestine. Afterwards, in vitro study revealed that several kinds of pathogens could be bound by the recombinant protein of OnCD302 (rOnCD302). Meanwhile, rOnCD302 could inhibit the growth of S. agalactiae, but had no inhibitory effect on A. hydrophila. However, the agglutinate ability of rOnCD302 to A. hydrophila and S. agalactiae was not observed in this study. Additionally, rOnCD302 reduced the ability of macrophages to phagocytose S. agalactiae and A. hydrophila. Summarily, our results indicated that CD302 get involved in fish immunization activities to bacterial infection.

Key words: CD302 Nile tilapia Streptococcus agalactiae Aeromonas hydrophila

凡纳滨对虾新的 C 型凝集素参与抗弧菌感染的天然免疫反应

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摘要：c 型凝集素(CTLs)作为模式识别受体的一员，在无脊椎动物消除微小入侵者的先天免疫反应中起着至关重要的作用。本研究成功克隆了一个新的凡纳滨对虾 CTL 基因，即 LvCTL7，其开放阅读框为 501 bp，编码 166 个氨基酸。Blast 分析表明，LvCTL7 与日本囊对虾 MjCTL7 的氨基酸序列相似性为 57.14%。LvCTL7 主要在肝胰腺、肌肉、鳃和眼柄中表达。哈氏弧菌能显著影响肝胰腺、鳃、肠和肌肉中 LvCTL7 的表达水平($p < 0.05$)。LvCTL7 重组蛋白可与革兰氏阳性菌(枯草芽孢杆菌)和革兰氏阴性菌(副溶血弧菌和哈维氏弧菌)结合。它能引起溶藻弧菌和哈维氏弧菌的凝集，但对无乳链球菌和枯草芽孢杆菌无作用。添加 LvCTL7 蛋白的攻击组 SOD、CAT、HSP 70、Toll 2、IMD 和 ALF 基因的表达水平较直接攻击组稳定($p < 0.05$)。此外，通过双链 RNA 干扰敲除 LvCTL7 下调了保护抵

关键词：凡纳滨对虾；c 型凝集素；免疫调节；微生物抑制活性

A novel C-type lectin for Litopenaeus vannamei involved in the innate immune response against Vibrio infection

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Abstract: C-type lectins (CTLs), as a member of pattern recognition receptors, play a vital role in the innate immune response of invertebrates to eliminate micro-invaders. In this study, a novel CTL of Litopenaeus vannamei, namely, LvCTL7, was successfully cloned, with an open reading frame of 501 bp and a capability to encode 166 amino acids. Blast analysis showed that the amino acid sequence similarity between LvCTL7 and MjCTL7 (Marsupenaeus japonicus) was 57.14%. LvCTL7 was mainly expressed in hepatopancreas, muscle, gill and eyestalk. Vibrio harveyi can significantly affect LvCTL7 expression levels in hepatopancreases, gills, intestines and muscles ($p < 0.05$). LvCTL7 recombinant protein can bind to Gram-positive bacteria (Bacillus subtilis) and Gram-negative bacteria (Vibrio parahaemolyticus and V. harveyi). It can cause the agglutination of V. alginolyticus and V. harveyi, but it had no effect on Streptococcus agalactiae and B. subtilis. The expression levels of SOD, CAT, HSP 70, Toll 2, IMD and ALF genes in the challenge group added with LvCTL7 protein were more stable than those in the direct challenge group ($p < 0.05$). Moreover, knockdown of LvCTL7 by double-stranded RNA interference downregulated the expression levels of genes (ALF, IMD and LvCTL5) that protect against bacterial infection ($p < 0.05$). These results indicated that LvCTL7 had microbial agglutination and immunoregulatory activity, and it was involved in the innate immune response against Vibrio infection in L. vannamei.

Key words: Litopenaeus vannamei; C-type lectin; Immune regulation; Microbiostatic activity

溶藻弧菌 HY9901△gr 减毒活疫苗对珍珠龙胆石斑鱼（♀Epinephelus fuscoguttatus × ♂Epinephelus lanceolatu）的免疫保护作用

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摘要：溶藻弧菌是水产养殖中一种严重的细菌病原体，被其感染的石斑鱼会出现行动迟缓、溃疡、肝脏充血等症状。这种病原体还会导致人类腹泻、中耳炎和伤口感染。因此，开发有效的疫苗预防弧菌病是非常重要的。本研究通过腹腔注射珍珠龙胆石斑鱼评价了溶藻弧菌 gr 缺失株作为减毒活疫苗候选疫苗的效力。实时荧光定量 pcr 检测免疫后 MHC-Iα、TNF-α、IL-1β、IL-6 和 MyD88 的基因水平，并检测血清抗体效价的变化。与对照组相比，接种石斑鱼的免疫组织中免疫相关基因的表达水平较高，接种 6 周后仍可检测到特异性 IgM。此外，免疫组超氧化物歧化酶(SOD)、过氧化氢酶(CAT)和溶菌酶(LZM)的活性也有所提高。△gr 作为减毒活疫苗，免疫保护率达到 73.08%。这些结果表明△gr 可作为一种潜在的石斑鱼疫苗和控制珍珠龙胆石斑鱼溶藻弧菌的有效活疫苗。

关键词：谷胱甘肽还原酶；溶藻弧菌；减毒活疫苗；珍珠龙胆石斑鱼

A live attenuated strain of HY9901Δgr provides protection against Vibrio alginolyticus in pearl gentian grouper (♀Epinephelus fuscoguttatus × ♂Epinephelus lanceolatu)

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Abstract：Vibrio alginolyticus is a severe bacterial pathogen in aquaculture. The grouper infected by it will have symptoms such as slow movement, ulcer and liver congestion. This pathogen can also cause diarrhea, otitis media and wound infection in humans. Therefore, it is very important to develop effective vaccines to prevent vibriosis. In this study, The efficacy of gr deletion strain of Vibrio alginolyticus as a candidate vaccine for attenuated live vaccine was evaluated by intraperitoneal injection of pearl gentian grouper. Real-time fluorescence quantitative pcr was used to detect the gene dynamics of MHC-Iα, TNF-α,IL-1β,IL-6 and MyD88 after immunization, and to detect the change of serum antibody titer. Compared with the control group, the expression level of immune-related genes in the immune tissues inoculated with grouper was higher, and specific IgM could still be detected after 6 weeks of inoculation. In addition, the activities of superoxide dismutase (SOD), catalase (CAT) and lysozyme (LZM) in the immune group were also increased. △gr is an attenuated live vaccine, and its immune protection rate reaches 73.08%. These results indicate that △gr can be used as a potential pearl grouper vaccine and an effective live vaccine for controlling Vibrio alginolyticus in grouper.

Key words: Glutathione reductase; Vibrio alginolyticus; Attenuated live vaccine; Pearl gentian grouper

铜胁迫下罗氏沼虾肝胰腺的转录组分析

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摘要：罗氏沼虾是我国重要的淡水养殖对虾之一。铜是水生生态系统中普遍存在的环境污染物，且可能对水生生物的生理功能产生负面影响。然而，罗氏沼虾肝胰腺对铜胁迫的分子响应仍缺乏系统的研究。本研究将罗氏沼虾暴露于含铜水体中 0 小时（对照组）、3 小时和 48 小时后取其肝胰腺组织，用 RNA-seq 技术筛选出与应激反应相关的潜在基因和通路。0h vs 3h 组筛选出 7288 个上调和 3876 个下调的差异表达基因，0h vs 48h 组筛选出 6630 个上调和 4307 个下调的差异表达基因，这表明机体内有更多的基因被诱导以抵抗铜毒性。KEGG 富集分析发现，细胞周期、错配修复和核苷酸切除修复途径中多个关键基因的表达被抑制，表明铜可能通过干扰 DNA 损伤修复途径破坏肝胰腺的基因组稳定性。同时，机体试图通过调节代谢、铜离子稳态、解毒、免疫和细胞凋亡过程来减少铜造成的损伤。研究结果为揭示罗氏沼虾对水体中铜胁迫的响应机制提供了理论依据。

关键词：罗氏沼虾；铜胁迫；转录组；肝胰腺；分子机制

Transcriptome analysis of the hepatopancreas in Macrobrachium rosenbergii under copper Stress

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Abstract：Macrobrachium rosenbergii is one of the important freshwater cultured prawns in China. Copper (Cu) is a widespread environmental contaminant in aquatic ecosystems, which may have a negative impact on the physiological functions of aquatic organisms. However, there is still a lack of systematic research on the molecular response of the hepatopancreas of M. rosenbergii under Cu stress. In this study, after exposure to water containing Cu for 0 h (control group), 3 h, and 48 h, the hepatopancreas of M. rosenbergii were taken and identify potential genes and pathways related to stress response by RNA sequencing (RNA-seq) technique. Compared to the control group, 7288 up-regulated and 3876 down-regulated differentially expressed genes (DEGs) were identified at 3 h and 6630 up-regulated and 4307 down-regulated DEGs were revealed at 48 h, indicating that many genes in M. rosenbergii were induced to resist the toxicity caused by Cu exposure. Notably, KEGG enrichment analysis showed that multiple key genes in the Cell cycle, Mismatch repair, and Nucleotide excision repair pathways were inhibited, indicating that Cu may disrupt the genomic stability of the hepatopancreas by interfering with the DNA damage repair pathway. However, the organism attempted to reduce the damage caused by Cu by regulating metabolism, copper ion homeostasis, detoxification, immunity, and apoptosis processes. In summary, our research provides basic data and theoretical basis for revealing the molecular response mechanism of M. rosenbergii to Cu stress in aquatic environments.

Key words: Transcriptome; Macrobrachium rosenbergii; Hepatopancreas; Copper exposure; Molecular mechanism

鲤疱疹病毒 2 型（CyHV–2）ORF150 在病毒与宿主免疫调节中的作用研究

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摘要：TRIM 蛋白是一类 E3 泛素化连接酶，在病毒与宿主的相互作用中发挥着重要的调节作用。鲤疱疹病毒 2 型（CyHV-2）ORF150 编码一种 TRIM 蛋白类似物，本研究克隆了 ORF150 基因，并研究了其在病毒感染中的作用。ORF150 基因共编码 605 个氨基酸，其中含有一个 RING 结构域（aa7-51）。在体外细胞中过表达 ORF150 能显著抑制病毒的复制，而缺失 RING 结构域后能显著降低这种抑制作用。此外，过表达 ORF150 能显著促进天然免疫相关因子 IRF2、IRF7、IRF9、Mx-1、IFN-α和炎性因子 IL-11 的转录，缺失了 RING 结构域后仅显著减弱了对 Mx-1 转录的促进作用，对其它因子的转录无影响。以上研究结果表明，ORF150 基因通过促进天然免疫反应和炎性反应对 CyHV-2 的感染起到负调节作用。研究为病毒与宿主的相互作用机制及病毒病的防控提供了理论基础。

关键词：鲤疱疹病毒 2 型；ORF150；RING 结构域；抗病毒

Study of the role of Cyprinid herpesvirus 2 (CyHV-2) ORF150 in the regulation of virus-host immunity

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Abstract：TRIM proteins are a class of E3 ubiquitinated ligases that play an important regulatory role in virus-host interactions. In this study, the ORF150 gene was cloned and its role in viral infection was investigated by cloning the ORF150 gene encoding a TRIM protein analogue encoded by Cyprinid herpesvirus 2,(CyHV-2). The ORF150 gene encodes a total of 605 amino acids, which contains a RING domain (aa7-51). Overexpression of ORF150 in cells in vitro significantly inhibited viral replication, while deletion of the RING domain significantly reduced this inhibition. In addition, overexpression of ORF150 significantly promoted the transcription of innate immune-related factors IRF2, IRF7, IRF9, Mx-1, IFN-α and inflammatory factor IL-11. These results suggest that ORF150 gene negatively regulates CyHV-2 infection by promoting innate immune response and inflammatory response. This study provides a theoretical basis for the interaction mechanism between viruses and hosts and the prevention and control of viral diseases.

Key words: CyHV-2; ORF150; RING domain; Antiviral

由星形胶质细胞条件培养液诱导的脑微血管内皮细胞的建立及应用：硬骨鱼脑部健康研究的新工具

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摘要：血脑屏障(blood-brain barrier, BBB)主要由内皮细胞组成，能够抵御有害物质，运输营养物质，维持脑环境的稳定。本研究成功建立了罗非鱼脑微血管内皮细胞系 TVEC-01。TVEC-01 从多个方面被鉴定为内皮细胞系。TVEC-01 具有超强的细胞迁移和体外合成血管的能力，可对硬骨鱼机体器官生长、胚胎发育和伤口愈合在内的多个生物过程所涉及的机制进行研究。此外，TVEC-01 还可用于模拟体内 LDL 的代谢机制以及构建体外血脑屏障模型。利用该模型证实了无乳链球菌可入侵 TVEC-01 细胞并在胞内存活，为无乳链球菌以跨细胞途径通过血脑屏障引起中枢神经损伤奠定了理论基础。综上所述，我们成功构建了硬骨鱼内皮细胞系，命名为 TVEC-01，该细胞系可用于多种体外实验。利用该模型证实了无乳链球菌通过跨细胞穿越途径突破硬骨鱼的血脑屏障并引起脑膜炎。

关键词：尼罗罗非鱼；内皮细胞系；BBB 星形胶质细胞条件培养基；胞内菌

A novel study of brain microvascular endothelial cells induced by astrocyte conditioned medium for constructing blood brain barrier model in vitro: a promising tool for teleost brain health research

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Abstract： The blood-brain barrier (BBB) is mainly composed of specialized endothelial cells, which can resist harmful substances, transport nutrients, and maintain the stability of the brain environment. In this study, an endothelial cell line from tilapia (Oreochromis niloticus) named TVEC-01 was successfully established. During the earlier establishment phase of the cell line, the TVEC-01 cells were persistently exposed to an astrocyte-conditioned medium (ACM). TVEC-01 cells were identified as an endothelial cell line. TVEC-01 cells retained the multiple functions of endothelial cells and were capable of performing various experiments in vitro. Furthermore, TVEC-01 cells efficiently expressed BBB-related tight junctions and key efflux transporters. From the results of the qRT-PCR, we found that the TVEC-01 cell line did not gradually lose BBB characteristics after persistent and repetitive passages, which was different from the vast majority of immortalized endothelial cells. The results showed that ACM induced up-regulation of the expression levels of multiple BBB-related genes in TVEC-01 cells. We confirmed that Streptococcus agalactiae was capable of invading the TVEC-01 cells and initiating a series of immune responses, which provided a theoretical basis for S. agalactiae to break through the BBB of teleost through the transcellular traversal pathway. In summary, we have successfully constructed an endothelial cell line of teleost, named TVEC-01, which can be used in many experiments in vitro and even for constructing BBB in vitro. Moreover, it was confirmed that S. agalactiae broke through the BBB of teleost through the transcellular traversal pathway and caused meningitis.

Key words: Nile tilapia; endothelial cell line; BBB; astrocyte-conditioned medium (ACM)； intracellular bacteria

虾肝肠胞虫增殖与宿主脂肪酸相关性研究

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摘要：本研究利用转录组、蛋白质组和靶向脂肪酸代谢组学技术，分析不同载量虾肝肠胞虫（EHP）感染对凡纳滨对虾初级代谢通路的影响，同时通过病原基因转录和蛋白表达特征，初步探究病原与宿主间的相互作用关系。我们发现初级代谢缺陷的 EHP 在对虾肝胰腺增殖过程中，严重破坏了宿主细胞的脂肪酸代谢，造成肝胰腺细胞内的游离脂肪酸显著减少，并且宿主细胞脂肪酸代谢的调控程度和脂肪酸含量的减少程度与 EHP 载量呈正相关。此外，鉴定的 479 个 EHP 蛋白中有 95 个为预测转运体，暗示了 EHP 对宿主物质和能量的高效利用。

关键词：虾肝肠胞虫；凡纳滨对虾；脂肪酸代谢

Study on the correlation of Enterocytozoon hepatopenaei proliferation and host fatty acid

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Abstract： In this study, transcriptomic, proteomics and targeted fatty acid metabolomics techniques were used to analyze the primary metabolism change of Litopenaeus vannamei after infected by different loads of Enterocytozoon hepatopenaei, and to explore the interaction between pathogens and hosts. We found that primary metabolism-deficient EHP severely disrupted the fatty acid metabolism of the host cells during its proliferation, resulting in a significant reduction of free fatty acids concentration in the shrimp hepatopancreas cells. Furthermore, the degree of regulation of fatty acid metabolism and the degree of reduction of fatty acid content were positively correlated with the EHP load. In addition, 95 of the 479 EHP proteins identified were predicted transporters, suggesting efficient utilizing of host materials and energy by EHP.

Key words: Enterocytozoon hepatopenaei; Litopenaeus vannamei; fatty acid metabolism

加州鲈水霉菌分离鉴定与中草药抑制研究

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摘 要： 淡水鱼水霉病（Saprolegniasis）常常于冬春季节暴发，病原菌主要为水霉属（Saprolegnia）和绵霉属（Achlya）的种类。水霉菌宿主范围广、传播迅速，可在短时间内造成大量养殖鱼或鱼卵暴发水霉病，经济损失巨大。近年来，实验室分别从来自广东和浙江的加州鲈鱼分离到多株水霉菌，经分子鉴定主要为多子水霉（Saprolegnia ferax）和绵霉（Achlya sp.）两个种类。多子水霉分离株（GLUD2110）与印度短盖肥脂鲤 (Piaractus brachypomus)多子水霉菌株的 ITS rDNA 序列一致性达到 100%，绵霉分离株（LM2109）与泰国尼罗罗非鱼（Oreochromis niloticus）绵霉属菌株单独聚为一支，与 GenBank 中所有已知种绵霉的 ITS rDNA 序列差异较大。两种菌株在生长条件和生长特性等方面存在较大差异：在马铃薯葡萄糖培养基（PDA）上，

关键词：加州鲈；多子水霉；绵霉；中草药；假单胞菌

Isolation and Identification of the Pathogen of Saprolegniasis in Largemouth Bass（Micropterus salmoides）and inhibition by Chinese herbal medicine

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Abstract： Abstract: Saprolegniasis in freshwater fish often breaks out in winter and spring, mainly caused by Saprolegnia sp. and Achlya sp.. Saprolegnia sp. has a wide host range and spreads rapidly. It can cause an outbreak of Saprolegniasis in a large number of farmed fish or fish eggs in a short period of time, causing huge economic losses. In recent years, several strains of Saprolegnia species were isolated from Micropterus salmoides perch from Guangdong and Zhejiang respectively. After molecular identification, they were mainly two species: Saprolegnia ferax and Achlya sp.. The ITS rDNA sequence identity between the S. ferax strain GLUD2110 and the isolate from Indian Piaractus brachypomus reached 100%, while the ITS rDNA sequence of the Achlya sp. isolate LM2109 and the Oreochromis niloticus strain from Thailand are clustered into a separate branch, significantly different from those of all known Saprolegnia species in GenBank. There are big differences between the two strains in terms of growth conditions and growth characteristics: on potato dextrose medium (PDA), S. ferax has a wider range of suitable growth temperatures, with the optimal temperature being about 25°C, whereas the suitable growth temperature of Achlya sp. is narrower, with the optimal temperature being about 18°C; S. ferax grows quickly and has slender hyphae, while Achlya sp. grows slowly and has thick hyphae. Correspondingly, the isolation rate of S. ferax is higher than that of Achlya sp., which is the main popular Saprolegnia species in China. We have isolated it many times from Micropterus salmoides in Guangzhou and, from Micropterus salmoides, grass carp and silver carp in Zhejiang, whereas only one strain of Achlya sp. was obtained. Subsequently, we investigated the growth inhibition effects of 8 kinds of Chinese herbal extracts and 14 Pseudomonas strains isolated from cultured environment on S. ferax. It was found that 8 kinds of extracts all had varying degrees of antibacterial effects on S. ferax, with Syzygium aromaticum having the best effect, followed by

Terminalia chebula Retz.. Pseudomonas strains also showed varying degrees of inhibitory effects on S. ferax. After culturing Pseudomonas stains and S. ferax in confrontation, the growth inhibition rate of S. ferax by 2 strains of Pseudomonas sp. reached 66.67% and 76.32% respectively. The research results not only enrich the biological characteristics and epidemiological data of Saprolegnia sp. in China, but also add selectivity to the development of green prevention and control drugs for freshwater fish Saprolegniasis.

Key words: Micropterus salmoides; Saprolegnia ferax; Achlya sp.; Chinese herbal medicine; Pseudomonas sp.

基于核酸纳米材料的水产品危险因子智能检测与阻控

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摘要：纳米材料依靠其独特的物理和化学特性，在水产品中危害物的检测应用方兴未艾。但因纳米材料高的比表面和反应活性，常在应用中出现不可控团聚、重复性差等问题。利用序列可编辑、生物兼容的核酸分子对纳米材料进行功能化和性质调控，可以大幅提升其在实际检测中的性能。此报告将介绍近期基于核酸纳米材料对重金属、微塑料和致病菌的快速智能检测研究，并利用其环境响应性能实现对致病菌的长期、可循环阻控。此外，由于核酸分子在细菌、水产动物细胞中的生物功能，核酸纳米材料的生物活性及功能也将初步讨论。

关键词：纳米材料；核酸；水产品；致病菌；重金属

Intelligent Detection and Inhibition of Hazardous Factors in Aquatic Products Based on Nucleic Acid Nanomaterials

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Abstract： The application of nanomaterials in the detection of hazardous substances in aquatic products is on the rise, thanks to their unique physical and chemical properties. However, their high surface area and reactivity often lead to issues such as uncontrollable aggregation and poor reproducibility in practical use. Enhancing their performance in real-world detection can be achieved by functionalizing and controlling their properties with sequence-editable, biocompatible nucleic acid molecules. In this presentation, I will introduce recent research on the rapid and intelligent detection of heavy metals, microplastics, and pathogenic bacteria using nucleic acid nanomaterials. They will also demonstrate how these materials can provide long-term, recyclable inhibition control of pathogenic bacteria, leveraging their environmentally responsive properties. Additionally, the biological activity and functions of nucleic acid nanomaterials in bacteria and aquatic animal cells will be preliminarily discussed.

Key words: Nanomaterials; nucleic acid; aquatic product; pathogenic bacteri; heavy metal ions

不同浓度虾肝肠胞虫侵染脊尾白虾能力差异分析

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摘要：为探究水体中虾肝肠胞虫（Ecytonucleospora hepatopenaei, EHP）数量与其侵染能力的关系，本研究通过设置 0（对照组）、101、102、103、104、105 等 6 个浓度组，探讨了不同 EHP 浓度对脊尾白虾组织（肝胰腺、鳃、肌肉和胃）中的 EHP 载量、肝胰腺组织结构、血淋巴中 iNOS 和 NO 含量的影响。结果表明：1）各组织中的 EHP 载量随着水体中 EHP 浓度的增加显著增加（$P < 0.05$），在 72 h 内同一侵染浓度下肝胰腺组织中 EHP 载量最大，且 EHP 载量与侵染时间成正相关；2）组织切片显示，EHP 浓度越高对肝胰腺组织损伤的程度越大，如仅 104 组、105 组发现了 EHP 侵染嗜碱性包涵体和孢囊；3）不同 EHP 浓度侵染会影响脊尾白虾的血淋巴中的 iNOS 活力和 NO 含量，在 24 h 内 iNOS 活力和 NO 含量呈现先升高后降低的趋势。本研究揭示了不同浓度 EHP 的感染能力存在显著差异。

关键词：脊尾白虾；虾肝肠胞虫；组织结构；侵染浓度；非特异性免疫酶活性

Analysis of the difference in Exopalaemon carinicauda with different concentrations of Ecytonucleospora hepatopenaei infection

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Abstract： In order to explore the relationship between the number of Ecytonucleospora hepatopenaei(EHP) and its infection ability in water, 6 EHP spores’concentrations of groups of 0 (control group), 101, 102, 103, 104, and 105 were set up .By analyzing the difference of EHP copy numbers in Exopalaemon carinicauda’s different tissues, hepatopancreas’ structure from E. carinicauda, inducible nitric oxide synthase and nitric oxide in hemolymph of E. carinicauda. As results showed:1)EHP copy numbers in each tissue increased significantly with the increase of EHP spores’concentration in water ($P<0.05$), and the highest EHP copy numbers was found in hepatopancreas at the same infection concentration within 72 hours, and the EHP copy numbers in hepatopancreas was positively correlated with infection time. 2) Histopathological results showed that the higher concentration of EHP, the deeper damage to hepatopancreas, for example, only the interstitial space of hepatic tubules increased in 101group at 12h after infection, while basophilic inclusions and cysts caused by EHP infection were found in 104,105groups.3) iNOS activity and NO content in hemolymph of E. carinicauda were affected by different EHP spores’concentrations,besides iNOS activity and NO content increased at first and then decreased within 24 hours. This study revealed that there were significant differences in the infection ability of different concentrations of EHP spores, and the presence of single-digit EHP spores per milliliter of water could lead to shrimp infection with EHP.

Key words: Exopalaemon carinicauda; Ecytonucleospora hepatopenaei; Organizational structure; Infection concentration; Non-specific immunoenzyme activity

鰤鱼诺卡氏菌减毒株的诱导及其作为鱼类诺卡氏病活疫苗的试验

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摘要：鰤鱼诺卡氏菌是一种革兰氏阳性兼性胞内寄生菌，已被确定为鱼类诺卡氏菌病，导致大量鱼类死亡和发病。基于此现状，迫切需要针对这种病原体的有效疫苗来控制水产养殖的重大损失。为了诱导减毒菌株开发具有潜在潜力的活疫苗，从野生型菌株 ZJ0503 中分别通过连续传代和紫外线（UV）照射获得了具有诱变性的序列 N.seriolae 菌株 S-250 和 U-20。此外，S-250 和 U-20 菌株的生物学特性、毒力、稳定性、介导免疫反应和对杂交鳢的保护作用都在本研究中确定。结果表明，U-20 菌株在形态特征上发生了显著变化，对杂交乌鱼的毒力显著下降，而 S-250 菌株则与 ZJ0503 菌株相比无明显差异。当用 ZJ0503、S-250 和 U-20 菌株各自的亚临床剂量注射杂交鳢腹膜内时，非特异性免疫的参数如（血清 LYZ、POD、ACP、AKP 和 SOD 活性），特异性抗体（IgM）的产生和免疫相关基因（CC1、CC2、IL-1β、IL-8

关键词：鰤鱼诺卡氏菌；鱼类诺卡氏菌病

Induction of attenuated Nocardia seriolae and their use as live vaccine trials against fish nocardiosis

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Abstract: Nocardia seriolae, a Gram-positive facultative intercellular pathogen, has been identified as the causative agent of fish nocardiosis, causing substantial mortality and morbidity of a wide range of fish species. Looking into that fact, the effective vaccine against this pathogen is urgently needed to control the significant losses in aquaculture practices. In order to induct attenuated strains for developing the potential live vaccines, the mutagenic N. seriolae strain S-250 and U-20 were obtained from wild-type strain ZJ0503 through continuous passaging and ultraviolet (UV) irradiation, respectively. Additionally, the biological characteristic, virulence, stability, mediating immune response and supplying protective efficacy to hybrid snakehead of the S-250 and U-20 strains were determined in the present study. The results showed that U-20 strain displayed dramatic changes in morpho logical characteristic and significant decreased in the virulence to hybrid snakehead, while that of S-250 strain had no obvious different in comparison to ZJ0503 strain. When hybrid snakehead were intraperitoneally injected with ZJ0503, S-250 and U-20 strains at their respective sub-clinical dosage, the non-specific immunity param eters (serum LYZ, POD, ACP, AKP and SOD activities), specific antibody (IgM) titers production and immune related genes (CC1, CC2, IL-1β, IL-8, TNFα, IFNγ, MHCIα, MHCIIα, CD4, CD8α, TCRα and TCRβ) expression were up-regulated, indicating that they were able to trigger humoral and cell-mediated immune responses. Furthermore, the protective efficacy in hybrid snakehead after vaccination with ZJ0503, S-250 and U-20 strains, in terms of relative percentage survival (RPS), were 28.85%, 56.89% and 89.65% respectively. Taken together, two attenuated N. seriolae strains S-250 and U-20 were obtained successfully and they could elicit strong immune response and supply protective efficacy to hybrid snakehead against N. seriolae, which suggested that these two attenuated strains were the potential candidates for live vaccine development to control fish nocardiosis in aquaculture.

Key words: Nocardia seriolae; Fish nocardiosis

患病加州鲈混合感染案例的病毒鉴定及 LMBV 水平传播途径初步研究

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摘要： 加州鲈是我国近年来发展最快的淡水养殖鱼类，但病害频发严重制约了该产业的健康发展。本研究用自行建立的加州鲈脑（MSH）细胞系，利用细胞分离、免疫组化、电镜观察、免疫荧光、基因测序等技术从患病加州鲈体内首次同时分离并鉴定出杂交鳢弹状病毒(HSHRV)和大口黑鲈蛙虹彩病毒(LMBV)，并评价这两种病毒对加州鲈致病性，结果表明 LMBV 是导致本次加州鲈发病的主要病原，且 HSHRV 与 LMBV 混合感染会导致感染鱼的死亡率增高。此外本研究通过浸泡人工感染方式模拟 LMBV 自然感染过程，利用 RT-qPCR 方法分析了感染鱼体内外各组织器官病毒载量动态变化规律。研究结果表明水体中的 LMBV 病毒是通过先感染鳃进入体内，然后在肝、肾、脾等器官中大量复制后，再通过血液循环扩散到鳃和皮肤粘液中，从而释放进入水体再次感染其他健康鱼。本研究结果为加州鲈多种病毒混合感染基础研究、多联疫苗开发及 LMBV 感染机制研究奠定理论基础

关键词：加州鲈；混合感染；蛙虹彩病毒；弹状病毒；传播途径

Identification of the virus form diseased Largemouth bass and preliminary study on the horizontal transmission route of Largemouthbass ranavirus

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Abstract: Largemouth bass is the fastest growing freshwater aquaculture fish in China in recent years, but the frequent occurrence of diseases has seriously restricted the healthy development of the industry. In this study, we used the self-established largemouth bass brain (MSH) cell line to isolate and identify both hybrid snakehead rhabdovirus (HSHRV) and Largemouthbass ranavirus (LMBV) from diseased largemouth bass by using cell isolation, immunohistochemistry, electron microscopy, immunofluorescence, and gene sequencing, and evaluated the pathogenicity of the two viruses to Largemouth bass. The results showed that LMBV was the main pathogen that caused the disease of Largemouth bass in this case, and the mixed infection of HSHRV and LMBV would lead to the increased mortality of infected fish. In addition, we simulated the natural infection process of LMBV by immersion artificial infection, and analysed the dynamic changes of viral load in various tissues and organs of infected fish in vivo and ex vivo by RT-qPCR. The results showed that the LMBV in the water column enters the body by first infecting the gills, and then after massive replication in organs such as the liver, kidney, and spleen, it spreads to the gills and skin mucus through the blood circulation, and is thus released into the water column to re-infect other healthy fish. The results of this study lay a theoretical foundation for the basic research on the mixed infection of multiple viruses in largemouth bass and the development of a multiplex vaccine as well as the study of the infection mechanism of LMBV.

Key words: Largemouth bass; mixed infections; LMBV; Rhabdoviridae; transmission routes

团头鲂源副炭疽芽孢杆菌 BC006 株致病性与耐药性的基因组解析

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摘要：基于全基因组测序，从致病性与耐药性上解析了 BC006 株特性。BC006 含 1 个染色体（CP119629）和 7 个质粒（CP119630 ~119636）。经 VFDB 预测到 48 个毒力基因（nhe、inhA、hlyIII,etc），经 CARD 预测到 16 个耐药基因(tet(45)、fexA、BcI,etc)；经 KEGG 预测到 48 个与人类抗微生物药物耐药性相关的基因（abcA、blaI、blaR1,etc），18 个与人类细菌感染相关的基因（dltD、dnaK、fliC，etc）。BC006 株对绵羊红细胞呈β溶血；对昆明系小白鼠、鳊、草金鱼和大口黑鲈的 LD50（105 cfu·g-1）依次为 4.22、4.68、45、147；对红霉素、林可霉素、甲硝唑、多西环素、四环素、头孢噻肟、甲氧嘧啶、青霉素 G、卡那霉素、丁胺卡那、利福平、诺氟沙星、恩诺沙星、氧氟沙星、环丙沙星、复方新诺明有耐药性。

关键词：副炭疽芽孢杆菌；全基因组序列；毒力基因；耐药基因；半数致死浓度；耐药性

Genome-wide analysis of pathogenicity and drug resistance of Megalobrama amblycephala-derived Bacillus paranthracis strain BC006

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Abstract：Based on whole genome sequencing, analyzing the characteristics of BC006 strain from the pathogenicity and drug resistance.BC006 contains 1 chromosome (CP119629) and 7 plasmids (CP119630 ~119636).The VFDB predicted 48 virulence genes(nhe、inhA、hlyIII、alo、esxB、essC、plcA、plcR、piplc、papR、pagR-XO1、sph、dhb、hal、ilsA、virR).The CARD to predict 16 resistant genes(VanT/VanG、VanW/VanI、VanY/VanM、VanY/VanB、VanY/VanF、tet(45)、fexA、qacJ、BcI、BcII、FosB、mphL、tetB(P)).The KEGG predicted 48 genes associated with human antimicrobial drug resistance(abcA、alr、amiABC、blaI、blaR1、bmrA、blaB、bla2、blm、ccrA、ddl、dltA、dltB、dltC、dltD、fmtC、mprF、mppA、mrcA、murF、murG、oppA、oppB、oppC、oppD、oppF、pbp2A、penP、vanY),18 genes associated with human bacterial infections(dltD、dnaK、fliC、frdA、groEL、hmp、HSPD1、HSPA9、inlA、pstS、sdhA、YHB1).BC006 strain showed β hemolysis on sheep red blood cells.The LD50 (105 cfu·g-1) of BC006 strain to Kunming mouse (~ 20 g),Megalobrama amblycephala (~ 16 g), grass goldfish (~12 g) and Micropterus salmoides (~12 g) were 4.22, 4.68, 45 and 147.BC006 strain can resist erythromycin、lincomycin、metronidazole、doxycycline、tetracycline、cefotaxime、trimethoprim、penicillin G、kanamycin、amikacin、rifampicin、norfloxacin、enrofloxacin、ofloxacin、ciprofloxacin、cotrimoxazole.

Key words: Bacillus paranthracis; the whole genome; virulence gene; drug resistance gene; median lethal dose; drug resistance

CgLITAF 通过调节 CgTNF 介导的细胞凋亡参与长牡蛎的免疫反应

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摘要：LPS 诱导的 TNF-α因子（LPS induced TNF-α factor, LITAF）是一种能诱导肿瘤坏死因子（Tumor necrosis factor, TNF）和其他细胞因子表达的转录因子。本研究从长牡蛎（Crassostrea gigas）中鉴定到一个具有保守锌指结构域的 CgLITAF，发现其在长牡蛎各组织中均有表达。LPS 处理后，血淋巴细胞中 CgLITAF mRNA 表达量的变化不显著，但 CgLITAF 蛋白发生明显的从细胞质向细胞核转位。注射 CgLITAF 的 siRNA 后，抑制了 CgLITAF 的表达，使血淋巴细胞的总凋亡率显著下降。同时使 CgTNF 及细胞凋亡相关分子的表达量显著降低。此外，CgTNF 还可以和受体 CgTNFR 的蛋白相互结合。这些结果表明，CgLITAF 可能通过介导 CgTNF 表达，进而与相应受体结合影响细胞凋亡相关因子的表达，在长牡蛎免疫应答过程中发挥着重要作用。

关键词：长牡蛎；LITAF；血淋巴细胞；凋亡

An LPS-induced TNF-α factor involved in immune response of oyster Crassostrea gigas by regulating CgTNF mediated apoptosis

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Abstract： LPS induced TNF-α factor (LITAF) is a transcription factor involved in activation of Tumor necrosis factor (TNF) and other cytokines in the inflammatory response. In the present study, a homologue of LITAF with the conserved zinc bind domain was identified from the Pacific oyster Crassostrea gigas. The transcripts of CgLITAF were detected in all examined tissues. An obvious nucleus translocation of CgLITAF protein was observed in haemocytes after LPS stimulation. While the mRNA level of CgLITAF changed slightly after LPS stimulation. The siRNA of CgLITAF was injected to inhibit its expression and the total apoptosis rate of haemocytes decreased observably after LPS stimulation. The expression of CgTNF and other apoptosis-related molecules was also significantly suppressed in CgLITAF-RNAi oysters. In addition, the CgTNF can bind to CgTNFR. These results indicated that CgLITAF regulated the expression of CgTNF, thereby binding with the corresponding receptor to affect the expression of apoptosis related factors and playing an important role in the immune response of oysters.

Key words: Crassostrea gigas; LITAF; haemocytes; apoptosis

聚ß–羟基丁酸酯(PHB)对异育银鲫抗氧化性能的调控作用及机制研究

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摘要：聚β-羟基丁酸酯(poly-β-hydroxybutyrate，PHB)是一种新型益生元，饲投 PHB 具有提高异育银鲫免疫力和抗病力的作用，但其调控机制尚不清楚。本文通过 mRNA-microRNA 联合分析、以及酶活指标测定揭示，PHB 显著增强异育银鲫抗氧化性能；与对照组相比，PHB 组异育银鲫脾脏共筛选获得 7005 个显著差异表达的 mRNAs 和 41 个 miRNAs，主要富集于 JAK/STAT 信号通路、B 细胞受体信号通路、Th1/Th2 细胞分化等 20 条免疫相关通路；以脾脏原代培养白细胞为模型，进一步研究显示 PHB 降低细胞内 NO 浓度和细胞毒性，提高白细胞抗氧化酶活性和降低 MDA 含量，对细胞具有较好的氧化保护作用；最后，通过酶活测定和 qRT-PCR 分析得出，代表性差异表达 miR-1971-x 参与 PHB 对免疫细胞抗氧化性能的调控作用。如上结果为深入揭示 PHB 的益生作用奠定基础。

关键词：异育银鲫；聚ß-羟基丁酸酯(PHB)；抗氧化性能；mRNA-microRNA 联合分析

Effects of dietary PHB supplementation on the antioxidative function of gibel carp (Carassius auratus gibelio) and its mechanism

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Abstract：Poly-β-hydroxybutyrate (PHB), as a kind of novel probiotics, can improve the immunity and disease resistance of gibel carp (Carassius auratus gibelio). However, the modulatory mechanism of PHB in aquatic animals is still unclear. Compared with the control group, 7005 differentially expressed (DE) mRNAs and 41 DE-miRNAs were screened in the PHB group. These DE-miRNAs and DE-mRNAs are involved in 20 immune-related pathways, such as JAK/STAT signaling pathway, B cell receptor signaling pathway, Th1 and Th2 cell differentiation, etc. PHB could reduce intracellular NO concentration and cytotoxicity, increase leukocyte antioxidant enzyme activity and reduce MDA content, reduce leukocyte oxidative damage, and show good protective effects on the oxidative damage of cells. Furthermore, the function of miR-1971-x in PHB regulation of leukocyte antioxidant activity was analyzed by enzyme activity determination and qRT-PCR. The results showed that miR-1971-x was involved in the regulation of antioxidant capacity of immune cells by PHB, and miR-1971-x negatively regulated the expression of target genes and downstream genes in JAK/STAT signaling pathway and Th1 and Th2 cell differentiation pathways. These results will provide a good guidance to illustrate the modulatory mechanism of PHB in aquatic animals.

Key words: Gibel carp; poly-β-hydroxybutyrate (PHB); anti-oxidant function; mRNA-microRNA analysis

鰤鱼诺卡氏菌多重 PCR 检测方法的建立

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摘要：鰤鱼诺鱼诺卡氏菌是鱼类肉芽肿性细菌性疾病诺卡菌病的致病因子，对水产养殖业的危害日趋严重。本研究筛选了 10 对引物和 7 组引物组合，选择其中 5 对引物组合建立多重 PCR 检测方法，用于鰤鱼诺卡氏菌的检测。然后对引物比例和退火温度进行了优化，对其灵敏度和特异性进行了测试，并在鱼体样品上进行了应用验证。结果表明，建立的多重 PCR 检测方法均表现出较强的特异性，可应用于鱼样品的检测。通过筛选鰤鱼诺卡氏菌的特异性引物，优化多重 PCR 体系的反应条件，成功建立了鰤鱼诺卡氏菌的多重 PCR 检测方法。为鰤鱼诺卡氏菌的快速检测提供了新方法，有助于鱼类诺卡氏菌病的防控。

关键词：鰤鱼诺卡氏菌；多重 PCR；特异性检测；鱼类诺卡氏菌病

Establishment of Multiplex PCR Assays for the Detection of Nocardia seriolae

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Abstract： Nocardia seriolae is the causative agent of fish nocardiosis, a granulomatous bacterial disease in fish, and is increasingly harmful to aquaculture. In this study, ten pairs of primers and seven sets of primer combinations were screened, and 5 primer combinations were selected to establish multiplex PCR assays for N. seriolae detection. Then the primer ratio and annealing temperature were optimized, the sensitivity and specificity were tested and the application on fish samples were verified. The results showed that the primer ratios of combinations 1, 2, 4, 6 and 7 were Chen-F/R: Miyoshi-F/R: Jiang-F/R= 1:2:1, Chen-F/R: 4296-F/R: Jiang-F/R= 1:2:1, Labrie-F/R: Chen-F/R: Jiang-F/R= 1:1:1, 4296-F/R: 4001-F/R: 4299-F/R= 2:1:2, Labrie-F/R: Chen-F/R: 4298-F/R= 1:1:2. The optimal annealing temperature of combinations 1, 2, 4, 6 and 7 were 57°C, 53°C, 48.4°C, 53°C, 64°C. The sensitivity of multiplex PCR assays based on combinations 1, 2, 4, 6 and 7 were 1 ng/μL, 62.5 pg/μL, 250 pg/μL, 500 pg/μL and 1.2 ng/μL, respectively. The established multiplex PCR assays all showed strong specificity and can be applied to fish sample detection. By screening the specific primers of N. seriolae and optimizing the reaction conditions of multiplex PCR system, the multiplex PCR assays for N. seriolae detection were successfully established. It provides a new method for the rapid detection of N. seriolae and helps the prevention and control of fish nocardiosis.

Key words: Nocardia seriolae; multiplex-PCR; specific detection; fish nocardiosis; accurate discrimination

大口黑鲈心脏细胞系的建立、应用及蛙虹彩病毒三种疫苗初步研究

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摘要：大口黑鲈蛙虹彩病毒（LMBV）病严重制约鲈鱼养殖业的健康发展,针对其基础研究薄弱、缺乏有效防治方法等问题。本研究一是建立大口黑鲈心脏细胞系 MSH，并开展其对外源基因表达效率及病毒感染诱导的免疫应答等研究；二是开发了针对 LMBV 的细胞灭活（In）、MCP 亚单位（Su）和 DNA 疫苗，并采用不同免疫策略接种大口黑鲈进行免疫效果评价。结果表明， MSH 细胞系可用于外源基因的表达研究，且对 LMBV 等 7 种病毒敏感，但 NNV 感染时可诱导I型干扰素表达而表现抗性，表明 MSH 细胞可用于多种鱼类病毒的病原学研究和疫苗开发。各疫苗免疫组鱼均诱导产生了不同程度的特异性和非特异性免疫应答，其中 DNA-DNA 组最强；DNA-DNA、DNA-Su、Su-Su、In-In 和对照组对 LMBV 强毒致死性感染的免疫保护率分别为 80%、63.3%、46%、43.3%和 10%。表明 DNA 疫苗可能是 LMBV 较为有开发前景的疫苗产品。

关键词：大口黑鲈；蛙虹彩病毒；心脏细胞系；疫苗

Establishment and application of heart cell line from largemouth bass and development of three types of vaccines against Largemouth bass ranavirus virus

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Abstract：Largemouth bass is among the most important cultured fish species in China and various viral diseases have greatly affected the largemouth bass industry. In this study, a permanent cell line from the heart of M. salmoides (MSH) was successfully established. MSH cells were successfully transfected with a GFP reporter gene and showed susceptibility to many fish viruses but were resistant to NNV, indicating that these cells that can be useful for future genetic, virological and immunological studies. In addition, cell-inactivated (In) vaccine, MCP subunit (Su) and DNA vaccines against LMBV were developed and evaluated for immunological effects using different immunological strategies to vaccinate largemouth bass. The results showed that all vaccine-immunised fish induced different degrees of specific and non-specific immune responses, with the highest in the DNA-DNA group; the immune protection rates of DNA-DNA, DNA-Su, Su-Su and In-In were 80%, 63.3%, 46% and 43.3%, respectively. This suggests that DNA vaccines may be a more promising vaccine product for LMBV. The results providing a direction and reference for the subsequent development of efficient vaccines for LMBV.

Key words: Largemouth bass; LMBV ; fish cell line; vaccine

第五专题：可持续捕捞

应用三种数据有限方法对印度洋近海金枪鱼类和马鲛类资源评估

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摘要：（2.近些年来印度洋近海金枪鱼类和马鲛类捕捞量上升较快，但因捕捞者多为个体手工渔业或小型工业渔业，渔业统计不完善，缺少传统资源评估所需数据。为了更好地掌握资源状况，本研究使用 1950—2020 年捕捞量数据，运用 CMSY 模型、DB-SRA 模型和 OCOM 模型三种数据有限评估方法对圆舵鲣、扁舵鲣、巴鲣、青干金枪鱼、斑点马鲛、康氏马鲛这六个鱼种资源状况进行评估。扁舵鲣和斑点马鲛的当前资源状态较为健康，圆舵鲣和巴鲣处于捕捞型过度捕捞状态，青干金枪鱼和康氏马鲛既处于捕捞型过度捕捞又处于资源型过度捕捞状态中。敏感性分析显示，参数 r 以及 Bend/K 的先验设定均会对 CMSY 模型结果产生较大的影响；DB-SRA 模型对 Bt/K 敏感，对 K 较为稳健。从结果上来看，三种模型均可以用于对近海小型金枪鱼和马鲛类的资源评估。建议在使用数据有限的评估方法时，采用多组参数以及多个方法进行比较分析，以更全面的获得种群资源状况。

关键词：近海金枪鱼；马鲛类；资源状况；数据有限评估方法；印度洋

Application of three data-limited methods for stock assessment of neritic tunas and mackerels in the Indian Ocean

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Abstract： Neritic tuna and mackerels catches in the Indian Ocean have increased rapidly in recent years, whereas these species currently lack comprehensive assessment due to their predominant capture in artisanal or small-scale fisheries, where fishery statistics are insufficient and the necessary data required for routine stock assessment are lacking.This study applied three data-limited methods (Monte carlo catch-msy,Depletion-based stock reduction analysis,Optimized catch-only assessment method) to analyze six neritic tunas and mackerels stock in the Indian Ocean. The size species assessed included Bullet tuna, Frigate tuna, Kawakawa, Longtail tuna, Indo-Pacific King Mackerel, and narrow-barred Spanish mackerel. Results showed that the Frigate tuna and Indo-Pacific King Mackerel had a healthy status, Bullet tuna and Kawakawa were at a higher risk of being subjected to overfishing ,Longtail tuna and narrow-barred Spanish mackerel was at a higher risk of being overfished and subjected to overfishing. Sensitivity analyses showed that both the priori setting of r and Bend/K had a large impact on the CMSY results; DB-SRA was sensitive to Bt/K and more robust to K. All three models are applicable for neritic tunas and mackerels stock assessment. It is recommended that when using data-limited assessment methods, multiple sets of parameters as well as comparative analyses of multiple methods are used to obtain a more complete picture of the status of the stock's resources.

Key words: neritic tunas; mackerels; stock status; data limited method; Indian Ocean

基于 DNA 条形码的全国市场鲨鱼唇物种鉴定

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摘要：本研究旨在通过 COI 基因 DNA 条形码（FDB，652 bp）和 mini DNA 条形码（MDB，127 bp）对 252 个鲨鱼唇样品进行物种鉴定，从而开展全国性调查。尽管鱼唇样品经过加工，但样品的总 DNA 呈现中低破碎度，99.2%的样品成功获得 FDB，另外 2 个样品获得 MDB。96.4%的样本鉴定到种。在已鉴定的 7 种鲨鱼中，大青鲨的检出率最高（65.5%），其他 6 种分别为镰状真鲨（11.5%）、路氏双髻鲨（6.7%）、锤头双髻鲨（3.6%）、灰鲭鲨（3.6%）、长鳍真鲨（3.2%）和沙拉真鲨（2.4%）。其中 3 种鲨鱼为濒危或极度濒危物种，4 种鲨鱼受全球商业管制。同时，FDB 和 MDB 也显示了一些真鲨属（Carcharhinus spp.）物种的鉴定受限问题。本研究结果强调了建立较完善的中国水产品可追溯系统的必要性。

关键词：鲨鱼；DNA 条形码；物种鉴定

DNA barcoding for the identification of shark lips: A nationwide survey for analyzing a never investigated product in the Chinese market

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Abstract： A nationwide survey conducted in China aimed at authenticating species in shark lips products (鱼唇) (n = 252) by full DNACOI barcoding (FDB; 652 bp) is presented. In addition, the efficiency of the FDB and of the mini DNA barcode (MDB; 127 bp) proposed by Fields et al. (2015) (PloS one, 10, e0114844.) in identifying the shark species detected in this study was compared. Despite the manufacturing process, the total DNA of the samples presented a medium low fragmentation degree, and the FDB was obtained from almost all the samples except for two (99.2%) from which the MDB was instead successfully obtained. Samples were allocated to species level in 96.4% of the cases. This confirms the importance to perform a preventive evaluation of the level of DNA degradation before selecting cost and time-consuming procedures. Of the 7 identified species, Prionace glauca was the most recovered (65.5%). The other six detected species were Carcharhinus falciformis (11.5%), Sphyrna lewini (6.7%), S. zygaena (3.6%), Isurus oxyrinchus (3.6%), C. longimanus (3.2%) and C. sorrah (2.4%), 5 of which are threatened and 4 are subject to global commerce regulation. Overall, issues in discriminating among some Carcharhinus spp. were highlighted both using the FDB and the MDB. Outcomes of this study confirms the need to improve the Chinese traceability system. In fact, even though a legislation for seafood labelling supported by an official system for name attribution not always ensure the sector safeguarding from frauds, absent or weak traceability system certainly facilitate illegal practices.

Key words: shark; DNA barcoding; species identification

马达加斯加西海岸捕虾拖网 CPUE 时空分布及其与环境因子关系分析

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摘要：马达加斯加西海岸是世界著名的虾类渔场，是我国过洋性拖网渔业的重要渔场之一。基于 GAM 模型分析主要渔获种类（印度白虾（Fenneropenaeus indicus）、独角新对虾（Metapenaeus monoceros）和短沟对虾（Penaeus semisulcatus））CPUE 的时空分布及其与主要环境因子的关系。结果表明：印度白虾的 CPUE 从三月份开始呈逐月递减的趋势，而独角新对虾和短沟对虾 CPUE 呈先升后降的趋势；空间上，印度白虾和独角新对虾 CPUE 在经度上自东向西、纬度上自南向北呈现出逐渐上升的趋势，而短沟对虾 CPUE 在渔场南北端较高；水深对短沟对虾（$P<0.05$）具有显著的影响；马达加斯加西海岸主捕虾类资源丰度具有明显的时空异质性，易受海洋环境、降水和径流等因素影响，研究结果为开展该海域渔业资源丰度评估、规范渔业管理、养护渔业资源，保障渔业可持续发展提供科学依据。

关键词：马达加斯加西海岸；拖网；印度白虾；独角新对虾；短沟对虾；CPUE；环境因子

Temporal and spatial distribution of CPUE of shrimp trawl fisheries and its relationship with environmental factors along the west coast of Madagascar

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Abstract：As a world famous shrimp fishing ground, the west coast of Madagascar has become one of Chinese important distant-water fishing grounds in Africa. In recent years, the catch per unite effort of the target shrimp in the coast of Madagascar has fluctuated and decreased significantly, and the proportion of by-catch species has increased, indicating a state of overexploitation of shrimp resources in the sea area. For offshore fishery, fishery resources are affected by runoff and precipitation. Runoff and precipitation can explain the change of offshore fishery resources. However, the current research on this aspect is not perfect. In this paper, shrimp trawl fishery yield statistics of representative office in Madagascar of China National Fisheries Corp., from 2012 to 2019 was used to analyze the spatial and temporal distribution of CPUEs of the main target catch species (Fenneropenaeus indicus, Metapenaeus monoceros and Penaeus semisulcatus) and their relationship with major environmental factors based on Generalized additive model (GAM). In the process of data processing, the fishery production data was first standardized by CPUE, transformed the resolution of environmental data to get the preprocessed data, and then used R software to build GAM model. The results showed that the CPUE of F. indicus showed a decreasing trend month by month from March, while CPUEs of M. monoceros, and P. semisulcatus presented increased firstly and then decreased with month. This difference indicates that the reproduction and supplement of the three main shrimp species on the west coast of Madagascar may not be synchronized in time, that is, as a dominant species, F. indicus may reproduce before the other two species. As for spatial distribution, the CPUEs of F. indicus and M. monoceros increased from south to north in latitude as well as from east to west in longitude. The higher CPUE of P. semisulcatus was found in the north and south section of the fishing ground. In the north-south direction, the CPUE of the three shrimp species reflects the trend of high in the north and low in the south, this study shows that there is a preference for the distribution of the three main shrimp species in this sea area, and the three shrimp species prefer higher SST in this sea area. Significant effect of depth on CPUEs of for M. monoceros ($P<0.05$) was detected, CPUE showed an obvious increasing trend with water depth from shallow to deep. For environmental factors, significant positive correlation between runoff on CPUEs for M. monoceros ($P<0.05$) and P. semisulcatus ($P<0.05$), CPUE of both shrimps increased with the increase of runoff. while significant effect of precipitation on CPUEs for F. indicus ($P<0.05$) and P. semisulcatus ($P<0.05$) was detected, CPUE of both shrimps increased with precipitation. And a CPUE for M. monoceros increased significantly with sea surface temperature (SST, $P<0.05$), but significant effect of SST on CPUEs for other shrimp species was not found, the reason for this phenomenon may be that the sea area is in a tropical region, with high water temperature and small variation, and the water depth is shallow. CPUEs of M. monoceros ($P<0.05$) and P. semisulcatus ($P<0.05$) decreased significantly with the increase of sea surface height anomaly (SSHA). Only significant effect of chlorophyll a concentration on CPUEs for all shrimps was detected. ($P<0.05$). There was a significant positive correlation between chlorophyll a concentration and CPUE of F. indicus and M. monoceros, while there was a significant negative correlation between chlorophyll a concentration and CPUE of P. semisulcatus. In conclusion, the abundance of main shrimps resource along the west coast of Madagascar has obvious temporal and spatial heterogeneity, and susceptible to the environmental factors, such as the oceanographical factors, precipitation, runoff, and so on. The significance of this study is to provide a scientific basis for assessing the abundance of fishery resources, standardizing fishery management, maintaining fishery resources and ensuring the sustainable development of fishery.

Key words: west coast of Madagascar; trawl; Fenneropenaeus indicus; Metapenaeus monoceros; Penaeus semisulcatus; CPUE; environmental factors

基于 CO I 基因的西北太平洋日本鳀群体遗传结构研究

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摘要：为了解西北太平洋海域日本鳀的群体遗传结构，更好地对西北太平洋海域的日本鳀资源进行开发和管理，本研究利用线粒体 CO I 基因，对西北太平洋海域 8 个群体共 203 条日本鳀样本进行群体遗传多样性和变异研究。结果显示，8 个群体总的单倍型多样性指数（h）为 0.9508±0.0083，核酸多样性指数（π）为 0.00670±0.00027，总体呈现较高的单倍型多样性水平和相对较低的核苷酸多样性水平。分子方差分析（AMOVA）结果表明 99.26%的遗传变异发生在群体内部，群体间的遗传分化指数（Fst）均小于 0.05，表明群体间不存在显著的遗传分化。基因流 Nm 数值较大（10.19910~inf），表明群体间基因交流频繁。核苷酸错配曲线呈现明显单峰，推测西北太平洋日本鳀在历史上可能经历过快速的群体扩张事件，群体扩张时间大约发生在 0.260Ma 年前。西北太平洋海域的洋流活动可能是导致日本鳀群体间遗传分化小的重要因素

关键词：日本鳀；CO I 基因；遗传结构；遗传多样性；西北太平洋

Genetic structure of Engraulis japonicus populations in the northwest Pacific Ocean based on CO I gene

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Abstract： In order to investigate the population genetic structure of Engraulis japonicus in the northwest of the Pacific Ocean and to better develop and utilize resources of E. japonicus, mitochondrial CO I genes were used to analyze the population genetic structure and variation of 203 E. japonicus samples from 8 sampling locations in this region. The results showed that the total haplotype diversity (h) and nucleotide diversity (π) of the 8 groups of E. japonicus were 0.9508±0.0083 and 0.00670±0.00027, respectively, indicating a higher haplotype diversity and a relatively lower nucleotide diversity. The results of molecular variance analysis suggested that 99.26% of the genetic variation occurred within population, while the Fst values among the populations were less than 0.05, showing that no significant genetic differentiation existed among the 8 groups of E. japonicus. The gene flow (Nm) values were large (10.19910~inf), suggesting that the gene exchanges among populations were frequent. There was a distinct single peak in the curve of nucleotide mismatch distribution, indicating that the E. japonicus in the northwest Pacific might have experienced a population expansion, and around 0.260 Ma years ago. The ocean currents in the northwest Pacific Ocean may be an important factor leading to low genetic differentiation among E. japonicus populations. Therefore, it is suggested that in the management of fishery resources, the E. japonicus in the Northwest Pacific should be regarded as a management unit.

Key words: Engraulis japonicus；CO I gene；Genetic structure；Genetic diversity；the northwest Pacific Ocean

基于质量谱模型评估捕捞对蜈支洲岛海洋牧场鱼类群落的影响

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摘要：本研究在蜈支洲岛海域构建了海洋牧场质量谱模型（SSM），反映了海洋牧场中食物网的复杂结构以及种间的相互作用，以评估捕捞对海洋牧场鱼类群落的影响。研究通过对两种管理策略（单物种管理和多物种管理）的模拟，分析了特定种类的捕捞死亡率改变对鱼类群落产生的影响，并利用 5 种群落生态指标监测了鱼类群落的特征状态。单物种管理策略结果显示，蜈支洲岛海洋牧场生态系统呈现下行控制效应，肉食性鱼类对浮游生物食性鱼类存在着强烈的调控作用。捕捞死亡率变化后，不同物种间竞争捕食等复杂的相互作用产生营养级联效应。多物种管理策略结果显示，灰海鳗的捕捞死亡率对群落质量谱斜率影响最大，大头狗母鱼和灰海鳗的捕捞死亡率对鱼类群落生物量和群落结构及功能的影响最大。研究结果对于保护和维持鱼类群落稳定方面具有重要意义，能够帮助管理者更好地了解捕捞死亡率变化对鱼类群落产生的潜在影响，从而根据物种对渔业的重要性制定可行且有效的保护和管理策略

关键词：质量谱模型；海洋牧场；管理策略；生态指标；营养级联

Assessing the impacts of fishing on fish community in marine ranch of Wuzhizhou Island based on size-spectrum model

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Abstract：In this study, a marine ranch Size-Spectrum Model (SSM) was built in the waters of Wuzhizhou Island. which reflects the complex structure of food webs and interspecies interactions in marine ranch, to assess the impacts of fishing on the fish community in marine ranch. The study analyzed the effects of changes in species-specific fishing mortality on fish community by simulating two management strategies (single-species management and multispecies management) and monitored the state of fish community characteristics using five community ecological indicators: the total biomass of the community, the slope of size spectrum, the mean maximum weight, the mean weight, and the large fish index. The results of the single-species management strategy showed that the marine ranch ecosystem of Wuzhizhou Island showed top-down control, and there was a strong regulatory effect of carnivorous fish on plankton-feeding fish. Complex interactions such as competitive predation among different species produce trophic cascade effects after changes in fishing mortality. The results of the multispecies management strategy showed that fishing mortality of Muraenesox cinereus had the greatest effect on the slope of size spectrum, and that fishing mortality of Trachiocephalus myops and Muraenesox cinereus had the greatest effect on fish community biomass and community structure and function. The results of this study have important implications for the conservation and stabilization of fish community, and can help managers to better understand the potential impacts of changes in fishing mortality rates on fish communities, so that viable and effective conservation and management strategies can be developed based on the importance of the species to the fishery.

Key words: Size-Spectrum Model; marine ranch; management strategies; ecological indicators; trophic cascading effects

栅条间距与栅栏倾角对圆形栅栏水动力及周围流场特性影响

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摘要：栅栏是栅型兼捕减少装置最重要的构件，其结构参数和姿态的变化影响着栅栏水动力特性和分隔装置的效果。为了明晰栅栏装置的水动力和周围流场分布规律，实现栅型兼捕装置的优化设计，本研究采用 CFD 数值模拟和动水槽模型试验探究了栅栏倾角和栅条间距对圆形栅栏的水动力和周围流场的影响规律。结果表明：（1）栅栏阻力随着流速和栅栏倾角的增大而增大，随着栅条间距的增大而减小。（2）栅栏前后部的流速差与倾角和栅条间距的变化有关，流速衰减率随着栅条间距的增大而减小，但随着栅栏倾角的增大而增大。（3）栅栏的上下端以及栅条之间存在流速增强区，栅栏尾部存在上升流和涡流，随着栅栏倾角的增大，涡流和尾迹效应增强。

关键词：圆形栅栏；栅条间距；倾斜角度；流场分布；CFD

The effects of grid bar spacing and inclination grid angle on flow field and hydrodynamic characteristics of grid device

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Abstract：The grid is a crucial component in the construction of grid-type bycatch reduction devices. The structural characteristics and orientation of the grid have a significantly impact on the hydrodynamic characteristics and the efficacy of the separation device. Therefore, it is essential to thoroughly understand of the hydrodynamic characteristics and flow field of the grid device to optimize its structure. Thus, this study investigated the effects of inclination grid angles and grid bar spacing on hydrodynamic forces and flow field around a circular grid using CFD numerical simulation and flume tank experiments. The results indicated that the hydrodynamic forces acting on the circular grid increased with higher flow velocity and inclination grid angle, while they decreased with smaller grid bar spacing. Both the inclination grid angle and grid bar spacing influenced the changes in flow velocity around the circular grid. The velocity reduction decreased with increasing grid bar spacing but increased with increasing inclination grid angle. Flow velocity enhancement zones were observed at the upper and lower ends of the grid, as well as between the grid bars. Additionally, upwelling and vortices were present at the back of the grid. It was found that an increase in the inclination grid angle enhanced the vortex and wake effects.

Key words:：circular grid, grid bar spacing, inclination grid angle, flow field distribution, CFD

黑潮流轴的位置变化对东海鲐鱼补充量的影响模拟研究

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摘要：东海鲐鱼(Scomber japonicus)是我国近海中上层暖水性经济鱼种，年际资源量波动较大。黑潮是暖水流，其路径变动对鱼卵仔幼鱼资源补充量影响很大，但其内在动力学因素尚不清楚。本文运用基于个体的东海鲐鱼生长初期生态模型，模拟 1990-2013 年东海鲐鱼资源补充量受黑潮流轴位置变动的影响。模拟发现，4 月份鱼卵仔鱼所处的海洋物理环境（黑潮流轴位置）对东海鲐鱼最终的资源补充量起到重要作用，4 月底鱼卵仔幼鱼的存活量基本上决定了东海鲐鱼最终的资源补充量。当东海 PN 断面黑潮流轴偏向西北时，有利于鱼卵仔幼鱼的存活，反之，当流轴位置偏向东南时，不利于鱼卵仔幼鱼的存活。最后，分析了黑潮流轴位置变动影响东海鲐鱼资源补充量的内在机制。模拟发现黑潮流轴位置变动是通过影响仔幼鱼的滞留分布、所处水温及其早期输运过程间接影响鱼卵仔幼鱼的存活量。

关键词：东海鲐鱼；黑潮流轴；基于个体模型；补充量；早期输运；

A simulation study on the effect of positional changes of the Kuroshio Current axis on the recruitment of chub mackerel in the East China Sea.

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Abstract： Chub mackerel (Scomber japonicus) is a warm-water pelagic economic fish species in China's offshore waters, with large interannual fluctuations in resources. The Kuroshio current is a warm-water current, and its path changes have a great influence on the recruitmentof the egg-laden juvenile resource, but its intrinsic dynamics are not clear. In this paper, we applied an individual-based ecological model (IBM) of the early stage of growth ofchub chub mackerel in the East China Sea to simulate the effects of the Kuroshio Current on therec ruitment of chub mackerel in the East China Sea from 1990 to 2013. It was found that the physical environment of the spawning fish in April (the position of the Kuroshio axis) played an important role in the final recruitment of mackerel in the East China Sea, and the survival of spawning fish at the end of April basically determined the final recruitment of chub mackerel in the East China Sea. When the Kuroshio current axis in the East China Sea PN section was biased to the northwest, it was favourable to the survival of juvenile mackerel, and conversely, when the current axis position was biased to the southeast, it was unfavourable to the survival of juvenile mackerel. Finally, the mechanism by which the position of the Kuroshio current axis affects the recruitment of chub mackerel stocks in the East China Sea was analysed. It was found that the change in the position of the Kuroshio current axis indirectly affects the survival of egg-laden juveniles by influencing the retention distribution of juveniles, the water temperature and the early transport process.

Key words: chub mackerel (Scomber japonicus); Kuroshio current axis; individual-based model; recruitment; early transport

西印度洋大青鲨繁殖生物学和分布研究

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摘要：目前印度洋海域大青鲨生物学研究存在一定局限性，缺乏生物样本信息，对其繁殖生物学和分布了解并不清晰，因此本文通过 2010-2020 年在西印度洋海域收集的大青鲨生物学数据及捕获位置等相关信息，对其叉长分布、性成熟长度、繁殖力和时空分布等信息进行分析研究，以期为未来的种群评估、资源保护提供帮助。本研究共收集西印度洋海域 791 尾雄性（33-249.5cmFL）和 803 尾雌性（12-349.6cmFL）大青鲨样本，研究结果显示，利用逻辑斯蒂曲线估计西印度洋海域雄性大青鲨 50% 性成熟体长为 161.4cmFL（192.4cmTL），雌性为 179.3cmFL（213.9cmTL）；怀孕大青鲨平均产仔数为 33.7 尾；不同季度不同性成熟度大青鲨个体的分布均存在显著差异（P<0.05）。本研究认为一季度和四季度印度洋赤道附近海域可能为大青鲨的交配场所，印度洋温带海域是大青鲨产仔和幼鱼生长的海域，因此建议在这些海域采取更科学合理的作业方式。

关键词：大青鲨；印度洋；繁殖生物学；时空分布

Reproductive Biology and Distribution of the Blue Shark (Prionace glauca) in the Western Indian Ocean

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Abstract： Due to the limited biological research on the blue shark in the Indian Ocean, such as the lack of a clear understanding of its reproductive biology and distribution, our study analyzed and evaluated the fork length distribution, sexual maturity length, reproductive capacity, and spatiotemporal distribution of blue sharks based on biological data and capture location information collected in the western Indian Ocean from 2010 to 2020. The objective of this study is to provide reliable biological information important in performing future stock assessments vital for species conservation in this region. A total of 791 male (33–249.5 cm FL) and 803 female (12–349.6 cm FL) blue sharks were collected in the West Indian Ocean. We used the morphology of the sexual organs to ascertain their sexual maturity. Results show that the observed size at 50% sexual maturity of male blue sharks in the West Indian Ocean was 161.4cm FL (192.4 cm TL) for males and 179.3 cm FL (213.9 cm TL) for females based on logistic curve analysis. The average litter size of pregnant blue sharks was 33.7 pups. There were significant differences in the distribution of blue shark individuals with different sexual maturity levels in different quarters ($p < 0.05$). This study suggests that the area near the equator in the Indian Ocean from October to March of the following year may be the mating ground for blue sharks, while the temperate waters in the Indian Ocean are the nursery ground and parturition ground for pregnant and juvenile throughout the whole year. Therefore, it is recommended to adopt a more scientific and reasonable operational method in these areas.

Key words: blue shark; Indian Ocean; reproductive biology; spatiotemporal distribution; fishery observer program; pelagic fisheries; habitat

不同水平扩张比和模拟渔获物对南极磷虾拖网整体形态的影响

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摘要：为了解不同工况条件下的网具形态变化，以南极磷虾捕捞船“龙腾”轮采用的四片式拖网为研究对象，基于修正的田内准则制作 1/35 的模型网进行循环动水槽试验，考察流速(v)、水平扩张比(L/S)和渔获物对网具(整体形态、阻力和能耗系数)的影响。结果表明：当 L/S=0.35、v=30 cm/s 时，网口形态最佳，网囊中有或无模拟渔获物时的网口形状变化情况相似；在低流速、高水平扩张比条件下，有模拟渔获物时的网口面积随流速、L/S 改变而变化的程度较空网时更小；流速不变时，随 L/S 的增大，网具阻力增加，能耗系数减小，且二者的变化程度均呈减缓态势；而 L/S 不变时，随流速的增大，网具阻力和能耗系数均增大，有模拟渔获物时的网具阻力与能耗系数较空网时更大，且流速越大，网具能耗系数与空网时的差异越大。研究表明，当 L/S=0.35、v=3.0 kn 时，可使网具以较佳作业性能运行。

关键词：南极磷虾；拖网；形态；渔获量；水平扩张比

Effects of horizontal opening ratio and simulated catch on whole configuration of Antarctic krill trawl net

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Abstract： In order to probe into configuration changes of the trawl configuration gears under different working conditions, the effects of current speed (v), horizontal opening ratio (L / S) and catch on the mouth opening overall shape, drag and energy consumption coefficient were investigated in A 1 / 35 scale four - pieces krill (Euphausia superba)trawl by the Antarctic krill fishing vessel “Longteng” manufactured based on modified Tauti’s law and tested in a flume tank. The tank had the circulating sink with main dimension is 22. 0 m (length) ×8. 5 m (width) ×2. 7 m (height), the side observation scale of 9. 0 m (length)×2. 2 m (width) ×1. 6 m (standard water depth), and a length of 7. 3 m, width 1. 5 m viewing window at sink bottom. The flow rate in the sink was measured by a propeller type flow meter (Tokyo Measurement Technology Co. , Ltd.) for 10-200 cm / s with an accuracy of 2%. The results showed the shape of net mouth tended to be “compressed” with the increase in v and L / S, with the best shape of mouth at L / S = 0. 35, and v = 30 cm / s, without significant effect of the catch on the shape of mouth. The area of the mouth was found to be increased with the increase in L / S at constant v and decreased with the increase in v at constant L / S. There was less change in the area of mouth with simulated catch than that in the empty with the change in current speed, and L / S under the condition of low velocity and high horizontal opening. The net body shape also tended to be “ compressed” with the increase in current speed and L / S and the change in L / S had a greater impact on it, the end of net body with simulated catch rose more obviously than that in empty net and the length of net was also increased obviously than it. The trawl net drag force was increased with the increase in L / S, while the energy consumption coefficient was decreased and the change degree of both showed a slowing down trend, both the trawl net drag force and the energy consumption coefficient were increased with the increase in current speed. There were greater drag force and energy consumption coefficient in the trawl net with simulated catch than those in the empty and the larger current speed, and the difference in energy consumption coefficient between net with catch and the empty net was great at high current speed. The finding suggests to keep L / S of 0. 35 and the towing speed of 3. 0 kn so that the trawl can operate with better fishing performance.

Key words: Antarctic krill; trawl; shape; catch; horizontal opening ratio

基于拉格朗日质点方法的黄海鲐鱼幼体早期输运初步研究

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摘要：本研究基于 2000-2011 年间海洋模型模拟数据，利用 FVCOM 模型生成三维物理场，基于个体模型参数化黄海鲐鱼的早期生物过程，采用拉格朗日方法耦合生成 4-8 月物理场和生物模型，构建其早期输运动力学模型。通过对模拟结果的统计分析，探讨了黄海鲐鱼在常规条件下的早期输运、密度分布和滞留时间，分析了鲐鱼鱼卵和仔鱼在各年份间产生的输运分布差异，确定了黄海鲐鱼的主要聚集区，研究了其对中韩渔业区域的资源补充。结果表明：所构建模型成功地模拟了黄海鲐鱼鱼卵和仔鱼的输运过程、密度分布和在黄海海区的滞留时间。分布在青外产卵场的鲐鱼鱼卵和仔鱼主要沿东北方向运移，不同年份释放粒子在空间分布上存在显著差异。夏季期间的黄海冷水团直接影响鲐鱼鱼卵和仔鱼的输运和分布，并于六月末影响不同年份间的鲐鱼鱼卵和仔鱼产生空间分布差异。黄海鲐鱼的主要聚集地在 34°～36°N、121°～123°E 海域内。

关键词：鲐鱼；IBM 模型；早期输运；滞留

Preliminary Study on Early Transport of Larvae of chub mackerel (Scomber japonicas) in the Yellow Sea Based on Lagrangian Particle Tracking

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Abstract：Based on Yellow Sea chub mackerel (Scomber japonicas) fisheries resource survey data from 2000 to 2011, by adopting the global multi-scale ocean model simulated 3-D physical field and based on the biological processes of chub mackerel (Scomber japonicas) in its early life history from the individual-based biological model，the individual-based ecological model for S． japonicas at its early growth stages in the Yellow Sea was constructed through coupling the physical field in April-August with the biological model by the method of Lagrange particle tracking.Explored the early transport, density distribution, and residence time of the Yellow Sea mackerel under conventional conditions, and analyzed the differences in transport distribution of mackerel eggs and larvae between different years.Based on the statistical analysis of simulation results, the main gathering areas of chub mackerel in the Yellow Sea were identified, and their resource replenishment research for the China South Korean fishery region was analyzed.The results showed that the model successfully simulated the transport process, density distribution, and retention time of chub mackerel eggs and larvae in the Yellow Sea area. The eggs and larvae of chub mackerel distributed in the Qingdao-Waihai spawning ground mainly migrate along the northeast direction, and there were significant differences in the spatial distribution of particles released in different years. The Yellow Sea cold water mass during summer directly affects the transportation and distribution of mackerel eggs and larvae,and the Yellow Sea cold water mass is the main reason for the spatial distribution differences of mackerel eggs and larvae in different years. The main accumulation areas of chub mackerel in the Yellow Sea were 34 ° ~36 ° N and 121 ° ~123 ° E, and the main retention areas of larvae included the shoal of Haizhou Bay and Shidao ground.The distribution of mackerel larvae and larvae contributed a lot to the replenishment of Sino-Korean agreement waters, and the spawning ground in the northern part of the South Yellow Sea was of great significance to the replenishment of fishery resources in the southern part of the South Yellow Sea.

Key words: chub mackerel (Scomber japonicas); individual-based model; early transport ; retention

基于动水槽试验：不同网线材料、占空率、结节类型和下纲配重对网片沉降性能的影响

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摘要：网片是构成网渔具的主要单元，其沉降性能决定着围网和罩网等渔具的捕捞效率。为探究不同因素对网片沉降性能的影响，本研究利用动水槽模型试验分析下纲配重、网线材料、结节类型和占空率对网片沉降性能（沉降深度、沉降速度）的影响规律，并基于广义加性模型（GAM）分析各因素对网片沉降性能的影响权重。结果显示：下纲配重与网片沉降深度和沉降时间均呈正相关关系，但当下纲配重超过 69.5 g 时，网片最大沉降深度达到极限值且不再继续增加；沉降初期，随下纲配重增加，各网片的沉降速度大幅度提高，随后呈递减趋势；在相似占空率下，涤纶网片达到最大沉降深度所需时间较尼龙和聚乙烯网片分别减少 33.3%和 42.9%，且其平均沉降速度较尼龙网片快 8.5%，平均沉降时间最短。GAM 模型分析显示，下纲配重对网片沉降性能影响最为显著。为确保网片能够达到最大沉降速度，建议采用占空率小的涤纶材料制作渔具并增加下纲配重。

关键词：网片；沉降速度；下纲配重；占空率；动水槽试验

Sinking Behavior of Netting Panels Made with Various Twine Materials, Solidity Ratios, Knot Types, and Leadline Weights in Flume Tank

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Abstract：Netting is an important component of fishing gear design, and its ability to sink determines the effectiveness of fishing gears such as purse seines, falling nets, and stick-held nets. Therefore,it is crucial to thoroughly investigate the sinking parameters (sinking depth and sinking speed) of the netting panel as a function of the leadline weights using various twine materials, knot types, and solidity ratios. In this study, a generalized additive model (GAM) was utilized to analyze the impact of each factor on the sinking performances of the netting. The results revealed that the sinking depth of the netting was positively correlated with sinking time and leadline weight. However, the netting featured a maximum sinking depth limit, indicating that the sinking depth would not increase beyond a leadline weight of 69.5 g. During the initial phase of the sinking process, the sinking velocity of each netting panel initially increased but gradually decreased over time. The incorporation of a leadline weight reduced sinking time. Thereby, polyester netting exhibited the shortest average sinking time. A comparison of netting types with similar solidity ratios showed that the maximum sinking depth of the nylon netting was 13.20% and 10.11% greater than that of polyethylene and polyester nettings, respectively. In addition, nylon nets' time average sinking speed was 64.58% and 4.62% greater than that of polyethylene and polyester nettings, respectively. The analysis of the GAM model clearly showed that the leadline weight has a significant effect on the netting sinking speed and depth. To ensure that the netting can reach its maximum sinking speed, it is strongly recommended to use nylon and polyester nettings with a low solidity ratio, i.e., a lower twine diameter and greater mesh size with a higher leadline weight, when constructing fishing gear such as purse seines with higher net leadline weights.

Key words: netting; sinking speed; leadline weight; solidity ratio; flume tank experiment

阿蒙森海冰间湖晶磷虾资源密度分布及环境分布特征

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摘要：摘要：晶磷虾作为南极生态系统中具有重要生态价值的的关键种，其资源密度状况与环境变化密切相关。通过阿蒙森海冰间湖内两条断面的综合调查，对晶磷虾资源密度分布及相关环境特征开展调查。资源密度通过对声学回声数据的后处理获得，其中晶磷虾的声学目标强度基于 SDWBA 模型及晶磷虾样本数据计算所得。结果显示：调查区域内晶磷虾的资源密度范围为 0.96 至 11.01g/m2，资源密度均值为 5.77g/m2，这表明晶磷虾仍是冰间湖内最主要的磷虾品种，但调查结果表明其资源密度较以往调查结果已出现明显下降。尽管其它环境参数诸如海表温度及盐度均会对晶磷虾资源的空间分布产生影响，但导致本次调查期间晶磷虾资源密度出现波动的主要原因应是冰间湖内浮游植物爆发规模与往年差异所致。此外，晶磷虾的虾群密度及厚度在昼夜间几乎未出现明显的差异。根据 GLM 模型拟合结果，2022 年夏季阿蒙森海冰间湖内晶磷虾的资源量估计为 17.5 万吨。

关键词：晶磷虾；资源密度；环境特征；阿蒙森海冰间湖；声学调查

Distribution of ice krill resource density and environmental characteristics in the Amundsen Sea coastal polynya

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Abstract：Abstract: The density of ice krill (Euphausia crystallorophias), a species of key ecological value, and related environmental factors were observed along two transects in the Amundsen Sea Coastal Polynya (ASCP) in Antarctica. The distribution of ice krill was processed using two-frequency acoustic backscatter data identification, and the target strength of ice krill was calculated via stochastic distorted-wave born approximation（SDWBA）based on the ice krill sample. The ice krill density ranged from 0.96 to 11.01 g/m2 for each transect (the mean value was 5.77 g/m2 for the entire survey). These results were a lower order of magnitude than those of a previous study in the same sea area, although the ice krill was still the dominant krill species in this polynya. We predict that this difference was mainly caused by the extent of phytoplankton bloom, while other hydrologic parameters such as surface temperature and salinity would have some effect on the spatial distribution of ice krill abundance. Meanwhile, the density and height of ice krill abundance suggested that the diurnal effect on the ice krill was almost negligible. According to the fitted results of the regression model, the predicted abundance of ice krill in ASCP in 2022 summer was 175,000 tons.

Key words: ice krill (Euphausia crystallorophias); krill density,; environmental factors; Amundsen Sea Coastal Polynya; acoustic survey

不同姿态下仔稚鱼采样网用台字形沉降板水动力特性研究

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摘要：定量仔稚鱼采样网的使用有利于评估渔业资源补充量和群体数量的动态变化，为进一步提升渔业资源的可持续利用提供决策依据。为掌握采样网用沉降板水动力特性本研究利用水槽模型试验探究仔稚鱼采样网用台字形沉降板在不同倾斜姿态下（内、外、前、后）的水动力性能变化，并利用 OpenFOAM 的数值模拟方法分析不同姿态下沉降板周围流场变化。结果显示: (1) 不同姿态下沉力系数随倾角和冲角增大均呈先增大后减小趋势，其均在倾角 5°时达到最大，内、外倾斜下最大值分别为 1.75 和 1.77（α=25°），前、后倾斜下最大值均为 1.78（α=25°）；阻力系数随倾角增大逐渐减小，随冲角增大逐渐增大；沉阻比随倾角和冲角增大均呈先增大后减小趋势，内、外倾斜下分别在倾角 20°和 10°时最大，为 3.73 和 3.76（α=20°），前、后倾斜下均在倾角 5°时最大，分别为 3.67 和 3.71（α=20°）。

关键词：台字形沉降板；倾角；水动力性能；水槽试验；数值模拟；流场分布

Hydrodynamic characteristics of frustum type depressor for sampling midwater trawl with different positions

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Abstract：The sampling trawl of quantitative sampling of larval and juvenile fish is advantageous for assessing the dynamic changes in fishery resource replenishment and population numbers. It provides a decision-making basis for further enhancing the sustainable utilization of fisheries resources. This study employs a flume tank experimental method to investigate the hydrodynamic performance variations of frustum type depressor for sampling trawl with different inclined positions (inward, outward, tilt). Furthermore, numerical simulations using OpenFOAM are employed to analyze the alterations in the flow field around the depressor under different positions. The results show: (1) the sinking coefficient of depressor was initially increasing and then decreasing with increasing angle of attack and heel angle, and both reaching their maximum at a heel angle of 5°. The maximum values for inward and outward inclined were 1.75 and 1.77 (α=25°), respectively, and the maximum values for tilt were both 1.78 (α=25°). The drag coefficient gradually decreases with increasing heel angle, and increasing with increasing angle of attack. The ratio of sinking force to drag was initially increasing and then decreasing with increasing angle of attack and heel angle. The maximum values were reached at heel angles of 20° and 10° for inward and outward inclined, with values of 3.73 and 3.76, respectively (α=20°). The maximum values were reached at a heel angle of 5° for tilt, with values of 3.67 and 3.71, respectively (α=20°). The pressure center coefficient remains relatively constant at different angle of attack, and Cpc gradually increases with increasing heel angle, Cpb remains constant with increasing heel angle. (2) The flow velocity on the outer side of the depressor gradually decreases as the heel angle increases. Under outward inclination, the boundary layer separation point on the depressor gradually moves toward the leading edge of the plate. In both forward and backward inclination states, the flow velocity decay region at the rear of the depressor gradually expands as the heel angle increases. This study elucidates the hydrodynamic performance variations of the depressor under different inclination states, providing a scientific basis for further rational installation and adjustment the working positions of the depressor.

Key words: frustum type depressor; heel angle; hydrodynamic characteristics; fluent tank experiment; numerical simulation; flow field distribution

基于数值模拟的定常流下定置底刺网水动力特性及对生态的影响

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摘要：底置刺网由柔性网片组成，广泛用于在全世界沿海水域捕捞水生生物。然而，在实际操作中，由于外力导致的形态和网目开口的变化会显著影响其效率和选择性。本研究基于质量弹簧模型，采用数值模拟方法，对定常流下的无结尼龙定置底刺网进行了综合研究。通过模拟，我们可以计算出不同流速下刺网的形态结构、网目张开和张力分布。结果表明，随着流速的增加，刺网系统内的张力呈递增趋势，网衣对角张力较高。网衣的垂直投影面积或有效作业面积随着流速的增加而减小，同时网目张开形态不均匀。模拟结果与在循环动水槽中进行的一组模型测试中获得的实验测量结果非常吻合。通过结构优化的模拟，我们发现尺寸较窄的定置底刺网呈现出垂直拉伸形态，网目以菱形形态均匀张开。这些发现对改进底层刺网设计和减轻海洋动物的生态风险具有重要意义。

关键词：定置底刺网；数值模拟；质量-弹簧模型；模型试验；网目张开；兼捕

Numerical simulation-based hydrodynamic interaction of bottom-set gillnet with current and ecological implications

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Abstract：Bottom-set gillnets, consisting of flexible netting, are extensively utilized in coastal waters worldwide for capturing aquatic organisms. However, their efficiency and selectivity can be significantly affected by changes in shape and mesh opening due to external forces during practical operations. In this study, a comprehensive investigation of knotless nylon bottom-set gillnets under uniform current conditions was conducted using numerical simulations based on the mass-spring model. The simulations allowed us to calculate the netting configuration, mesh opening, and tension distribution of gillnets under different current velocities. The results suggest that with the increase in current velocity, the tension within the gillnet system shows a progressive increment, with higher tension observed at the diagonal corners. The vertical projection area, or effective operation area, of the netting diminishes with increasing current velocity, which is accompanied by a less uniform distribution of mesh openings. The simulation outcomes are in strong agreement with experimental measurements obtained from a set of model testing carried out in a circulating flume tank. Through simulations of structural optimization, we observed that low-profile gillnets with narrower dimensions exhibit a vertically stretched configuration resembling a wall, with meshes uniformly opened in a diamond-shaped pattern. These findings hold significant implications for the improvement of bottom-set gillnet design and the mitigation of ecological risks posed to marine fauna.

Key words: bottom-set gillnet; numerical simulation; mass-spring model; model testing; mesh opening; bycatch

基于 GA–BP 神经网络的
南太平洋长鳍金枪鱼 CPUE 标准化研究

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摘要：长鳍金枪鱼（Thunnus alalunga）是大范围洄游性鱼类，其时空分布与多种环境因子的存在一定联系。根据 2016-2021 年的南太平洋长鳍金枪鱼延绳钓渔捞日志，利用南方涛动指数（SOI）、海表温度（SST）、叶绿素浓度（CHLA）等海洋遥感资料，把时空和环境因子作为输入层，把单位努力捕捞量（CPUE）作为输出层，采用遗传算法（GA）优化 BP 神经网络，并基于 GA-BP 对长鳍金枪鱼进行 CPUE 标准化研究近年来其资源丰度的时空变动。敏感性分析显示，SST 和 DO 对长鳍金枪鱼的变动有较大影响，最适的 SST 范围为 18℃-20℃，DO 的浓度为 210ml/L 以上。研究表明，利用 GA-BP 神经网络能够较好地预测 CPUE 时空分布，为相关渔业管理政策的实施提供参考。

关键词：长鳍金枪鱼；遗传算法；BP-神经网络；标准化；南太平洋

Study on CPUE Standardization of South Pacific Albacore Based on GA-BP Neural Network

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Abstract： The albacore (Thunnus alalunga) is a kind of large-scale migratory fish, and its spatiotemporal distribution is related to various environmental factors. Based on the South Pacific albacore fishing logs from 2016 to 2021, ocean remote sensing data such as Southern Oscillation Index (SOI), Sea Surface Temperature (SST), and Chlorophyll Concentration (CHLA) were utilized, the spatiotemporal and environmental factors were used as input layers, and the catch per unit yield (CPUE) was used as output layers. Genetic algorithm (GA) was applied to optimize the BP neural network, then GA-BP was applied to standardize the CPUE of long finned tuna to study the spatiotemporal changes in its resource abundance in recent years. Sensitivity analysis showed that SST and DO had a significant impact on the variation of albacore, with an optimal SST range of 18 ℃ - 20 ℃ and a DO concentration of over 210ml/L. The spatiotemporal distribution of fishing grounds predicted using GA-BP neural network was consistent with the actual fishing grounds. Research had shown that GA-BP neural networks could effectively predict the spatiotemporal distribution of CPUE and provide reference for the implementation of relevant fisheries management policies.

Key words: Albacore; Genetic algorithm; BP neural network; Standardization; South Pacific

模拟渔获物形状对网囊振荡特性的影响

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摘要：渔获物作为影响网囊水动力特性的重要因素，随着其在网囊内不断堆积，不仅造成网囊阻力增加，也易导致网囊产生振荡。渔获量的大小决定着含有渔获物的网囊形状，一般可简单划分为凹槽型、半圆型及圆球型等。为了探究渔获物形状对网囊振荡性能的影响，本研究利用循环动水槽试验，对含有凹槽型和球型等两种形状模拟渔获物的网囊的阻力、形态和振荡变化进行测试，并与海上实测结果进行了对比分析。结果表明，含有凹槽型模拟渔获物的网囊阻力小波系数最先在 0.07 s 周期尺度开始振荡，且相较于含球型模拟渔获物的网囊阻力小波系数振荡更加剧烈。采用注水乒乓球代替真实渔获物，其模型网囊振幅和周期与实测网囊的相关性系数分别为 91%和 89%，基本符合海上实测网囊振荡规律。本研究结果可为模型试验中模拟渔获物的选取、提高网囊水动力特性和改善网囊选择性提供基础科学数据。

关键词：网囊；模拟渔获物；阻力特性；振荡特性

The Oscillating Behavior of Trawl Codends Including Various Geometric Configurations of Simulated Catch

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Abstract： As an important factor affecting the hydrodynamic characteristics of the codend, the catch not only increases the resistance of the codend, but also easily causes the codend structure to oscillate with its accumulation in the end of codend. The size of the catch determines the geometric configuration of the codend with catch, which can be simply divided into grooves, semicircles and spheres. In order to investigate the effect of the geometric configuration of catch on oscillating characteristics of codend, the resistance, shape and oscillation change of codend containing groove type and spherical type of simulated catch were tested by using the circulating flume tank experiment, and compared with the results of sea trials in this study. The resistance wavelet coefficient of the codend with the groove-type simulated catch began to oscillate at the 0.07s period scale at first and oscillated more intensive than the codend containing the spherical simulated catch. In terms of displacement oscillation characteristics, the table tennis filled with water was an approximate substitute for real catch during the sea trial, because the difference in wavelet coefficients for the codend displacements in amplitude and period between the model codend with table tennis filled with water and the full scale codend was 91% and 89%, respectively. The results of this study confirm the feasibility of using simulation catch with similar shape replace real catch to carry out model test, and can provide basic scientific data for improving the hydrodynamic characteristics and the selectivity of the codend structure.

Key words: codend, simulated catch, resistance characteristics, oscillation

基于 DLNM 的气候变化对中西太平洋围网黄鳍金枪鱼 CPUE 影响的滞后效应

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摘要：热带金枪鱼种群分布与资源丰度对气候变化所引起的海洋环境变动很敏感，厄尔尼诺与南方涛动事件（ENSO）是影响热带中西太平洋（WCPO）黄鳍金枪鱼（Thunnus albacares）种群分布和变动等的主要气候事件，且环境变化对金枪鱼种群动态的影响存在滞后效应。为了探索气候异常和振荡对低龄黄鳍金枪鱼群体丰度影响的滞后效应，本研究基于中西太平洋渔业管理委员会（WCPFC）1982 年至 2021 年的围网渔业黄鳍金枪鱼单位捕捞努力量的渔业数据，采用分布滞后非线性模型（DLNM）分析了不同滞后的海洋尼诺指数（ONI）对渔业 CPUE 的影响。结果显示，热带 WCPO 南北不同海域的低龄黄鳍金枪鱼群体对 ONI 的响应存在月度尺度上的滞后，表明 DLNM 在种群丰度与环境因素之间的滞后效应分析方面的适用性。

关键词：黄鳍金枪鱼；CPUE；海洋尼诺指数；滞后效应；DLNM；中西太平洋；围网

Lag effect of influence of climate change on the CPUE of Yellowfin Tuna in the Western and Central Pacific Ocean Purse Seine Fisheries

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Abstract：Tropical yellowfin tuna (Thunnus albacares) populations and the abundance variations are highly sensitive to climate change-induced oceanic environmental changes. The El Niño-Southern Oscillation (ENSO) events are the primary climatic events that influence the population distribution and dynamics of yellowfin tuna in the Western and Central Pacific Ocean (WCPO). Moreover, there is a lag effect in the impact of environmental changes on the dynamics of tuna populations. In order to explore the lag effect of climate anomalies and oscillations on the abundance of young yellowfin tuna populations, this study analyzed the catch per unit effort (CPUE) data of yellowfin tuna from purse seine fisheries, collected by the Western and Central Pacific Fisheries Commission (WCPFC) from 1982 to 2021. The analysis was conducted using a Distributed Lag Nonlinear Model (DLNM) to examine the effects of the Oceanic Niño Index (ONI) at different time lags on the CPUE. The results indicate that there is a lag effect at a monthly scale in the response of young yellowfin tuna populations in different regions of the tropical WCPO to ONI, demonstrating the applicability of DLNM in analyzing the lag effect between population abundance and environmental factors.

Key words: Thunnus albacares; CPUE; Oceanic Niño index; lag effect; DLNM; western and central Pacific Ocean; purse seine

基于圆形统计和时间序列的 月相对两种拖网渔业 CPUE 的影响

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摘要：利用 2016—2019 年马达加斯加西海岸底拖网独角新对虾 Metapenaeus monoceros 和 2017—2020 年西白令海中层拖网狭鳕 Theragra chalcogramma 的渔业生产数据，结合基于圆形统计的广义线性模型(GLM)和基于时间序列的广义加性模型(GAM)2 种不同的月相量化和统计方法，分析月相对拖网渔业 CPUE 的影响。结果表明：月相对独角新对虾的 CPUE 具有显著的影响，2 种方法影响趋势较为一致，较高 CPUE 出现在上弦月。交叉验证显示，基于圆形统计的 GLM 平均绝对误差(MAE)和均方根误差(RMSE)均小于基于时间序列的 GAM，决定系数 R2 大于基于时间序列的 GAM，表明前者拟合具有更好的准确性、稳定性和拟合优度。研究表明，当周期性循环变量(月度、月相、小时等)具有较弱的显著性时，使用基于圆形统计的 GLM 更能反映月相对拖网渔业 CPUE 影响。

关键词：月相；拖网；CPUE；圆形统计；时间序列；交叉验证

Study of the effects of lunar phases on CPUEs of trawl fisheries based on circular statistics and time series

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Abstract： In order to understand and grasp the pattern of effect of lunar phase on fishery yield or CPUEs (catch per unit effort), the daily CPUEs of Metapenaeus monoceros in the bottom trawl fisheries along the west coast of Madagascar from 2016 to 2019 (from March 2 to November 29 each year) and Theragra chalcogramma in midwater trawl fisheries in the western Bering Sea from 2017 to 2020 (from June 15 to October 9 each year) were used to analyze the impact of lunar phases on CPUEs of trawl fisheries, combined with two distinct methods of quantification of lunar phases, including generalized linear model (GLM) based on circular statistics method and generalized additive model (GAM) based on time series method. The results showed that the lunar phases had significant effect on the daily CPUEs of M. monoceros, and the trends of two methods were consistent. The higher CPUEs were found in the first quarter moon period. The model fit of GLM based on circular statistics showed that the lunar phases had significant effect on the CPUEs of T. chalcogramma, and the higher CPUEs were found in the new moon phase. However, insignificant effect of lunar phases on CPUEs of T. chalcogramma was detected in model fit of GAM based on time series. Analysis of cross-validation indicated that both the mean absolute error (MAE) and root mean square error (RMSE) of GLM based on circular statistics were less than those of GAM based on time series, while the coefficient of determination (R2) of GLM was larger than that of the GAM, which means the former model fit was of better accuracy, stability, and fit superiority. The findings show that the circular statistical quantification method is more likely to reflect the influence of lunar phases on the CPUEs of trawl fisheries when periodic cyclic variables (monthly, lunar phase, hourly, etc.) are weakly significant.

Key words: Lunar phase; trawl; CPUE; circular statistics; time series; GLM; GAM; cross-validation

西北太平洋公海日本鳀的摄食生态和汞积累

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摘要：为了研究日本鳀（*Engraulis japonicus*）摄食生态与个体生长对重金属 Hg 含量的关系。本研究根据 2021 年 6～7 月在西北太平洋公海（39°2′N～42°30′N，154°02′E～161°29′E）采集的 143 尾日本鳀样本，测定其肌肉的碳、氮稳定同位素比值及 Hg 含量。结果显示，日本鳀 $\delta^{13}C$、$\delta^{15}N$ 值在不同体长组之间差异显著（$P<0.05$），随个体的生长，$\delta^{13}C$ 呈现先下降后上升的趋势，$\delta^{15}N$ 呈现逐渐上升的趋势。其次，生态位宽度呈现先增大后减小趋势，在 111～120mm 生态位宽度最大（0.80）；体长小于 120mm 日本鳀营养生态位重叠较大，相反，大于 120mm 生态位重叠较小。Hg 含量随日本鳀的生长呈逐渐上升的趋势，Hg 含量与 $\delta^{13}C$ 值呈正相关，Hg 含量随着 $\delta^{15}N$ 值呈现先上升后稳定再上升的趋势。研究表明，不同生活史阶段日本鳀的摄食会发生转变，同时摄食与栖息地环境的转变是可能导致 Hg 含量变化的主要原因。

关键词：日本鳀；摄食生态；汞积累

Feeding ecology and mercury accumulation of Japanese anchovy （Engraulis japonicus）in the high seas of the Northwest Pacific Ocean

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Abstract：In this study, 143 samples of Engraulis japonicus were collected from the high seas of the Northwest Pacific Ocean (39 ° 2'N ~ 42 ° 30'N, 154 ° 02'E ~ 161 ° 29'E) from June to July 2021. The stable isotope ratios of carbon and nitrogen and mercury content in muscle were measured. The feeding characteristics, nutritional niche and mercury content of Engraulis japonicus were analyzed by multivariate statistical analysis and niche overlap index method. The relationship between feeding ecology and individual growth and heavy metal mercury accumulation of Engraulis japonicus was explored.The results showed that the δ13C and δ15N values of Japanese anchovy were significantly different among different body length groups ($P < 0.05$). The δ13C showed a trend of first increasing, then decreasing and then increasing at different growth stages, and the δ15N showed a trend of first stable and then increasing at different growth stages. The niche width increased first and then decreased with the growth of Japanese anchovy, and the maximum niche width of 111 ~ 120mm in the body length group was 0.8. The niche overlap rate of 90 ~ 120mm was higher, and decreased with the growth niche overlap rate. The trophic level (2.85-3.11) showed a fluctuating upward trend, and the body length of 90 ~ 110 mm changed little. When the body length was greater than 110 mm, the trophic level increased rapidly with the increase of body length. Hg content was positively correlated with δ13C value. The mercury content increased first, then stabilized and then increased with the δ15N value. In the range of δ15N value 7-9.5, the Hg content remained almost unchanged. The results showed that the stable isotope values of carbon and nitrogen and niche breadth were significantly affected by the feeding changes of Japanese anchovy in the growth stage. There is a correlation between carbon and nitrogen stable isotope values and mercury content, which may be due to the influence of marine mesoscale processes and feeding species in the migratory waters of Japanese anchovy.

Key words: Japanese anchovy ; feeding ecology ; mercury accumulation

秘鲁外海涡旋的时空分布及其与茎柔鱼资源丰度的关系分析

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摘要：茎柔鱼(Dosidicus gigas)是短生命周期的头足类种类, 对环境变化极其敏感, 秘鲁外海是茎柔鱼重要的作业渔场, 该海域广泛分布的中尺度涡对其有何影响尚不清晰。本研究基于角动量涡旋检测与追踪算法获得的涡旋追踪数据分析了秘鲁外海涡旋的时空分布, 并进一步采用茎柔鱼渔业数据、涡旋追踪数据和环境数据评估中尺度涡及其引起的环境变化对秘鲁外海茎柔鱼资源丰度和分布的影响。结果表明, 秘鲁外海的涡旋主要分布在沿岸海域和 15°S 以南的海域, 存在一定的月间变化, 年际变化不明显。反气旋涡中的茎柔鱼丰度优于气旋涡, 涡旋边缘的茎柔鱼丰度高于涡旋内部; 反气旋涡中的适宜环境占比高于气旋涡, 涡旋边缘的适宜环境占比高于涡旋内部。此外, 反气旋涡中相对较低的海表面温度和 50 m 水层温度产生了更多的适宜栖息地, 导致反气旋涡中茎柔鱼丰度更高。

关键词：中尺度涡；环境变化；茎柔鱼；资源丰度；秘鲁

Analysis of the spatial and temporal distribution of eddies off Peru and their relationship with the abundance of jumbo flying squid, Dosidicus gigas

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Abstract：Dosidicus gigas, a short-lived cephalopod species, is extremely sensitive to environmental changes. The waters off Peru are an important fishing ground for D. gigas; nonetheless, mesoscale eddies are ubiquitous throughout this region. However, the impacts of eddies off Peru on D. gigas remain unclear. In this study, we first analyzed the spatial and temporal distribution of eddies off Peru using an angular momentum eddy detection and tracking algorithm (AMEDA) based on an eddy tracking dataset; we then used fishery data, an eddy tracking dataset, and environmental data to evaluate the impacts of mesoscale eddies and eddy-induced changes in the environmental conditions on the abundance and distribution of D. gigas off Peru. It was found that eddies off Peru were primarily distributed in the coastal waters and south of 15°S, with some inter-monthly variability; nonetheless, interannual variability was not significant. The influence range of the anticyclonic and cyclonic eddies was divided into internal (0–R) and marginal (R–2R) regions. The corresponding analysis showed that the abundance of D. gigas in the anticyclonic eddy regions was higher than that in the cyclonic eddy regions; further, the abundance of D. gigas at the edge of the eddies was higher than that in the center of the eddies.

Correspondingly, the percentage of suitable environments in the anticyclonic eddies was higher than that in the cyclonic eddies, and the percentage of suitable environments at the edges of the eddies was higher than that in the center. In addition, the relatively lower sea surface temperature (SST) and 50 m water temperature (T50 m) in the anticyclonic eddies yielded more suitable habitats, leading to a high abundance of D. gigas at anticyclonic eddy sites. Our results suggested that the variation of suitable environments in the interior and edges of different types of eddies affects the abundance and spatial distribution of D. gigas.

Key words: mesoscale eddy; environmental variations; Dosidicus gigas; abundance; Peru

西北印度洋雄性鸢乌贼个体繁殖力特性研究

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摘要：为深入了解西北印度洋鸢乌贼雄性个体有效繁殖力特性，对印度洋雄性鸢乌贼的繁殖力、性腺成熟度以及精荚特性进行研究。根据 21 年 11-12 月、22 年 3-5 月的西北印度洋鸢乌贼样本进行测定。对个体性腺发育过程中有效繁殖力特性、精荚囊与精荚随性腺发育的变化规律进行了分析。鸢乌贼雄性性腺指数为 0.20-2.73 %，精荚复合体指数为 0.08-2.63 %；个体繁殖力范围为 1-220 条；精荚囊长度范围为 49.32-171.6mm，重量范围为 0.082-5.141g，；精荚长为 5.45-70.99 mm，精荚重为 0.2-19.5 mg，两者呈现幂函数关系。研究表明，西北印度洋鸢乌贼雄性个体的性腺指数和精荚复合体指数随着性腺发育而增大；个体有效繁殖力、精荚囊和精荚均随着性腺发育而不断增大，并都与胴长、体重呈显著的函数关系；精荚长度与重量均随着胴长和体重的增大而增大。

关键词：鸢乌贼；有效繁殖力；繁殖生物学；西北印度洋

The effective fecundity in male Sthenoteuthis oualaniensis in the northwest Indian ocean

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Abstract: Sthenoteuthis oualaniensis is an economically important Cephalopod in the Indian Ocean, and the research of fecundity can provide insight into the adaptive characteristics of organisms or populations to survive in the environment.In order to deeply understand the effective fecundity characteristics of male S.oualaniensis in the northwest Indian Ocean, according to the samples of S.oualaniensis in the northwest Indian Ocean from November to December 2021 and from March to May 2022, the effective fecundity characteristics, the changes of spermatophore sac and spermatophore with gonad development were analyzed. The results showed that the gonad index was 0.20-2.73 %, and the spermatophore complex index was 0.08-2.63 %. The individual fecundity ranged from 1-220, and the relative fecundity of mantle length ranged from 0.006 -1.073 mm each. The length of spermatophore sac ranged from 49.32-171.6 mm, and the weight ranged from 0.082-5.141 g. The length and weight of spermatophore sac increased with the increment of individual mantle length and body weight. The length of spermatophore was 5.45-70.99 mm, and the weight of spermatophore was 0.2-19.5 mg, which showed a power function relationship. The length and weight of spermatophore scaled up with growing carcass length and body weight. The above results showed that the gonad index and spermatophore complex index of male S.oualaniensis in the northwest Indian Ocean magnified with gonad development. Individual effective fecundity, spermatheca and spermatheca increased with the development of gonad, and had significant functional relationship with individual carcass length and body weight. In this research, male S.oualaniensis in the northwest Indian Ocean were studied to analyze their gonadal development patterns and effective fertility characteristics in order to gain insight into the reproductive biology of S.oualaniensis and provide a basis for subsequent male S.oualaniensis in the northwest Indian Ocean resource assessment and sustainable development.

Key words: Sthenoteuthis oualaniensis; effective fecundity; reproductive biology; northwest Indian Ocean

网囊设计参数和网片属性对中层拖网网囊振荡特性的影响

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摘要：为研究网囊设计参数和网片属性对中层拖网网囊水动力特性、网囊形态及振荡特性影响，本研究设计制作了 13 顶不同参数（网目尺寸、网线直径、网囊长度、结节方向、网线材料及内衬网有无结节）网囊，采用快速傅立叶变换获取各网囊阻力和位置振荡特性（频率和振幅），并利用统计模型分析各因素对网囊阻力和位置振荡特性影响权重。结果显示：空网条件下，各网囊在 V≤0.6 m/s 的速度下为完全展开，在 V≥0.7 m/s 的速度下网衣全部展开，中部截面积随着网目尺寸、网线直径和网囊长度的增加而增加；采用 T90 结节和聚乙烯(PE)材料可有效扩张网囊网目。网囊阻力振幅随网囊线面积的增大而增大。当网囊存在渔获物时，网囊形状变化主要为在网囊前部闭合，后部隆起，其中 T90 结节是保证网目张开最有效方法。此外，网囊在 X 和 Z 方向上的位置振荡频率为 0.28-0.48 Hz。阻力振荡频率为 0.29-0.50 Hz，且与位置运动同步。

关键词：属性参数；网囊振荡；形态；影响权重

The profile and fluttering characteristics of mid-water trawl codend with different properties and design parameters

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Abstract： To investigate the effects of the codend parameters and simulated catch on hydrodynamic characteristics, net cross-section, and fluttering motions of the codend in the flume tank. Thus, 13 codends with varying parameters (mesh size, bar diameter, codend length, knot direction, twine material and liner net) were designed. Fourier analysis was performed via the fast Fourier transform (FFT) method to observe the frequency and amplitude of the codend fluttering motions and time evolution of the drag forces, and the generalized additive models (GAMs) to evaluate the effect weight of each design parameter on the oscillation characteristics (frequency and amplitude) of codend. The results showed that at the empty stage, each codend is folded at V≤0.6 m/s but fill at V≥0.7 m/s, the middle cross-sectional area increases as the mesh size, the bar diameter and the codend length increase; using the T90 and polyethylene (PE) codend can effectively expand the mesh opening. The drag force amplitude increased with the twine area increase of empty codend. For the codend with simulated catch, the shape of each codend was closed at the front of the mesh and bulging at the rear contour, the T90 knot is the most efficient method to ensure the mesh opening. Additionally, the codend position oscillates frequency was 0.28–0.48 Hz in X and Z directions. The drag oscillation frequency was mainly 0.29–0.50 Hz and synchronized with the position motion.

Key words: property parameter; fluttering motion; profile; effect weight

基于随机森林模型的秘鲁外海茎柔鱼资源丰度与环境因子研究

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摘要：本研究基于秘鲁外海 2018-2021 年 9-12 月茎柔鱼的渔捞日志数据，并结合环境因子海表温度、海表盐度、海表高度、叶绿素数据，运用 ArcGIS 和随机森林模型分析秘鲁外海茎柔鱼资源丰度与环境因子之间的关系。研究表明，2018-2021 年 9-12 月茎柔鱼渔场重心分布范围集中于 76°W~87°W、13°S~21°S 海域，9-12 月渔场重心呈现西北向东南方向移动。随机森林模型结果显示，各月环境因子对秘鲁外海茎柔鱼资源丰度和分布的影响存在一定的差异性，最适 SST 为 16.3~18.5℃，最适 SSH 为 0.55~0.60m，最适 Chla 范围 0.18~0.46mg/m³。研究结果对于了解该海海域茎柔鱼资源变动规律、指茎柔鱼生产具有重要意义。

关键词：茎柔鱼；随机森林模型；资源丰度；环境因子

Study on resource abundance and environmental factors of Dosidicus gigas in Peru based on random forest model

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Abstract：Dosidicus gigas (D. gigas) in the Southeast Pacific Ocean off Peru is an important part of China’s pelagic fishery, and it is important to explore the relationship between its resource abundance and environmental factors. This study was based on the fisheries data of D. gigas in Peru from September to December 2018-2021, combined with the environmental factors sea surface temperature (SST), sea surface salinity (SSS), sea surface height (SSH), and chlorophyll-a (Chla) data collected by satellite remote sensing. ArcGIS and the random forest model were used to analyze the relationship between the abundance of D. gigas resources and environmental factors in Peru. The results showed that from September to December 2018-2021, the distribution range of the center of gravity of the fishery was concentrated in the sea area of 13°S~21°S and 76°W~87°W, and the center of gravity of D. gigas shifted towards the southeast from September to December. The results of the random forest model analysis showed that there were some differences in the effects of environmental factors on the abundance and distribution of D. gigas, and the optimal range of SST was between 16.3°C and 18.5°C. The optimal range of SSH is from 0.55 to 0.60m, and the optimal range of Chla is 0.18~0.46mg/m³. The results of this study are of great significance for understanding the variation of D. gigas resources in this area and guiding the sustainable production of D. gigas resources.

Key words: Environmental DNA(eDNA); Liuheng sea area; Species of fish community; Resource survey

基于物联网和 VMS 系统的
渔捞日志数据收集研究

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摘要：捕捞日志等相关记录是渔业生产过程中重要的数据记录，可用于鱼类生境研究、种群评估和渔业管理。为了更准确地收集捕捞日志等数据，本研究以秋刀鱼刀鱼渔业为例，开发了基于物联网技术的相关捕捞可追溯系统，并使用二维码测试和收集了一些物联网包装的捕捞信息。基于 VMS 数据与海表温度数据，提出了渔捞日志数据采集方法。结果表明:物联网系统可以提高渔业数据采集的可靠性和准确性， 在当前获取可靠的 VMS 数据的情况下，当晚作业期内所有 VMS 记录点的重心点可作为渔捞日志捕捞地点记录的最合适位置，且午夜后日期可作为渔捞日志作业日期的记录日期。

关键词：物联网；VMS 系统；渔捞日志

Data collection for fishing logbook by using Traceability System and VMS

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Abstract： Fishing logbook and other related records are important data records in the process of fishery production, which can be used in the study of fish habitat, stock assessment and fishery management. In order to collect fishing logbooks and other data more accurately, this study takes the Pacific saury fishery as a case study, develops a relevant catch traceability system based on IoT technology, and uses QR code to test and collect some IoT packed catch information. A Better data collection for fishing logbook was analyzed by combining VMS data and SST data. The results indicate that: IoT systems can improve the reliability and accuracy of fishing data collection. With reliable VMS data currently available, the center of gravity of all VMS recording points during the night operation can be used as the most appropriate location for logging sites, and the post-midnight date can be used as the logging date for logging dates

Key words: Traceability System; VMS; Fishing logbook

南海北部张网方形和菱形混合网目网囊的选择性研究

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摘要：为探索南海北部张网方形和菱形混合网目网囊的不同网目尺寸对主要渔获的网目选择性，使用套网法开展了4种不同网目尺寸（25mm、30mm、35mm和40mm）的方形和菱形混合网目网囊的选择性对比试验，根据相对重要性指数（IRI），确定风鲚作为选择性研究的指标种。使用Logistic模型拟合不同网目尺寸下风鲚的选择性曲线，采用极大似然法估算模型参数。结果显示，网囊网目尺寸为25mm、30mm、35mm和40mm时，风鲚的50%选择体长（\mathrm{L}_{\mathrm{0.5}}）分别为108.48mm、109.02mm、114.36mm和115.94mm，选择范围（\mathrm{SR}）分别为39.37mm、84.99mm、75.26mm和38.73mm；风鲚的\mathrm{L}_{\mathrm{0.5}}随着网目尺寸的增大而增大，而\mathrm{SR}逐渐减小；根据该\mathr

关键词：南海；张网；最小网目尺寸；选择性；套网法

Selective Study of combined square and diamond mesh codend of stow net in the Northern part of South China Sea

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Abstract：In order to evaluate the mesh selectivity of combined square and diamond mesh codend for the main catches of stow net in the northern part of South China Sea, comparative experiments were conducted using the covered net method with four different mesh sizes (25mm, 30mm, 35mm, and 40mm). The selectivity of combined square and diamond mesh was evaluated, and the target species, Trichiurus lepturus, was determined as the indicator species for the selectivity study based on the Importance Index (IRI). Logistic models were employed to fit the selectivity curves of T. lepturus under different mesh sizes, and model parameters were estimated using maximum likelihood estimation. The results showed that the 50% selection length(\mathrm{L}_{\mathrm{0.5}}) of T. lepturus for mesh sizes 25mm, 30mm, 35mm, and 40mm were 108.48mm, 109.02mm, 114.36mm, and 115.94mm, respectively. The selection range（\mathrm{SR}）for these mesh sizes were 39.37mm, 84.99mm, 75.26mm, and 38.73mm, respectively. \mathrm{L}_{\mathrm{0.5}}\ of T. lepturus increased with increasing mesh size, while SR gradually decreased. Based on this \mathrm{L}_{\mathrm{0.5}}\ and mesh size relationship, the minimum mesh size for T. lepturus was determined to be 47.03mm. The combined square and diamond mesh exhibited a higher release rate for T. lepturus, and their use effectively improved the selectivity of the fishing gear.

Key words: stow net; combined square and diamond mesh codend; codend; selectivity performance

不同气候条件下海洋环境对中西太平洋金枪鱼围网鲣资源影响的时空异质性研究

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摘要：鲣资源分布受厄尔尼诺-南方涛动（ENSO）的影响，表现出多种时空影响机制。为了探索不同气候条件下海洋环境对鲣资源丰度影响的时空非平稳性，本文利用中西太平洋渔业委员会 2004—2021 年的中西太平洋金枪鱼围网渔业和海洋环境数据，采用时空地理加权回归(GTWR)方法进行研究。研究结果表明：（1）GTWR 的表现优于 OLS、GWR 和 GAM 模型。(2）海面盐度和温度对鲣鱼丰度有影响显著，而海流速度（U55、V55）的影响相对较小。(3）环境因子的影响表现出不同的时空非稳定性。正常时期海平面异常影响的空间异质性降低，厄尔尼诺时期 U55 影响的空间异质性增加，拉尼娜时期混合层深度和 V55 影响的空间异质性增加。(4）东部海域的时间异质性大于西部海域，整个研究区的时间异质性在 2013 年后有所上升，这与 FADs 的使用及禁渔期延长有关。

关键词：鲣；中西太平洋；ENSO；时空地理加权回归模型；时空异质性

Spatiotemporal Non-stationarity of the Marine Environmental Impact on Skipjack Fishery Resources under Different Climate Conditions in the Western and Central Pacific

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Abstract: The skipjack tuna (Katsuwonus pelamis) is a significant fishery resource within purse seine fisheries in the Western and Central Pacific Ocean. The distribution of skipjack resources is influenced by the El Niño-Southern Oscillation (ENSO), exhibiting diverse spatiotemporal impact mechanisms. To investigate the spatiotemporal non-stationarity of how marine environments affect skipjack resource abundance under different climate conditions, we applied the geographically and temporally weighted regression (GTWR) model to skipjack catch rate and marine environmental data from 2004 to 2021. The findings reveal: (1) The GTWR outperformed ordinary least squares, geographically weighted regression, and generalized additive models, achieving an adjusted R2 value of 0.63. (2) Skipjack abundance was significantly affected by sea surface salinity and temperature (SSS, SST) as well as net primary production (NPP). Sea level anomaly (SLA) and mixed layer depth (MLD) had a moderate impact, whereas zonal and meridional current velocities (U55, V55) had a relatively minor influence. (3) The impact of environmental factors displayed varying spatial non-stationarity. Spatial heterogeneity was most pronounced for NPP, SSS, and V55, followed by SLA and SST, and least pronounced for MLD and U55. Notably, SLA spatial heterogeneity decreased during normal periods, U55 increased during El Niño, and MLD and V55 increased during La Niña. (4) Due to spatial differences influenced by ENSO, the eastern study area displayed more significant temporal heterogeneity than the western area. After 2013, the entire study area experienced increased temporal heterogeneity, attributed to the use of fish aggregating devices and extended fishing moratorium periods.

Key words: Skipjack; Western and Central Pacific Ocean; ENSO; Geographically and Temporally Weighted Regression model; Spatiotemporal heterogeneity

锚泊式人工集鱼装置在渔业中的应用

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摘要：锚泊式人工集鱼装置（AFADs）是定置于海洋中，用于聚集鱼群的人造漂浮物。本研究总结了 AFADs 的种类与结构及其在全球主要地区的应用历史与现状，介绍了利用 AFADs 作业的主要渔具及渔获种类。渔业中应用 AFADs 有利于近海渔业资源养护，提高 CPUE 并降低油耗，有助于大洋性渔业资源开发；能促进休闲游钓渔业发展；在太平洋岛国，还促进当地的食物供应与海上作业安全。此外，AFADs 配备科学仪器可成为监测海洋环境和渔业资源的平台。同时，针对 AFADs 存在的过度开发渔业资源、对海洋生态与环境产生负面影响、投放密度过高、潜在影响航运安全等问题，本研究总结了应对措施，包括：AFADs 海域建立禁渔期及渔具准入制度；使用可降解材料制作 AFADs 并改进结构减少意外丢失；规定 AFADs 间的最小距离或总量控制；禁止在航运繁忙的海域投放 AFADs。研究可为应用 AFADs 开发我国南海金枪鱼等大洋性渔业资源提供基础资料。

关键词：AFADs；金枪鱼；大洋性渔业

The application of Anchored Fish Aggregating Devices in fisheries

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Abstract： Anchored fish aggregating devices (AFADs) are artificial floating objects anchored in the ocean. They use the characteristics of tuna and other pelagic fishes that prefer to gather around floating objects to gather and catch fish schools. At present, there is no consensus on the reasons why tuna are attracted to floating objects. However, AFADs are widely used in tropical and subtropical waters and are effective auxiliary tools for developing tuna resources because they can reduce the time spent searching for fish schools and increase the catch per unit fishing effort (CPUE). This study summarized the types and structures of AFADs. According to the physical environment of the sea area, deployed AFADS could be divided into lagoon AFADs, nearshore AFADs and offshore AFADs. According to the position of the floatation, it could be divided into surface AFADs and subsurface AFADs. AFADs were composed of three parts: upper floatation system, main line system, and anchor system. The upper floatation of AFADs provides the buoyancy and floats were the most common buoyancy used for AFADs. The main line should show a catenary shape in the water or 1.25 times the depth of water to provide elasticity against the impact of tides, currents, and waves. Anchors were mostly cement anchors, and their weight needed to match the buoyancy of AFADs to prevent accidental loss. The study showed the history and current situation of AFADs in the Mediterranean and Caribbean sea, in the Western Pacific (Philippines and Indonesia), in the Central Pacific (Hawaii and Kiribati) and in the Indian Ocean (Maldives and Mauritius). The development of AFADs in the above-mentioned countries had been successful, but due to the lack of statistical data, it was difficult to accurately understand the current situation such as the number and location of AFADs in use. The study found the main fishing gears operating in the waters of AFADs included purse seine, rod line, handline, and troll line. In the Mediterranean, the target species of AFADs fishery was mahi mahi (Coryphaena hippurus), in other areas the target species was mainly tuna such as skipjack (Katsuwonus pelamis), yellowfin tuna (Thunnus albacares), etc. This study found AFADs had the following benefits:

benefiting coastal and coral reef resource conservation by shifting fishing effort to oceanic resources and improving economic benefits by improving CPUE and reducing fuel consumption; promoting the development of pelagic fishery (especially tuna fishery) and sport fishery; advancing food supply safety and operation safety at sea in Pacific Island countries and territories (PICTs); becoming a data monitoring platform by equipping with advanced electronic instruments such as echo-sounder buoy, wave buoy, ocean current profilers, GPS tracking devices, etc. However, AFADs also had the following disadvantages: there was a risk of overexploitation of fishery resources in some areas due to the high ratio of juveniles and spawning groups in the catches; loss of AFADs would have negative impacts on marine ecology and environment; excessive density of AFADs would be harmfull; AFADs might affect the safety of shipping. This study summarized corresponding measures to slove the above issues: building system of closed fishing season, fishing effort control and fishing gear access; using biodegradable materials to produce AFADs and optimizing the structure to reduce accidental loss; ensuring minimum distance between AFADs or total amount control; prohibiting the placement of AFADs in the aforementioned waters. Given its success in other countries, AFADs may become effective auxiliary tools for developing tuna resources in the South China Sea and this study will provide basic data for its application in the South China Sea.

Key words: AFADs; tuna; oceanic fishery

“十三五”秋刀鱼捕捞装备研究与标准规范的制定

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摘要：秋刀鱼渔业是我国远洋渔业的重要组成部分。根据秋刀鱼舷提网捕捞技术发展和产业升级要求，概述了“十三五”秋刀鱼捕捞装备研发和标准规范制定相关研究。基于秋刀鱼趋光行为特性，结合灯光理论模拟和照度实测，开展秋刀鱼多光谱集成可变光源集鱼灯研发、实船试验及系统优化，突破盲目增加功率和凭经验研制灯具等模式，满足船长对全船灯色分布和光照需求的实时调控；针对舷提网放网慢耗时问题，通过水槽模型试验、开放水域和近海全尺寸 1/6 段动力推进中试等研发动力装置，开展全方位主动式秋刀鱼舷提网网具系统研发和优化，突破被动放网的传统作业方式，提高捕捞效率 10-15%；基于物联网技术记录追踪渔获捕捞、转运和仓储等关键节点，研发秋刀鱼渔获物联网可追溯系统；制定秋刀鱼渔业灯具和网具标准，规范装备生产、装配等技术指标，确保产品优良可靠。研究成果已在国内秋刀鱼渔船应用推广，积极满足行业需求，实现生态高效节能捕捞，推动绿色可持续发展。

关键词：集鱼灯；舷提网渔具；标准规范；秋刀鱼渔业

Research on fishing equipment and formulation of standards and specifications for Pacific saury fishery in the 13th Five-Year Plan

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Abstract： Pacific saury fishery is an important part of Chinese pelagic fisheries. According to the requirements of the development of fishing technology and the upgrading of the saury fishery, the research on fishing equipment and the formulation of standards and specifications in the “13th Five-Year Plan” are summarized. Based on the phototropic characteristics of saury, the study of multi-spectrum integrated variable fishing lamps, onboard experiments and system optimization were carried out by combining with the theoretical simulation and illumination measurement of light source, which broke through the traditional modes of blindly increasing the power and empirical development of lamps. The newly designed fishing light system allows the captain to control the lamp color distribution and operational lighting needs on the vessel in real time. To solve the problem of slow and time-consuming release of the stick-held dip net, the electric-powered devices were investigated through flume tank model tests, open water and offshore full-size 1/6-section floater propel tests. An active propulsion fishing gear system was developed and optimized, which breaks through the traditional mode of passive to release the net and improves the catching efficiency by 10-15%. Using the Internet of Things (IoT) technology to record and track the key process of fishing, transport, and storage of catches, the IoT traceability system for saury catches was developed. The standards for fishing lamps and gears in the saury fishery were formulated to standardize the technical indicators including production and assembly process of equipment to ensure the reliable product performance. The above equipment had been applied and promoted in the domestic saury fishery, which helps to meet the needs of fishery industry, realize ecologically efficient and energy-saving fishing, and promote the sustainable development of the saury fishery.

Key words: Fishing lamp; Stick-held dip net; Standard and specification; Pacific saury fishery

捕捞数据不确定下剑尖枪乌贼渔业管理策略评估

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摘要：剑尖枪乌贼是海洋重要的渔业资源，是头足类主要经济物种之一，是海洋生态系统的关键组成，在我国海洋渔业生产中占有重要地位，但评估其资源变动的研究在国内较少。因此，调查东海海域剑尖枪乌贼的资源动态、种群水平，可以更好地开发、利用、保护东海剑尖枪乌贼资源。由于剑尖枪乌贼的渔业数据处于缺乏状态，自然死亡率等生物学参数没有明确研究，传统的渔业资源评估方法无法对其进行过评估，阻碍了渔业管理评估的发展进程。本研究使用包括输入控制和输出控制的 5 种不同基于渔获量、体长等的管理程序(management procedures, MP)对剑尖枪乌贼资源进行了评估。结果表明，在剑尖枪乌贼渔获量数据不确定性较大的情况，AvC 更适合于剑尖枪乌贼渔业等捕捞数据不确定性较大渔业的评估。本研究根据不确定性分析、敏感性分析以及管理策略综合评估，比较了上述的 5 种 MP，认为 AvC 能够使剑尖枪乌贼渔业资源可持续利用。

关键词：剑尖枪乌贼；DLMtool；管理策略评估；不确定性分析

Management strategy evaluation of mackerel swordtip squid (Uroteuthis edulis) fishery with uncertainty of catch data

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Abstract： As one of the main economic species of cephalopods and a key component of Marine ecosystem, Swordtip squid plays an important role in Marine fishery production in China. However, there are few studies on the assessment of its resource changes in China. Therefore, the investigation of resource dynamics and population level of the East China Sea can better develop, utilize and protect the resources of the East China Sea. Due to the lack of fishery data, natural mortality and other biological parameters have not been clearly studied, and the traditional fishery resources assessment methods have not been able to evaluate the squid, which has hindered the development of fishery management assessment. In this study, five different management procedures (MP) based on catch, body length, etc. were used to assess the swordtip squid resources, including input and output controls. The results show that AvC is more suitable for the evaluation of swordtip squid fishery when the fish catch data is more uncertain. Based on uncertainty analysis, sensitivity analysis and comprehensive evaluation of management strategies, this study compared the above 5 MP, and concluded that AvC can make the sustainable use of the fish resources of swordtip squid.

Key words: Uroteuthis edulis; DLM tool; management strategy evaluation; uncertainty analysis

基于结构方程模型的环境因子对鲣资源丰度的影响研究

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摘要：关于渔业资源丰度与环境因子关系研究是近年来一大热点，大量研究集中在环境因子如何直接影响渔业资源方面，但渔业资源变化通常取决于多个环境因素的综合作用，影响区域渔业资源的因素是复杂和有相关性的，有鉴于此，为了进一步深入了解影响渔业资源丰度与环境因子之间存在的关系以及存在复杂的关系。本研究以 2017-2019 年毛里塔尼亚鲣为研究对象，采用结构方程模型分析了鲣 CPUE 与海表温度(SST)、海表盐度(SSS)、海面高度异常(SLA)、溶解氧(DO)和叶绿素 a 浓度(Chl-a)等环境因子之间的关系。结果表明：SST 等环境因子均对鲣 CPUE 有直接影响，其中 DO 和 SLA 对 CPUE 显著正相关，SST、SSS 和 Chl-a 对 CPUE 显著负相关；SST 通过影响 SSS、DO 和 SLA，对鲣 CPUE 产生间接影响。因此，在后续研究环境因子和资源丰度时还需考虑环境因子间相互关系和环境因子影响渔业资源 CPUE 存在的潜在机制。

关键词：渔业资源；鲣；CPUE；SEM；环境因子

A study on the effect of environmental factors on the abundance of bongo resources based on structural equation modelling

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Abstract： Research on the relationship between fishery resource abundance and environmental factors has been a major hotspot in recent years, and a large number of studies have focused on how environmental factors directly affect fishery resources, but changes in fishery resources usually depend on the combined effects of multiple environmental factors, and the factors affecting regional fishery resources are complex and correlated. In view of this, in order to gain a deeper understanding of the relationship that exists between the factors affecting the abundance of fishery resources and the environmental factors and the existence of complex relationships. In this study, the relationship between skipjack tuna CPUE and environmental factors such as sea surface temperature (SST), sea surface salinity (SSS), sea surface altitude anomaly (SLA), dissolved oxygen (DO), and chlorophyll a concentration (Chl-a) were analysed using structural equation modelling for skipjack tuna from 2017-2019. The results showed that all the environmental factors, including SST, had a direct effect on skipjack CPUE, with DO and SLA significantly positively correlated with CPUE, and SST, SSS and Chl-a significantly negatively correlated with CPUE; and SST had an indirect effect on skipjack CPUE by affecting SSS, DO and SLA. Therefore, it is necessary to consider the interrelationships among environmental factors and the potential mechanisms of environmental factors affecting the CPUE of fishery resources in the subsequent study of environmental factors and resource abundance.

Key words: fishery resources; Katsuwonus pelamis; CPUE; SEM; environmental factors

基于地理加权主成分分析和多尺度地理加权模型的太平洋黄鳍金枪鱼渔获率环境影响机制研究

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摘要：黄鳍金枪鱼 (Thunnus albacares) 资源分布受环境影响明显，为探索环境对黄鳍金枪鱼渔获率影响的空间异质性特征，利用中西太平洋渔业委员会 (WCPFC) 和美洲间热带金枪鱼委员会（IATTC）公布的 2000-2020 年太平洋金枪鱼延绳钓 5°×5°渔业数据，建立了地理加权主成分分析和多尺度地理加权回归相结合的模型，揭示了太平洋黄鳍金枪鱼渔业资源空间变动。结果表明：1) 考虑环境多重共线性问题的 GWPCA-MGWR 拟合优度有所提升，拟合结果的空间分布更符合真实情况；2) 各环境因子对黄鳍金枪鱼资源分布存在显著的空间非平稳性影响。不同深度温度和盐度，以及净初级生产力（npp）、温跃层深度和溶解氧浓度等各海洋环境因子均对黄鳍金枪鱼渔获率分布空间异质性有所影响；3）不同年存在主成分偏离现象。2006、2002 及 2020 年受 ENSO 现象影响，环境因子主成分代表性减弱，整体回归出现偏离。

关键词：黄鳍金枪鱼、多尺度地理加权回归、地理加权主成分、中西太平洋

The Environmental Impact Mechanism of Pacific Yellowfin Tuna Catch Rate Based on Geographically Weighted Principal Component Analysis and Multiscale Geographically Weighted Models

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Abstract：The distribution of Yellowfin Tuna (Thunnus albacares) resources is notably influenced by environmental factors. To investigate the spatial heterogeneity of environmental effects on Yellowfin Tuna catch rates, a model was developed using a combination of Geographically Weighted Principal Component Analysis (GWPCA) and Multiscale Geographically Weighted Regression (MGWR). The model was constructed using fishing data from the Pacific Ocean, spanning from 2000 to 2020 and published by the Western and Central Pacific Fisheries Commission (WCPFC) and the Inter-American Tropical Tuna Commission (IATTC). This model revealed spatial variations in the distribution of Yellowfin Tuna fisheries resources.The results of the study are as follows:1) The GWPCA-MGWR model, which accounts for environmental multicollinearity, led to an improvement in the model's goodness of fit. The spatial distribution of the model's results more accurately reflects real-world conditions.2) Various environmental factors were found to have a significant spatial non-stationary impact on the distribution of Yellowfin Tuna resources. These factors include sea surface temperature and salinity at different depths, as well as net primary productivity (NPP), thermocline depth, and dissolved oxygen concentration. All of these factors influence the spatial heterogeneity of Yellowfin Tuna catch rates.3) In different years, variations in the principal components were observed. In years affected by ENSO events, such as 2006, 2002, and 2020, the representation of principal components of environmental factors weakened, resulting in deviations in the overall regression analysis.

Key words: Yellowfin Tuna; Multiscale Geographically Weighted Regression; Geographically Weighted Principal Component; Western and Central Pacific

秘鲁外海茎柔鱼（Dosidicus gigas）的脂肪酸组成：揭示摄食策略的多变性

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摘要：茎柔鱼（Dosidicus gigas）在海洋生态系统中扮演着重要角色，是东太平洋的重要商业物种。一般来说，根据成体的胴长（ML）可将其分为三个表型群。本文利用肌肉组织的脂肪酸分析，探讨了秘鲁外海不同表型群和内部性别的摄食策略。在脂肪酸组成方面，小型和中型群之间没有明显差异，而大型群与其他群体之间存在明显差异。C20:4n6 和（C18:2n6 + C18:3n3）的含量较高，表明大型群可能更频繁的在近岸和深海水域摄食。此外，大型群占据的营养位最广，其次是中型组，然后是小型组。有证据表明，小型组和中型组之间存在营养位重叠。在中小型群的性别差异方面，雌性和雄性之间的脂肪酸组成存在显著差异。在大型群中，雌性和雄性的脂肪酸组成相似，表明它们可能采取了相似的摄食策略。这项研究揭示了秘鲁专属经济区外三个大小群体茎柔鱼摄食策略的差异性。

关键词：茎柔鱼；稳定同位素；摄食器官形态；生态位；种群

Fatty Acid Profile of Jumbo Squid (Dosidicus gigas) off the Peruvian Exclusive Economic Zone: Revealing the Variability of Feeding Strategies

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Abstract: Jumbo squid Dosidicus gigas plays a critical role in marine ecosystems and is an important commercial species in the East Pacific. Generally, three size groups have been distinguished on the basis of the mantle length (ML) of an adult. Here, fatty acid (FA) analyses of muscle tissues were used to explore the feeding strategies of D. gigas off the Peruvian exclusive economic zone in terms of different size groups and sexes. There was no significant difference in fatty acid composition between the small- and medium-sized groups, whereas the large-sized group differed significantly from other groups. The higher content of C20:4n6 and C18:2n6 + C18:3n3 indicates that the large-sized group may feed more frequently in nearshore and deep waters. Furthermore, the niches of the three size groups were consistent with the results of fatty acid composition, with the large-sized group occupying the widest trophic niche, followed by the medium-sized group, and then the small-sized group. In addition, there was evidence of trophic niche overlap between the small and medium groups. In terms of sexual variability among the small and medium groups, the fatty acid composition significantly differed between females and males. In terms of sexual variation among the large group, the fatty acid composition between females and males was similar, indicating that similar feeding strategies may be adopted by them. This study revealed the variability of the feeding strategies of three size groups of D. gigas off the Peruvian exclusive economic zone.

Key words: Dosidicus gigas; group; feeding strategy; fatty acid; trophic niche

基于双重拔靴法拟合拖网网囊选择性的不确定性

杨炳忠

摘要：研究拖网网囊选择性对于渔业的科学管理和资源的合理利用都有重要意义。拖网网囊选择性的研究一般先开展捕捞试验，然后使用选择性模型拟合和处理试验数据，最后得出选择性参数和选择性曲线。主要的选择性参数包括 50%选择体长（L50）和选择范围（SR）。但是，仅仅提供选择性参数和曲线是不够的，还需要拟合它们的不确定性，并以置信区间的形式展现。双重拔靴法是拟合网囊选择性不确定性的重要方法。本文在阐述双重拔靴法基本原理的基础上，选取 2 组试验数据为实例，用常规方法和双重拔靴法进行拟合，通过比较拟合结果诠释双重拔靴法的特点和优势。结果表明，双重拔靴法能够很好地拟合网囊选择性参数 L50、SR 和曲线的不确定性。同时，文章还就应用双重拔靴法的重大误区进行了分析和讨论。本文可为研究人员开展渔具选择性研究提供方法参考，以提升研究的理论水平，更好地为海洋渔业的可持续发展服务。

关键词：拖网；网囊选择性；双重拔靴法；不确定性

Estimation uncertainties of the size selectivity of trawl codends based on the double-bootstrapping technique

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Abstract： Codend size selectivity is the keystone for management of trawling fisheries and sustainable exploitation of fisheries resources. In order to assess the size selectivity of trawl codends, experimental sea trials are often conducted and fishing data is manipulated using some mathematical models to obtain selectivity parameters, such as 50% retention length (L50) and selection range (SR), and selectivity curves. Providing the values of this information, however, is highly inadequate. It needs to account for the uncertainties in size selectivity and represent them in confidence intervals. To do this, the double-bootstrapping technique is intensively applied in fishing gear selectivity studies. In this study, the basic principle of the double-bootstrapping was firstly introduced, then two set of fishing data involved two different fishing species were used as case studies to show and compare how this technique was used to estimate the uncertainties of codend size selectivity. Our results demonstrated that the uncertainties of codend size selectivity could be easily estimated applying the double-bootstrapping technique. Additionally, the most commonly wrong practice of using the double-bootstrapping technique was discussed. Our study will provide a guideline for conducting trawl codend selectivity studies, improve the level of selectivity researches, and contribute to the sustainable development of marine fisheries in China.

Key words: trawl; codend selectivity; double-bootstrapping technique; uncertainties

热带中西太平洋围网 FSC 和 DFADs 鱼类群落结构与环境因子的响应差异

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摘要：中上层鱼类群落在鱼类组合中占主导地位，并且由于其高丰度、垂直洄游行为和全球分布而构成海洋生态系统的重要组成部分。本研究使用 2018—2020 年 WCPO 围网渔业数据并结合环境特征数据，采用 VPA 分析、Procrustes 分析、Mantel 检验和共生网络分析等分析方法分析了围网自由鱼群(Free-swimming school, FSC)和漂流人工集鱼装置(Drifting fish aggregating devices, DFADs) 两种不同捕捞策略下的中上层鱼类群落的结构特征、构建机制、共生关系及环境响应。VPA 分析表明，环境因子对群落分布的影响大于地理变量，地理变量只对 FSC 鱼类群落有影响。Procrustes 分析结果显示，环境因子与围网 FSC 和 DFADs 中上层鱼类群落结构之间均存在显著相关性($p < 0.01$)。本研究可为 WCPO 围网生物多样性保护提供理论依据。

关键词：围网；鱼类群落；FSC；DFADs；Mantel 检验；环境响应

Differences in FSC and DFADs fish community structure and response to environmental factors in the tropical Western and Central Pacific Ocean purse seine

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Abstract ： Pelagic fish communities dominate fish assemblages and constitute an important component of marine ecosystems due to their high abundance, vertical migratory behavior, and global distribution. In this study, using the 2018-2020 Western and Central Pacific Ocean purse seine fishery data and combining it with environmental characteristics data, we analyzed the free-swimming school (FSC) and drifting fish aggregating devices (DFADs) in the purse seine by using analytical methods, such as VPA analysis, Procrustes analysis, Mantel test, and Co-existence network analysis. VPA analysis showed that environmental factors had a greater effect on community distribution than geographic variables, and geographic variables only had an effect on the FSC fish community. Procrustes analysis showed significant correlations ($p< 0.01$) between environmental factors and the structure of pelagic fish communities in both seine FSCs and DFADs. This study may provide a theoretical basis for biodiversity conservation in the WCPO purse seine.

Key words: Purse seine; fish community; FSC; DFADs; Mantel test; environmental response

西北太平洋渔业物种的生活史策略研究

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摘要：生活史特征及其变化是海洋渔业和海洋生态系统研究的重要内容，对基本生活史信息的了解被认为是渔业管理和保护的基本标准。本文从已发表的文献中收集了西北太平洋海域渔业生物的生活史特征(即繁殖和生长动态)。根据生活史策略的理论分类，对一百多种生物的生活史特征进行了分类。PC1 即体型和生长因子，受最大长度、最大年龄、性成熟长度和生长系数的影响最大，得分为正的物种代表体型大、生长慢、寿命长、体型成熟大的物种。生殖因子 PC2 受繁殖力和成熟卵径的影响最大，表现为繁殖力低、卵大。研究结果提供了管理选择的概念框架，可用于对典型种群反应进行分类，为渔业的可持续发展提供科学依据。

关键词：渔业管理；生活史特征；西北太平洋

Study on life history strategies of fishery species in the northwest Pacific

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Abstract: The characteristics and changes of life history are important content in the study of marine fisheries and marine ecosystems, and the understanding of basic life history information is considered a basic standard for fisheries management and protection. A suite of life history traits (i.e. reproduction and growth vital statistics) of fishery species in the Northwest Pacific Ocean were collected from reliable published literatures. The life history traits of more than 100 species were grouped according to the theoretical classifications of life history strategies. The PC1, namely size and growth factor, was most influenced by the maximum length, maximum age, length at sexual maturity and growth coefficient, with positive scores representing species that are large, slow growing, long-lived and mature at large size. The PC2, namely reproductive factor, was most influenced by the fecundity and matured egg diameter, representing low fecundity and large eggs. The research results provide a conceptual framework of management options, they can be used to classify typical population responses and provide scientific basis for the sustainable development of fisheries.

Key words: fisheries management; life history trait; the northwest Pacific

远洋鱿鱼钓机集中控制系统研发进展

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摘要：鱿鱼钓机是远洋鱿钓渔业的核心装备之一，长期以来，该装备依赖进口，是我国远洋渔业“卡脖子”技术难题之一。在“十三五”国家重点研发与浙江省重点研发计划计划项目支持下，课题组联合装备企业逐步突破了鱿鱼钓机单机控制系统，实现了钓机单机系统及核心部件与材料的国产化，研制了鱿鱼钓机集中控制系统第一代产品。该集控系统采用模块化、层次化设计思路，基于 WINDOWS10 平台开发，采用工业总线拓扑结构，通过通信模块实现集控主机与多台鱿钓机之间的信息交换，达到准确控制钓机及反馈钓机实时运行状态的目的。该系统可靠性高，拓展性强，具有较好的人机交互。系统第一代产品的成功研制为后期产品功能完善和升级奠定了基础，对打破国外鱿钓机领域的垄断，保障我国远洋鱿钓渔业的安全和可持续发展具有重要意义。

关键词：鱿鱼钓机；集中控制系统；远洋鱿钓

Research and development progress of centralized-control system for distant-squid jigging Machin

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Abstract：Squid fishing machine is one of the core equipments of distant-squid fishery. For a long time, the equipment relies on imports, which is one of the "bottleneck" technologies of Chinese distant-squid fishery. Under the support of the "13th Five-Year" National Key Research and Development and Key Research and Development Programme of Zhejiang Province, the research group and equipment enterprise gradually broke through the single control system of the squid jigging machine, realized the localization of the single control system, core components and materials of squid jigging machine, and developed the first generation of the centralized-control system of the squid jigging machine. The centralized-control system were designed based on the modular and hierarchical idea, and the WINDOWS10 platform, which brought about the information exchange between the centralized-control host and multiple squid fishing machines through the communication module on the industrial bus topology structure, to achieve the purpose of accurately controlling and real-timely feeding back the running state of the jigging machine. The system has high reliability, strong expansion, and good human-computer interaction. The successful development of the first generation system will lay a foundation for the function improvement and promotion of the coming systems, which is of great significance for breaking the monopoly in the field of squid fishing machine and ensuring the safe and sustainable development of Chinese distant-squid fishery.

Key words: squid jigging machine; centralized-control system; distant-squid fishery

不同捕捞策略对海水青鳉不同发育阶段生长的影响

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摘要： 以海洋模式物种—海水青鳉(Oryzias melastigma)为研究对象, 设置了 90%大个体捕捞(H-B)、 90%随机捕捞 (H-R)、 75%大个体捕捞(M-B)、 75%随机捕捞(M-R)、 50%大个体捕捞(L-B)、 50%随机捕捞(L-R)、 75%小个体捕捞 (M-S) 7 种捕捞策略处理组, 用以研究海水青鳉的生长特征在不同捕捞策略、不同世代(F1、 F2 和 F3)之间的差异。结果表明, 同代际不同捕捞策略条件下, 海水青鳉卵径和仔鱼全长呈极显著性差异($P<0.01$); 不同代际间, 高强度捕捞处理组(90%捕捞策略) 卵径增大, 低强度捕捞处理组(50%捕捞策略)卵径变小, 但不同世代对下一代鱼卵的孵化率和存活率影响较小。 不同代际间, 低强度捕捞处理组在幼鱼时期增长率高于其余处理组; 同代际间仔鱼发育阶段, 高强度捕捞处理组生长迅速, 前期增长率明显高于后期, 其在仔幼鱼阶段其增长率低。随着外界捕捞压力的增加, 同代际间高强度捕捞处理组瞬时增长率最低; 低强度大个体捕捞策略组瞬时增长率在代际间较稳定。 与现阶段捕捞策略相同, 高强度大个体捕捞会导致鱼类生物学性状在 3 代中产生极大差异。因此本研究通过模拟不同捕捞策略探讨鱼类发生的生物学性状变化, 旨在为预测鱼类进化趋势的深入研究提供依据。

关键词：海水青鳉；捕捞策略；生长；肥满度

Preliminary study on the growth of Oryzias melastigma with different fishing strategies

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Abstract：Different fishing strategies have different effects on the adaptive changes of morphological characteristics of this species. In order to evaluate the impact of different fishing strategies on the growth characteristics of fishery organisms , taking the marine model species-Oryzias melastigma as the research object, set 90% large individual fishing (high-intensity large individual fishing, H-B), 90% random fishing (high-intensity random fishing, M-R), 75% large individual fishing (middle-intensity large individual fishing, H-B), 75% random fishing (middle-intensity random fishing, M-R), 50% large individual fishing (low-intensity large individual fishing, L-B), 50% random fishing (low-intensity random fishing, L-R), 75% small individual fishing (middle-intensity small individual fishing, M-S), 7 fishing strategies, studied the growth characteristics of O. melastigma in different fishing strategies, different generations (F1-F3). The results showed that the egg diameter and larval length of O.melastigma were significantly different under different fishing strategies in the same generation ($P<0.01$). Among different generations, the egg diameter increased in the high intensity fishing treatment group (90% fishing strategy condition), and decreased in the low intensity fishing treatmentgroup (50% fishing strategy condition). However, different generations had little effect on the hatchability and survival rate of the next generation eggs. The growth rate of the low-intensity fishing treatment group was higher than that of the other treatment groups in juvenile stage among different generations. During the intergenerational larval development stage, the growth rate of the high-intensity fishing treatment group increased rapidly, and the growth rate of the high-intensity fishing treatment group was significantly higher in the early stage than in the late stage, but the growth rate of the high-intensity fishing treatment group was lower in the larval and juvenile stage. With the increase of external fishing pressure, the instantaneous growth rate of high intensity fishing treatment group was the lowest among the same generation. The instantaneous growth rate of low intensity and large individual fishing strategy group was stable among generations. Similar to the current fishing strategy, high intensity and large individual fishing will lead to great differences in the biological characteristics of fish in three generations. Therefore, it is of great significance for the sustainable utilization of fishery resources to study the changes in biological traits of fish caused by fish-induced evolution under the simulation of different fishing strategies, and to predict the development trend of fish evolution.

Key words: Oryzias melastigma; fishing strategy; growth and development; fishery resources

辽东湾多锚单片张网鱼虾分离网片的选择性研究

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摘要：为掌握分离网片对多锚单片张网渔获分离效果的影响，解决鱼虾混获问题，采用主网衣网目尺寸为 18 mm 及加装 35 mm 网目尺寸的分离网片试验网，在辽东湾海域进行 4 网次有效生产试验研究。结果显示：网兜中的渔获种类以鱼类为主，约占网兜总渔获数量的 85.0 %，其中棘头梅童鱼（Collichthys lucidus）和斑尾刺虾虎鱼（Acanthogobiu sommaturus）的尾数分离率为 79.76 %、82.90 %，优势体长组主要集中在 91~110 mm 和 101~120 mm；网囊中的渔获种类以虾类为主，占网囊总渔获数量的 80.0 %以上，葛氏长臂虾（Palaemon gravieri）与中华安乐虾（Eualus sinensis）的尾数分离率为 85.92 %、85.47 %，优势体长组主要集中在 51~70 mm 和 31~50 mm。研究表明，加装分离网片后，试验网对渔获优势种分离效果明显，且能够为渔民带来较好的经济效益，本研究成果可为中国多锚单片张网的结构优化提供参考。

关键词：多锚单片张网；鱼虾分离网片；渔具选择性；海洋捕捞；辽东湾

The selectivity about separating mesh for fishes and shrimps of multi-anchored monolithic trap in Liaodong Bay

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Abstract： In order to grasp the effect of separating mesh on the catch separation effect of multi-anchor monolithic trap and to solve the problem of mixed catch of fish and shrimp, a test net with a mesh size of 18 mm for the main net jacket and a 35 mm mesh size separating mesh was used to conduct a four-network effective production test study in the sea area of Liaodong Bay. In this study, the main purpose of designing a multi-anchor monolithic trap device for separating fish and shrimp is to be used for separating different species of catches caught in the open-net operation. In this sea trial, due to the influence of various factors such as changes in offshore fishery resource stocks, operating seasons, operating locations, tides, and so on, the main dominant species caught were Collichthys lucidus , Acanthogobiu sommaturus , Palaemon gravieri and Eualus sinensis. The results showed that fish were the main species caught in the covered net, accounting for more than 85.0 % of the total number of catches, the average separation rates of Collichthys lucidus and Acanthogobiu sommaturus were 79.76 % and 82.90 %, respectively; and the dominant length groups were concentrated in the range of 91~110 mm and 101~120 mm, respectively. Shrimp were the main species caught in the codend net, accounting for more than 80.0 % of the total number of catches The average separation rates of Palaemon gravieri and Eualus sinensis were 85.92 % and 85.47 %, respectively; and the dominant length groups were mainly concentrated in 51~70 mm and 31~50 mm, respectively. The study shows that the test net has obvious effect on the separation of the dominant species after the installation of the separation net, and can bring better economic benefits to the fishermen, and the results of this study can provide a reference basis for the optimization of the structure of multi-anchor monolithic trap in China.

Key words: Multi-anchor monolithic trap; Fish and shrimp separation net; Fishing gear selectivity; Marine fishing; Liaodong Bay

在渔业中使用时空立方体模型和时空热点分析--金枪鱼围网的案例研究

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摘要：鲣是中西太平洋金枪鱼围网捕捞的重要资源，确定其资源分布的冷、热点对于有效的资源管理至关重要，但鱼类的行为特征意味着其分布的冷、热点并非恒定不变。本文利用中国大陆2010-2019年中国渔船围网渔捞日志数据构建时空立方体，采用时空热点分析工具探测鲣资源分布的冷、热点类型及其变动趋势。结果表明，鲣单位捕捞努力量冷、热点时空动态变化存在13种时空模式。热点模式集中在中部地区，主要表现为振荡热点。振荡热点东部位置的显著效应持续增强，继续影响其周边区域向东扩增。冷点模式主要表现为加强冷点。未检测到模式类型分布在冷点和热点之间。渔场存在着经度方向3°-6°、纬度方向1°-2°的振荡幅度。研究区内的冷、热点位置分布规律性极强，中西太平洋围网鲣资源的时空动态变化与ENSO现象密切相关。在2011-2016年期间，热点表现出向东扩展的趋势，受VDS体系等管理措施的影响，这一趋势在2017-2019年间继续。

关键词：鲣；中西太平洋；围网渔业；时空立方体；新兴热点分析；Mann-Kendall趋势检验

Use of Space-Time Cube Model and Spatiotemporal Hot Spot Analyses in Fisheries—A Case Study of Tuna Purse Seine

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Abstract： Katsuwonus pelamis, or skipjack, is a vital resource in purse seine fishing across the Central and Western Pacific. Identifying skipjack distribution hotspots and coldspots is crucial for effective resource management, but the dynamic nature of fish behavior means these spots are not constant. We used Chinese fishing logbook data from 2010 to 2019 to analyze skipjack resource hotspots and coldspots in a space-time cube. The study revealed 13 spatiotemporal patterns in skipjack Catch per Unit Effort (CPUE). Hotspots (36.53%) were concentrated in the central area, predominantly showing oscillating hotspots (21.25%). The significant effect of the eastern of the oscillating hotspot continues to enhanceand extends to the east. Coldspots constituted 63.47% of the distribution, mainly represented by intensifying coldspots (25.07%). The no-pattern-detected type (10.53%) are distributed between coldspots and hotspots. The fishing grounds exhibited longitudinal oscilla-tions of 3°–6° and latitudinal oscillations of 1°–2°. The spatial autocorrelation of cold and hot spot distribution was strong, and the spatiotemporal dynamic changes in skipjack resources were closely related to the El Niño-Southern Oscillation (ENSO) phenomenon. Notably, during 2011–2016, hotspots exhibited an eastward expansion trend, which continued from 2017–2019 due to the influence of fishery management measures, such as the Vessel Day Scheme (VDS) system.

Key words: Katsuwonus pelamis; central and western Pacific; purse-seine fishery; space-time cube; emerging hot spot analysis; Mann-Kendall trend test

塞内加尔近海渔业资源时空分布及其与环境因子关系研究

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摘要：为探究塞内加尔近海渔业资源的时空分布及其与环境因子的关系，本文根据 2018—2020 年我国入渔塞内加尔拖网渔船渔捞日志数据，结合海洋遥感海表温度(SST)及叶绿素(Chl-a)数据，结果表明，2018—2020 年塞内加尔近海渔业资源主要分布于 12°N~16°N、16.5°W~18°W 的海域，1—6 月渔场重心从南部渔场向北部渔场迁移，7—12 月渔场重心迁移回南部渔场；GAM 模型结果显示，年份、月份、纬度、经度、SST 和 Chl-a 对 CPUE 皆有着显著影响(P＜0.05)，其中影响最大的是经度和年份；渔场最适 SST 范围是 22~24℃，最适 Chl-a 浓度范围是 2~4mg/m3。研究结果对于了解塞内加尔近海渔业资源变动规律、指导远洋渔业捕捞生产具有重要意义。

关键词：塞内加尔；渔业资源；CPUE；GAM 模型

Spatial temporal distribution of cpue and its relation with environmental factors for offshore fishery resources from senegal

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Abstract： In order to explore the spatial and temporal distribution of offshore fishery resources in Senegal and their relationship with environmental factors, this paper based on the fishing log data of Chinese fishing trawlers in Senegal from 2018 to 2020, combined with Marine remote sensing sea surface temperature (SST) and chlorophyll (Chl-a) data, The temporal and spatial changes of fishery resources in Senegal were studied by using gravity analysis of fishery grounds and interpolation of geographical statistics. Generalized additive model (GAM) was used to investigate the relationship between spatial distribution of fishery resources and Marine environmental factors. The results show that from 2018 to 2020, the offshore fishery resources of Senegal are mainly distributed in the waters of 12°N~16°N and 16.5°W~18°W, and the center of gravity of the fishing ground shifts from the southern fishing ground to the northern fishing ground from January to June, and back to the southern fishing ground from July to December. The results of GAM model showed that year, month, latitude, longitude, SST and Chl-a all had significant effects on CPUE ($P < 0.05$), among which longitude and year had the greatest effects. The optimum range of SST is 22-24℃, and the optimum range of Chl-a concentration is 2-4mg/m3. The results of this study are of great significance for understanding the changes of offshore fishery resources in Senegal and guiding the production of pelagic fishery.

Key words: Senegal; fishery resources; CPUE; GAM model

基于简化基因组 GBS 技术的 中国海域香螺群体遗传结构及本地适应性研究

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摘要：采集了中国黄渤海沿海 6 个海域的香螺作为研究对象，采用简化基因组技术，研究了香螺群体遗传结构和遗传多样性水平，以明确香螺环境适应性的遗传变异格局。结果显示：经过质控过滤，共获得可用于群体基因组学分析的高质量离散位点 1992 个；6 个香螺群体的观测杂合度为 0.1551~0.1612、期望杂合度为 0.1064~0.1117；核苷酸多样性在 0.1120~0.1241；Fst 值为-0.04683~-0.02041；0.27%的遗传差异来源于群体间，100.80%的遗传差异来源于群体内；通过两种 Fst 值的筛选和一种与环境因子关联的方法共筛选了 331 个离散位点，表明香螺的不同群体间存在与本地适应性相关的信号。研究结果对于明确香螺遗传多样性水平和种质遗传背景，深入了解香螺环境适应的遗传学机制，以及对于香螺资源的恢复及管理具有重要的指导价值和重要的科学意义。

关键词：香螺；简化基因组；GBS 技术；SNP 位点；群体遗传结构；遗传多样性；遗传分化；本地适应性

Genetic structure and local adaptation of Neptunea cumingii crosse populations in China based on GBS technology

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Abstract： To identify the genetic characteristics and local adaptation mechanism of the snail Neptunea cumingii in different sea areas of China, specimens from six coastal areas of the Yellow Sea and Bohai Sea were collected. Simplified genome technology was used to study the population genetic structure and genetic diversity level of N. cumingii and to infer the genetic variation pattern of environmental adaptation of this species. In total, 1992 discrete loci with high quality were obtained used for population genomics analysis. The observed heterozygosity was 0.15510.1612, and the expected heterozygosity was 0.1064–0.1117. Nucleotide diversity ranged from 0.1120 to 0.1241, and fixation index values ranged from −0.04683 to −0.02041. A total of 330 discrete loci were screened based on two fixation index values and a method associated with environmental factors. Functional annotation showed that the genes of discrete loci were involved in the three major functions of cell composition, biological process, and molecular function, including growth and development and cell metabolism and catalytic activity. These results suggested that different populations of N. cumingii had loci that may be related to local adaptation. The results of this study helped to clarify the level of genetic diversity and the germplasm genetic background of N. cumingii. They also provided information about the genetic mechanism of environmental adaptation of N. cumingii that can be applied to the restoration and management of N. cumingii resources.

Key words:：Neptunea cumingii, simplified genome technology, GBS, SNPs, population genetic structure, genetic diversity, genetic differentiation, local adaptability

基于正交实验法的双翼型网板水动力性能研究

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摘要：采用正交实验法研究展弦比、前翼板弯度以及前后翼板的水平间距对双翼型网板水动力性能的影响。正交实验设计为三因素三水平，展弦比 A（1.0,1.5 和 2.0）、弯度 B（0.12,0.14 和 0.16）和间距比 C（0.25,0.30 和 0.35）通过风洞试验获取 9 块模型网板的阻力系数 Cx、升力系数 Cy、俯仰力矩系数 Cm、压力中心系数 Cp，并计算得到升阻比 Cy/Cx。选取工作冲角 30°对应的升阻比作为考察指标，采用直观分析法通过对各因素水平的均值分析和极差分析，结果表明水平组合为 A3B3C3，各因素的主次顺序为展弦比 A > 间距比 C > 弯度 B。结论表明，正交实验研究优化网板参数为展弦比（2.0）、前翼板弯度（0.16）、间距比（0.35），以展弦比对网板性能的设计影响最为显著。本实验结果可为双翼型网板的优化设计提供参考。

关键词：网板；水动力性能；风洞试验；正交实验法；拖网

Optimization of the Hydrodynamic Performance of a Double-Vane Otter Board Based on Orthogonal Experiments

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Abstract: An orthogonal experiment was conducted to study the effects of the aspect ratio, camber of the fore wing, and gap ratio of front and rear wing panels on the hydrodynamic performance of double-vane otter boards. The design of the orthogonal experiment comprised three factors (each having three levels), namely the aspect ratio (1.0, 1.5, and 2.0), camber (0.12, 0.14, and 0.16), and gap ratio (0.25, 0.30, and 0.35), the drag coefficient Cx and the lift coefficient Cy of nine otter board models obtained in a wind tunnel experiment, and the lift–drag ratio K obtained by calculation. The lift–drag ratio for a working angle of attack of 30° was selected as the inspection index, and the experimental data were analyzed in an orthogonal design-direct analysis. Analysis of each factor revealed that the optimal level combination of factors was A3B3C3 and that the decreasing order of the effects of the factors was A (aspect ratio) > B (gap ratio) > C (camber). The orthogonal experiment thus obtained an optimal otter board in terms of the aspect ratio (2.0), fore wing camber (0.16), and gap ratio (0.35), with the aspect ratio having the greatest effect on performance. The hydrodynamic performances of the otter board with the optimized structure and another otter board model were compared in numerical simulation, which verified the correctness of the analysis results. The experimental results provide a reference for the optimal de-sign of the double-vane otter board.

Key words: otter board; hydrodynamic; wind tunnel; orthogonal experiment; trawl

天然漂浮物对中西太平洋鲣适生区的指示作用

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摘要：热带金枪鱼如鲣（Katsuwonus pelamis）在洄游过程中会随附天然漂浮物形成集群，此特性常被围网渔业漂流物渔法利用。在尝试解释随附行为发生机制的诸多假说中最为可信的是“天然漂浮物指示物”假说，但针对该假说尚缺乏大洋尺度的量化研究。本研究使用来自中西太平洋渔业委员会的金枪鱼围网渔业数据，结合不同水层多种海洋环境数据，使用最大熵模型模拟鲣的栖息地适宜性时空分布，统计不同环境变量对模型的贡献率，并将栖息地适宜性指数与天然漂浮物密度进行空间相关性分析。结果表明影响鲣栖息地适宜性的环境变量前两位分别是海表面温度和 50 米水层净初级生产力，天然漂浮物往往出现在高栖息地适宜性的区域，约 55.3%的区域内天然漂浮物密度和栖息地适宜性存在明显的正相关性，高天然漂浮物密度区域会有更好的指示作用。本研究结果能为更好的理解金枪鱼随附行为发生机制以及对金枪鱼围网渔业可持续发展和养护管理等提供参考。

关键词：中西太平洋鲣；随附行为；流木指示物假说；栖息地适宜性；可持续捕捞；

The role of natural floating object as indicators of suitable distribution areas of skipjack tuna in the Central and Western Pacific Ocean

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Abstract： Tropical tuna, such as skipjack(Katsuwonus pelamis), will form attachment groups with natural floating object during migration, and this characteristic is often used in the floater fishing of Seine fishery. Among many hypotheses that try to explain the mechanism of associative behavior, the most credible one is the "log-indicator" hypothesis, but there is still a lack of quantitative research on this hypothesis at oceanic scale. The study used tuna Seine fishery catch data from the Western Central Pacific Fisheries Commission (WCPFC) as species occurrence data, combined with multiple Marine environmental data from different water layers. Maximum entropy mode (MaxEnt) was used to simulate the spatial and temporal distribution of habitat suitability of skipjack free swimming schools in the Central and Western Pacific Ocean and evaluate the accuracy. The difference in contribution rate of environmental variables in different water layers to the model was calculated, and the spatial correlation analysis was carried out between the habitat suitability index of free swimming schools and the density of natural floating object.The results showed that the top two environmental variables affecting the habitat suitability of the East and West Pacific free swimming schools of skipjack were Sea Surface Temperature (SST) and 50 m water layer Net Primary Production (NPP). About 55.3% of the area has a significant positive correlation between natural floating object density and habitat suitability index, natural floating object often appear in the area with high habitat suitability, and the area with high natural floating object density will have a better indication. The results of this study can provide a better understanding of the mechanism of tuna attachment behavior and provide a reference for the sustainable development, conservation and management of tuna Seine fisheries.

Key words: Skipjack tuna of the Central and Western Pacific; associative behavior; "log-indicator" hypothesis; Habitat suitability; sustainable fishing

基于水声学方法保护南海灯光罩网渔业中的点斑原海豚

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摘要：灯光罩网是南海外海的一种主要捕捞方式, 夜晚作业时点斑原海豚(Stenella attenuata)常常聚集在渔船周围进行捕食活动, 导致被网具兼捕死亡。本研究研发宽带声波驱豚系统（acoustic deterrent system, ADS）以驱赶点斑原海豚。研究表明，ADS 开启前的海豚单体信号数目小于开启后, 而离船平均间距大于开启后;水听器采集到的海豚声波信号表明，ADS 系统开启后,海豚 click 信号次数从每分钟 1502 次减少到 136 次，信号强度减少了 84%，即海豚远离了调查船。根据渔获数据，有效驱赶海豚的夜晚 CPUE 均值为 5.55±3.15 kg/min；驱赶无效的夜晚 CPUE 均值为 3.54±3.86 kg/min，表明海豚被有效驱赶后，渔获物重新聚集在渔船周围，产量得到提高，海豚声驱赶对于渔业没有不利影响。

关键词：灯光罩网；点斑原海豚；兼捕；声波驱赶

Protection of dolphins in the light-falling net fisheries in the South China Sea based on hydroacoustic methods

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Abstract：Light-falling net is a vital fishing method in the South China Sea; after the lights turn on at night, the dolphins often gather around and prey on net catches, which seriously affects fishing activities and makes them easy to be killed by net bycatch. We provided a self-developed acoustic deterrent system and conducted field experiments, suggesting its effectiveness as a potentially useful conservation tool to reduce bycatch. The acoustic echogram collected by the EY60 ecosounder indicates that the number of dolphin individual signals before ADS activation is smaller than after ADS activation, while the average distance from the ship is greater than after ADS activation. Additional evidence was reflected in acoustic recordings, showing the number of clicks emitted by dolphins decreased from 1,502 to 136 per minute after the ADS was activated. Meanwhile, click amplitude was reduced by 84%, indicating an increase in the distance between dolphins and the system. Based on catch data of the trial fishing vessel, The average CPUE of the effective deter nights (among the ADS used nights) is 5.55 ± 3.15 kg/min; The average CPUE of the ineffective deter nights is 3.54 ± 3.86 kg/min. Both K-S and T-tests showed significant differences under the two conditions ($P<0.05$). These combined results indicate that the system was effective in driving dolphins away from the fishing vessel to facilitate the conservation of the species by protecting them from potential bycatch, and this ADS system will not have adverse effects on fishing catch.

Key words: Light-falling net; Stenella attenuata; bycatch; ADS

福岛核泄漏对北太平洋海洋生物的影响研究进展

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摘要：2011年福岛核事故导致大量放射性物质进入太平洋，引起社会恐慌。本文总结了福岛核电站释放的人工放射性核素在北太平洋海域的运输分布情况，分析了福岛人工放射性核素对北太平洋不同营养级生物如鲯鳅(Coryphaena hippurus)、大青鲨(Prionace glauca)、柔鱼(Ommastrephes bartramii)等影响的研究进展，对比讨论了受福岛人工放射性核素影响的中高低营养级生物之间的普遍规律，梳理了福岛核电站事故在北太平洋海域影响的整体脉络，并提出人工放射性核素对生物影响研究的未来发展方向。

关键词：福岛核事故；人工放射性核素；海洋生物；北太平洋

Research Progress on Impact of Fukushima Nuclear Leakage on North Pacific Organisms

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Abstract：The Fukushima Nuclear Accident in 2011 caused a large number of radioactive substances to enter the Pacific Ocean, causing social panic. This paper summarizes the relevant research since the Fukushima Nuclear Power Plant Accident, briefly summarizes the transportation and distribution of artificial radionuclides released by Fukushima in the North Pacific, and focuses on the research progress of the effects of artificial radionuclides released by Fukushima on organisms in the North Pacific. The different trophic levels of Coryphaena hippurus, Prionace glauca and Ommastrephes bartramii in the North Pacific have been summarized and analyzed. The general law between high and low trophic organisms affected by artificial radionuclides in Fukushima was preliminarily compared and discussed. The overall context of the impact of Fukushima Nuclear Accident in the North Pacific Ocean was sorted out, and the future research on the impact of artificial radionuclides on organisms was discussed to provide effective reference.

Key words: Fukushima nuclear accident; artificial radionuclides; marine animals; North Pacific Ocean

可生物降解 PLA 刺网与传统 PA 刺网的物理性能和捕捞效率对比研究

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摘要：废弃渔具引发的幽灵捕捞和海洋塑料污染问题正受到全球的广泛关注。开发生态友好型可降解渔具是解决幽灵捕捞、保护海洋生态环境及渔业资源的有效途径之一。为探究可降解聚乳酸（PLA）材料在三重刺网渔业中的应用性，本研究通过室内试验测试比较了 PLA 刺网与传统商用尼龙（PA）刺网的物理性能，并在黄海海域进行了 PLA 刺网和 PA 刺网的捕捞性能对比试验。结果表明 PA 刺网的力学性能优于 PLA 刺网，但两种类型刺网对目标鱼种鲻鱼和梭鱼的捕捞效率并没有显著差异，这可能与三重刺网对鲻鱼和梭鱼的捕获模式有关。袋捕是两种鱼类的主要捕获模式，这种特定的捕获模式相较于其他捕获模式对网具材料的力学性能可能要求较低。初步研究结果表明 PLA 刺网可作为 PA 刺网的替代，应用于鲻鱼和梭鱼三重刺网渔业。

关键词：幽灵捕捞，海洋塑料污染，废弃渔具，可降解材料，三重刺网，捕捞效率

Comparison of physical properties and fishing efficiency between biodegradable PLA and conventional PA trammel nets

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Abstract： Marine plastic pollution and ghost fishing caused by abandoned, lost, or otherwise discarded fishing gear (ALDFG) are rising global concerns. Development and use of environmentally friendly biodegradable fishing gear has emerged as a promising strategy to limit ghost fishing and protect marine environment and fishery resources. To investigate the applicability of biodegradable resin, polylactic acid (PLA) in trammel net fishery, this study tested and compared the physical property of PLA and PA nets in the laboratory and conducted a comparative experiment on the fishing performance of PLA and PA trammel nets in the Yellow Sea. The results showed that although PA monofilament exhibited superior physical properties than PLA monofilament, no significant differences in catch efficiency were observed for target species, grey mullet (Mugil cephalus) and red-lip mullet (Liza haematocheila) between PA and PLA trammel nets. The observed similar catch efficiency may be related to the capture modes of both species by trammel nets. Fish of both species were mainly captured by pocketing. This specific capture mode may less dependent on the physical properties of netting materials compared to other capture modes. The initial results suggest a potential for applying biodegradable PLA materials in the commercial mullet trammel net fisheries for the replacement of PA materials.

Key words: Ghost fishing; Marine plastic pollution; ALDFG; Biodegradable materials; Trammel nets; Catch efficiency

基于环境 DNA 技术的

六横海域鱼类群落种类多样性研究

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摘要：鱼类组成多样性是水生生物多样性的重要组成部分，为了解六横海域主要鱼类群落种类和结构特征，本研究利用环境 DNA 技术对浙江省六横海域鱼类群落进行调查。提取环境 DNA，通过 PCR 的扩增和高通量测序分析，在 23 个环境 DNA 的样品中共检测到 37 种六横海域常见鱼类物种，隶属于辐鳍鱼纲中 8 个目的 18 个科 30 个属中 36 个种，软骨鱼纲中 1 个目的 1 个科 1 个属中 1 个种。其中，龙头鱼（Harpadon nehereus）、小黄鱼（Larimichthys polyactis）、褐菖鲉（Sebastiscus marmoratus）、海鳗（Muraenesox cinereus）、日本鳀（Engraulis japonicus）相对丰度较高。研究结果表明，环境 DNA 技术与传统调查方法的结果相似性较高，虽不能完全取代传统资源调查方法，但可以为六横海域鱼类资源多样性和种群结构多样性提供依据。

关键词：环境 DNA；六横海域；鱼类群落；物种多样性

Study on species diversity of fish community in Liuheng sea area based on environmental DNA technology

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Abstract： In order to understand the species and structural characteristics of the main fish communities in the Liuheng sea area, this study investigated the fish communities in Liuheng sea area of Zhejiang province by using environmental DNA technology. Through the collection of water samples, the extraction of eDNA, PCR amplification and high-throughput sequencing analysis, 37 common fish species of Liuheng sea area were detected in 23 eDNA samples, which belong to 36 species in 30 genera, 18 families, 8 orders of Chondrichthyes, and 1 species in 1 genus, 1 family, 1 order of Actinopterygii. Among them, Harpadon nehereus, Larimichthys polyactis, Sebastiscus marmoratus, Muraenesox cinereus and Engraulis japonicus have relatively high abundance. The research results showed that the eDNA technology can be combined with the traditional fish resource survey to assess the existing status of fish resources in the Liuheng sea area, and provided a basis for supplementing the diversity of fish resources and population structure in the Liuheng sea area.

Key words: Environmental DNA(eDNA); Liuheng sea area; Species of fish community; Resource survey

秋刀鱼资源丰度及渔场分布变动趋势的估计研究

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摘要：秋刀鱼广泛分布于西北太平洋，其在资源丰度和渔场分布上表现出很大的年际变化。本文根据中国秋刀鱼的生产调查数据，研究秋刀鱼栖息地所处海域2013-2022年平均北太秋刀鱼资源丰度、渔场重心与气候海洋条件变量的相关关系，使用线性回归、多项式回归和GAM三种模型，对秋刀鱼资源丰度、渔场重心的变化趋势进行估计。结果显示：1、GAM的拟合均较欠佳，线性拟合和多项式拟合优度较接近；2、影响CPUE年均值的海洋环境变量主要为SST、EKE、Chla；影响海区主要为WA、WOYE、EOYE；影响月份主要为春季（3—6月）及年平均值，均为负相关关系；3、影响经度重心年均值的海洋环境变量主要为SSTG；影响海区主要为WA、OY、WOYE、EOYE；影响月份主要为5、6月和年平均值，均为正相关关系。研究结果可为秋刀鱼资源与渔场变动的认知提供参考。

关键词：秋刀鱼；资源丰度；渔场重心；相关性分析；海况环境

Study on the estimation of the abundance of saury resources and the change trend of fishing ground distribution

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Abstract：Cololabis saira is widely distributed in the Northwest Pacific, and its resource abundance and fishery distribution show great interannual variation. Based on the production survey data of saury in China, this paper studies the correlation between the average abundance of saury resources in the sea area of saury habitat in the North Pacific and the center of gravity of fishing ground and the variables of climate and ocean conditions from 2013 to 2022. The linear regression, polynomial regression and GAM models are used to estimate the change trend of the abundance of saury resources and the center of gravity of fishing ground. The results show that : 1. The fitting of GAM is not good, and the goodness of linear fitting and polynomial fitting is close ; 2. The main marine environmental variables affecting the annual average value of CPUE are SST, EKE and Chla ; the main affected sea areas are WA, WOYE and EOYE. The influence months are mainly spring (March-June) and annual average, both of which are negatively correlated. The main marine environmental variables affecting the annual mean of longitude barycenter are SSTG ; the main influencing sea areas are WA, OY, WOYE and EOYE. The impact months are mainly May, June and annual averages, all of which are positively correlated. The research results can provide reference for the cognition of saury resources and fishing ground changes.

Key words: saury; fishery resource abundance; the center of gravity of fishing ground; correlation analysis; oceanographic environmental variables

大水面生态渔业活鱼起捕转运技术研究

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摘要：活鱼起捕转运是大水面生态渔业中重要环节，分析了大水面渔业特点和不同捕捞方式。基于千岛湖渔业介绍了大水面起捕机械化设施和起捕活鱼转运、计数装置工作原理和结构，分析了信息化在渔业生产中的应用，提升了渔业生产机械化水平，为大水面渔业养殖管理提供技术支撑。

关键词：大水面、生态渔业、捕捞、活鱼转运

Research on Fishing and Transportation technology for Ecological Fisheries on Large-water fisheries

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Abstract： The fishing and transportation of live fish is an important link in Large-scale fisheries. The characteristics of Large-scale fisheries and different fishing methods were analyzed. Based on the Qiandao Lake fishery, this article introduces the working principles and structures of mechanized facilities for Large-scale fishing, as well as the transportation and counting devices for catching live fish. It analyzes the application of information technology in fishery production, improves the level of mechanization in fishery production, and provides technical support for the management of open water aquaculture.

Key words: Large water; ecological fisheries; fishing; live fish transportation

秋刀鱼近成熟阶段的性腺发育特征研究

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摘要：秋刀鱼属颌针鱼亚目，竹刀鱼科，秋刀鱼属，寿命一般是 2 年，是一种重要的经济鱼类，广泛分布于北太平洋。掌握鱼类资源的生物学信息是进行资源评估的基础，因此不断增加秋刀鱼生物学的研究内容具有现实意义。秋刀鱼卵母细胞发育共分为VI个时相，其中第IV时相包含三个时相。秋刀鱼属于非同期卵发育。因此，秋刀鱼卵巢中同时存在不同发育时相的卵母细胞。本研究根据秋刀鱼这一卵巢发育特征，从秋刀鱼样本中提取卵巢组织，制备组织切片进行观察，旨在发现卵母细胞在卵巢中的发育规律，为以后的繁殖生物学研究提供参考。

关键词：秋刀鱼；繁殖生物学；性腺发育；卵母细胞

Study on gonad development characteristics in the near mature stage of saury

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Abstract： Saury belongs to the suborder of Gnathopsida, bamboo Saury family, Saury genus, life expectancy is generally 2 years, is an important economic fish, widely distributed in the North Pacific Ocean. To master the biological information of fish resources is the basis of resource assessment, so it is of practical significance to increase the research content of the biology of saury. There are six phases in oocyte development, of which the fourth phase contains three phases. The egg development of the saury is non-synchronous. Therefore, there are oocytes with different developmental phases in the ovaries of the saury. In this study, ovarian tissue was extracted from the samples of saury, and tissue slices were prepared for observation according to the developmental characteristics of ovary. The purpose of this study was to discover the development rules of oocytes in the ovary, and provide references for future reproductive biology studies.

Key words: Saury; reproductive biology; gonad development; oocyte

动力浮棒系统初步设计及水动力研究

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摘要：秋刀鱼舷提网捕捞时主要依靠风流使船体和浮棒分开，是一种被动式作业。为了提高秋刀鱼舷提网的放网速度和捕捞效率，本文设计了一种适用于浮棒的动力装置，试制了样机并安装在浮棒上（以下简称动力浮棒），开展了基于 RANS 的动力装置和动力浮棒的数值仿真和实物试验。数值仿真部分使用 solidworks 进行建模，并通过 ansys fluent 对推进器和动力浮棒的水动力特性进行仿真模拟，结果显示：（1）使用 Realizable k-E 和 SST k-ω 湍流模型可以很好地拟合推进器和动力浮棒的动力与转速之间的关系；（2）推进器仿真结果与实验数据吻合较好。这些结果为将来进一步研究奠定基础。

关键词：渔具设计；动力浮棒；推进器；计算流体力学；水动力分析

Preliminary Design and Hydrodynamic Study of Dynamic Bamboo Pole

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Abstract： The stick held net is a passive operation that mainly relies on the wind and current to separate the hull from the floating pole. To improve the release speed and fishing efficiency of stick held net, the study designs a power unit applicable to the floating pole, tries to make a prototype and installs it on the floating pole (hereinafter referred to as dynamic bamboo pole), and carries out the numerical simulation and physical test of the power unit and the dynamic bamboo pole based on RANS. The numerical simulation part uses solidworks for modeling and ansys fluent to simulate the hydrodynamic characteristics of the thruster and dynamic bamboo pole, and the results show that: （1） the relationship between the power and rotational speed of the thruster and the dynamic bamboo pole can be well fitted by using the Realizable k-E and SST k-ω turbulence models,（2）the thruster simulation results are in good agreement with the experimental data. These results provide a basis for further research in the future.

Key words: Fishing gear design; dynamic bamboo pole; thruster; computational fluid dynamics; hydrodynamic analysis

气候调控下赤道东部海域洪堡茎柔鱼栖息地变化

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摘要：本研究建立了东太平洋赤道海域茎柔鱼的综合栖息地适宜性指数模型，根据海表温度、海表盐度和叶绿素 a 浓度这三个关键环境变量，探讨气候影响下栖息地时空分布变化。结果发现，HSI 模型可以准确预测茎柔鱼的潜在栖息地。不同月份的栖息地适宜性差异明显，从 12 月到次年 2 月，栖息地适宜性逐渐提高，4 月高于 3 月和 5 月。此外，从 12 月到 5 月，渔场经度重心和 HSI 重心整体向东移动，纬度重心先北后南。与 2019 年厄尔尼诺事件相比，2018 年拉尼娜事件使 12 月至 5 月的适宜栖息地面积增加，从而 CPUE 显著增加。2018 年的潜在适宜栖息地主要分布在西部(12 月除外)，这导致 1 月至 5 月渔场经度重心的分布更加偏西。2018 年 12 月至 2 月适宜栖息地向北移动，3 月至 5 月向南移动，而 2019 年的纬度移动较小。茎柔鱼丰度和分布年间变化可能受到 SST 的调控。研究表明，茎柔鱼栖息地有明显的月间和年间变化，受到气候引起的环境变化影响。

关键词：茎柔鱼；环境因素；栖息地建模方法；时空分布；赤道海域

Climate-related habitat variaions of Humboldt squid in the eastern equatorial waters

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Abstract： An integrated habitat suitability index (HSI) model was developed in this study for Dosidicus gigas in the eastern equatorial waters of the Pacific Ocean to explore climate-related spatial and temporal variability in the habitat distribution pattern based on three crucial environmental variables: sea surface temperature (SST), sea surface salinity (SSS) and chlorophyll-a concentration (Chl-a). Results revealed that the HSI model could accurately predict potential habitats for D. gigas. The habitat suitability varied significantly by month, it progressively improved from December through February, and was higher in April than that in March and May. Besides, from December to May, the longitudinal gravity center of the fishing grounds (LONG) and the HSI overall shifted eastward and the latitudinal gravity center shifted northward then southward. In comparison to the El Niño event in 2019, the La Niña event in 2018 produced increased suitable habitat from December to May, leading to a significantly higher CPUE. Prospective high-quality habitats in 2018 primarily occurred in the western regions, with the exception of December, which resulted in a more westward distribution of LONG from January to May. High-quality habitats moved northward from December to February and southward from March to May 2018, compared to minor latitudinal movement in 2019. It was inferred that annual variations in squid abundance and distribution were largely affected by the SST-related habitat pattern of D. gigas in the eastern equatorial waters. Our findings suggested that D. gigas habitats clearly varied by month and year and were greatly influenced by climate-induced environmental changes.

Key words: Dosidicus gigas; environmental factor; habitat modeling approach; spatio-temporal distribution; the equatorial waters

中尺度涡调节全球中纬度海域人类捕捞活动

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摘要：理解捕捞活动的变动及其驱动因子对于设计和实施有效的海洋管理至关重要。据报告，公海捕捞活动在局地水域具有高度的空间变异性；然而，目前尚不清楚这种变化是随机的还是受海洋变化调节。中尺度涡旋是一种普遍存在的高能旋转流体，其如何影响捕捞活动一直不清楚。这限制了从涡旋到鱼类和人类捕捞活动的自下而上的调控来理解捕捞活动的时空变动。通过结合深度学习的全球捕捞活动和卫星监测的海洋涡旋大数据集，本研究发现在全球中纬度海洋中，捕捞活动的空间变化与中尺度涡旋密切相关，证明了主要针对金枪鱼的捕捞活动聚集在反气旋涡核心而远离气旋涡核心。这种涡旋引起的捕捞活动与卫星观测到的初级生产相反，但与海洋中层的温度和溶解氧含量很好地对应。通过整合现有证据，我们提出了一个合理的假说来解释这一现象：反气旋涡中温暖且富氧的次表层水缓解了金枪鱼潜水捕食的热和缺氧限制，而在寒冷且缺氧的气旋涡会加剧这种限制。

关键词：中尺度动力过程；渔场变动；金枪鱼；次表层水温；溶解氧；

Mesoscale eddies modulate the dynamics of human fishing activities in the global midlatitude ocean

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Abstract： Understanding the changes in fishing activities and their driving factors is crucial for designing and implementing effective ocean management. According to reports, high seas fishing activities exhibit high spatial variability in local waters; However, it is currently unclear whether this change is random or regulated by ocean changes. Mesoscale eddies are a ubiquitous high-energy rotating fluid, and it has been unclear how they affect fishing activities. This limits the bottom-up control of fishing activities from eddies to fish and humans to understand the spatiotemporal changes in fishing activities. By combining deep learning-based global fishing activities and satellite monitoring of ocean eddies, this study found that spatial changes in fishing activities are closely related to mesoscale eddies in global mid latitude oceans, proving that fishing activities mainly targeting tuna concentrate at the core of anticyclonic eddies and stay away from them. The eddy-induced fishing activity pattern is opposite to the primary production observed by satellites, but well corresponds to the temperature and dissolved oxygen content in the subsurface ocean. By integrating existing evidence, we propose a reasonable hypothesis to explain this pattern: the warm and oxygen-rich subsurface water in anticyclonic eddies alleviates the thermal and hypoxic limitations of tuna diving predation, while in cold and hypoxic cyclonic eddies, this limitation is exacerbated.

Key words: Mesoscale dynamic processes; Changes in fishing grounds; Tuna; Subsurface water temperature; Dissolved oxygen

近 40 年中国远洋渔场海表温度异常年际变化分析

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摘要：基于美国国家海洋大气管理局的最优插值月平均海表温度数据（1982~2021 年）与澳大利亚气象局发布的南方涛动指数，分别对中国 7 个主要远洋渔场 1982~2021 年的海表温度异常的时间序列进行年纪变动分析，使用傅里叶变换计算时间序列的显著变动周期，并对 SSTA 与 SOI 进行了相关性分析。结果表明，1982~2021 年中国七个远洋渔场的总体海表温度异常的波动范围在-0.39℃~0.37℃之间，波动周期为 3~4 年，与同期的 SOI 时间序列相对比，两者的波动呈现出相反的升降趋势，做显著性分析得到七个渔场的总体年平均海表温度异常值与 SOI 时间序列在 0.05 的显著水平上呈现出负相关，相关指数为 0.351；从渔场 SSTA 升降趋势来看，七个渔场均呈现出上升的趋势，但东太平洋的上升趋势平缓，且波动范围大；去趋势后与 SOI 时间序列进行相关性分析得到，东太平洋、中大西洋、西北太平洋和东印度洋均存在显著的相关性。

关键词：中国远洋渔场；海表温度异常；南方涛动指数

Analysis of the interannual variability of sea surface temperature anomalies in Chinese offshore fishing grounds over the past 40 years.

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Abstract： Based on monthly average sea surface temperature data obtained from the National Oceanic and Atmospheric Administration (NOAA) of the United States for the period 1982 to 2021, and the Southern Oscillation Index (SOI) released by the Australian Meteorological Administration, we conducted age variation analysis on the time series of sea surface temperature anomalies in seven main ocean fishing grounds in China. Fourier transform was employed to calculate significant periodic changes in the time series, and a correlation analysis was performed between sea surface temperature anomalies (SSTA) and SOI. The findings reveal that the overall fluctuation range of sea surface temperature anomalies in these seven fishing grounds ranged from -0.39 °C to 0.37 °C over the period of 1982 to 2021, with a fluctuation period of 3-4 years.Moreover, the fluctuations observed in SSTA and SOI during the same period demonstrated opposing trends of increasing and decreasing. Significance analysis indicated a negative correlation between the annual average sea surface temperature anomalies and the SOI time series in all seven fishing grounds, with a correlation coefficient of 0.351, which was statistically significant at a level of 0.05. When examining the upward and downward trends in SSTA, it was observed that all seven fishing grounds exhibited an overall upward trend, but the trend in the Eastern Pacific was more gradual and exhibited a wider fluctuation range. After detrending, the correlation analysis with the SOI time series displayed significant correlations in the East Pacific, Central Atlantic, Northwest Pacific, and East Indian Oceans.

Key words: China's pelagic fishing ground; Sea Surface Temperature Anomalies; Southern Oscillation Index

南海北部短尾大眼鲷资源评估研究

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摘要：为探明南海北部短尾大眼鲷（Priacanthus macracanthus）资源的利用状况，利用 2008—2020 年南海北部渔获产量渔港抽样调查数据，分析各作业方式分功率段单位捕捞努力量（CPUE）状况，基于 6 种剩余产量模型估算短尾大眼鲷最大可持续产量（MSY），按照决策原则和图解法估算总允许捕捞量（TAC），基于 Kobe 图判断短尾大眼鲷资源利用状态。结果表明：短尾大眼鲷拖网年捕捞量占比最高，平均为 79.36%；近十年捕捞量整体呈现波动性下降趋势；3 种剩余产量模型对短尾大眼鲷 CPUE 数据具有较好的适用性（平均绝对百分比误差 MAPE<100%），估算的 MSY 范围（2.5~3.2）×104 t，平均为 2.9×104 t；TAC 范围（2.4~3.0）×104 t，平均为 2.7×104 t；Kobe 图表明南海北部短尾大眼鲷资源状态处于安全限度内，未发生过度捕捞。

关键词：南海北部；短尾大眼鲷；剩余产量模型；渔业管理；最大可持续产量

A study on the stock assessment of Priacanthus macracanthus in the Northern South China Sea

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Abstract： To investigate the status of utilization of Priacanthus macracanthus resources in the northern South China Sea, we utilized data from a sample survey of fishing port catches in the region between 2008 and 2020. We analyzed the CPUE (Catch Per Unit Effort) status of each fishing method at different power levels and estimated the maximum sustainable yield (MSY) of P. macracanthus based on six residual production models. Subsequently, we calculated the total allowable catch (TAC) using decision-making principles and graphic methods, and assessed the utilization status of P. macracanthus resources through Kobe plots.The results showed that the annual catch of P. macracanthus by trawling was the highest, with an average of 79.36%. In the past decade, the overall catch showed a fluctuating downward trend. The Schaefer model, Fox model, and D-FOX model were found to be highly applicable to the CPUE data of P. macracanthus (MAPE＜100%). Our estimates suggest an MSY range of (2.5~3.2) × 104 t, with an average of 2.9 × 104 t, and a TAC range of (2.4~3.0) × 104 t, with an average of 2.7 × 104 t. Kobe plot analysis indicated that the resource status of P. macracanthus in the northern South China Sea was within safe limits and there was no overfishing.

Key words: Northern South China Sea; Priacanthus macracanthus; Surplus production models; Fisheries Management; Maximum Sustainable Yield

青岛近岸海域渔业资源群落结构特征的初步研究

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摘要：本研究基于青岛近岸海域 2022 年 7-8 月和 11-12 月的渔业资源底拖网调查数据，研究了该海域渔业资源密度及群落结构动态特征，并进一步构建了食物网拓扑结构。研究发现，夏季共捕获 92 种渔业生物，优势种为戴氏赤虾(Metapenaeopsis dalei)、方氏云鳚(Enedrias fangi)和大泷六线鱼(Hexagrammos otakii)，冬季捕获 86 种渔业生物，优势种为戴氏赤虾、枪乌贼(Loligo spp.)、鹰爪虾(Trachypenaeus curvirostris)、双斑蟳(Charybdis bimaculata)和尖海龙(Syngnathus acus)，总更替率为 42.48%。通过构建食物网拓扑结构发现，该海域渔业生物关键种为黄鮟鱇(Lophius litulon)和戴氏赤虾，食物网结构相对稳定。研究表明夏、冬两季青岛近岸海域渔业生物群落存在较强的抗扰动能力。

关键词：青岛近岸；群落结构；渔业生物；关键种；食物网拓扑结构

Structural insights into fishery resources communities in the coastal waters of Qingdao: A preliminary analysis

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Abstract：The warm-temperate coastal waters of Qingdao, including Aoshan Bay, Jiaozhou Bay and Lingshan Bay, serve as crucial spawning and feeding grounds for diverse fishery organisms, as well as the important fishing grounds. These vital areas have experienced significant ecological shifts due to escalated human activities, intensified marine pollution, and increased fishing pressure, leading to the evolution of fishery resources towards miniaturization and diminished value. Consequently, the present study analyzed the composition, community structure, ecosystem stability and biodiversity of fishery resources within the coastal waters of Qingdao, which was based on the data from the surveys on fishery resources conducted during the summer (July~August) and winter (November~December) of 2022. Furthermore, the keystone species were identified, which are crucial for regulatory function of marine ecosystem. A total of 92 and 86 fishery species were collected during the summer and winter, respectively, with a notable turnover rate of 42.48%. Specifically, Metapenaeopsis dalei emerged as the predominant species in both seasons. The study also highlighted the seasonal dominance of Enedrias fangi and Hexagrammos otakii in summer and Loligo spp., Trachypenaeus curvirostris, Charybdis bimaculate and Syngnathus acus in winter. Moreover, there has been a discernible shift in the structure of fishery resources, with an increasing dominance of invertebrates and a trend towards miniaturization and devaluation across fish, crustaceans and cephalopods. In terms of biodiversity indices, Shannon-Weaver (H') and Pielou evenness (J') indices were significant higher in summer, while the Margalef richness index (D) was higher in winter. In comparison with coastal waters of other areas in China, the coastal waters of Qingdao exhibited normal ecosystem diversity, demonstrating stable seasonal horizontal structures and consistent community compositions. There has been notable ecological improvement over the past decade, with measures to restore fishery resources yielding positive outcomes. The constructed food web topology for the ecosystem of the coastal waters of Qingdao, developed based on the feeding relationships of local feeding relationships, incorporated

26~29 major species (S) and 116~165 feeding relationships. The topology exhibited substantial variations between summer and winter. The node density (Dd) in summer was superior (0.22>0.18), while other indices, including average path length (1.17<1.27), interspecific connectance (C) (0.17<0.20), and clustering coefficient (Cl) (0.18<0.25), were lower than in winter. According to the comprehensive topological index ranking (D, Dout, Din, BC, CC, IC, TI1, TI3, TI5, K, Kb, Kt, F, and DF), Lophius litulon and Metapenaeopsis dalei were identified as key species, with the former being a primary predator and the latter a principal bait species. Overall, the food web of coastal waters of Qingdao exhibited high connectivity and complexity, presenting strong stability and resilience against disturbances, thereby ensuring the provision of vital ecosystem services. The findings furnished by this study offer indispensable data and a robust scientific foundation for understanding the structure of the marine food web and biodiversity conservation in the coastal waters of Qingdao. Furthermore, the observed seasonal changes in fishery resource communities provide a scientific basis for the prudent conservation and management of fishery resources in this pivotal region.

Key words:：Coastal waters of Qingdao; Community structure; Fishery organisms; Keystone species; Food-web topological structure

舟山市灯光带鱼钓渔具渔法调查分析

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摘要：为了应对海洋渔业捕捞以及现代渔业技术的发展，改进和创新传统有效的带鱼钓捕方式，对舟山市灯光带鱼钓渔具结构、装配方法、操作技术、渔期渔场、主要捕捞对象、经济效益与存在问题等进行调研分析。结果表明，灯光带鱼钓受伤事故较低，是省能耗、产值大、效益高的一种新型作业方式；不会破坏海底的生态系统，对渔获物有较强选择性，是一种生态、绿色、环保的环境友好型渔具。灯光带鱼钓作业存在明显的淡、旺季，产值在 7、8 月的集中度高，最高月产值达到 70 多万，年平均产值 250 万左右，总体经济效益良好。基于研究结果，建议渔民要着力提高钓捕技术，提高捕捞作业的经济效益；政府要加大政策扶持力度，提高燃油补贴，调动渔民积极性，促进渔业资源的可持续利用。

关键词：灯光带鱼钓；渔具渔法；环境友好型；调查；舟山市

Investigation and analysis of fishing gear and fishing method of light belt fishing in Zhoushan City

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Abstract： In order to cope with the development of Marine fishery and modern fishery technology, improve and innovate the traditional and effective belt fishing methods, the structure, assembly method, operation technology, fishing grounds, main fishing objects, economic benefits and existing problems of light belt fishing gear in Zhoushan City were investigated and analyzed. The results show that the light strip fishing is a new type of operation with low injury accident, saving energy, large output value and high benefit. It will not destroy the ecosystem of the seabed, and has strong selectivity for the catch, which is an ecological, green and environmentally friendly fishing gear. The light fishing operation has obvious light and peak season, the output value is high in July and August, the highest monthly output value reaches more than 700,000, the average annual output value is about 2.5 million, and the overall economic benefits are good. Based on the research results, it is suggested that fishermen should focus on improving fishing techniques to improve the economic benefits of fishing operations. The government should increase policy support, increase fuel subsidies, mobilize the enthusiasm of fishermen, and promote the sustainable use of fishery resources.

Key words: Light with fish fishing; Fishing gear fishing method; Environmentally friendly; Investigate; Zhoushan City

刚性分隔栅对宽口涡螺（Cymbium pepo）分隔性能的水槽试验研究

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摘要：宽口涡螺（Cymbium pepo）是毛塔底拖网渔业中常见兼捕种类，网具中加装刚性分隔栅可分离宽口涡螺，提高渔获物品质、提升捕捞效率。为探究不同栅型（横栅、竖栅、圆栅）和布设角度（30°、45°、60°）对宽口涡螺的分隔性能的差异，利用 3D 打印技术制作了宽口涡螺模型，在水槽中进行了捕捞模拟试验，利用分隔效率模型对数据进行拟合，结果表明：（1）圆栅具有最大的个数分隔率，分隔效果最好，其次为竖栅、横栅；（2）随着角度增大，选择率 SR 增大，L50 减小；接触概率减小，增大；（3）分隔效率受选择率与接触概率共同影响，角度越大，分隔效率越高。本研究可为分隔栅的设计优化提供理论依据。

关键词：宽口涡螺；刚性分隔栅；分隔性能

Flume Experiment on Separating Performance for Cymbium pepo of Sorting Grid

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Abstract: Cymbium pepo is a by-catch species in bottom trawl fishery in Mauritania. The sorting grid rigged in beam trawls can effectively separate snails, improving the quality of catches and enhancing the fishing efficiency. In order to analyze the separation performance of different grid types (transverse grid, vertical grid, circular grid) and layout angles (30°,45°, 60°). Snails' model was made using 3D printing technology, The fishing simulation test was conducted in the flume, The separation efficiency model was used to fit the data, The main results are as follows: (1)The circular grid has the largest number separation rate, and the separation effect is the best, followed by vertical grid and horizontal grid; (2)As the angle increases, the selectivity parameters SR increases and L50 decreases. The change trend of contact probability parameters is opposite to the selectivity parameters. This study can provide a theoretical basis for the design and optimization of sorting grid.

Key words: Cymbium pepo; sorting grid; Separation performance

基于体长世代分析法估算秋刀鱼生物量和捕捞死亡系数的初步研究

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摘要：秋刀鱼（Cololabis saira）是我国远洋渔业主要的捕捞目标鱼种之一。为了对其资源状态进行科学评估，本文利用 2014~2018 年太平洋秋刀鱼的渔获体长组成（CAS）样本数据，结合秋刀鱼生活史参数，检验了 LCA 模型和 B-LCA 模型的拟合能力，并进行敏感性分析；使用蒙特卡罗模拟方法估算模型参数均值及其 95%的置信区间，基于 LCA 模型和 B-LCA 模型估算秋刀鱼年度生物量和每个体长组的捕捞死亡系数。结果表明在 LCA 模型和 B-LCA 模型中，体长间隔越小，模型性能越好；基于数量的渔获体长组成数据适用于传统的 LCA 模型，基于重量的渔获体长组成数据更适用于 B-LCA 模型；种群生物量估算值对生长参数 b 和 L_\infty 的改变最为敏感；2014~2018 年秋刀鱼种群总年均生物量的波动范围为 0.527-1.635\times{10}^6 吨，捕捞死亡系数的波动范围为 0-2.86。

关键词：太平洋秋刀鱼，渔获体长组成，LCA 模型，B-LCA 模型

Preliminary Study on Estimating Biomass and Fishing Mortality Coefficient of Pacific Saury Using Length based Cohort Analysis

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Abstract： Cololabis saira is one of the main fishing target species in China's offshore fisheries. This study utilizes Catch-at-size (CAS) sample data of Pacific saury from 2014 to 2018 to scientifically assess the resource status of Cololabis saira. By integrating the life history parameters of Pacific saury, the fitting abilities of the LCA model and B-LCA model were tested, alongside sensitivity analysis. The Monte Carlo simulation method was employed to estimate the mean values and 95% confidence intervals of model parameters. Based on the LCA model and B-LCA model, the annual biomass of Pacific saury and the fishing mortality coefficient of each length class were estimated. The results indicated that both the LCA model and B-LCA model performed better with smaller size intervals. The LCA model was suitable for numbers-based data, while the B-LCA model was more suitable for biomass-based data. The estimated population biomass was most sensitive to changes in the growth parameters b and L_\infty. The fluctuation range of the total annual average biomass of Pacific saury from 2014 to 2018 was 0.527 to 1.635 million tons, and the fluctuation range of the fishing mortality coefficient was 0 to 2.86.

Key words: Pacific saury; Catch-at-size; LCA model; B-LCA model

渔用平面网片水动力学特性研究

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摘要：网渔具是经济性水生生物的渔业生产装备，是我国建设“蓝色粮仓”，践行“大食物观”的承接载体。开展渔用网片水动力载荷及其流场分布研究是探究柔性透空网衣水动力形成机制，研发高品质智能捕捞装备，发展绿色生态渔业的基础性研究，具有重要的学术和应用价值。本研究团队通过三种不同网片水动力测量装置，测量冲角 0-90°和流速范围 0.4-1.1 m/s 工况下网目系数 0.075-0.75 的渔用平面网片水动力系数，提出了适用范围更广泛、预估更准确的平面网片水动力系数经验公式。结合多孔介质模型与流体力学数值模拟方法，完成平面网片水动力与流场精度验证后，计算得到了网目系数 0.1-0.72 范围内平面网片多孔介质模型参数的拟合关系式与不同平面网片流场云图。流场结果显示大网目系数平面网片的流速衰减率随距网片中心距离的增大而减小，随网目系数和冲角的增大而增大，但小冲角时流速衰减率增大趋势并不显著。

关键词：平面网片；水动力特性；流速衰减；网目系数；冲角

Study on hydrodynamic characteristics of net panel for fishing gears

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Abstract： Fishing nets that provide economic aquatic organisms stably play an essential role in the implementation of the Blue Granary Plan and the Great Food Strategy in China. The hydrodynamics and the relative flow characteristics of the fishing nets are necessary to be investigated to explore the nature of the hydrodynamic mechanisms, contributing to developing intelligent fishing equipment and promoting ecological fisheries. Three hydrodynamic measurement devices were employed to measure the hydrodynamic forces of fishing net panels with the solidity ratios of 0.075-0.75, in the angles of attack of 0-90°, and current velocities of 0.4-1.1 m/s. Newly empirical formulas of hydrodynamic coefficients of the fishing nets were proposed with the enhancement of applicability and predictive accuracy. Subsequently, the porous model of the net panel integrated with the porous coefficient matrix at the range of solidity ratio of 0.1-0.72 was successfully established, when the validation of the computational fluid dynamics simulation test was confirmed. The flow counters around the fishing net panel indicated that the ratio of velocity reduction Ur [= (setting velocity-local velocity)/setting velocity] decreased with an increasing distance from the center of the net panel with solidity ratio. Ur increased with solidity ratio and attack of angle, but that trend of Ur was less significant for small angles of attack.

Key words: Net panel; Hydrodynamic characteristic; The ratio of velocity reduction; Solidity ratio; Angle of attack

柔性风筝形装置对拖网网囊网目扩张的影响研究

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摘要：拖网是一种主动型的过滤渔具，具有作业灵活、捕捞效率高等特点，但传统拖网网囊网目在拖曳张力作用下，网目常趋于闭合，具有较差的选择性，不利于幼体逃逸。帆布是一种柔性材料，在水流作用下能够提供扩张力。为了避免网目闭合，改善拖网渔获性能，提高拖网对幼鱼的释放能力，本研究拟在传统拖网网囊上安装柔性扩张装置（风筝形装置）使网囊网目扩张，提高拖网渔具的选择性，以达到更好的释放幼鱼和保护渔业资源的目的。

关键词：柔性风筝形装置；水槽实验；单船底拖网；网囊扩张性能；渔具选择性

Effect of flexible kite-shaped device on mesh expansion and codend selectivity of a trawl net

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Abstract： The trawl is an active filter fishing equipment with dexterity and great fishing efficiency. However, the meshes of traditional trawls frequently shut under drag tension, resulting in poor selectivity, which prevents juvenile fish from escaping. Canvas is a flexible material that provides expansion force under the influence of water. To prevent mesh closure, improve trawl catch performance, and enhance the trawl's ability to release juvenile fish. This study suggests installing a flexible expansion device (a kite-shaped device made of canvas) on the codend to expand the meshes and improve the codend selectivity of trawl gear, to achieve better release of juvenile fish to protect fishery resources.

Key words: flexible kite-shaped device; flume tank experiment; single bottom trawl; mesh expansion performance; codend selectivity

基于树莓派嵌入式开发的 CTD 数据快速处理和查询软件

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摘要：本文介绍了一款基于树莓派开发的快速处理和查询 CTD（Conductivity, Temperature, Depth）数据的软件。该软件旨在为海洋学和环境科学领域的研究人员以及从事渔业捕捞人员提供一个方便且高效的工具，以处理和分析复杂的海洋观测数据。

软件基于树莓派的开发旨在充分利用硬件性能，以实现数据的快速处理和查询，以便用户能够迅速获得有关水体的温度和深度相关信息。树莓派的底成本和便携性使得此方案适用于远海研究和实时的数据搜据。目前软件提供直观的用户界面，使用户可以直接接入 CTD 获取数据，并对数据进行操作，例如数据的清洗，校准和格式转换。软件还具备快速查询功能，以及展示温度与深度的曲线，许用户以多种方式筛选和分析数据。并且基于此信息软件通过算法实现温跃层的判定，满足用户特定的研究需求。

关键词：树莓派，CTD，温跃层

Software for Rapid Processing and Querying of CTD Data based on Raspberry Pi Embedded Development

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Abstract: This article introduces a software developed based on Raspberry Pi for rapid processing and querying of CTD (Conductivity, Temperature, Depth) data. The software aims to provide a convenient and efficient tool for researchers in the fields of oceanography and environmental science, as well as professionals in the fishing industry, to handle and analyze complex oceanographic data.

The development of the software on Raspberry Pi is aimed at fully utilizing the hardware performance to achieve fast data processing and querying, allowing users to quickly obtain temperature and depth-related information about the water. The low cost and portability of Raspberry Pi make this solution suitable for offshore research and real-time data retrieval.

Currently, the software provides an intuitive user interface, allowing users to directly connect to the CTD device to retrieve data and perform various operations such as data cleaning, calibration, and format conversion. The software also features fast querying capabilities and provides visualization of temperature-depth profiles, enabling users to filter and analyze data in multiple ways. Additionally, the software utilizes algorithms to determine thermoclines based on this information, fulfilling the specific research requirements of users.

Key words: Raspberry Pi; CTD; thermocline

粤西海域毛虾渔业生物学特征

及其与环境因子的关系

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摘要：为掌握粤西海域毛虾渔业生物学特征，于 2022 年 2 月-4 月在阳江东平海域随机采集毛虾样品，对毛虾种类进行鉴定，并测定其全长、体质量，鉴定了毛虾性别，根据阳江东平海域实时监测获取的海洋环境信息，分析毛虾捕捞量与环境因子的的关系。结果显示，本次监测共采集日本毛虾(Acetes japonicus)3500 尾、中国毛虾(Acetes chinensis)849 尾，同期采集的中国毛虾普遍大于日本毛虾，中国毛虾平均全长为 31.8±2.9mm，日本毛虾为 26.8±3.2mm；监测期间毛虾全长总体呈增长趋势。同时，两种毛虾的雌性个体均多于雄性个体，其中日本毛虾雌雄性比平均为 1.6:1，中国毛虾性比平均为 1.4:1。根据 GAM 拟合采样海域环境因子对毛虾捕捞量影响发现，毛虾捕捞量与海表温度、海表盐度、浊度和潮位差均有季节性的显著相关（p＜0.05）。相关研究结果为粤西海域毛虾资源可持续利用及海洋生态灾害防控提

关键词：中国毛虾；日本毛虾；渔业生物学特征；环境因子；广义线性可加模型

The relationship between biological characteristics and environmental factors of Acetes in western Guangdong Sea Area

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Abstract：In order to understand the biological characteristics of the Acetes fishery in the waters of western Guangdong, we randomly collected Acetes samples from February to April 2022 in the Dongping Sea of Yangjiang, identified the species of Acetes, measured their full length and body weight, and identified the Acetes. Gender, based on the marine environment information obtained through real-time monitoring in the Dongping Sea Area of Yangjiang, the relationship between Acetes population dynamics and environmental factors was analyzed. The results showed that a total of 3,500 Acetes japonicus and 849 Acetes chinensis were collected during this monitoring period. The Acetes chinensis collected during the same period were generally larger than the Acetes japonicus. The average total length of the Acetes chinensis was 31.8±2.9 mm, the Acetes japonicus is 26.8±3.2mm; during the monitoring period, the overall length of the Acetes showed an increasing trend. At the same time, there are more females than males in both species. The average male-to-female ratio of Acetes japonicus is 1.6:1, and the average sex ratio of Acetes chinensis is 1.4:1. According to the influence of GAM fitting sampling sea area environmental factors on the amount of Acetes resources, it was found that the amount of Acetes resources has a seasonal significant positive correlation with sea surface temperature, sea surface salinity, turbidity and tidal range difference ($p<0.05$) . Relevant research results provide basic data for the sustainable utilization of Acetes resources in western Guangdong waters and the prevention and control of marine ecological disasters.

Key words: Acetes chinensis; Acetes japonicus; fishery biology characteristics; Environmental factors; generalized additive model

舟山市六横沿岸延绳钓产业

可持续发展策略探究

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摘要：近海延绳钓是浙江海洋渔业中较为传统的捕捞方式，由于相对拖网、围网等渔业方式缺乏竞争力等原因，很长一段时间都未得到较好发展。近年来，受到禁渔区、禁渔期措施的进一步影响，延绳钓渔业越来越受到关注，其原因在于延绳钓属于钓渔具，具有较好的保护渔业资源并和极强的选择性等诸多优点，被允许常年进行作业，不受禁渔期限制。本文结合舟山市六横岛沿岸渔业资源的特点和当前主要延绳钓作业方式，围绕该渔业发展中的一些问题，从政府部门的产业介入、延绳钓渔具性能改进、开发配套新渔船、促进产业链延伸等方面，提出推动六横沿岸延绳钓可持续发展的建议和对策。

关键词：延绳钓；绿色渔具；可持续发展策略；六横；沿岸

Inquiry strategy of sustainable development strategies of the six -horizontal coast of Zhoushan City

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Abstract：The offshore long -seeds fishing is a more traditional fishing method in Zhejiang marine fisheries. Due to the lack of competitiveness such as the relative fishery methods such as dragging nets and fences, it has not been able to develop well for a long time. In recent years, it has been further affected by the measures of the ban on fishing areas and the ban on fishing. Waiting for many advantages, it is allowed to perform operations all year round without restrictions on the fisheries period. This article combines the characteristics of fishery resources along the Liheng Island along Zhoushan City and the current main long -term fishing operation method, focusing on some problems in the development of the fishery, from the industrial intervention of government departments, the improvement of the performance of the long rope fishing fishing gear, the development of supporting new fishing vessels, promoting the promotion In terms of industrial chain extension, suggestions and countermeasures for promoting the sustainable development of the six -horizontal coast are the sustainable development.

Key words: Landic fishing; green fishing gear; sustainable development strategies; six horizontal; coastal

材料与结构类型对金枪鱼围网人工集鱼装置漂流速度影响

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摘要：人工集鱼装置（FAD）的漂流速度和漂流轨迹影响着其下方金枪鱼的随附行为。渔民基于海上的生产经验对 FAD 的结构进行优化以期降低 FAD 的漂流速度，从而提高下方随附鱼群的集群稳定性。然而，目前有关量化 FAD 制作材料与结构类型对漂流速度影响的试验研究相对较少。为此，本研究基于动水槽模型试验在 5 种流速条件下测试了 10 中不同类型的 FAD，并采用威尔科克森检验两两比较模型的漂流时间。结果表明：10 种模型中 FAD-F2-Cc 的漂移速度最快，FAD-Br-C1 和 FAD-Br-Nb 的漂移速度最慢；在浮体结构相同的情况下，采用单根棉绳和网束作为水下结构的 FAD 模型的漂流速度最慢，且漂移速度几乎相同；当水下结构相同时，采用竹筏作为浮体结构可以减缓 FAD 的漂流速度。综合来看，我们建议制作低漂流速度的 FAD 时采用相同直径的棉绳代替网束制作 FAD 的水下结构，并采用竹筏制作浮体结构，从而降低合成材料在 FAD 中的比例。

关键词：人工集鱼装置；模型试验；漂流速度；威尔科克森检验；金枪鱼渔业

Effects of material and structure types on drifting speed of fish aggregation devices (FAD) in tuna purse seine fishery

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Abstract： The associative behavior of tunas around fish aggregation devices (FAD) in influenced by the drifting speed and trajectory. Based on expertise, fishermen modify the structural specifications to slow down drifting speed of FADs, which enhances the aggregation stability of tuna aggregation around FADs. However, few trials and experiments have been developed to quantify the effects of material and structure types on drifting speed. To address this gap, 10 different types of FAD models were tested under 5 different current velocities in a flume tank and compared drifting times using pairwise Wilcoxon tests. Results showed that FAD-F2-Cc exhibited the fastest drifting speed, while FAD-Br-C1 and FAD-Br-Nb had the slowest drifting speed. When floating structures are the same, FAD models with Cotton rope (1) and Netting bundle submerged structure had the slowest and almost the same drifting speeds. When submerged structures are the same, using Bamboo raft as the floating structure can slow down the drifting speed. Results suggested that it is feasible to replace the netting bundle with the cotton rope of the same diameter for constructing submerged structure and use bamboo to construct floating structure to slow down drifting speed, thus reducing the proportion of synthetic materials in FAD construction.

Key words: Fish aggregation devices; FAD; Model test; Drifting speed; Wilcoxon test; Tuna purse seine fishery

热带中西太平洋延绳钓黄鳍金枪鱼 CPUE 分布及其与主要环境因子的关系

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摘要：研究更为先进的方法以尽量减少寻找渔场的时间，对提高公海渔业的捕捞效率和捕捞成功至关重要，它可以尽量减少操作成本和捕鱼时间。了解黄鳍金枪鱼对时空因子和环境因子的喜好是解决捕捞不确定性的重要方面，从而确保在短时间内获得预期的渔获量。本文利用热带中西太平洋金枪鱼漂流延绳钓 2016-2018 年的实际生产数据和美国国家海洋和大气管理局提供的环境数据，研究各种因素对黄鳍金枪鱼 CPUE 分布的影响。，通过广义相加模型构建 CPUE 与各环境因子关系，研究各因子对黄鳍金枪鱼分布的影响。结果表明，时空因子和环境因子与黄鳍金枪鱼渔获率之间存在非线性关系，主要在海面温度（SST）29.5-30℃之间的区域发现较高的 CPUE，相应的海表面高度距平（SSHA）在-0.05~0.2m 之间，叶绿素 a 浓度（Chl-a）在 0.03~0.20mg/m3 之间。从广义相加模型（GAM）得到的结果表明，时空因素的影响远高于海洋环境因素。

关键词：黄鳍金枪鱼；中西太平洋；延绳钓；CPUE；环境因子

Distribution of CPUE in tropical western and central Pacific longline yellowfin tuna and its relationship with major environmental factors

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Abstract：Research into more advanced methods to minimize the time spent searching for fishing grounds is essential to improve fishing efficiency and fishing success in high seas fisheries by minimizing operational costs and fishing time and ensuring fish quality. Understanding the preferences of yellowfin tuna for spatial and temporal factors and environmental factors is an important aspect of resolving fishing uncertainty, thus ensuring the desired catch in a short time. This paper examines the effects of various factors on the CPUE distribution of yellowfin tuna using actual production data from 2016-2018 from the tropical Central and Western Pacific tuna drift longline and environmental data provided by the National Oceanic and Atmospheric Administration. , the relationship between CPUE and each environmental factor was constructed by GAM (generalized summation model) to study the effects of each factor on the distribution of yellowfin tuna. The results showed that there was a non-linear relationship between spatial and temporal factors and environmental factors and yellowfin tuna catch rate, and higher CPUE was mainly found in the area between 29.5-30℃ of sea surface temperature (SST), with corresponding sea surface height anomaly (SSHA) between -0.05 and 0.2m and chlorophyll a concentration (Chl-a) between 0.03 and 0.20mg/m3. The results obtained from the generalized summation model (GAM) indicate that the influence of spatial and temporal factors is much higher than that of marine environmental factors.

Key words: Yellowfin tuna; Central and Western Pacific Ocean; Longline; CPUE; Environmental factors

第六专题：水生生物资源养护与水域生态修复

海水养殖池塘 CO2 和 CH4 通量：底质改良剂对碳排放的潜在影响

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摘要：本研究测定了养殖期间使用和未使用底质改良剂的蟹-虾养殖池塘（分别表示为 SAPs 和 NSPs）水-气界面 CO2 和 CH4 通量。结果显示，养殖期间 SAPs 和 NSPs 均表现为 CO2 的汇和 CH4 的源。CO2 通量与净初级生产力和水体 pH 值显著相关，而 CH4 通量主要受水温的调控。氧化型底质改良剂的应用能显著减少养殖池塘水-气界面 CH4 排放，但对 CO2 通量无显著影响。底质改良剂的应用降低了底泥有机质含量，提高了底泥 pH 值和氧化还原电位，这可能间接减少了底泥中 CH4 的产生。氧化型底质改良剂能促进底泥有机物的氧化，产生的 CO2 可能通过较强的光合作用被吸收，这导致 SAPs 和 NSPs 之间 CO2 通量差异不显著。结果表明，养殖期间底质改良剂的应用可减少海水养殖池塘水-气界面碳排放，特别是 CH4。基于持续变化全球增温潜势(SGWP)和冷却潜势(SGCP)计算模型，以 20 年尺度计，底质改良剂的应用有助于缓解全球变暖。

关键词：海水养殖池塘；二氧化碳通量；甲烷通量；底质改良剂；氧化作用

Carbon dioxide and methane fluxes from mariculture ponds: The potential of sediment improvers to reduce carbon emissions

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Abstract： The CO2 and CH4 fluxes across the water-air interface were determined in two groups of swimming crab-ridgetail white prawn polyculture ponds with and without oxidation-based sediment improver application (referred to as SAPs and NSPs, respectively). During the farming season, both the SAPs and NSPs acted as CO2 sinks and CH4 sources. CO2 fluxes were significantly related to net primary production and water pH. CH4 fluxes were mainly regulated by water temperature. The application of sediment improver had a positive effect on reducing the CH4 emissions but had no effect on CO2 fluxes. The sediment improver reduced the organic matter contents and improved the sediment pH and redox potential, which may have facilitated a decrease in CH4 production in the sediment. The CO2 produced by the oxidation of organic matter in the sediment may have been absorbed by strong photosynthesis, resulting in a nonsignificant difference in CO2 fluxes between the two groups. The results indicated that the application of sediment improvers in polyculture ponds can reduce carbon emissions, especially CH4 emissions, during the farming period and could help mitigate global warming with regard to the sustained-flux global warming potential and global cooling potential models over a 20-year time horizon.

Key words: Mariculture ponds; CO2 flux; CH4 flux; Sediment improver; Oxidation

南海典型岛礁渔业资源群落结构、食物网和系统承载力

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摘要：报告介绍了南海典型珊瑚礁鱼类的群落结构和种群生物学的长期变化及礁栖鱼类的利用状况。当前，南海珊瑚礁鱼类正遭受过度捕捞。西沙群岛七连屿珊瑚礁生态系统 Ecopath 模型分析表明当前七连屿生态系统的成熟度和稳定性偏低，系统对于外界的干扰抵抗能力较弱，各功能组中珊瑚、双壳类和植食性鱼类的生态承载力仍具有较大的增殖空间。南海珊瑚礁是多种经济鱼类的产卵场，并且可能是黄鳍金枪鱼在南海的产卵场之一。最后针对南海珊瑚礁鱼类衰退问题，提出了资源养护建议。

关键词：珊瑚礁鱼类；多样性；种群生物学；食物网；生态承载力

Community structure, food web dynamics, and ecosystem capacity of fishery resources in representative coral reefs in the South China Sea

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Abstract： This report presents a comprehensive analysis of the long-term changes in community structure and population biology of reef fishes, as well as the current status of their utilization. It is evident that overfishing has become a pressing issue for coral reef fish populations in this region. By employing an Ecopath model to assess the coral reef ecosystem of Qilianyu Island in Xisha Islands, it was found that the ecosystem's maturity and stability are currently low, rendering it vulnerable to external disturbances. Furthermore, there exists significant untapped potential for breeding among corals, bivalves, and phytophagous fish within each functional group. The ecological carrying capacity of corals, bivalves, and herbivorous fishes across all functional reproductive expansion. The coral reefs in the South China Sea are vital spawning grounds for numerous economically significant fish species, potentially including yellowfin tuna in the region. Lastly, considering the declining population of coral reef fish in this area, recommendations for resource conservation are proposed.

Key words: Coral reef fish; Diversity; Population biology; Food web; Ecological carrying capacity

三疣梭子蟹早期生活史关键阶段的海水温度对后期产量的影响

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摘要：早期生活史对三疣梭子蟹的群落资源起着至关重要的作用，为了分析三疣梭子蟹不同幼虫期海面温度（SST）与相应产量之间的相关性，我们利用环流模型和拉格朗日粒子追踪实验模拟了 2014 年至 2022 年幼虫的迁移和分布。在五年（2014、2015、2016、2019 和 2020 年）中，粒子向西北方向迁移，并向低海温方向移动。在 大眼幼体阶段（M 阶段），粒子分布在温度较低的区域。2017 年、2018 年和 2021 年，粒子向东北方向迁移，但这几年粒子没有随低 SST 梯度移动，最后 M 阶段的粒子位于此时段 SST 处于峰值的区域。2022 年，大部分粒子分布在浙江西南沿海，小部分粒子向西北方向迁移，少量粒子分布在浙江北部沿海区域。各幼虫阶段的 SST 与相应年份产量的相关性表明，三疣梭子蟹产量随 M 阶段 SST 的增加而显著下降（R=-0.772，p =0.015）

关键词：东海；三疣梭子蟹；早期生活史；大眼幼体阶段；拉格朗日质量跟踪；时空分布；海面温度

Effect of sea surfer temperature during the critical stage in the early life history of Portunus trituberculatus on later yield

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Abstract： Early life history plays a critical role in the community resources of marine organisms. Portunus trituberculatus, an important crustacean species in China, holds significant importance in fishery resources and is therefore of great economic value. However, few studies have considered the response of the early larval stages of P. trituberculatus to later yield. To analyse the correlation between sea surface temperature (SST) during different larval stages and the corresponding yield of P. trituberculatus, we simulated the transport and distribution of larvae from 2014 to 2022 by employing circulation models and Lagrangian particle tracking experiments (LPTE). In five years (2014, 2015, 2016, 2019 and 2020), particles were transported in a northwestern direction and moved in the direction of low SST. The distribution of particles in the Magalopa stage (M stage) were located in the region of the lower temperature. In 2017, 2018 and 2021, the particles were transported in a northeastern direction but they did not move with the gradient of low SST in these years, and the particles in the last M stage were located in the region where the SST was at the peak of the time period at this moment. In 2022, the distribution was observed for most of the particles in southwestern of Zhejiang coast, a small part of them were transported in the northwestern direction and a small amount of particles was distributed offshore along the northern area of the Zhejiang coast. The correlations between the SST at each stage of larvae with the corresponding year's yield showed that the yield of P. trituberculatus decreased significantly (R=-0.772, p =0.015) with increasing SST at the M stage. This study preliminarily explains the correlation between SST at the larval stage and the yield of P. trituberculatus and provides essential information for scientific stock enhancement in the future.

Key words: East China Sea; Portunus trituberculatus; Early life history; Magalopa stage; Lagrangian mass tracking; Spatial and temporal distribution; Sea surface temperature

江苏省七个湖泊翘嘴鲌群体的

遗传多样性和遗传结构分析

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摘要：为了解江苏省主要湖泊的翘嘴鲌遗传资源状况，采用线粒体 D-loop 基因分析 7 个湖泊的翘嘴鲌群体遗传多样性和遗传结构。结果显示：D-loop 序列长度为 934-936bp，碱基 A+T 含量(66.0%)明显高于 G+C 含量(34.0%)。300 尾翘嘴鲌共检出 42 个单倍型，平均单倍型多样性和核苷酸多样性分别为 0.885± 0.010 和 0.00348± 0.00012。42 个单倍型在各群体中随机分布，没有形成特定的地理谱系结构。分子方差分析(AMOVA)显示，群体内遗传变异(84.15%)远大于群体间遗传变异(15.85%)。群体间 Fst 显示同水系群体间遗传分化较弱(P>0.05)，而不同水系群体间有中度到高度的遗传分化(P<0.01)。中性检验显示，整个翘嘴鲌群体的 Tajima’s D 和 Fu’s Fs 值均为显著性负值(P<0.05)，且核苷酸歧点分布曲线呈明显的单峰型，表明翘嘴鲌历史上发生过显著的种群

关键词：翘嘴鲌；线粒体控制区；遗传多样性；遗传结构

Genetic diversity and genetic structure of Culter alburnus populations from seven freshwater lakes in Jiangsu province

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Abstract：In this study, the genetic diversity and genetic structure of C. alburnus populations from seven freshwater lakes (Tai Lake, Ge Lake, Changdang Lake, Gaoyou Lake, Baima Lake, Hongze Lake and Luoma Lake) in Jiangsu province were analyzed based on mitochondrial D-loop gene. The results showed that the full length of D-loop gene was 934-936bp, and the content of A+T was higher than that of G+C. 42 distinct haplotypes were defined in 300 individulas of C. alburnus, and the average haplotype diversity (Hd) and nucleotide diversity (π) were 0.885± 0.010 and 0.00348± 0.00012, respectively; The genetic diversity of Gaoyou Lake population was the highest (Hd: 0.901±0.023, π: 0.00341± 0.00030), and that of Luoma Lake population was lowest(Hd: 0.470±0.089, π: 0.00178± 0.00053) among seven populations. The Neighbor- Joining phylogenetic tree and haplotypes network both revealed that haplotypes were randomly distributed in seven populations and there was no geographic genetic structure. Analysis of molecular variance (AMOVA) suggested that most of thegenetic variation occurred within the populations (84.15%), and only the 19.55% of genetic variation occurred among the populations groups; Pairwise Fst showed that genetic differentiation among populations in the same river system was weak (P>0.05), while moderate to high genetic differentiation occurred among populations in different river systems (P<0.01). The neutral tests showed that the Tajima’s D and Fu’s Fs values of C. alburnus were significant negative (P<0.05), and mismatch ditribution curve showed obvious single peak, which both indicated that C.alburnus had experienced population expansion in history.

The research results showed that the genetic structure of seven lake populations was consistent with the distribution pattern of river system. The genetic diversity of C.alburnus from freshwater lake was low, and it was urgent to take measures to restore the natrual resources and genetic diversity of C. alburnus in Jiangsu province.

Key words: Freshwater Fisheries Research Institute of Jiangsu Province; Nanjing Normal University, Nanjing

Cyt b 和 12S rRNA 基因条形码在灯笼鱼科鱼类物种鉴定中的应用

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摘要：灯笼鱼科鱼类种类繁多，且同属鱼类形态学相近，因此利用分子标记对灯笼鱼进行准确的物种鉴定具有重要价值。为探讨线粒体细胞色素 b 基因（Cyt b）和 12S rRNA 基因在灯笼鱼科物种鉴定中的适用性，对西北太平洋采集的 56 尾灯笼鱼进行扩增，并进行序列对比与系统发育分析。研究表明，采集的样本包括 6 种灯笼鱼，分别为瓦氏角灯鱼（Ceratoscopelus warmingii）、长体标灯鱼（Symbolophorus californiensis）、粗鳞灯笼鱼（Myctophum asperum）、细泰勒灯鱼（Tarletonbeania crenularis）、日本背灯鱼（Notoscopelus japonicus）以及某背灯鱼属鱼类。核苷酸多态性分析显示，Cyt b 基因的种内与种间核苷酸多态性差距比 12S rRNA 基因更明显。比较灯笼鱼科 2 种基因序列的结构特征，发现 Cyt b 基因的种间平均遗传距离

关键词：灯笼鱼科；Cyt b 基因；12S rRNA 基因；物种鉴定；系统进化分析

Identification analysis of DNA barcoding based on mitochondrial Cyt b and 12S rRNA genes in Myctophidae fishes

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Abstract： The Myctophidae with a huge amount of resources are widely distributed in the mesopelagic oceans of the world, and play a significant role in the pelagic food chain due to its vertically migrating behavior. Myctophidae have wide varieties and the morphological differences between genus are not obvious. Therefore, the ability to identify Myctophidae using molecular markers would be very useful. In this study, 56 Myctophidae samples collected from the Pacific Northwest were amplified based on Cyt b and 12S rRNA genes. The sequences obtained from the amplification were used for phylogenetic analyses with sequences of 29 other Myctophidae species in 18 generas from the Genbank database. And we also explored the applicability of Cyt b and 12S rRNA genes in identification of Myctophidae species. Results indicate that the 56 samples belonged to 6 species,i.e. Ceratoscopelus warmingii, Symbolophorus californiensis, Myctophum asperum, Tarletonbeania crenularis, Notoscopelus japonicus, and Notoscopelus sp. The difference of nucleotide polymorphism between individuals within a species and between different species in Cyt b gene was revealed to be more obvious than those in 12S rRNA gene. The genetic difference between the average interspecific and intraspecific genetic distances of Cyt b and 12S rRNA gene were 25 and 26 times, respectively. These results indicated that both genes meet the basic requirements for using as DNA barcodes. Phylogenetic analysis showed that the six Myctophidae species respectively form an independent clade based on Cyt b and 12S rRNA gene sequences; however, in the evolutionary tree based on Cyt b gene, each fish was better clustered with sequences in the Genbank database. In summary, Cyt b and 12S rRNA genes could be used as DNA barcodes for Myctophidae species identification , and Cyt b genes was particularly suitable for phylogenetic relationships analysis.

Key words: Myctophidae; Cyt b gene; 12S rRNA gene; Species identification; Phylogenetic analysis

中华鲟的灭绝旋涡和逃出旋涡的可能性

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摘要：中华鲟是长江水生生物旗舰种之一，1981 年葛洲坝截流截断了中华鲟传统的洄游繁殖路径至今，中华鲟野外种群持续萎缩，并出现自然繁殖中断，岌岌可危。针对其自然种群演替，本研究提出中华鲟在葛洲坝截流之后就已陷入了灭绝旋涡的假设，并用基于中华鲟生活史的自然种群演替建模检验了该假设，计算了中华鲟逃出灭绝旋涡的可能性。模型计算显示，葛洲坝截流后导致的中华鲟对环境改变的不适应（受精率、怀卵量降低，性腺发育节律失配）已使得中华鲟陷入了灭绝漩涡，三峡蓄水导致的滞温效应、坝下涉水工程导致的产卵场退化对中华鲟自然繁殖中断、自然种群萎缩有一定影响，但不是决定性影响。中华鲟种群恢复（形成可持续种群）的关键是其能够适应葛洲坝截流导致的环境条件改变（受精率、怀卵量、性成熟状况能够恢复），同时要完成水温调控（基本消除滞温）、产卵场修复（容量≥♀14），然后进行短期的年 30 万放流。

关键词：中华鲟；自然繁殖；野外种群；灭绝漩涡；增殖放流；产卵场修复；水温调控

The chance of escaping from the extinction vortex for Chinese sturgeon, Acipenser sinensis

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Abstract：Chinese Sturgeon (Acipenser sinensis) is one of the flagship species of the Yangtze River aquatic ecosystem and has been an indicator species of the degradation of the Yangtze River aquatic ecosystem in recent decades. The Gezhou Dam, constructed in 1981, blocked the traditional spawning migration route of Chinese Sturgeon, and the spawning section located about 600 kilometers upstream in the upper reaches of the Yangtze River and downstream of the Jinsha River was reduced to a section of about 3.5 kilometers under the Gezhou Dam, which greatly affected the entire spawning migration process of Chinese Sturgeon. Subsequently, a number of river engineering projects also had further impacts on the natural spawning activities of Chinese Sturgeon. Although national and local governments took a series of protective measures, the wild population of Chinese Sturgeon continued to decline. Natural spawning activity of Chinese Sturgeon in the wild has been interrupted in 2013, and there has been no natural spawning detected for 6 consecutive years from 2017 to 2022, making the wild population extremely endangered. Why does Chinese Sturgeon fall in such a situation, and what are the key influencing factors? There has been much debate about this in the academic community. In the current study, we propose that Chinese Sturgeon may have fallen into an extinction vortex after the Gezhou Dam was closed, and subsequent human activities further pushed it towards extinction. Based on the life cycle of Chinese Sturgeon, we constructed a simple modeling to estimate the dynamic of the natural population of Chinese Sturgeon and to test this hypothesis and explore the possibility of Chinese Sturgeon escaping from the extinction vortex. The results showed that: 1) river engineering projects in the spawning ground under the Gezhou Dam had a small contribution to the natural spawning failure (one year earlier). 2) The temperature hysteresis effect caused by water storage at the Three Gorges Dam brought about a 15-year earlier natural spawning failure. 3) Artificial propagation and release implemented over the past 40 years had little effect on natural spawning (one year later), but had some contributions on the spawning migration population (postponing extinction time by 31 years). 4) Assuming that water temperature regulation and spawning ground restoration can be completed in 2025 and one million Chinese Sturgeon juveniles are released each year, natural spawning may be reappeared in 2025, but may once again failures in both 2029 and 2030, and then natural spawning would be restored once again. However, natural spawning and spawning migration populations will still heavily rely on artificial propagation and release. If artificial propagation and release was stopped, natural spawning will fail again in approximately 38 years later, with a complete loss of spawning migration population after 46 years. 5) Assuming that water temperature regulation and spawning ground restoration can be completed in 2025, Chinese Sturgeon can adapt to the environmental changes caused by Gezhou Dam, with fertilization rate, egg production rate, and gonadal development rhythm recovered, then 300,000 Chinese Sturgeon juveniles only need to be released until 2027, and Chinese Sturgeon can form a small-scale sustainable population. However, the size of the spawning migration population is positively correlated with the duration of artificial propagation and release, but there is an inherent ceiling (♀217 & ♂197), mainly limited by the capacity of spawning ground (♀90). Moreover, there is a minimum value (♀14) for the capacity of spawning ground. If the capacity of spawning ground is lower than the minimum value, the sustainable wild population of Chinese Sturgeon would not appear. It is recommended to carry out the water temperature regulation and spawning ground restoration under Gezhou Dam as soon as possible, and continue to release 300,000 Chinese Sturgeons juveniles per year.

Key words: Chinese sturgeon; natural spawning; wild population; extinction vortex; artificial propagation and release; spawning ground restoration; water temperature regulation

我国淡水增养殖系统温室气体排放的时空特征研究进展

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摘要：【目的】综述我国稻渔综合种养、粗放、半集约化和集约化 4 种主要淡水增养殖系统温室气体（N2O、CO2 和 CH4）排放的特征及其时空差异性原因，结合现有研究数据，估算 4 种典型增养殖系统单位面积和单位产量温室气体排放系数和增温潜势，最后根据各增养殖系统温室气体排放特征及生产特征，提出了相应减排措施。【方法】从 4 种养殖模式的温室气体时空排放特征、温室气体区域排放量、淡水养殖系统低碳发展措施及建议【结果】稻渔综合种养、粗放、半集约化养殖温室气体排放均存在明显的时空变化特征：不同模式温室气体排放存在南北差异，各养殖水域内部存在空间变异性；时间排放特征主要受温度影响，在夏秋高温季节排放强度更大，同时存在明显的昼夜变化。【结论】大水面增殖系统可通过增加放流滤食性鱼类的比例摄食藻类，降低水中氮磷；稻渔综合种养可通过恰当的田间水管理达到温室气体减排目的；曝气、换水能减少养殖过程沉积物的矿化，达到养殖过程中减排。

关键词：淡水增养殖；温室气体；增温潜势；时空特征；排放通量

Spatial and temporal characteristics of greenhouse gas emissions from freshwater aquaculture systems in China

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Abstract：【Objective】This article reviewed the main research results of the greenhouse gas (N2O, CO2 and CH4) emission characteristics and causes of differences in four major freshwater aquaculture systems, including rice-fish system, extensive, semi-intensive and intensive system in China, and estimate the greenhouse gas emission factors and warming potential per unit area and per unit yield of these typical aquaculture systems. Finally, according to the emission situation and production characteristics of each aquaculture system, the corresponding emission reduction measures are proposed to help the agricultural field to achieve "carbon peak and carbon neutrality" as soon as possible.【Methods】A series of research results were introduced from four aspects: spatial and temporal greenhouse gas emission characteristics of four systems, regional emission of greenhouse gas, low-carbon development measures and suggestions of freshwater aquaculture system, and future prospects.【Results】In addition to intensive system, therice-fish system, extensive and semi-intensive system all had obvious spatio-temporal emission characteristics. Taking Qinling Mountains and Huaihe River as the boundary, there were north-south differences in greenhouse gas emissions in each systems, and there were also high-resolution spatial emission characteristics in each water area.

The temporal emission characteristics are mainly affected by temperature, and the emission flux of CH4, CO2 and N2O is greater in the summer and autumn high temperature seasons, and there are obvious diurnal variations. 【Conclusion】 freshwater aquaculture system in our country requires certain measures to reduce greenhouse gas emissions emissions. The extensive system can reduce nitrogen and phosphorus in the water by increasing the proportion of released filter-feeding fish by eating algae. During the breeding process, The suitable feed for fish can increase feed utilization. In addition, rice-fish farming system can reduce greenhouse gas emissions by avoiding sewage irrigation and proper field water management; By using an oxygen pump and water exchange, the mineralization of sediments during the breeding process can be reduced, thereby, reducing greenhouse gas emissions from semi-intensive and intensive farming systems, intensive farming can also achieve low-carbon development by regulating water temperature.

Key words: Freshwater aquaculture; Greenhouse gases; Warming potential; Spatio-temporal characteristics; Emission flux

湛江港皮氏叫姑鱼种群生物学特征和资源开发状态研究

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摘要：为探究湛江港皮氏叫姑鱼（Johnius belangerii）生物学特征和资源开发状态。本研究根据2016-2021年湛江港海域底拖网调查数据，使用ELEFAN I、pauly经验公式、长度转换捕获曲线法等方法，研究了该海域皮氏叫姑鱼体长体重分布状况、生长死亡参数、开发率以及种群资源开发状态等内容。结果显示，湛江港海域皮氏叫姑鱼群体体长分布范围为27.03-182.00mm，体重分布范围为0.19-137.34g。体长与体重的关系式为W=2.52×10-5L3.04（R2=0.96），生长方程为Lt=185.85[1-e-0.61(t+0.27)]，自然死亡率（M）为0.75，总死亡系数（Z）为2.40，捕捞死亡系数（F）为1.65，开发率（E）为0.69，体重生长拐点年龄（ttp）为1.55龄。湛江港海域皮氏叫姑鱼存在小型化、低龄化趋势，面临的捕捞压力较大，开发程度高，种群处于过度捕捞状

关键词：皮氏叫姑鱼；生物学特征；资源开发状态研究；湛江港

Study on population biological characteristics and resource exploitation status of Johnius belangerii in Zhanjiang Bay

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Abstract：To explore the biological characteristics and status of Johnius belangerii in Zhanjiang Bay, length and weight distribution, growth and death parameters, exploitation rate, and exploitation status of Johnius belangerii in Zhanjiang Bay were studied using ELEFAN I, Pauly empirical formula and length conversion capture curve methods, based on the bottom trawl survey data in Zhanjiang Bay waters from 2016 to 2021. The results showed that the distribution of length and weight ranged from 27.03-182.00mm and 0.19-137.34g. The relationship between length and weight was W=2.52×10-5L3.0398 (R2=0.9588) and the growth equation was Lt=185.85[1-e-0.61(t+0.27)]. The estimated natural mortality (M), total mortality (Z) and fishing mortality (F) was 0.75,2.40,1.65 respectively. The exploitation rate (E) was 0.69, and the body mass growth turning point age (ttp) was 1.55. The study showed that there is a tendency of miniaturization and younger age of Johnius belangerii in the waters of Zhanjiang Bay, and the population subjected to relatively high fishing pressure and are highly exploited. This study will help to reveal the life history characteristics of Johnius belangerii and provide a reference for the sustainable utilization and scientific management of the resources.

Key words: Johnius belangerii; biological characteristics; exploitation status; Zhanjiang Bay

聚苯乙烯纳米塑料对淡水螯虾肠道微生物和氧化应激防御的影响

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摘要：塑料垃圾的广泛产生和积累已成为全球公认的问题。然而，关于纳米材料对淡水甲壳动物不利影响的报道有限。本研究检测了 75 nm 聚苯乙烯纳米塑料暴露 48 h 后，不同浓度(0、5、10、20 mg / L)对淡水小龙虾肠道微生物和氧化应激参数的急性影响。高通量测序分析揭示了聚苯乙烯纳米塑料暴露克氏原螯虾肠道微生物的丰富度、多样性和组成。在属水平上，Lactobacillus、Faecalibaculum、Niveibacterium 和病原菌 Bacilloplasma 的丰度差异显著。乳酸杆菌丰度的降低可能通过数量劣势影响肠道微生物的平衡，进而导致克氏原螯虾免疫力降低。

关键词：乳杆菌；益生菌；病原菌；16S rRNA；淡水螯虾；抗氧化反应

The effect of a polystyrene nanoplastic on the intestinal microbes and oxidative stress defense of the freshwater crayfish, Procambarus clarkii

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Abstract： The widespread generation and accumulation of plastic waste has become a globally recognized problem. However, there are limited reports on the adverse effects of nanomaterials on freshwater crustaceans. This study tested the acute effects of different concentrations (0, 5, 10, and 20 mg/L) after 48 h exposure of 75 nm polystyrene nanoplastic on intestinal microbes, and oxidative stress parameters of freshwater crayfish, Procambarus clarkii. High-throughput sequencing analysis revealed the richness, diversity, and composition of intestinal microbiota in P. clarkii exposed to polystyrene nanoplastic. At the genus level, abundances of Lactobacillus, Faecalibaculum, Niveibacterium, and Candidatus Bacilloplasma were significantly different. The reduced abundance of Lactobacillus could affect the balance of intestinal microbes through quantitative disadvantage, which may lead to reduced immunity of P. clarkii. Streptococcus salivarius, Clostridium butyricum and Lachnospiraceae bacterium10–1 in intestinal tract reached maximum abundance at a polystyrene concentration of 20 mg/L. The increase in the number of some pathogenic bacteria may upset the balance of intestinal microorganisms through the number of dominance, and the decrease in the relative abundance of lactic acid bacteria. Probiotics, such as Lactobacillus salivarius, Lactobacillus murinus, Lactobacillus gasseri, Lactobacillus reuteri, Lactobacillus iners AB-1,and Lactobacillus crispatus in the intestinal tract reached the lowest value at a concentration of 10 mg/L. The reduced abundance of Lactobacillus can affect the balance of intestinal microbes through quantitative disadvantage, which may lead to reduced immunity in P. clarkii. At nanoplastic 10 mg/L, the relative abundance of intestinal pathogens increased, while the relative abundance of lactic acid bacteria and other probiotics decreased. With increases in nanoplastic concentrations, the values of glutathione (GSH), superoxide dismutase (SOD), acid phosphatase (ACP), lysozyme (LZM), alkaline phosphatase (AKP), peroxidase (POD), glutathione peroxidase (GPX), and protein carbonylation were significantly changed. Our data suggested that Lactobacillus may play an adjunctive role in the treatment of oxidative stress in P. clarkii exposed to 75 nm polystyrene. This study represents an important step towards a better understanding of the toxic effects of nanoplastics on aquatic crustaceans.

Key words: Lactobacillus; Probiotics; Pathogenic bacteria; 16S rRNA; P. clarkii; Antioxidant response

黄海南部海域鱼类组成及
生物量粒径谱特征

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摘要：为了解黄海南部海域鱼类组成及生物量粒径谱特征，根据 2017—2018 年底拖网调查资料，分析了黄海南部海域 4 个季节鱼类组成、优势种、资源密度，构建了鱼类生物量粒径谱。结果显示, 全年共采集鱼类 133 种，隶属于 20 目 64 科，全年优势种为小黄鱼、银鲳、日本鳀、带鱼，不同季节优势鱼种存在一定差异；全年鱼类平均资源密度为(1258.85±796.92) kg/km2，资源密度分布呈现季节差异；ABC 曲线显示春、秋季鱼类群落处于严重干扰状态，夏、冬季处于中等干扰状态；鱼类 Sheldon 型粒径谱存在明显的季节差异，波峰对应的粒径级为高丰度粒径级小的鱼种；鱼类生物量标准化粒径谱拟合曲线呈抛物线型，曲率均高于稳定理论值−1，曲线偏陡，说明鱼类群落以小型个体为主，群落中的营养循环效率低。总体上，黄海南部海域鱼类群落处于不稳定状态，这可能与环境因素、鱼类生理习性以及人类捕捞影响有关。

关键词：黄海南部；鱼类组成；ABC 曲线；资源密度；粒径谱特征

Fish composition and biomass particle size spectrum in the southern Yellow Sea

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Abstract: Fish is the main object of study in fishery resources and one of the important sources of human food. In the fishery ecosystem, the fish community can reflect the energy conversion of the fishery ecosystem. The southern Yellow Sea is influenced by the interaction of the Yellow Sea warm current, coastal current and the Yellow Sea cold water mass, and has a complex ecological environment and rich fish resources. In order to comprehend the fish community composition and characteristics of fish biomass particle size spectrum in the southern Yellow Sea, an analysis was conducted based on trawl survey data from 2017 to 2018. The study examined the fish community composition, dominant species, resource density in four seasons, and constructed a fish biomass particle size spectrum. The findings revealed that annually, a total of 133 fish species were collected belonging to 64 families and 20 orders. and the dominant species were Larimichthys polyactis, Pampus argenteus, Engraulis japonius and Trichiurus lepturus, with some differences in the dominant species in different seasons. The annual average resource density of fish was recorded as (1258.85±796.92) kg/km2 with seasonal variations observed throughout summer, spring, autumn, and winter. ABC curve indicated that fish communities experienced significant disturbance during spring and autumn while moderate disturbance occurred during summer and winter. Notably, there were distinct seasonal differences in the Sheldon type particle size spectrum of fish with high abundance observed among small-sized individuals at specific particle size levels corresponding to peaks. Furthermore, the fitting curve for standardized fish biomass particle size spectrum exhibited a parabolic shape with curvatures higher than the stable theoretical value -1, indicating dominance by small individuals within the fish community along with low nutrient cycling efficiency. Overall, it can be concluded that the unstable state of the fish community in the southern Yellow Sea may be attributed to environmental factors, physiological habits of fishes as well as human fishing.

Key words: The southern Yellow Sea; fish species; ABC curve; resource density; particle size spectrum

贝藻养殖系统沉积有机碳来源、再矿化和埋藏过程的研究

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摘要：以近海贝藻养殖为代表的养殖活动对近海生态系统的碳循环结构、功能和演化产生了重要影响，而目前该系统的碳循环工作多关注可移出碳汇功能，有关其生物地化过程的研究相对不足。本研究以典型贝藻养殖系统——皱纹盘鲍-海带综合养殖系统为研究对象，对沉积有机碳来源、再矿化和埋藏影响研究开展了系统研究。

研究表明：1. 在研究区域内，细颗粒物（粉砂和黏土）占主导地位；粒径从养殖区到对照区出现升高的分布趋势，养殖活动可以降低沉积颗粒物的粒径；2. TOC、TN 和 13C 由养殖区向对照区逐渐降低，而 C/N 逐渐增加，表明养殖活动增强了有机质的积累并改变了其来源；3. 在厌氧培养过程中，养殖区沉积物孔隙水中溶解无机碳的垂直剖面浓度和生产率均高于对照区，表明养殖活动增加了有机碳再矿化的速率; 4. 放射性同位素研究表明养殖区沉积物的沉积速率为 0.95 cm·a-1 约是对照区域的 3-4 倍,显著加强了有机质的沉积和埋藏。

关键词：贝藻养殖；沉积有机碳；源解析；再矿化；埋藏

Study on the source, remineralization and burial of sedimentary organic carbon in shellfish and seaweed polyculture systems

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Abstract： Aquaculture activities represented by coastal shellfish and seaweed farming have had an important impact on the carbon cycle structure, function and evolution of coastal ecosystems. However, the current carbon cycle work in this system focuses more on the function of removable carbon sinks, while research on its biogeochemical processes is relatively insufficient. This study took a typical shellfish farming system - the Abalone chinensis-kelp integrated farming system as the research object, and conducted a systematic study on the sources, remineralization and burial effects of sedimentary organic carbon.

Research shows that: 1. In the study area, fine particulate matter (silt sand and clay) dominates; the distribution trend of particle size increases from the breeding area to the control area, and breeding activities can reduce the particle size of sedimentary particles; 2. TOC , TN and δ13C gradually decreased from the breeding area to the control area, while C/N gradually increased, indicating that breeding activities enhanced the accumulation of organic matter and changed its source; 3. During the anaerobic culture process, the pore water of the sediment in the breeding area The vertical profile concentration and productivity of dissolved inorganic carbon are higher than those in the control area, indicating that farming activities increase the rate of organic carbon remineralization; 4. Radioisotope studies show that the sediment deposition rate in the farming area is 0.95 cm·a-1, which is approximately 3-4 times that of the control area, significantly enhancing the deposition and burial of organic matter.

Key words: Shellfish and seaweed polyculture systems; sedimentary organic carbon; source apportionment; remineralization; burial

江苏近海鮸胃含物初步分析

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摘要：根据 2018 年 11 月（秋季）与 2019 年 4 月（春季），在江苏近海中南部采集到的鮸胃含物样品进行其摄食习性的研究分析。结果表明，从鮸胃含物中共鉴定出 4 大类 19 种生物饵料。并且生物饵料的秋季多样性指数 H’值为 2.31，均匀度 J’值 0.76，优势度指数 D 值为 4.34；春季的多样性指数 H’值为 1.23，均匀度 J’值为 0.42，优势度指数 D 值为 4.12。采取百分比相对重要性指数（IRI%）和综合指标优势度指数（Ip）分析结果较一致，鱼类和虾类是江苏中南部近海鮸秋季和春季主要的生物饵料，其相对重要性指数百分比和综合指标优势度分别为 35.79% 和 59.15、16.73%和 11.17。优势饵料生物为矛尾虾虎鱼（IRI%=6.65%，Ip=13.83）和凤鲚（IRI%=9.37%,Ip=12.46）。经过相似性分析，秋季和春季鮸食性组成相似性显著，说明两个季节上鮸胃含物组成基本一致。

关键词：鮸；食性分析；胃含物；江苏近海

Feeding Habits of Miichthys miiuy in Jiangsu Costal Waters

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Abstract： Miichthys miiuy is one of the important economic fishes in the Jiangsu offshore. According to the study of feeding habits in November 2018 (autumn) and April 2019 (spring), samples of gastric contents collected in the central and southern areas of Jiangsu offshore. The results showed that 19 species of bait organisms were identified from the stomach contents of Miichthys miiuy. The autumn diversity index H' value was 2.31, the evenness J' value was 0.76, and the dominance D value was 4.34; otherwise the spring diversity index H' value was 1.23, the evenness J' value was 0.42, and the dominance D value was 4.12.The analysis results using the percentage relative importance index (IRI%) and the index of preponderance (Ip) are more consistent. Fishes and shrimp are the main biological food in the spring and autumn of the central and southern Jiangsu province. The percentage relative importance index and The index of preponderance are 35.79% and 59.15%,16.73% and11.17%, respectively.The dominant diets species were Chaemrichthys stigmatias (IRI%= 6.65, Ip =13.83) and Coilia mystus (IRI%= 9.37, Ip= 12.46). According to similarity analysis, there was ignificant similarity in diet composition between spring and autumn.

Key words: Miichthys miiuy；food analysis；gastric contents；Jiangsu Costal Waters

鱼类 eDNA metabarcoding PCGs 标记的筛选

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摘要：本研究对 2 纲、56 目、260 科、656 属、951 种鱼类线粒体基因组全序列进行了比对，从 2×250 bp 测序读长范围内筛选出 8 个 PCGs 相对保守区块，以此为基础设计了 71 条简并引物；基于 2 纲、19 目、82 科、139 属、144 种鱼类对上述 71 条简并引物进行了 PCR 验证；使用 160 个水环境样品对 PCR 成功率=100%的引物组合进行了高通量测序比较；使用 2 纲、20 目、52 科、106 属、935 种鱼类线粒体序列分析了本研究筛选的 PCGs 标记与 MiFish-U 等标记的属内近缘物种识别率。本研究将充实鱼类多样性研究内容，为推进 eDNA metabarcoding PCGs 标记开发提供参考。

关键词：鱼类，eDNA metabarcoding，PCGs 标记，物种识别率，通用引物

Screening of PCGs markers for fish eDNA metabarcoding

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Abstract：In this study, the complete mitochondrial genome sequences of 951 fish species belonging to 2 classes, 56 orders, 260 families, 656 genera were compared; Eight relatively conservative PCGs blocks were selected from the reading length range of 2×250 bp, and 71 degenerate primers were designed; PCR validation was conducted on the 71 degenerate primers based on 144 fish species belonging to 2 classes, 19 orders, 82 families, 139 genera; A high-throughput sequencing comparison was then conducted using 160 water samples for the primer pairs with a PCR success rate of 100%; Mitochondrial sequences of 935 fish species belonging to 2 classes, 20 orders, 52 families, 106 genera were used to analyze the identification rates of PCGs markers screened in this study and MiFish-U markers. This study will enrich the research content on fish diversity and provide reference for the development of eDNA metabarcoding PCGs markers.

Key words: fish; eDNA metabarcoding; PCGs markers; species recognition rate; universal primers

崖州湾海洋牧场渔业资源调查

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摘要：崖州湾海洋牧场是海南热带海洋学院集科研与教学为一体的热带海域海洋牧场，为了解海洋牧场建设前渔业资源状况，本研究开展了游泳动物生物多样性内容调查。结果显示崖州湾海洋牧场共采集到获游泳动物 100 种，隶属于 13 目 55 科，其中鱼类为 8 目 42 科 75 种，头足类为 3 目 4 科 4 种，甲壳类 2 目 9 科 21 种。游泳动物的平均渔获率为 4.861 kg/h 和 372ind/h。根据扫海面积法估算，评价区及附近海域目前游泳动物的资源密度约为 2665.975kg/km2 和 209602ind/km2，其中鱼类约为 2416.031kg/km2 和 188901ind/km2，头足类 47.550kg/km2 和 1490ind/km2，甲壳类约为 202.394kg/km2 和 18209ind/km2。调查的优势渔获种类共有 16 种。通过本次对崖州湾海洋牧场的游泳动物调查，了解其建设前的生物资源量，为后期的海洋牧场效果评估提供参考数据。

关键词：崖州湾，渔获率，资源密度，优势种类

Investigation of fishery resources of Marine ranch in Yazhou Bay

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Abstract： Yazhou Bay Marine Ranch is a integrates scientific research and teaching of tropical marine ranch at Hainan Tropical Oceanography University. In order to assess fishery resources before establishment marine ranch, this study conducted a survey on the biodiversity of swimming animals. The results revealed that a total of 100 species of swimming animals, 13 orders and 55 families, were collected in Yazhou Bay Marine Ranch. This included 75 species of fish from 8 orders and 42 families, 4 species of cephalopods from 3 orders and 4 families, and 21 species of crustaceans from 2 orders and 9 families. The average catch rate for swimming animals was recorded as being approximately 4.861 kg/hour and 372 individuals/hour. According to estimates using the swept area method, the current resource density for swimming animals in both the evaluation area and nearby waters is approximately 2665.975 kg/km2 and 209602 ind/km2 respectively; with fish accounting for about 2416.031 kg/km2 and 188901 ind/km2; Cephalopods accounting for 47.550 kg/km2 and 1490 ind/km2; while crustaceans account for 202.394 kg/km2 and 18209 ind/km2. A total of 16 dominant fish species were identified through this investigation. In conclusion, the survey on swimming animals in Yazhou Bay Marine Ranch provided an understandingof the biological resources before its construction, and also served as reference data for future evaluations regarding the impact of the marine ranch.

Key words: Yazhou Bay; Fishing rate; Resource density; Dominant species

基于 eDNA metabarcoding 技术的海南岛淡水鱼类多样性调查

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摘要：本研究使用 5 种 eDNA metabarcoding 标记对海南岛淡水鱼类多样性进行调查，共获得 1593 个鱼类 OTUs；结合 Genbank、Mitofish 数据库及历史分布纪录，共注释出 69 种土著淡水鱼类及 25 种外来入侵鱼类。eDNA metabarcoding 结果还暗示虾虎鱼科等类群存在未定种或遗传分化种。本研究将有助于了解海南岛淡水鱼类多样性及时空分布格局。

关键词：海南岛鱼类，eDNA metabarcoding，土著鱼类，入侵鱼类，未定种

Investigation of freshwater fish diversity in Hainan Island based on eDNA metabarcoding

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Abstract： In this study, five eDNA metabarcoding markers were used to investigate the diversity of freshwater fish in Hainan Island. A total of 1593 OTUs were obtained. Combined with Genbank and Mitofish databases and historical distribution records, a total of 69 indigenous freshwater fish species and 25 invasive alien fish species were annotated. eDNA metabarcoding results also suggest the existence of undetermined or genetically differentiated species in Gobiidae and other groups. This study will help to understand the diversity and spatial and temporal distribution pattern of freshwater fishes in Hainan Island.

Key words: Hainan fish; eDNA metabarcoding; indigenous fish; invasive fish; undetermined species

基于环境 DNA 宏条形码的南极宇航员海表层鱼类多样性首次评估

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摘要：在中国第 38 次南极科学考察航次（CHINARE-38）期间，我们采集了南极宇航员海 38 个站位的海水和表层沉积物样本，并首次同时基于 12S rRNA 和 16S rRNA 分子标记对南大洋鱼类生物多样性进行了分析评估。两种标记共检测到 48 种鱼类，其中 12S rRNA 和 16S rRNA 标记分别检测到 30 种和 34 种，涵盖了南大洋鱼类主要类群。这不仅超过了本航次鱼类生物拖网结果的 19 种，也超过了国外“BROKE-WEST”航次的历史调查记录的 16 种。我们的研究结果显示，甘纳勒斯海脊海域和恩德比地外海之间的鱼类群落组成存在一些不显著的差异，与此同时，宇航员海的鱼类多样性也比以往的报道也更为丰富，但其整体群落组成和分布模式与东南极鱼类群落一般类型趋近。通过本次研究尝试，我们认为，环境 DNA 方法可作为气候变化背景下极地生态传统研究手段的一种重要且有益的补充。

关键词：气候变化，南大洋，宇航员海，鱼类多样性，环境 DNA 宏条形码

First pelagic fish biodiversity assessment of Cosmonaut Sea based on environmental DNA

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Abstract： The Cosmonaut Sea is a typical marginal sea in East Antarctica that has not yet been greatly impacted by climate change. As one of the least explored areas in the Southern Ocean, our knowledge regarding its fish taxonomy and diversity has been sparse. eDNA metabarcoding, as an emerging and promising tool for marine biodiversity research and monitoring, has been widely used across taxa and habitats. During the 38th Chinese Antarctic Research Expedition (CHINARE-38), we collected seawater and surface sediment samples from 38 stations in the Cosmonaut Sea and performed the first, to our knowledge, eDNA analysis of fish biodiversity in the Southern Ocean based on the molecular markers of 12S rRNA and 16S rRNA. There were 48 fish species detected by the two markers in total, with 30 and 34 species detected by the 12S rRNA and 16S rRNA marker, respectively. This was more than the trawling results (19 species) and historical survey records (16 species, “BROKE-West” cruise). With some nonsignificant differences between the Gunnerus Ridge and the Oceanic Area of Enderby Land, the Cosmonaut Sea had a richer fish biodiversity in this research compared with previous studies, and its overall composition and distribution patterns were consistent with what we know in East Antarctica. We also found that the eDNA composition of fish in the Cosmonaut Sea might be related to some environmental factors. Our study demonstrated that the use of the eDNA technique for Antarctic fish biodiversity research is likely to yield more information with less sampling effort than traditional methods. In the context of climate change, the eDNA approach will provide a novel and powerful tool that is complementary to traditional methods for polar ecology research.

Key words: Climate Change; Southern Ocean; Cosmonaut Sea; fish biodiversity; eDNA metabarcoding

利用角质颚形态判别东太平洋茎柔鱼
3 个不同种群的可行性研究

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摘要：为了探究利用角质颚形态对茎柔鱼三个种群(大、中、小种群)判别的可行性,本研究基于2018 年 7 月—2020 年 12 月中国鱿钓船在东太平洋公海采集的茎柔鱼样本,测定了其胴长、体质量以及角质颚的 12 个形态参数,分析了不同性别和不同种群间角质颚形态的差异。结果显示,在雌、雄间差异性方面, 除了上翼长、下头盖长,大种群雌、雄间的角质颚形态参数差异均显著(P<0.05),3 个种群的雌性个体的角质颚形态参数均大于雄性;主成分分析显示,角质颚形态在雌、雄种群之间存在差异。在种群间差异性方面,角质颚各形态参数在 3 个种群间差异极显著(P<0.01),大种群的角质颚最大,其次是中种群,小种群最小。利用标准化后的角质颚形态参数进行逐步判别分析,大、中、小 3 个种群的判别正确率分别为 100%、93.2%和 98.6%。研究表明,,茎柔鱼 3 种群的角质颚形态参数存在差异,角质颚形态可以用于判别茎 柔鱼 3 个不同的种群。

关键词：茎柔鱼;种群判别;角质颚;形态

A study on feasibility of discriminating three jumbo squid(Dosidicusgigas) populations inhabiting eastern Pacific Ocean using beak morphology

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Abstract： In order to explore the feasibility of using the morphology of beaks to distinguish the different sized populations of D. gigas, based on the samples of squids collected by Chinese squids fishing vessel in the high seas of the Eastern Pacific Ocean (79°26'W - 120°32'W, 02°19'N-20°24' S) from July 2018 to December 2020, the ML, BM, and 12 morphological parameters of beaks were measured. The morphological differences of beaks between different sexes and different populations were analyzed. Results showed that the variability of morphological parameters of beaks between females and males for small and medium populations were significant except lower hood length (LHL) ($P < 0.05$), while the differences of beak morphometrics between females and maless of large population were significant except upper wing length (UWL) and lower head hood length (LHL) ($P < 0.05$); Results of principal component analysis (PCA) showed that there were differences in beak morphology between females and males. Compared with small and large populations, the overlap between females and males was larger for middle population. The standardized morphological parameters of beaks were used for stepwise discriminant analysis (SDA). Results showed that the discriminant accuracy of large, medium, and small populations were 100%, 93.2%, and 98.6%, respectively. This study indicated that there were differences in the morphological parameters of beaks among three populations of D. gigas, and the beak morphology can be used to distinguish three populations of D. gigas.

Key words: Dosidicus gigas; population discrimination; beak morphometrics

基于稳定同位素分析法研究日本鲐与远东拟沙丁鱼之间的营养关系

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摘要：日本鲐和远东拟沙丁鱼广泛分布于日本沿海、西北太平洋海域，两个物种是重要的捕捞对象。为了研究两个物种之间的营养关系，本研究根据 2021 年 6～7 月在西北太平洋公海采集的（38°59′N～43°00′N，150°30′E～161°48′E）日本鲐和远东拟沙丁鱼肌肉样本，应用稳定同位素示踪技术，分析了在不同体长和性别的日本鲐、远东拟沙丁鱼种间和种内稳定同位素的差异性。对于种内差异，日本鲐和远东拟沙丁鱼的$\delta^{13}C$、$\delta^{15}N$ 值在雌、雄个体间均无显著差异（$P>0.05$）；日本鲐的$\delta^{15}N$ 值在不同体长组间无显著差异（$P>0.05$），$\delta^{13}C$ 值差异显著（$P<0.05$），远东拟沙丁鱼$\delta^{13}C$、$\delta^{15}N$ 值在不同体长组间的差异均显著（$P<0.01$）。对于种间差异，日本鲐和远东拟沙丁鱼的$\delta^{13}C$、$\delta^{15}N$ 值在对应体长组间均存在显著差异（$P<0.01$）。GAM 模型结果显示，随体长的增加，日本鲐的$\delta^{13}C$ 和$\delta^{15}N$ 值逐渐增大；远东拟沙丁鱼的$\delta^{13}C$ 和$\delta^{15}N$ 值呈现先减小后增大的趋势。随着个体的生长，日本鲐和远东拟沙丁鱼营养生态位重叠总体呈减小趋势。日本鲐$\delta^{15}N$ 值总体上高于远东拟沙丁鱼，远东拟沙丁鱼的生态位宽度大于日本鲐。日本鲐与远东拟沙丁鱼种内生态位重叠和生态位宽度在生长发育的过程中呈现出先增大后减小的趋势。研究表明，日本鲐平均营养级高于远东拟沙丁鱼，但远东拟沙丁鱼摄食资源的多样性更高，两个鱼种通过食性分化减小种间和种内的竞争压力从而实现共存。

关键词：日本鲐；远东拟沙丁鱼；摄食生态；稳定同位素；生态位；营养关系

Based on stable isotope analysis, the nutritional relationship between Scomber japonicus and Sardinops melanostictus was studied.

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Abstract：Scomber japonicus and Sardinops melanostictus are widely distributed in the coastal waters of Japan and the northwest Pacific Ocean. They are one of the main economic species with the highest yield in the world and are the key fishing targets in many countries. In this study, samples of chub mackerel (38 ° 59 ′ N ~ 43 ° 00 ′ N, 150 ° 30 ′ E ~ 161 ° 48 ′ E) and sardines were collected in the high seas of the Northwest Pacific Ocean from June to July 2021 by the ocean fishery resource survey ship ' Songhang '.The carbon and nitrogen stable isotope ratios of muscle were measured, and the effects of body length and sex on the carbon and nitrogen stable isotope ratios between the two species were analyzed by GAM model. At the same time, the differences of stable isotopes between S. japonicus and S .melanostictus in different body lengths and genders were analyzed. The results showed that the δ13C and δ15N of S. japonicus and S. melanostictus were significantly different among different body length groups ($P < 0.05$). The results of GAM model showed that the δ13C value increased with the increase of body length. The δ15N value showed a trend of decreasing first and then increasing.With the increase of body length, δ13C and δ15N showed a trend of decreasing first and then increasing. The niche breadth of S. melanostictus (SEAc = 3.998 ‰) was much smaller than that of P.sardines (SEAc = 11.735 ‰), and the overlap rate was 34.89 %. The niche overlap area of the two species decreased first and then increased slowly with the increase of body length. The average trophic level (TL = 3.36) of S. japonicus was significantly higher than that of Far East sardines (TL = 2.88) among all body lengths.

Key words: Scomber japonicus; Sardinops melanostictus; feeding ecology; stable isotope; ecological niche; nutritional relationship

沅江-西洞庭湖鱼类早期资源密度和群聚的时空动态

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摘要：沅江-西洞庭湖区是鱼类度过早期生活史的重要场所，不同生境具有不同的功能。本研究在河流江段（常德河洑）、河湖交汇区（常德牛鼻滩）和静水区（西洞庭湖区）采集样品。结果发现河洑江段和西洞庭湖鱼卵出现时间（5-7 月）长于牛鼻滩江段（5-6 月），河洑的鱼卵密度最高，其次是西洞庭湖。河洑、牛鼻滩江段和西洞庭湖鱼卵产浮性和漂流性卵的鱼类（9 种）、河湖洄游性和喜流水性鱼类 10 种多于其它两个江段。三个江段的于鱼卵都以赤眼鳟和鳊为主，河洑和牛鼻滩江段鱼卵以原肠期为主，西洞庭湖以器官形成期为主。河洑和牛鼻滩江段仔鱼密度只有一个高峰期，西洞庭湖区仔鱼密度从 6 月至 8 月较高。最高仔鱼密度出现在牛鼻滩江段，其次是西洞庭湖。牛鼻滩江段产浮性卵、漂流性卵鱼类（17 种）和喜流水性、河湖洄游性鱼类（17 种）多于其它两个江段。说明河流江段是鱼类的重要繁殖场，河湖交汇区是早期仔鱼的重要育幼场，鱼卵和仔鱼进入西洞庭湖进行发育和生长。

关键词：仔鱼；鱼卵；洞庭湖；鱼类群落

Spatio-temporal variation of fish egg and larval density and assemblages in Yuanjiang-West Dongting Lake continuum

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Abstract： Many fish spend early life history in Yuanjing-West Dongting Lake, where different habitats may play different roles in different developmental stages. In this study, ichthyoplankton was collected in lotic (Hefu), slow water-flows (Niubitan) and lentic (lake area) habitats in the Yuanjiang River and West Dongting Lake from April to September in 2021 and 2022. Egg density was highest in July (2021) and June (2022), and was the highest in Hefu and followed by lake area. Fish eggs were identified as nine, seven and six species at Hefu, Niubitan and lake area. Most of these species are fish of pelagic and drifting eggs and rheophilic and river-lake migratory fish. Squaliobarbus curriculus is the most abundant in the egg compositions in the three sections, and followed by Parabramis pekinensis. Larval density was highest in July 2021 and June 2022 at Hefu and Niubitan, but high in June and July 2021 and from June through August in 2022 at lake area. Larval density during peak period was the highest at Niubitan, and it is the highest in the West Dongting Lake in the later spawning period. There were more fish species of pelagic and drifting eggs at Niubitan than at Hefu and lake area, and more rheophilic and river-lake migratory fish at Niubitan than at Hefu and lake area. These results suggested that lotic habitat (Hefu) served as an important spawning ground and egg-drift sites, slow water-flows habitat (Niubitan) was nursery ground for preflexion larvae of rheophilic and river-lake migratory fish; pelagic eggs and larvae drift into lentic lake area (the West Dongting Lake) for development and growth.

Key words: Egg; larvae; Dongting Lake; Fish assemblag

浮游动物稳定同位素研究进展

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摘要：浮游动物是海洋浮游食物网、物质循环和能量流动的关键组成部分，其生物量水平和类群结构在很大程度上影响经济鱼类的产量。稳定同位素技术在海洋生态研究中的应用十分广泛，利用稳定同位素技术便于深入探究鱼类等的摄食生态及食物网结构特征。本文比较分析了国内外浮游动物稳定同位素研究进展，概括总结了浮游动物稳定同位素特征与粒径、环境因子的关系，及其在评估海洋生态系统的营养级和食物网结构中的作用，有助于深入研究鱼类的生活史和洄游路线，完善海域生态系统渔业资源的基础生物学资料，对海洋环境和渔业资源的保护具有重要意义。

关键词：浮游动物；稳定同位素；食物网

Advance in stable isotopes of zooplankton

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Abstract：Zooplankton is a key component of the marine planktonic food web, material cycle and energy flow, and its biomass level and taxa structure greatly affect the production of economic fish. Stable isotope technology is widely used in marine ecological research, and its use facilitates in-depth investigation of the feeding ecology and food web structure of fishes and other species. In this paper, we compare and analyze the progress of zooplankton stable isotope research at home and abroad, and summarize the relationship between zooplankton stable isotope characteristics and particle size, environmental factors, and their roles in evaluating the trophic level of marine ecosystems and the structure of food webs, which can help to study the life history and migratory routes of fishes in-depth, and to improve the basic biology of the fishery resources of marine ecosystems and have great significance for the protection of the marine environment and the fishery resources. It is of great significance to the protection of the marine environment and fishery resources.

Key words: Zooplankton; Stable nuclide; Food web

基于集成模型模拟长江口刀鲚栖息地适宜性变化

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摘要：河口地区渔业资源正逐渐衰退，保护鱼类栖息地成为全球关注的科学问题。物种分布模型(Species Distribution Models, SDMs)已被用于鱼类栖息地模拟，这种评估通常基于单一模型，这可能会增加模型拟合的不确定性。本研究以长江口刀鲚(Coilia nasus)为研究对象，基于 2017-2021 年底拖网资源监测调查数据，将水温、叶绿素 a、盐度等七个变量作为预测因子，使用三种指标对比评估八种单一模型和采用加权平均法的集成模型(Ensemble model, EM)的性能表现。结果表明：(1)EM 模型是除随机森林(Random Forest, RF)、梯度提升机(Gradient Boosting Machine, GBM)模型以外性能最佳的模型，且具有良好的鲁棒性；(2)温度、叶绿素 a 是影响长江口刀鲚栖息地分布的重要因素；(3)长江口刀鲚的栖息地分布范围自春季到冬季逐渐增大。

关键词：物种分布模型；集成模型；长江口；刀鲚；栖息地适宜性

Modeling habitat suitability of Coilia nasus in the Yangtze River Estuary with Ensemble Model

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Abstract： The high biological productivity and rich fishery resources extremely in estuaries are gradually declining, due to the impacts of human activities and global climate change. The protection of the ecological health of fish habitats has become a scientific issue of global concern. Species Distribution Models (SDMs) have been used for fish habitat simulation and prediction of potential species distributions; however, such assessments are often based on single models which will increase uncertainty in habitat suitability models, leading to inaccurate predictions of species distributions in the future. In this study, we took Coilia nasus in the Yangtze River Estuary as the research object and based on the trawl resource monitoring survey data from the end of 2017-2021.We used seven natural environment explanatory variables such as water temperature, chlorophyll a, salinity, and chemical oxygen demand as predictors. Three evaluation metrics, Area Under receiver operating character Curve (AUC), Kappa, and True skill statistic (TSS) were used to compare and evaluate the performance of eight single models with ensemble model (EM) using the weighted averaging method. The results showed that: (1) EM is the best performance model in addition to the two types of machine learning models, namely random forest (RF) and gradient boosting machine (GBM) and has relatively good robustness; (2) In the analysis of the contribution of environmental factors, the simulation results of EM, RF and GBM were highly similar. Temperature and chlorophyll a were the important factors affecting the habitat distribution of Coilia nasus in the Yangtze River Estuary; (3) The spatial distribution of the habitat of Coilia nasus in the Yangtze River Estuary shows seasonal changes, as evidenced by the gradual increase of the habitat range from spring to winter, and the higher habitat suitability in the waters of the South Branch North Harbor and at the mouth of the Yangtze River. This study will provide a reference basis for the investigation and evaluation of fishery resources in the Yangtze River Estuary and the design of conservation strategies.

Key words: Species distribution model; Ensemble model; Yangtze River Estuary; Coilia nasus; Habitat suitability

鱼类野化训练策略的有效性评估

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摘要：近年来，各种野化训练方法被广泛应用于提高增殖放流鱼类的生态适应性，但其有效性尚未被量化评估。本研究采用 meta 分析方法广泛搜集历史文献并汇编数据集，借助多种统计模型对此开展整合分析。主要结果显示，环境丰容、生存技能训练和软放流均能显著提高放流鱼类的适应性，但其效果受到适合度评价指标、放流鱼种营养级、放流鱼类发育阶段等因素的影响。本研究首次系统评估了野化训练策略在提升鱼类适应性当中的有效性，研究结果将为进一步优化增殖放流实施框架提供理论依据。

关键词：增殖放流；环境丰容；生存技能训练；软放流；meta 分析

Effectiveness of conditioning strategies in improving fish fitness

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Abstract： Although conditioning strategies are widely used to increase fish post-release adaptability in stock enhancement projects, their effectiveness has not been systematically evaluated. Using a global-scale meta-analysis, we demonstrate that three major conditioning strategies, including environmental enrichment, life skills training, and release tactic, can significantly improve fish individual fitness, although high heterogeneity is observed. Our findings indicate the necessity of conditioning procedures and highlight the need to enact context-dependent strategies in practical release projects.

Key words: hatchery release; environmental enrichment; life skills training; soft release; meta-analysis

不同印度洋偶极子模态下西南印度洋深海散射层生物热点栖息地分布

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摘要：为了探究不同印度洋偶极子模态（IOD）下西南印度洋深海散射层（DSL）生物热点栖息地分布，研究选取 2012 年 10 月—2020 年 7 月的西南印度洋海域声学调查数据，利用热点分析方法和最大熵模型，分析不同 IOD 模态下 DSL 生物热点栖息地的变动规律。 结果显示，不同 IOD 模态的最大熵模型精度均大于 0.9，模型预测效果较好，其中溶解氧是对栖息地分布贡献率最高的因子，平均贡献率为 50.88%。DSL 热点适宜栖息地的重心主要在西北-东南方向移动，第 1 个 IOD 冷相位时期热点适宜栖息地重心变动最为明显。DSL 热点的适宜栖息地分布在 30°~45°S 与 11 和 22℃等温线之间。研究表明，不同 IOD 模态下 DSL 热点受溶解氧等变化的影响，其适宜栖息地变动明显，最大熵模型可以较好的预测 DSL 热点栖息地的分布。本研究可为阐明 DSL 中渔业资源的空间分布和变动规律提供新的参考。

关键词：深海散射层；印度洋偶极子；栖息地；西南印度洋

Potential habitats distribution on hotspots of deep scattering layer in the southwestern Indian Ocean under different Indian Ocean dipole modes

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Abstract：Based on the acoustic data from October 2012 to July 2020 in the southwestern Indian Ocean, hotspot analysis and maximum entropy model were used to study on the potential habitats' distribution on hotspots of deep scattering layer under different IOD. The results showed that the maximum entropy model had a good performance with the accuracy of the model was larger than 0.9. Dissolved oxygen had the highest contribution rate to the habitat distribution, and the average contribution rate was 50.88%. The gravity center of in DSL hotspot habitats mainly moved in the northwest to southeast direction, and the most significant change was observed during the first cold phase of IOD. DSL hotspot habitat was distributed between 30 ° - 45 ° S and 11 ℃ - 22 ℃ isotherms, which indicated a certain latitude correlation. Research showed that the changes of suitable habitat on hotspots of DSL were influenced by dissolved oxygen. The maximum entropy model can effectively predict the distribution of DSL hotspots' habitats. This study can provide new references for elucidating the spatial distribution and resource variation patterns of DSL.

Key words: deep scattering layer; Indian Ocean dipole; habitats; southwestern India Ocean

鱼类信息素对大型溞诱导型防御特征的影响

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摘要：自然界中捕食者对猎物诱导型防御特征存在一定影响，为探究捕食信息素对枝角类表型可塑性是否存在剂量效应，本试验使用孔雀鱼（Poecilia reticulata）作为捕食者，大型溞（Daphnia magna）作为被捕食者，设立 0%（M0）、10%（M1）、50%（M2）、100%（M3）四种信息素浓度，连续测量三代。试验结果显示，信息素处理下大型溞体长、体高绝对长度显著减小（$P<0.01$）、壳刺相对长度显著增加（$P<0.01$），产幼数显著增加（$P<0.01$）；信息素处理下，体型有逐代减小趋势（$P>0.05$）；连续三代个体中，M3 处理组体长、体高均最小，壳刺相对长度最大；信息素处理下产幼数均比对照组高，以第三代 M1 处理组最高。试验结果表明，信息素对枝角类表型形态的影响存在剂量效应，随着浓度的增加体型变小，但产幼数不存在剂量效应，只存在有或无的效应。

关键词：大型溞；孔雀鱼；信息素浓度；表型可塑性；剂量效应

Effects of fish kairomones on inducible defense characteristics of Daphnia magna

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Abstract：Predators in nature have a certain influence on the characteristics of prey induced defense. In order to explore whether there is a dose dependent response of predator kairomones on phenotypic plasticity of Cladocerans, this experiment used Poecilia reticulata as predator and Daphnia magna as prey. Four kairomones concentrations of 0 % (M0), 10 % (M1), 50 % (M2)and 100 % (M3)were set up, and three generations of continuous measurement were carried out. The results showed that the absolute length of body length and body height of D.magna decreased significantly ($P<0.01$), the relative length of the mucrone increased significantly ($P<0.01$), and the number of offspring increased significantly ($P<0.01$). Under kairomones treatment, the body size showed a decreasing trend from generation to generation ($P>0.05$). Among the three consecutive generations of individuals, the body length and body height of the M3 treatment group were the smallest, and the relative length of the mucrone was the largest. The number of offspring under kairomones treatment was higher than that of the control group, and the third generation M1 treatment group was the highest. The resulte showed that there was a dose dependent response of predator kairomones on the phenotypic morphology of Cladocerans, with the increase of concentration, the body size became smaller, but there was no dose dependent response effect on the number of offspring, and there were only on off response.

Key words:： Daphnia magna; Poecilia reticulata; kairomones concentration; phenotypic plasticity; dose dependent response

长江口浮游植物群落特征及影响因素分析

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摘要：为了解长江口浮游植物群落组成与结构特征、时空分布格局及关键影响驱动因子，基于2018-2020年8月（夏季）与11月（秋季）长江口浮游植物调查数据，运用群落多样性分析指标及广义加性模型（GAM）探究了长江口浮游植物群落特征及与各影响因子间的关系。结果表明：本次调查共采集浮游植物8门99属185种，硅藻、蓝藻和绿藻是主要的浮游植物类群，优势种主要包括中肋骨条藻（Skeletonema costatum）、颗粒直链藻（Aulacoseira granulata）、具槽直链藻（Melosira sulcata）、小环藻（Cyclotella sp.）和衣藻（Chlamydomonas sp.）等，其中中肋骨条藻长期占绝对优势；在时间上，夏季浮游植物丰度和种类数显著高于秋季（$P<0.05$），但秋季浮游植物群落多样性指数和丰富度指数更高，分布更均匀；在空间上，浮游植物平均丰度整体上呈现“东滩>南支>北支”的分布格局；GAM分析显示，在夏季，水温（Tem）、酸碱度（pH）和氮磷比（TN/TP）是显著影响长江口浮游植物丰度分布的环境因子（$P<0.05$），其中TN/TP的贡献率最高，为71.86%；在秋季，盐度（Sal）、溶氧（DO）和化学需氧量（COD）是显著影响长江口浮游植物丰度分布的环境因子（$P<0.05$），其中DO的贡献率最大，为48.48%。研究表明，长江口浮游植物群落的组成、结构、格局及影响因素存在季节差异，研究结果可为掌握长江口浮游植物资源动态提供参考依据。

关键词：浮游植物；群落特征；影响因素；广义加性模型；长江口

Analysis of phytoplankton community characteristics and influencing factors in the Yangtze River Estuary

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Abstract： In order to understand the composition and structural characteristics, spatiotemporal distribution pattern and key impact drivers of phytoplankton communities in the Yangtze River Estuary, based on the survey data of phytoplankton in the Yangtze River Estuary from August (summer) to November (autumn) from 2018 to 2020, community diversity analysis indicators and generalized additive model (GAM) were used to explore the characteristics of phytoplankton communities in the Yangtze River Estuary and the relationship between them and each influencing factor. The results showed that a total of 185 species of phytoplankton were collected in 8 phyla, 99 genera, and diatoms, cyanobacteria and green algae were the main phytoplankton groups, the dominant species mainly include Skeletonema costatum, Aulacoseira granulata, Melosira sulcata, Cyclotella sp. and Chlamydomonas sp., among them, Skeletonema costatum has long been overwhelming; In terms of time, the abundance and species of phytoplankton in summer were significantly higher than those in autumn ($P<0.05$), however, in autumn, phytoplankton communities have a higher diversity index and richness index and are more evenly distributed; Spatially, the average phytoplankton abundance showed the distribution pattern of “East Beach > South Branch > North Branch” as a whole; The GAM analysis showed that water temperature (Tem), pH and nitrogen-phosphorus ratio (TN/TP) were the environmental factors ($P<0.05$) that significantly affected the abundance distribution of phytoplankton in the Yangtze River Estuary in summer, among which TN/TP had the highest contribution rate of 71.86%; Salinity (Sal), dissolved oxygen (DO) and chemical oxygen demand (COD) were the environmental factors ($P<0.05$) that significantly affected the abundance distribution of phytoplankton in the Yangtze River Estuary in autumn, among which DO contributed the most, 48.48%. The results show that there are seasonal differences in the community composition, structure, pattern and influencing factors of phytoplankton in the Yangtze River Estuary, and the research results can provide references for understanding the dynamics of phytoplankton resources in the Yangtze River Estuary.

Key words: phytoplankton; community characteristics; influencing factors; generalized additive models; Yangtze River Estuary

西南大西洋海洋生态系统的长期变化及其对气候强迫的响应

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摘要：近年来，气候变化对环境与社会层面的影响以及随之而来的生态系统结构与功能的改变越来越受到国际社会的关注。探究气候变化对西南大西洋生态系统内渔业资源的影响，可以帮助建立一种基于生态系统的渔业资源保护和合理的利用方法。本研究使用 1950-2018 年的长期渔业数据、环境数据和气候数据探索西南大西洋生态系统的稳态转换和渔业资源对气候变化的响应。研究结果表明，西南大西洋生态系统在 1976/1977 年、20 世纪 80 年代末和 20 世纪末发生了 3 次稳态转换。此外，温度、海表面高度、径流量和云量是西南大西洋生态系统内对渔业资源影响最大的环境变量。此外，在气候指数方面，渔业资源对全球平均陆地-海洋温度指数和南极海冰覆盖范围的响应最为明显；大西洋年代际涛动对低纬度地区产生强烈影响。本研究对西南大西洋生态系统的非线性变化进行了系统描述，探究了环境和气候对生态系统影响的渐进关系。

关键词：西南大西洋；海洋生态系统；气候变化；稳态转换

Long-term variability of the large marine ecosystems in Southwest Atlantic and its responses to climatic regime shifts

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Abstract：The climate-induced environmental and social variations, as well as the accompanying ecosystem changes, have received increasing attention from the global community in recent years. The southwest Atlantic Ocean is one of the most important fishing areas in the world with considerably high primary productivity. Exploring the impacts of climate variability on the fishery ecosystems in the southwest Atlantic is conducive to establishing an ecosystem-based approach for the protection and rational utilization of fishery resources. Therefore, in this study, long-term fishery data, 23 environmental data from the entire Southwest Atlantic, and 25 global climate data have been used to explore the regime shift of the ecosystem and the response of fishery resources to climate change from 1950 to 2018. The research results indicate that changes in the ecosystem of the Southwest Atlantic exhibit a significant nonlinear trend, and there are three noteworthy regime shifts in 1976/1977, the late 1980s, and the late 20th century. Additionally, temperature, sea surface height (SSH), water runoff, and cloudiness are the environmental variables with the greatest impact on fishery resources within the southwest Atlantic ecosystem, while zonal wind speed and air temperature have a more significant impact on low latitude areas. Furthermore, in terms of climate indices, fishery resources have the most obvious response to the Global Mean Land-Ocean Temperature Index and Antarctic Sea Ice Extent, and the Atlantic Multidecadal Oscillation has an intense impact on low latitude areas concurrently. The study highlights the nonlinear changes in the ecosystem of the Southwest Atlantic and the progressive relationship between environmental and climate impacts on the ecosystem. Understanding the relevant mechanisms of the influence between fishery resources, the environment, and climate can help complete fisheries management based on the ecosystem.

Key words: Southwest Atlantic Ocean; large marine ecosystem; climate change; regime shift

盐度对夜光藻生长及抗氧化酶能力的影响

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摘要：盐度是影响海洋藻类生长的重要因素。本研究以常见赤潮生物夜光藻（Noctiluca scintillans）为研究对象，设置盐度梯度为 18、22、26、30、34、38、42，测定夜光藻的生长、细胞大小、SOD、CAT 活性和 GSH 含量。结果显示，盐度对夜光藻生长影响显著（P<0.05），盐度 26 时，细胞密度最高为 3.3×104 个/L；盐度 42 时，细胞密度最高仅有 2.67×103 个/L。盐度对夜光藻细胞大小影响显著（P<0.05），盐度 18～22 时，夜光藻细胞直径变大，最大为（914.97±25.97）μm，盐度 38～42 时，细胞直径变小，最小为（350.94±4.66）μm；盐度对夜光藻 SOD、CAT 活性和 GSH 含量有显著影响（P <0.05），盐度 18 和盐度 42 时，夜光藻细胞内的 SOD、CAT 活性显著升高，均高于其他盐度组。盐度 18 时，GSH 含量低于其他盐度组。

关键词：盐度；夜光藻；生长；抗氧化酶

Effects of salinity on the growth and antioxidant enzyme activities of Noctiluca scintillans

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Abstract： Salinity is an important factor affecting the growth of marine algae. In this study, the common red tide organism Noctiluca scintillans was used as the research object, and the salinity gradient was set to 18,22,26,30,34,38 and 42. The growth, cell size, SOD, CAT activity and GSH content of Noctiluca scintillans were determined. The results showed that salinity had a significant effect on the growth of Noctiluca scintillans (P < 0.05). The highest cell density was 3.3 × 104 cells / L at salinity 26. When the salinity was 42, the highest cell density was only 2.67 × 103 cells / L. Salinity had a significant effect on the cell size of Noctiluca scintillans (P < 0.05). When salinity was 18 ~ 22, the cell diameter of Noctiluca scintillans became larger, the maximum was (914.97 ± 25.97) μm, and when salinity was 38 ~ 42, the cell diameter became smaller, the minimum was (350.94 ± 4.66) μm. Salinity had a significant effect on SOD, CAT activity and GSH content of Noctiluca scintillans (P < 0.05). At salinity 18 and 42, SOD and CAT activities in Noctiluca scintillans cells increased significantly, which were higher than those in other salinity groups. At salinity 18, the GSH content was lower than that of other salinity groups.

Key words: Salinity ; night light algae ; growth ; antioxidant enzymes

基于环境 DNA 技术对长江口鱼类生物多样性的调查

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摘要：长江口作为西北太平洋最大的河口，具有丰富的鱼类资源和生物多样性，是有重要的研究价值的河口功能区域。准确监测鱼类多样性的动态变化是开展资源评估和管理的基础。本研究在 2022 年 11 月利用环境 DNA（Environmental DNA, eDNA）与传统拖网对长江口水域进行了调查，并比较两种调查方式的差异以评估 eDNA 技术在长江口水域鱼类多样性研究的应用前景。结果显示，两种调查方式在 11 月共检出 39 种鱼类，eDNA 检出 26 种，拖网检出 20 种，其中只有 7 种物种两种监测方式均有检出，eDNA 识别的优势物种为焦氏舌鳎（Cynoglossus joyneri），拖网识别的优势物种则是刀鲚（Coilia nasus）。虽然 eDNA 技术较拖网可检出更多物种种类，但种类存在差异，因此二者多样性也有所不同。因此，eDNA 技术可能并不能完全替代拖网作为长江口多样性调查的工具，但可以为某些物种的调查提供补充信息。

关键词：eDNA；拖网；长江口；物种多样性

Investigation of Fish Biodiversity in the Yangtze River Estuary Based on Environmental DNA Technology

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Abstract： As the largest estuary in the Pacific Northwest, the Yangtze River Estuary is rich in fish resources and biodiversity, and is an estuarine functional area with important research value. Accurate monitoring of the dynamic changes in fish diversity is the basis for resource assessment and management. In this study, we conducted a survey of the Yangtze River Estuary using Environmental DNA (eDNA) and traditional trawl in November 2022, and compared the differences between the two survey methods to evaluate the prospects of applying eDNA technology in fish diversity studies in the Yangtze River Estuary. The results showed that 39 fish species were detected by the two survey methods in November, 26 species were detected by eDNA and 20 species were detected by trawl, of which only 7 species were detected by both monitoring methods，the dominant species identified by eDNA was predominantly Cynoglossus joyneri, while the dominant species identified by trawl was Coilia nasus. Although the number of species detected by eDNA technology was more than that by trawl, there were large differences in the types, and the results of the species diversity. Therefore, eDNA technology may not completely replace trawl as a tool for diversity surveys in the Yangtze River Estuary, but it can provide complementary information for surveys of certain species.

Key words: eDNA; trawl; Yangtze River Estuary; species diversity

自然灾害对雅鲁藏布江大峡谷墨脱段鱼类群落结构和多样性的影响

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摘要：雅鲁藏布江大峡谷为世界第一深峡谷，位于西藏林芝派镇至巴昔卡的雅鲁藏布江下游段，属于热带雨林-常绿阔叶林地区。墨脱段的生态环境较为脆弱，海拔落差较大、地质构造复杂，极易受到地震、泥石流滑坡等自然灾害的威胁。墨脱江段部分鱼类为当地的特有种，分布范围较窄，一旦遭到破坏，种群很难恢复。本文根据 2017-2019 年及 2022-2023 年等五年对墨脱江段鱼类资源的科考结果，分析了雅鲁藏布江大峡谷墨脱江段鱼类种类组成、优势种、相对生物量及多样性的时空分布特征。2017 年 9 月雅鲁藏布江大峡谷内墨脱江段上游发生了较大的泥石流，2018 年 10 月林芝堰塞湖的形成。本文通过对比自然灾害前后大峡谷墨脱段的鱼类群落结构和生物多样性特征，探讨了自然灾害对鱼类资源的影响，以期为揭示雅鲁藏布江大峡谷鱼类资源在外界因素干扰下的演变状况提供背景资料，为雅鲁藏布大峡谷国家自然保护区鱼类物种多样性的保护及渔业资源管理提供科学依据。

关键词：雅鲁藏布江大峡谷；自然灾害；鱼类；群落结构；多样性

Effects of natural disasters on structural and diversity characteristics of fish communities in the Motuo reach of the Yarlung Zangbo Grand Canyon，China

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Abstract： The Yarlung Zangbo River Grand Canyon is the deepest canyon in the world, and located in the lower reaches of the Yarlung Zangbo River from Pai Town of Linzhi city to Bashika in Xizang of China, and it is a tropical rainforest - evergreen broad-leaved forest area. The ecological environment of Motuo reach is relatively fragile, and the altitude drop is large and the geological structure is complex, so extremely vulnerable to natural disasters such as earthquake, mud-rock flow and landslide. Some fish are endemic species in the Motuo reach, and the distribution range is narrow, and once damaged, the population is difficult to recover. The paper is based on the results of the five years from 2017 to 2019 and from 2022 to 2023 on the fish resources of the Motuo reach. The spatial and temporal distribution characteristics of fish species composition, dominant species, relative biomass and diversity were revealed in the Motuo reach of Yarlung Zangbo River Grand Canyon. In September 2017, a large mudslide occurred on the Motuo reach of the Yarlung Zangbo River Grand Canyon, and formation of Linzhi reach barrier Lake in October 2018. The fish community structure and biodiversity characteristics were compared before and after two natural disasters in Motuo reach, and the impact of natural disasters on fish stocks was discussed. In order to provide background information for revealing the evolution of fish resources in the Yarlung Zangbo River Grand Canyon under the interference of external factors, and further provides scientific basis for the protection of fish species diversity and the management of fishery resources in Yarlung Zangbo Grand Canyon National Nature Reserve.

Key words: Yarlung Zangbo Grand Canyon; natural disasters; fish; Community structure; diversity

长江口龙头鱼时空分布特征及其与环境因子的关系

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摘要：本研究根据 2017~2022 年 8 月(夏季)和 11 月(秋季)长江口及其邻近水域资源与环境调查数据，运用广义加性模型(generalized additive models, GAM)探析了龙头鱼(Harpadon nehereus)相对资源量与环境因子的关系，并对 2022 年龙头鱼资源的时空分布进行预测。结果显示，夏秋两季最佳模型偏差解释率分别为 64.89%和 49.90%，交叉验证回归线斜率的平均效应分别为 0.75 和 0.70。水温和盐度是影响长江口龙头鱼相对资源量分布的关键环境因子。研究表明，2022 年长江口龙头鱼相对资源量的预测值与实测值大小范围相近且呈现的空间分布特征相似，呈现夏季龙头鱼相对资源量明显高于秋季，北支水域的相对资源量明显高于南支水域，远岸水域高于近岸水域。本研究揭示了龙头鱼的时空分布特征及与环境因子的关系，以期为长江口龙头鱼资源的养护管理和可持续利用提供科学依据。

关键词：龙头鱼；GAM；时空分布；环境因子；长江口

Spatial-temporal distribution characteristics of Harpadon nehereus in the Yangtze River Estuary and its relationship with environmental factors

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Abstract：To investigate the spatial-temporal distribution characteristics of Harpadon nehereus in the Yangtze River Estuary and its relationship with environmental factors, this study utilized data from resource and environmental surveys conducted in the Yangtze River Estuary and adjacent waters during August (summer) and November (autumn) from 2017 to 2022. Generalized additive models (GAM) were employed to analyze the relationship between relative abundance of H. nehereus and environmental factors, and to predict the spatial-temporal distribution of H. nehereus resources in 2022. The results showed that the best model deviance explained 64.89% and 49.90% of the variability in summer and autumn, respectively, with average effect sizes of 0.75 and 0.70 for cross-validated regression slope. Water temperature and salinity were identified as key environmental factors influencing the relative abundance distribution of H. nehereus in the Yangtze River Estuary. Overall, there were notable seasonal differences in the relationship between relative abundance of H. nehereus and environmental factors. In summer, both water temperature and salinity exhibited multi-modal nonlinear relationships with the relative abundance of H. nehereus. In autumn, the relative abundance of H. nehereus showed a positive linear relationship with water temperature, and a nonlinear relationship with salinity, with an increasing trend followed by a decreasing trend as salinity increased. The study demonstrated that the predicted values of relative abundance of H. nehereus in 2022 closely matched the actual values and displayed similar spatial distribution patterns. There were evident spatial-temporal differences in the distribution of relative abundance of H. nehereus in the Yangtze River Estuary, with higher relative abundance in summer compared to autumn, and higher relative abundance in the northern branch than the southern branch, as well as higher relative abundance in offshore areas compared to nearshore areas. This research revealed the spatial-temporal distribution characteristics of H. nehereus and their relationship with environmental factors, aiming to provide scientific basis for conservation management and sustainable utilization of H. nehereus resources in the Yangtze River Estuary, thereby contributing to the restoration and management of fisheries resources in the region.

Key words: Harpadon nehereus; GAM; spatial-temporal distribution; environmental factors; Yangtze River Estuary

基于 PIV 技术的鳗鲡游动涡量研究

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摘要：为探究鳗鲡（Anguilla japonica）在自由游动状态下涡量的传递和变化过程，本文利用粒子图像测速技术对鳗鲡在不同速度下直线游动过程中的涡量变化以及涡流传递效率进行了分析。结果表明：（1）鳗鲡游动时产生的涡是沿着身体从头部向尾部进行传递，其游动频率与涡的脱落周期保持一致，随着鳗鲡游泳速度的升高，其产生的正、负涡度之比逐渐减小；（2）鳗鲡游动时头部和体部分别只聚集一个涡，两个涡旋转方向相反，随着鳗鲡游泳速度的升高，体部与头部聚集的涡度之比逐渐增大，同时尾部会聚集两个涡，一个正涡，一个负涡，但当鳗鲡以较低的速度游动时，尾部的正涡起主要作用；（3）鳗鲡游动时头部的涡流传递效率最大，体部次之，尾部最小，最高可达 2.98：1.76：1，头部在鳗鲡游动过程中具有重要作用。本研究结果有助于了解鳗鲡式游动鱼类的运动学机理，同时为仿生机器鱼的运动特性提供研究方向。

关键词：鳗鲡；粒子图像测速技术（PIV）；涡量；游泳速度

Study on the swimming vorticity of eel based on PIV technology

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Abstract: In order to explore the process of vorticity transfer and change of Anguilla japonica in free swimming state, this paper uses particle image velocimetry to analyze the vorticity change and eddy current transfer efficiency of Anguilla japonica during linear swimming at different speeds. The results show that : (1) The vortex generated by the eel swimming is transmitted from the head to the tail along the body, and its swimming frequency is consistent with the shedding period of the vortex. With the increase of the swimming speed of the eel, the ratio of positive and negative vorticity gradually decreases ; (2) The vortex generated by the eel swimming is transmitted from the head to the tail along the body, and its swimming frequency is consistent with the shedding period of the vortex. (2) When the eel swims, the head and body parts of the eel gather only one vortex separately, and the two vortices turn in the opposite direction. As the swimming speed of the eel increases, the ratio of the vorticity gathered by the body to the head gradually increases. At the same time, the tail will gather two vortices, a positive vortex and a negative vortex. However, when the eel swims at a lower speed, the positive vortex at the tail plays a major role ; (3) When the eel swims, the eddy current transfer efficiency of the head is the largest, followed by the body, and the tail is the smallest, up to 2.98 : 1.76 : 1. The head plays an important role in the swimming process of the eel. The results of this study are helpful to understand the kinematics mechanism of eel-like swimming fish, and provide research directions for the motion characteristics of bionic robotic fish.

Key words: eel; particle image velocimetry (PIV); vortex; swimming speed

乙醇保存对头足类角质颚几何形态的影响：以金乌贼为例

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摘要：越来越多的研究人员认识到生物标本的保存可能对生物体及其软组织和硬组织的形态测量和其他分析产生重大影响。头足类的角质颚常被保存在乙醇试剂中，然而，目前缺乏详细且定量的研究来检查乙醇保存对角质颚几何形态的影响。本研究以金乌贼为例，利用几何形态测量学工具表征和量化不同保存时间的角质颚几何形态的变化，并测试保存对下游统计分析的影响。研究结果显示从新鲜样本到保存 720 天后金乌贼角质颚的略微缩小，保存会导致角质颚的喙、头盖、翼部和侧壁形状产生一定差异。更重要的是，保存潜在影响了角质颚形态的性别分类。研究结果表明头足类金乌贼角质颚的形状和大小会随着保存时间的推移而产生的一定程度的变化，同时保存时间过久还会对下游的统计分析产生潜在影响。因此，我们建议在尽量减少其他误差的前提下提取新鲜角质颚的形态特征用于科学研究。本研究可为其他水生生物物种的相关研究提供参考，同时也为水生生物资源的养护和管理提供科学依据。

关键词：乙醇保存；头足类角质颚；几何形态测量学；金乌贼；测量误差

Effect of ethanol preservation on cephalopod beaks geometric morphometrics over time: Sepia esculenta as a case

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Abstract： Increasingly, researchers have realized that biological specimen preservation can have significant effects on morphometry and other analysis of animals and their soft and hard tissues. Although cephalopod beaks are often preserved in ethanol reagents, there is a lack of mentioned and quantitative studies to investigate the effect of ethanol preservation on beak morphology. We used geometric morphometrics to characterize and quantify the geometric morphology of beaks at different preservation times in this study, and we tested the effect of preservation on downstream statistical analysis. The results of the investigation demonstrated that the beaks of the Sepia esculenta were slightly reduced after 720 days of storage from fresh samples, and the preservation caused certain variations in the morphology of the rostrum, hood, wing and lateral wall. In particular, the preservation of sex classifications that may have influenced palate morphology. These results confirmed that the shape and size of Sepia esculenta beaks changed to some amount over time, and that preservation time had a potential impact on downstream statistical analysis. For the sake of scientific research, we thus advise preserving the morphological features of a fresh beak while reducing any additional defects to avoid preservation-related mistakes. However, we can evaluate the impact of preservation on preserved specimens prior to using them when needed because of sample shortage, etc. This research can be used as an example for similar studies on other hydrobios and offer a solid scientific foundation for the preservation and management of hydrobios resources.

Key words: ethanol preservation; cephalopod beaks; geometric morphometrics; Sepia esculenta; measurement error

东海生态群落关键种识别

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摘要：关键种(Keystone species)对于维持群落稳定性和物种多样性至关重要。识别关键种并探究其生态调节将有助于优先研究重要物种并且更好地了解群落稳定机制。本研究基于食物网构建拓扑生态网络，旨在揭示我国东部水域生态系统中的关键种并量化其生态功能。根据十项拓扑网络指数的主成分分析结果，我们识别出海鳗(Muraenesox cinereus)、细螯虾(Leptochela gracilis)和带鱼(Trichiurus lepturus)为该水域的关键物种。移除分析表明，关键种的丧失可能对东海食物网的复杂性和稳定性产生负面影响。因此，海洋生态系统中应优先考虑关键种的保护。

关键词：关键种；网络分析；食物网；东海

Identification of Keystone Species in Ecological Communities in the East China Sea

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Abstract： Keystone species are critical to preserving community stability and species diversity. Identifying key species and investigating their ecological regulation will help to prioritize important species and gain a better understanding of community stability mechanisms. Based on food web structures, this study constructs a topological ecological network with the aim to reveal critical species within the eastern aquatic ecosystem of China, and further quantify their ecological functions. We identified Muraenesox cinereus, Leptochela gracilis, and Trichiurus lepturus as keystone species in the region based on the results of principal component analysis of ten network indices. The removal analysis performed suggested that the loss of keystone species might have a negative impact on the complexity and stability of the food web in the East China Sea. As a result, protecting keystone species should be prioritized in marine ecosystems.

Key words: keystone species; network analysis; food webs; East China Sea

鸢乌贼不同地理种群耳石形态差异及轮廓可视化研究

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摘要：耳石是头足类的重要硬组织之一，不同群体或种类的耳石外部形态存在显著差异。本文运用逐步判别分析法对于东印度洋、中东太平洋、西北印度洋 3 个不同海域的鸢乌贼的耳石外部形态差异进行研究，并通过傅里叶分析法和地标点法对其轮廓进行可视化重建。逐步判别分析结果表明，基于传统测量法的总体正确率为 84.4%，傅里叶分析法的总体正确率为 82.9%，地标点法为 87.3%。轮廓可视化结果表明，中东太平洋海域的鸢乌贼耳石个体较小，侧区弧度最为明显；东印度洋海域的耳石侧区弧度分化最为平缓；西北印度洋海域的耳石吻区形态发育较短小，背区边缘更平滑。重建结果表明，不同海域鸢乌贼的耳石外部形态存在显著性差异。本文研究表明 3 种方法对于种群判别均有效，地标点法对于不同种群的判别要优于传统测量法。利用傅里叶变换和地标点法对于耳石轮廓的重建给耳石形态分类学提供了重要的科学依据。

关键词：耳石形态；椭圆傅里叶变换；地标点法；种群识别；鸢乌贼；轮廓可视化

Morphological differences and contour visualization of statoliths in different geographic populations of purpleback flying squid (Sthenoteuthis oualaniensis)

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Abstract： Statoliths are important hard tissues in cephalopods. Significant differences are found in the external morphology of statoliths in different groups or species. In this study, stepwise discriminant analysis was used to investigate the external morphological differences in purpleback flying squid statoliths in three different marine regions comprising the East Indian Ocean (5°S–2°N, 82°–92°E), Central East Pacific Ocean (02°37′S–0°59' N, 99°44′W–114°19′W), and Northwest Indian Ocean (17°04′N–17°18′N, 61°05′E–61°32′E). The contours of statoliths were reconstructed visually by using Fourier analysis and the landmark method. The results obtained by stepwise discriminant analysis showed that the overall accuracy was 84.4% for the traditional measurement method, 82.9% for the Fourier analysis method, and 87.3% for the landmark method. The contour visualization results showed that the purpleback flying squid statoliths were small in the Central East Pacific Ocean, and the curvature of the side region was the most obvious. The radian differentiation of statoliths was most gentle in the East Indian Ocean. In the Northwest Indian Ocean, the rostral region of statoliths was shorter and the dorsal region was smoother. The reconstruction results detected significant differences in the outer morphology of statoliths in different marine regions. The results obtained in this study show that all three methods are effective for identifying populations, but the landmark method is better than the traditional measurement method. The reconstruction of statolith contours by using the Fourier transform and landmark methods provides an important scientific basis for conducting taxonomy according to statolith morphology.

Key words: Contour visualization; Elliptic Fourier transform; Landmark method; Population identification; Purpleback flying squid; Statolith morphology

分子标记在渔业资源增殖放流效果评估中的应用研究

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摘要：渔业资源增殖放流是指对野生鱼、虾、蟹、贝类等进行人工繁殖、养殖或捕捞天然苗种在人工条件下培育后，释放到渔业资源出现衰退的天然水域中，使其自然种群得以恢复。与传统的增殖放流效果评估方法相比，分子标记具有避免鱼体损伤、标记不丢失、且检测过程不受生长和活动影响等优势，同时可以长期监测增殖放流活动对野生群体的遗传学影响。

本研究基于线粒体控制区和微卫星等分子标记，开展了中国对虾、三疣梭子蟹、黑鲷等重要增殖放流物种的增殖放流效果评估。结果表明：（1）中国对虾群体遗传多样性较低，不同世代群体间的遗传分化不显著；回捕样品中放流苗种的比例为 5.31%。（2）三疣梭子蟹回捕比例达 14.81%，但不同育苗单位的增殖放流效果差异较大。（3）舟山岛礁周边海域的黑鲷回捕比例约为 10%，但广州、深圳海域的黑鲷放流效果明显，回捕比例高达 24.5%。以上研究为中国对虾等重要渔业资源修复及其渔业可持续发展提供了基础依据。

关键词：渔业资源；增殖放流；分子标记；效果评估

Application of Molecular Markers in Fishery Stock Enhancement and Effect Evaluation

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Abstract： Stock enhancement is a positive fishery management tool to increase the biomass of depleted fishery resources by releasing the artificial reproduction, cultivation, or capture of natural fry of wild fish, shrimp, crabs, shellfish, etc. Compared with traditional markers, molecular markers could avoid direct damage to fish body and not be lost. The individual identification will not be affected by their growth and activity, and moreover it can monitor the genetic impact of stock enhancement for a long time.

In this study mitochondrial DNA control region and microsatellite markers were employed to conduct the effect evaluation of stock enhancement for the economically important species including Fenneropenaeus chinensis, Portunus trituberculatus and Acanthopagrus schlegelii. The results indicated that: (1) the population genetic diversity of F. chinensis was relatively low, and the genetic differentiation among different generations was not significant; the proportion of released individuals was estimated to be 5.31% for all the recaptured individuals. (2) the recapture rate of P. trituberculatus reached 14.81%, but the effect of stock enhancement in different breeding nurseries varied greatly. (3) the recapture rate of A. schlegelii in the coastal waters of Zhoushan Island was about 10%, but it was

24.5% in the coastal waters of Guangzhou and Shenzhen. The results of the present study provides a fundamental basis for the restoration of important fishery resources and their sustainable development.

Key words: Marine fishery resource; Stock enhancement; Molecular markers; Effect evaluation

长江口中华绒螯蟹仔蟹食性和肠道菌群的时空差异分析

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摘要：长江口是中华绒螯蟹的重要产卵场，近岸潮间带水域能够为幼体提供适宜地栖息生境。仔蟹阶段是中华绒螯蟹变态发育且生活习性改变的重要时期，然而还没有关于其在野外食性变化的相关研究。本研究从食性和肠道菌群的角度揭示仔蟹的食物种类组成、肠道菌群结构及其在不同空间和时间上的差异。在2022年6月至12月每月大潮期间分别在长江口崇明岛南支上游（绿华）、中游（南门）以及下游（陈家镇）潮滩区域收集中华绒螯蟹仔蟹。肠胃含物样品通过18S和16S高通量测序，分析仔蟹的食性与肠道菌群组成。研究结果表明，中华绒螯蟹仔蟹阶段的食物组成包括链型植物门、节肢动物门（17.1%）、绿藻门（3.4%）。肠道菌群包括软壁菌门（39.5%）、变形菌门（36.6%）、拟杆菌门（13.5%）、厚壁菌门（7.5%）。总体来说，中华绒螯蟹仔蟹时期主要以植物碎屑为食，肠道微生物中软壁菌门和变形菌门存在一定的相互作用。

关键词：长江口；中华绒螯蟹仔蟹；食性；肠道菌群

Temporal and Spatial Differences in the Diet and Gut Microbiota of Chinese Mitten Crab Zoea in the Yangtze River Estuary

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Abstract： The Yangtze River Estuary serves as a critical spawning ground for the Chinese mitten crab, and the intertidal zone near the coast provides suitable habitats for the larvae. The zoeal stage is a crucial period in the Chinese mitten crab's life cycle, involving morphological development and changes in behavior. However, there is a lack of research regarding its altered dietary habits in the wild. This study aimed to investigate the food composition and intestinal microbiota of zoeal crabs across different spatial and temporal dimensions. Zoeal crab specimens were collected during each high tide from June to December 2022 at specific areas in the Yangtze River Estuary, including the upstream (Lvhua) and midstream (Nanmen) regions of Chongming Island and the downstream area (Chenjiazhen). Stomach content samples underwent 18S and 16S high-throughput sequencing to analyze the dietary preferences and the microbiota composition in the crabs' intestines. Results indicated that the food composition during the zoeal stage of the Chinese mitten crab included the Phylum Arthropoda (17.1%), Chlorophyta (3.4%), and Plantae. The microbiota consisted of the Phyla Bacteroidetes (39.5%), Proteobacteria (36.6%), Actinobacteria (13.5%), and Firmicutes (7.5%). In conclusion, the primary diet of the zoeal stage of the Chinese mitten crab comprises plant detritus, and there is a certain level of interaction between the Bacteroidetes and Proteobacteria in the intestinal microorganisms.

Key words: Yangtze River Estuary; larvae of Eriocheir sinensis; Diet; Gut Microbiota

东海剑尖枪乌贼春生群体个体发育对环境变化响应研究

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摘要：掌握种群生长对环境变动的响应关系有助于全面了解其生活史特征。通过平衡石日龄及每日增量宽度分析春生群体的生长规律，并采用梯度森林法和广义可加性混合模型探究环境因素对生长的影响权重及效应关系。结果表明，根据每日增量到核心的距离将春生群体划分四个生长阶段（胚-仔期 S1、稚鱼期 S2、亚成鱼期 S3、成鱼期 S4）；温度和盐度在 S1 阶段对生长影响的累计权重最大，温度和流速在 S2 阶段的累计权重最大，温度在 S3 阶段的权重最大，混合层深度、温度和盐度在 S4 阶段的累计权重最大；T25 与日生长呈先正（S1、S2）后负（S3）再正（S4）的相关关系；春生群体的生长效益随 MLD 的加深而逐渐减少（30-50 m），随 SSS 的升高而逐渐减少（S3—S4 阶段，32.2-33.2 ‰），随流速的升高而逐渐增加（S1 阶段，0.1-0.2 m/s）。分析认为：春生群体在生长不同阶段对环境因素响应的差异可能导致生长体征的变动。本研究为全面了解剑尖枪乌贼的生活史特征提供科学依据。

关键词：东海；剑尖枪乌贼；生长阶段；每日生长增量；环境因素

Ontogenetic growth responses to the environmental changes of Uroteuthis edulis spring stock in the East China Sea

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Abstract： Population growth response to environmental variations will help to understand their life history traits. In this study, the daily growth of the spring stock was analyzed based on the age and increment width of statolith. The gradient forest method (GFM) and generalized additive mixed models (GAMMs) were used to explore the changes in the weights of environmental variables and the relationships between daily growth and environmental variables in various growth stages. According to the distance from daily increment to core in the statolith, the life history of the spring stock was divided into four growth stages (embryo-larval stage S1, juvenile stage S2, sub-adult stage S3, and adult stage S4). The cumulative weight of temperature and salinity was the largest in S1 stage; the cumulative weight of temperature and velocity was the largest in S2 stage; the cumulative weight of temperature was the largest in S3 stage; the cumulative weight of mixed layer depth (MLD), temperature, and salinity was the largest in S4 stage. The relationship between temperature at the depth of 25 m (T25) and daily growth of the spring stock was firstly positive correlation (S1-S2), then negative correlation (S3), and finally positive correlation (S4). The relationship between environment variable and growth of the spring stock gradually decreased with the increase in MLD (30 to 50 m) and SSS (S3-S4, 32.2‰ to 33.2‰) and gradually increased with the increase in the velocity of currents (S1, 0.1 m/s to 0.2 m/s). The differences in the responses of the spring stock to environmental variations in different growth stages might lead to the changes in the growth traits for the spring stock. This study provides a scientific basis for a comprehensive understanding of the life history traits of Uroteuthis edulis (U. edulis).

Key words: East China Sea; Uroteuthis edulis; Growth stage; Daily growth increment; Daily growth increment; Environment

不同温度驯化对铜鱼幼鱼温度耐受性影响研究

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摘要：以铜鱼幼鱼为研究对象，探究其在不同温度(低温组 14 、18 ℃；中温组 22 ℃；高温组 26、30℃)下耐受性影响及肠道微生物变化。结果表明低温组临界温度分别为 2.22±0.37℃、4.19±0.15℃，29.82±0.39℃、31.02±0.88℃；中温组为 7.86±0.71℃，35.11±0.15℃；高温组临界温度分别为 9.42±0.36℃、10.64±0.17℃，36.03±0.35℃、37.42±0.19℃。临界低温随驯养温度降低而降低，临界高温随驯养温度升高而升高，临界低温和临界高温与驯化温度呈正相关 。肠道微生物菌群丰度排名前十菌门相同，低温组临界低温和 30℃高温组铜鱼幼鱼临界高温时肠道微生物 OTU 数量增加，30℃组鱼临界温度的 Alpha 多样性较低温驯养组和中温驯养组显著降低。综合以上结果认为驯化温度可以改变铜鱼幼鱼温度耐受性，临界温度对铜鱼幼鱼肠道形态和肠道微生物会造影响。

关键词：铜鱼；温度驯化；热耐受性；肠道微生物菌群。

Study on the Effect of Different Temperatures Domestication on the Temperature Tolerance of Young Coreius heterodon

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Abstract： Coreius heterodon fish were studied at different temperatures (low temperature group 14, 18 ℃; Middle temperature group 22 ℃; Effects of tolerance and changes of intestinal microbiome in high temperature group (26, 30℃). The results showed that the critical temperatures of the low temperature group were 2.22±0.37℃, 4.19±0.15℃, 29.82±0.39℃, 31.02±0.88℃, respectively. The medium temperature group was 7.86±0.71℃ and 35.11±0.15℃. The critical temperatures of the high temperature group were 9.42±0.36℃, 10.64±0.17℃, 36.03±0.35℃, 37.42±0.19℃, respectively. Critical low temperature decreased with the decrease of domestication temperature, critical high temperature increased with the increase of domestication temperature, critical low temperature and critical high temperature were positively correlated with domestication temperature. The abundance of intestinal microbial flora was the same as that of the top ten bacterial groups. The number of intestinal microbial OTU increased at critical low temperature in the low temperature group and 30℃ high temperature group, and the Alpha diversity at critical temperature in the 30℃ group was significantly lower than that in the low temperature domestication group and the medium temperature domestication group. Based on the above results, it is concluded that acclimation temperature can change the temperature tolerance of Coreius heterodon fish, and the critical temperature can affect the intestinal morphology and intestinal microorganisms of Coreius heterodon fish.

Key words: Coreius heterodon; Temperature domestication; Thermal tolerance; Intestinal microbiota.

虾夷扇贝应答日本蟳捕食的行为特征及相关生理生态响应研究

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摘要：本实验研究了不同规格虾夷扇贝应对日本蟳捕食时的行为特征，鳃、闭壳肌和外套膜的超氧化物歧化酶，过氧化氢酶，精氨酸激酶和章鱼碱脱氢酶活力变化，并选取以上差异显著的组织转录组测序，查找关键基因并验证。结果显示：（1）扇贝会通过持续闭壳或运动的方式躲避日本蟳捕食，扇贝规格越大则闭壳力越大，同规格受日本蟳刺激后闭壳力更大，随着实验时间的延长，各规格扇贝闭壳能力均呈下降趋势。（2）捕食刺激后虾夷扇贝各组织酶活均有显著变化，中规格扇贝闭壳肌酶活差异最显著。（3）对中规格扇贝闭壳肌进行转录组分析，共识别到 C1ql4，CHRNA2，KIF13B，HMCN1，PROM1A 等 780 个差异基因在日本蟳刺激时差异表达，推测这些基因可能与虾夷扇贝受刺激后肌肉的运动及调节相关。综上，虾夷扇贝在受到敌害生物刺激时，其行为特征和相关生理生态指标会发生显著变化，研究结果对于虾夷扇贝在底播养殖过程中投苗规格提供了科学参考。

关键词：日本蟳，虾夷扇贝，测力计法，行为特征，转录组

Behavioral characteristics and related physiological and ecological indexes of cultured scallops (Mizuhopecten yessoensis) in response to predation by the crab Charybdis japonica

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Abstract：To investigate the effects of predation of the paddle crab Charybdis japonica on the culture and survival of scallops (Mizuhopecten yessoensis) during bottom culture, we investigated the behavioral characteristics of three sizes (small, medium, and large) of scallops in response to exposure to crabs. We also measured the activities of superoxide dismutase, catalase, arginine kinase, and octopine dehydrogenase in the gill, adductor muscle, and mantle of scallops before and after exposure to predation. Tissues that showed significant differences between control and test specimens were selected for deep sequencing of the transcriptome to identify and validate the key genes that were sensitive to predation. We found that scallops escaped from crab predation by continuous shell closure or movement. Shell closure force increased with scallop size, and scallops of the same size that were stimulated by the presence of crabs closed their shell more frequently than control scallops. The shell closure ability of scallops of all sizes decreased with increasing duration of the experiment. The enzyme activities of the three scallop tissues changed significantly after continuous stimulation, and the trend was particularly obvious in the enzyme activities of the adductor muscles of the medium-sized scallops. Transcriptome analysis of the adductor muscles of medium-sized scallops revealed 780 differentially expressed genes (322 up-regulated and 458 down-regulated), and expression levels of C1ql4, CHRNA2, KIF13B, HMCN1, and PROM1A changed after stimulation by crabs. Their sequencing results were verified by quantitative real-time PCR. We hypothesize that these genes may be related to muscle movement and regulation in M. yessoensis after stimulation. In conclusion, when M. yessoensis is stimulated by the presence of predators, its behavioral characteristics and related physiological and ecological indexes undergo significant changes. The results are relevant for developing specifications for M. yessoensis seedling casting during bottom culture.

Key words: C. japonica; M. yessoensis; dynamometer method; behavioral traits; transcriptome

万佛湖水域水生生物多样性研究

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摘要：水环境中生物种类组成复杂，有些种类个体微小、数量较少、不同生长阶段个体差异大，在进行调查时难以捕获、鉴定，这给湖泊资源调查工作带来诸多困难。环境 DNA（eDNA）技术可从环境样品中直接提取 DNA 片段，并对其进行扩增和高通量测序，从而用于湖泊生物多样性检测、群落分布和资源评估等方面。本研究结合传统采样法和 eDNA 技术对万佛湖水域鱼类繁殖期和索饵期 9 个点的水生生物进行多样性研究，并分析了水环境的理化特性如溶氧、温度等对水生生物多样性的影响。传统采样法与 eDNA 技术均显示繁殖期与索饵期水生生物多样性的类型存在差异，eDNA 技术显示更高的多样性水平。传统采样法在种群数量较大的物种采样方面有较高准确性，同时物种的分类信息相对确定，而 eDNA 技术鉴定得到的分类单元更多，但很多种类只能精确到属水平的分类。综上，本研究显示将传统采样与 eDNA 技术结合进行资源评估可以获得更加准确的物种多样性信息。

关键词：环境 DNA；理化因子；底栖动物；鱼类；浮游生物

Research on aquatic biodiversity in the waters of Wanfo Lake

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Abstract： The composition of biological species in the aquatic environment is complex, and some species are small, small in number, and have large individual differences in different growth stages, which are difficult to capture and identify during investigation, which brings many difficulties to the investigation of lake resources. Environmental DNA (eDNA) technology can be used to extract DNA fragments directly from environmental samples, amplify them, and sequence them with high throughput sequencing for lake biodiversity monitoring, community distribution, and resource assessment. In this study, the diversity of aquatic organisms at 9 points during the fish breeding period and the feeding period in the waters of Wanfo Lake was studied by combining traditional sampling method and eDNA technology, and the effects of physical and chemical characteristics of the water environment, such as dissolved oxygen and temperature, on aquatic biodiversity were analyzed. Both the traditional sampling method and eDNA technology showed that there were differences in the types of aquatic biodiversity during the breeding period and the foraging stage, and the eDNA technology showed a higher level of diversity. The traditional sampling method has high accuracy in sampling species with large populations, and the taxonomic information of species is relatively certain, while the eDNA technology can identify more taxa, but many species can only be classified accurately at the genus level. In summary, this study shows that combining traditional sampling with eDNA technology for resource assessment can obtain more accurate information on species diversity.

Key words: eDNA; Physicochemical factors; Benthic fauna; Fish; Plankton

基于零膨胀模型的温台渔场黄鲫资源时空分布特征

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摘要：为从零值处理的角度建立环境因子与黄鲫丰度分布的关系，本研究根据 2018-2019 年 4 季浙南近海（温台渔场）调查数据，采用零膨胀泊松（ZIP）模型和零膨胀负二项（ZINB）模型建立黄鲫丰度与环境因子的关系。通过比较，利用最优模型预测了 2020 年春、夏、秋三季黄鲫资源的时空分布。交叉验证结果表明，ZINB 模型在环境数据处理的两个部分中表现相对较好，在 ZINB 模型的两部分环境数据处理过程中，温度+深度和温度+深度+盐度是 AIC 最合适的建模组合。模型预测结果表明，从时间分布上看，2020 年夏季黄鲫的资源量高于春季。从空间分布来看，黄鲫资源分布呈现出从近岸海区向开阔海区递减的趋势。ZINB 模型预测的春、夏、冬三季较高的黄鲫丰度大致分布在温州和台州近岸海域。该研究拓展了渔业资源时空分布特征的研究思路，为有效保护和可持续利用黄鲫资源提供了科学依据。

关键词：黄鲫；环境因素；资源时空分布；零膨胀模型；养护和管理

Spatio-temporal distribution characteristics of Setipinna taty resources in Wentai fishing ground based on zero-inflated model

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Abstract：In order to establish the relationship between environmental factors and S. taty abundance distri-bution from the perspective of zero value processing, in this study, according to the survey data in the south inshore of Zhejiang (Wentai fishing ground) in 4 seasons from 2018 to 2019, zero-inflated poisson (ZIP) model and zero-inflated negative binomial (ZINB) model were used to establish the relationship between S. taty abundance and environmental factors. By comparing, an optimal model was used to predict the spatio-temporal distribution of S. taty resources in spring, summer and autumn in 2020. The results of cross-validation showed that the performance of ZINB model was relatively good in the two parts of environmental data processing procedures of the ZINB model, the temperature + depth and temperature + depth + salinity is the most suitable combination for modeling by AIC. y. Higher S. taty abundance was distributed in the depth of 20-40 m and salinity of 26-34‰. The prediction results of the model showed that the S. taty resource level was higher in summer than that in spring in 2020 from the perspective of temporal distribution. From the perspective of spatial distribution, the distribution of S. taty resources demonstrated a decreasing trend from inshore areas to open sea areas. The higher S. taty abundances predicted by ZINB model in spring, summer and winter were roughly distributed in the inshore waters of Wenzhou and Taizhou. This study ex-panded the ideas for the study of spatio-temporal distribution characteristics of fishery resources, explored the relationship between the distribution of S. taty resources and environmental factors and provided a scientific basis for the effective conservation and sustainable utilization of S. taty resources in Wentai fishing ground in the south inshore of Zhejiang, China by predicting the spa-tio-temporal distribution of the S. taty through the model.

Key words: Setipinna taty; Environmental factor; Spatio-temporal distribution of resources; Zero-inflated model; conservation and management

基于耳石几何形态测量学的野生鲢鳙群体识别研究

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摘要：为了解鲢鳙耳石的形态特征，以及微、星耳石在种间和种内的识别效果，本研究采取基于地标点法的几何形态测量学手段，分别对采自于长江九江段、铜陵段、芜湖段的鲢以及长江九江段、同里湖、鄱阳湖的鳙的微、星耳石进行了分析。结果显示，对于鲢、鳙种间差异，星耳石和微耳石判别正确率均为 100%；而对于种内鲢种群的星耳石和微耳石的判别正确率均为 100%，鳙种群在星耳石和微耳石的判别正确率分别是 100%和 75%。结果表明两种耳石均能有效的区别鲢和鳙；同时无论是对于长江干流间隔约 220 km（九江至铜陵段）至 86 km（铜陵至芜湖段）的不同鲢群体，还是对于长江下游干流、湖泊等的不同鳙群体，基于星耳石几何形态测量学分析方法均可以有效地识别，这将为进一步开发非法渔获物查证溯源方法提供重要的技术支撑。

关键词：鲢；鳙；星耳石；微耳石；几何形态测量学分析

Wild population identification for Hypophthal michthysmolitrix and Aristichthys nobilis based on otolith geometric morphometric analysis

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Abstract： In order to reveal the otolith morphological characteristics of silver carp (Hypophthal michthysmolitrix) and bighead carp (Aristichthys nobilis), as well as identification effects on the inter- and intra- species, the landmark-based geometric morphometric analysis was utilized to comparatively study asteriscus and lapillus of silver carp from Jiujiang, Tongling and Wuhu sections of the Changjiang River, as well as bighead carp from the Jiujiang section of the Yangtze River, Tongli Lake and Poyang Lake, respectively. The results showed that for the inter-species differences between silver and bighead carp, both the discriminant accuracy of asteriscus and lapillus were 100%; while for the intra-species, the discriminant accuracy of asteriscus and lapillus were 100% for silver carp, while they were 100% and 75% for bighead carp, respectively. The results indicated that both asteriscus and lapillus were effective in identifying the inter-species difference, and the asteriscus also had a high discriminant accuracy in the intra-species. The aforementioned findings suggest that the landmark-based geometric morphometric characteristics of asteriscus is able to effectively discriminate the stocks of not only silver carps in difference section of the Changjiang River with an interval of 220km (Jiujiang section to the Tongling section) to 86 km (Tongling section to Wuhu section), but also the bighead carps from the main stream and lakes in lower reach of the Changjiang River. The present study also provide important technical support for the further development of illegal catch verification and traceability methods.

Key words: Hypophthal michthysmolitrix; Aristichthys nobilis; asteriscus; lapillus; Geometric morphometric analysis

热胁迫对中华绒螯蟹亲蟹的影响机制

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摘要：全球变暖导致水体暖化问题日益严重，热胁迫将影响众多生物赖以生存的水生态系统。水温是影响中华绒螯蟹亲蟹生存的关键生境因子，高温会导致氧化应激问题，影响其正常生命活动，从而改变野外资源数量和栖息地分布。本研究分析了不同热胁迫下亲蟹的热耐受性能、组织结构和抗氧化系统的变化情况，并通过转录组学和蛋白组学技术挖掘鳃内响应急性热胁迫的关键基因、蛋白和通路。结果表明超 30℃热胁迫下亲蟹的鳃组织结构明显改变，抗氧化酶活性显著降低，抗氧化系统受到破坏。进一步地，多组学联合分析发现鳃内热休克蛋白 70 和谷胱甘肽巯基转移酶在基因和蛋白水平上均显著上调，参与抗热胁迫的调控过程；Relaxin 信号通路的显著激活表明 Relaxin 可能是减轻热胁迫引起的鳃氧化损伤的重要因子。本研究结果可为阐明热胁迫对中华绒螯蟹亲蟹的影响研究提供一定参考，为热胁迫下蟹类分子机制解析提供基础。

关键词：中华绒螯蟹，高温胁迫，氧化应激，分子机制

The influencing mechanism of heat stress on parent Eriocheir sinensis

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Abstract: Global warming leads to the increasingly serious problem of water body warming, and heat stress will affect the water ecosystem on which many organisms depend for survival. Water temperature is a key habitat factor affecting the survival of parent Eriocheir sinensis. High temperature will lead to oxidative stress, affect the normal life activities of parent E. sinensis, and thus change the quantity of wild resources and habitat distribution. In this study, the changes of thermal tolerance, tissue structure and antioxidant system of parent crabs under different heat stress were analyzed. The key genes, proteins and pathways in gills response to acute heat stress were explored by transcriptomics and proteomics techniques. The results showed that the structure of gills in parent crab was changed obviously under heat stress, and the activity of antioxidant enzyme was decreased significantly, destroying the antioxidant system. Further, the multi-omics analysis indicated that heat shock protein 70 (HSP 70) and glutathione s-transferase (GST) were significantly up-regulated at both gene and protein levels, and participated in the regulation process of heat stress resistance. The significant activation of relaxin signaling pathway suggested that relaxin may be an important factor in alleviating oxidative damage induced by heat stress in gills. This study can provide a reference for the influence study of parent crabs under heat stress, and provide a basis for the molecular mechanism analysis of crabs under heat stress.

Key words: Chinese mitten crab; high temperature stress; oxidative stress; molecular mechanism

气候变化对洪堡洋流生态系统结构的影响分析

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摘要：洪堡洋流生态系统易受年际和年代际气候变化的扰动。此前，有关该生态系统结构长期动态的研究大都集中于优势种更替的物种层面上，对生态系统整体结构的变化知之甚少。本研究收集了气候、区域环境变量以及生态系统不同功能组产量数据，旨在较为全面地了解气候变化驱动下洪堡洋流生态系统结构的长期变化特征。结果表明，洪堡洋流生态系统结构跃变集中发生于20世纪70年代前中期、80年代中期和90年代后期，较好地响应了气候和生态系统区域环境于上述年代期中的跃变。在众多气候和环境变量中，气候指数第一、第三主成分以及区域环境变量第一主成分对洪堡洋流生态系统结构变化的生态系统重要性更大，表明阿留申低压和厄尔尼诺-南方涛动的变化极大地影响了生态系统区域内以热量和风速为代表的区域环境的变化，进而影响生态系统结构功能组的变化。本研究可促进从整体角度理解气候变化引起的生态系统结构的变化，为基于生态系统的渔业管理提供依据。

关键词：东南太平洋；海洋生态系统；稳态变化；生物群落；气候变化；局部环境变化

Analysis of the impact of climate variability on the structure in the Humboldt Current System

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Abstract: Influenced by external stressors such as climate or ecology, marine ecosystem structure and function may undergo significant changes. The Humboldt current system (HCS) is of great interest because it supports for the world's largest pelagic fishery and is vulnerable to disturbances from interannual and decadal climate variability. Previous pioneering studies on the long-term dynamics in structure in the HCS have mostly focused on the replacement of the dominant species such as Engraulis ringens and the Sardinops sagax at the species level, and comprehensive understanding of the overall changes in ecosystem structure has been limited. Therefore, datasets were collected on climate, regional environmental variables and catches of different functional groups in this study, aiming to comprehensively understand the effects of climate variability on the long-term changes in ecosystem structure in the HCS. The results indicated that significant decadal-scale changes in the ecosystem structure in the HCS, aligning with inferred regime shifts in the early to mid-1970s, mid-1980s and late 1990s, which well responded to climate and regional environment regime shifts. Among the climatic and environmental variables studied, the first and third principal components of the climate index, as well as the first principal components of the regional environmental variables, showed higher ecological importance for ecosystem structure variations of the HCS. This suggested that the fluctuations in the Aleutian Low and El Niño-Southern Oscillation significantly affected the regional environment characterized by heat and wind speed, consequently influencing alterations in the ecosystem structure. This study could enhance a holistic understanding of long-term changes in ecosystem structure driven by climate variability, providing a robust foundation for ecosystem-based fisheries management.

Key words: Southeast Pacific; marine ecosystem structure; regime shifts; long-term change; climate variability; regional environmental changes

秘鲁外海茎柔鱼渔业生物学特性年际变化及其对 ENSO 的响应：2008–2020

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摘要：茎柔鱼作为一种短生命周期的头足类，其个体生长、资源量变动等对气候及海洋环境变化极为敏感。本文根据 2008-2020 年在秘鲁外海采集的 7514 尾茎柔鱼样本，对其个体大小、性腺成熟度、初次性成熟胴长等渔业生物学特性进行分析，探究 ENSO 对其个体生长的影响。研究结果显示，不同年份雌、雄个体胴长-体重关系、性腺成熟度组成存在显著差异（P<0.05）。拉尼娜事件有利于茎柔鱼个体生长、性腺发育变慢，产生中大体型群；厄尔尼诺事件会抑制茎柔鱼生长，加速个体的性成熟，产生较小体型群。在 2008-2020 年间，小型群胴长下降了 46mm，而中型群胴长增长了 28mm；雌性茎柔鱼初次性成熟胴长下降了 201.2mm，雄性初次性成熟胴长下降了 143mm。研究认为，2008-2020 年间由于气候变化引起的海洋环境发生的变化，对秘鲁外海茎柔鱼种群结构、生长发育均产生了重要的影响。

关键词：茎柔鱼 秘鲁外海 种群结构 性成熟度 ENSO

Long-term series variation in fishery biology of Dosidicus gigas off Peru: Response to ENSO from 2008 to 2020

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Abstract： As a cephalopod with a short life cycle, the Dosidicus gigas (Jumbo flying squid) is extremely sensitive to changes in climate and marine environment in terms of individual growth and resource changes. Based on 7,514 D. gigas samples collected off Peru from 2008 to 2020, the fishery biological characteristics such as size, sexual maturity, and the mantle length at the first sexual maturity were analyzed to explore the effects of ENSO on individual growth. The results showed that there were significant differences in the relationship between mantle length and body weight and in the composition of sexual maturity between male and female individuals in different years ($P<0.05$). La Niña events were conducive to the individual growth of D. gigas and slowed down their sexual maturity, producing D. gigas groups in medium and large sizes; El Nino events inhibited the individual growth of D. gigas and accelerated their sexual maturity, producing D. gigas groups in smaller size. From 2008 to 2020, the mantle length of the small-size group decreased by 46mm, while that of the medium-size group increased by 28mm. The mantle length at the first sexual maturity of female D. gigas decreased by 201.2mm and that of male D. gigas decreased by 143mm. The study concluded that the changes in the marine environment caused by climate change from 2008 to 2020 have had a significant impact on the population structure, growth, and development of the D. gigas off Peru.

Key words: Dosidicus gigas; off Peru; Population structure; sexual maturity; ENSO

东海渔业生物群落营养级链效应

及驱动因素

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摘要：大量证据表明人类活动（捕捞和增殖放流）和气候变化改变了渔业生态系统功能及群落结构。当前，东海正经历着渔业捕捞整治和渔业资源增殖放流措施改革，这些管理活动对东海渔业群落结构的影响知之甚少。为了解东海渔业生物群落结构的现状，营养级关系及变化趋势，本文利用近十年的东海中北部渔业拖网调查数据、渔船努力量和舟山增殖放流量数据，进行渔业生物粒径谱与营养级链接关系的研究。结果表明。东海的渔业生物可根据鱼类粒径大小，斜率的变化特征，分为大鱼（捕食性或底层鱼）、小鱼（饵料鱼或中生层鱼）、虾、蟹四类。结合多元序列模型，量化了各类群之间的营养级关系，分析了东海渔业生态系统的营养级链的变化趋势及驱动因素。秋季鱼类受到上行效应控制，虾蟹类受到下行控制。春季鱼类受到下行控制，虾蟹类受到上行控制为主。根据 MAR 自回归分析，当前的食物链上行效应受到增殖放流和捕捞强度的控制发生较大变化，上行效应减弱，下行效应逐渐增强。

关键词：粒径谱；鱼类；营养级；上行效应；下行效应

size spetrum; fisheries; trophic level; bottom-up; top-down

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Abstract： A large amount of evidence shows that human activities (exploitation and enhancement) and climate change have changed fishery ecosystem functions and community structure. Currently, the East China Sea is experiencing reforms in fishery regulation and fishery resource enhancement and release measures. Little is known about the impact of these management on the fishery community structure in the ECS. In order to understand the current status of the fishery community structure, trophic level relationships and changing trends in the ECS, this study made use of decadal time series trawl survey in the central and northern ECS, fishing vessel effort and release data to investigate size spectra and trophic levels of the fisheries resources. The trophic link were analyzed through size and taxanomic groups separated by size spectrum and ecological functions. The results showed that marine organisms can be divided into four categories: large fish (predatory or bottom fish), small fish (forage fish or mesozoic fish), shrimp, and crabs based on the size spectrum and the changing characteristics of the slope. Combined with the multivariate time series model, the trophic level relationship between various groups was quantified, and the changing trends and driving factors of the trophic level were analyzed. In autumn, fish species interactions are under bottom-up control, while shrimps and crabs are under top-down control. In spring, trophic control were reversed, indicating the release pressure of fishing effort and enhancement. During last decades, the bottom-up effect has weakened and the top-down effect has gradually increased.

Key words: size spectrua;fish; tropic level; bottom-up control; top-down control

河川沙塘鳢早期个体食性转化和异速生长研究

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摘要：河川沙塘鳢（Odontobutis potamophila）野生资源衰退严重，因其较高的经济价值，人工繁育迫在眉睫，掌握早期阶段的食性转换和生长是苗种培育的基础。本研究对早期个体的食性分析表明, 出膜第 2 天即可摄食，枝角类和桡足类是最主要的饵料类群；聚类分析发现全长小于 6 mm 的个体主要摄食无节幼体；6-8 mm 的个体主要摄食枝角类和桡足类；8-9 mm 的个体摄食的枝角类的比例下降, 桡足类增加；而大于 9 mm 的个体，只摄食枝角类和大个体桡足类，结果显示随个体生长存在明显的食性转换。分析早期个体的生长发现，刚出膜个体全长达 6.53±0.51 mm, 体重 1.93±0.56 mg，头部、躯干部、尾部及运动器官都呈现先正异速后负异速生长的模式，各形态生长拐点集中在 10 日龄，与食性转化时间耦合。研究结果将为河川沙塘鳢的苗种培育提供科学指导。

关键词：河川沙塘鳢；食性转换；异速生长

Study on early individual diet shift and allometric growth of Odontobutis potamophila

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Abstract： The wild resources of Odontobutis potamophila are rapidly dwindling. Artificial breeding is going to become more and more common due to its great economic worth. The goal of breeding is to acquire early development and diet transformation. The feeding habits of early individuals showed that they could feed on the second day after hatching, and cladocerans and copepods were the primary food categories. Cluster analysis revealed that individuals with a total length of less than 6 mm primarily dined on nauplius. The 6–8 mm individuals mostly consume copepods and cladocerans. Copepods increased while the percentage of cladocerans feeding on 8–9 mm individuals dropped. Individuals larger than 9 mm, however, exclusively consume giant copepods and cladocerans, and the results showed a significant change in diet with growth. The findings revealed that during the early stage, individuals hatched at 6.53 ± 0.51 mm in total length and 1.93 ± 0.56 mg in body weight. The head, trunk, tail, and locomotor organs displayed a positive allometric growth pattern, followed by a negative one. Morphological inflection points first appeared around 10 days, coinciding with the start of the change in feeding habits. The findings provide scientific guidance for O. potamophila breeding.

Key words: Odontobutis potamophila; diet shift; allometric growth

基于环境 DNA 技术的长江口鱼类多样性研究

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摘要：由于人类活动和环境变化，长江口的渔业资源急剧下降，导致生态系统受到了破坏，不少珍稀鱼类也濒临灭绝。环境 DNA（eDNA） 技术已被许多研究证明在研究和揭示物种生物多样性方面具有很高的潜力，是一种极具推广应用前景的新型技术。本研究采用 eDNA 技术和底拖网相结合方法对长江口水域物种组成和多样性进行分析，同时对两种方法进行比较 。结果表明，利用 eDNA 技术和底拖网两种方法均检测到 18 种鱼类，其中有 6 种鱼是两种检测方法共同检测出来的，均以鲈形目(Perciformes)最多。根据 Alpha 多样性指数显示，eDNA 技术检测长江口鱼类群落多样性均显著大于底拖网方法。综上所述，eDNA 技术可以很好的应用于长江口鱼类多样性评估，为该地区鱼类多样性调查提供了一个重要补充手段，具有重要意义和良好应用前景。

关键词：长江口；环境 DNA；底拖网；鱼类多样性

Study on fish diversity in the Yangtze Estuary based on environmental DNA technology

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Abstract： Due to anthropogenic activities and environmental changes, the fishery resources in the Yangtze River Estuary (YRE) have experienced a significant decline, leading to ecosystem degradation and the extinction of numerous rare fish species. Environmental DNA (eDNA) technology has been extensively validated through various studies for its high potential in studying and revealing species biodiversity. It is an emerging technology with promising prospects for widespread adoption and application. In this study, we employed a combination of eDNA technology and bottom trawling method to analyze species composition and diversity in the waters of the Yangtze Estuary, while also comparing these two methods. The findings revealed that both eDNA technology and bottom trawling detected 18 fish species, with 6 common detections between them; Perciformes being the most frequently observed group. Furthermore, based on Alpha diversity index analysis, eDNA technology demonstrated significantly higher fish community diversity compared to bottom trawling method. To summarize, our results highlight that eDNA technology can effectively contribute towards assessing fish diversity in the Yangtze Estuary by providing an important supplementary approach for investigating this area's fish biodiversity; thus holding substantial significance with promising applications.

Key words: Yangtze River Estuary; Environmental DNA (eDNA); Bottom Trawl; Biodiversity

东海春夏季浮游植物群落生态特征及其影响因子分析

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摘要：为获得近年东海浮游植物群落的生态学特征，通过 2015-2017 年 5 月（春季）和 8 月（夏季）对东海海域浮游植物和环境要素进行调查，本文分析了东海浮游植物群落结构特征及其与典型环境因子（水文、营养盐、CODMn、悬浮物浓度等）之间的关系。研究表明，春季浮游植物优势种主要由虹彩圆筛藻（Coscinodiscus oculus-iridis）、琼氏圆筛藻（Coscinodiscus jonesianus）和中肋骨条藻（Skeletonema costatum）组成，夏季的主要优势种为中肋骨条藻。受长江冲淡水、钱塘江、东海沿岸流等影响，东海近岸海域环境浮游植物数量明显高于东海大陆架海域。冗余度分析结果显示，2015-2017 年春季，对调查海域浮游植物丰度影响较大的环境因子是活性磷酸盐；2015-2017 年夏季，对研究海域浮游植物丰度影响较大的环境因子是无机氮、活性磷酸盐和化学需氧量。

关键词：东海；浮游植物群落；生态特征；环境因子；春夏季

Ecological characteristics and influencing factors of phytoplankton community in spring and summer in East China Sea

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Abstract： In order to understand the ecological characteristics of phytoplankton community in East China Sea in recent years, the characteristics of phytoplankton community in East China Sea was analyzed by investigating the basic elements of phytoplankton and environment in May and August from 2015 to 2017. The results showed that the nitrogen phosphorus ratio in the study area of East China Sea in spring was 20 ~35. The dominant species of phytoplankton in spring were mainly composed of Coccinodiscus oculus-iridis, Coccinodiscus jonesianus and Skeletonema costatum. The ratio of nitrogen to phosphorus in summer was higher than that in spring and much higher than 16:1. The dominant species in summer was Skeletonema costatum. According to the investigation, the number of phytoplankton in the coastal waters of the East China Sea was significantly higher than that in the continental shelf of East China Sea. The redundancy analysis results showed that from the spring of 2015 to 2017, the environmental factor that had a great impact on phytoplankton in the investigated sea area was active phosphate. From the summer of 2015 to 2017, the environmental factors that had a great impact on phytoplankton in the investigated sea area were inorganic nitrogen, active phosphate and chemical oxygen demand.

Key words: East China Sea; Phytoplankton community; Ecological characteristics; Environmental factors; Spring and summer

富里酸（FA）对 MC–LR 的光敏降解作用及相关环境条件研究

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摘要：淡水池塘蓝藻水华频发，微囊藻毒素（MCs）会对养殖动物造成直接危害。光降解是自然水环境消减微囊藻毒素危害的有效途径。富里酸（FA）为池塘水环境中广泛存在的光敏剂。通过模拟太阳光照试验，探究不同浓度 FA 对 MC-LR 的光敏化降解作用及相关环境条件因素。结果表明：MC-LR 能在去离子水中发生直接光解反应。不同浓度（2.5、5、7.5 和 10 mg L-1）FA 对 MC-LR 的光解均有促进作用，其中 7.5 mg L-1FA 对 MC-LR 的光敏降解作用最强，180 min 时降解率达 52.65%。FA 对 MC-LR 的光敏降解过程符合二级反应动力学，其光敏降解产物与去离子水中直接光解产物相同。不同 pH 值和不同光照强度下，FA 对 MC-LR 的光敏降解作用分别为 pH6 > pH7 > pH8 > pH9 和 350 W > 500 W> 200 W。结果表明 pH 值和光照强度均会影响富里酸（FA）对 MC-LR 的光敏降解作用。

关键词：富里酸；MC-LR；光敏降解

Photosensitized degradation of MC-LR by fulvic acid (FA) and its related environmental conditions

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Abstract： Cyanobacteria bloom frequently occurs in freshwater ponds, and microcystins (MCs) can cause direct harm to farmed animals. Photodegradation is an effective way to reduce MCs-caused harm in natural waters. Fulvic acid (FA) is a widely existing photosensitizer in ponds. Effects of different concentrations of FA on the photosensitized degradation of MC-LR and its related environment conditions were investigated under simulated solar light. The results showed that the direct photolysis of MC-LR occurred in deionized water. Different concentrations (2.5, 5, 7.5 and 10 mg L-1) of FA promoted the photolysis of MC-LR, of which 7.5 mg L-1FA had the best photosensitized degradation effect. The degradation rate reached 52.65% after 180 min. The photosensitive degradation of MC-LR by FA conformed to the second-order reaction kinetics, and the photosensitive degradation products are the same as the direct photolysis products in deionized water. Under different pH values and light intensities, the photosensitive degradation effects of FA on MC-LR were pH6>pH7>pH8>pH9 and 350 W>500 W>200 W, respectively. The results showed that both pH value and light intensity affected the photosensitized degradation of FA on MC-LR.

Key words: fulvic acid; MC-LR; photosensitized degradation

基于张网作业调查的
漳浦近海口虾蛄生物学特征初步研究

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摘要：根据 2022 年 8 月—2023 年 4 月福建漳浦近海张网作业调查数据，对主要渔获物口虾蛄（Oratosquilla oratoria）368 尾样品的体长、体质量、摄食强度、雌性卵巢发育程度、雌雄比例和肥满度等生物学特征进行了研究，以期为口虾蛄资源的利用和保护提供参考。研究表明，张网作业渔获物中，口虾蛄雌雄比例为 1：1.115，口虾蛄体长优势组为 110~130 mm，体质量优势组为 15.0~25.0 g，雌、雄样品平均体长、平均体质量差异均不显著（P>0.05）。口虾蛄体长和体质量关系为 W=2.140×10-5L2.882（R2=0.946，n=368）。雌性口虾蛄性腺成熟度在I-III期之间，III期个体主要出现在 2—4 月。口虾蛄摄食等级平均为 1.44 级，其中 1 级最多。口虾蛄群体肥满度指数平均值为 1.226，雄性略大于雌性。

关键词：口虾蛄；张网；生物学特征；漳浦近海

A preliminary study on the biological characteristics of Oratosquilla oratoria based on the survey of stow net in Zhangpu offshore waters

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Abstract： Mantis shrimp (Oratosquilla oratoria), the main catches of stow net fishing vessel in Zhangpu, Fujian, was followed and sampled monthly from August 2022 to April 2023. A total of 368 ind samples were used to determine body length and body weight, to characterize feeding intensity and female ovarian development, and to calculate the ratio of males to females in the catch, in order to analyze the fishery biology of O. oratoria.The results showed that the ratio of female to male was 1∶1.115 in the catch of O. oratoria, and the body length advantage group was 110~130 mm, and the body weight advantage group was 15.0~25.0 g， and there was no significant difference in average body length and average body weight between male and female samples. The relationship between body length and body weight was W = 2.140×10-5L2.882 (R2 = 0.946, n = 368). The gonadal maturity of female O. oratoria was between stage I-III, and stage III individuals mainly appeared from February to April. The average feeding grade of O. oratoria was 1.44, of which grade 1 was the most. The average annual condition factor index of O. oratoria was 1.226, and the male was slightly larger than the female.

Key words: Oratosquilla oratoria; stow net; biological characteristics; Zhangpu offshore waters

小球藻共生菌的分离鉴定及

藻菌共生系统的构建

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摘要：通过优化水环境中藻-菌群落，合理构建藻-菌体系，实现微藻与细菌的协同作用对水体净化与资源利用具有重要意义。本研究从稳定培养的普通小球藻藻际环境中分离获得细菌并进行基因测序、形态学观察和生化试验，确定细菌种类及生化特性，并考察不同菌株对小球藻生长的影响，筛选出微藻促生长菌与最优藻菌接种比例，构建稳定藻菌共培养体系。结果表明，在小球藻藻际环境中共分离鉴定 3 株菌，分别为发酵海鲜异希瓦氏菌、贝莱斯芽胞杆菌、红球菌属。3 株菌均可促进小球藻生长，且藻菌体系 Fv/Fm 均显著高于小球藻纯培养体系（$P<0.05$），贝莱斯芽胞杆菌与小球藻构建的藻菌共培养体系中，藻细胞密度达 29.65×106 cells/mL，显著高于其它藻菌体系（$P<0.05$）。相同培养条件下藻菌接种比例为 1:3 时小球藻 Chla 含量在第 8 d 达 5.68 mg/L，藻细胞密度为 33.05×106 cells/mL，显著高于其它比例组。

关键词：普通小球藻；共生菌；藻菌体系

Isolation and identification of symbiotic bacteria of Chlorella vulgaris and construction of algae-bacteria co-culture system

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Abstract：The synergistic effect of algae-bacteria is achieved by optimizing the algae and bacteria community in the water environment and constructing the algae-bacteria system reasonably, which is important for water purification and resource utilization. Bacteria were isolated from phycosphere of Chlorella vulgaris, and gene sequencing, morphological observation and biochemical test were carried out to determine the bacterial species and biochemical characteristics in this study. Moreover, a stable algal bacterial co-culture system was constructed based on examined the effects of different bacterial strains on the growth of C. vulgaris, and screened algae growth promoting bacteria and optimal inoculation ratios.

The results showed that three strains of bacteria were identified as Alishewanella jeotgali, Bacillus velezensis and Rhodococcus corynebacterioides, and all the three strains of bacteria could promote the growth of C. vulgaris. The Fv/Fm of the three algal-bacteria systems were significantly higher than that of C. vulgaris ($P<0.05$). The the algal cell density of C. vulgaris amounted to 29.65×106 cells/mL in the algae-bacteria system constructed by B. velezensis, was significantly higher than that of other algae-bacteria systems ($P<0.05$). Under the same culture conditions, Chl-a content of C. vulgaris reached at 5.648 mg/L on the 8th day when the inoculation ratio of C.vulgaris and B. velezensis was 1:3. The algal cell density reached 33.05×106 cells/mL, which was significantly higher than that of other combinations of ratios ($P<0.05$).

Key words: Chlorella vulgaris; commensal bacteria; algae-bacteria system

气候变化事件对头足类的影响研究进展

——繁殖、年龄生长与早期生活史

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摘要：头足类是重要的渔业资源之一，其渔业生物学特性极易受到海洋环境变化的影响。气候能量主要的储存载体是海洋，近年来频发的气候变化事件引发海洋环境因子变动，直接或间接地改变了头足类的渔业生物学特性，对头足类的渔业生产造成影响。为此，本文归纳和总结了气候变化对头足类繁殖、年龄生长与早期生活史三个方面的影响，并提出了展望。结果表明，气候变化事件的发生极易影响头足类动物的渔业生物学特性，海洋环境因子中的温度和初级生产力变动为主要影响因素。目前，相关研究对象多为柔鱼类和枪乌贼类等经济种，选用的海洋环境因子也多为海洋环境温度，今后应结合其它海洋环境数据研究气候变化事件对其它种类的影响。本文旨为研究气候变化事件对头足类渔业生物学特性的影响提供理论依据，为近年来气候变化事件频发下头足类渔业的可持续发展提供科学指导。

关键词：气候变化事件；头足类；渔业生物学；繁殖；年龄生长；早期生活史；影响

Review on the impact of climate change events on cephalopods—— reproduction, age and growth and early life history

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Abstract： Cephalopod is one of the most important fishery resources, which its fishery biology characteristics were easily affected by marine environmental changes. Ocean was the main storage carrier of climate energy. The changes of marine environmental factors in recent years were caused by frequent climate change events, which have directly or indirectly influenced the fishery biology characteristics and even fishery of cephalopods. Therefore, three aspects in this paper were summarized in previous studies from reproduction, age and growth and early life history. The results were shown that the fishery biology characteristics of cephalopods were easily affected by the occurrence of climate change events mainly through temperature and primary productivity in marine environmental factors. At present, the objectives of correlated researches were mostly concentrated on Ommastrephidae and Loliginidae, and marine temperature was mostly used to select for analysis from major marine environmental factors. In the future, long-term marine environmental data should be applied into the researches for impact of climate change on other cephalopods species. The purpose of this study was to provide a theoretical basis for analyzing the impact of climate change events on fishery biology characteristics of cephalopods, and to provide scientific direction for sustainable development of cephalopod fishery under frequent climate change events in recent years.

Key words: Climate change events; cephalopods; fishery biology; reproduction; age and growth; early life history; impact

江苏近海南部海域渔业生物群落结构的年际变化

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摘要：为了解江苏近海南部渔业生物群落结构的年际变化，利用 2014—2018 年春、秋两季在江苏近海南部的底拖网调查数据，运用聚类分析（Cluster）、多维标度法（MDS）、相似性百分比分析（SIMPER）和 RDA 分析等方法分析了江苏近海南部渔业生物群落结构的年际变化及其与环境因子的关系。结果表明：共捕获江苏近海南部渔业生物 114 种，隶属于 3 纲 17 目 59 科 94 属，优势种主要为棘头梅童鱼、鮸、葛氏长臂虾、口虾蛄、和三疣梭子蟹。Cluster 与 MDS 分析表明，研究期间春季可分为 A、B 两年份组，秋季可划分为 C、D 两年份组，A、B 组与 C、D 组的组间相异性系数分别为 65.49、55.33。SIMPER 分析显示，A 组与 B 组的组间分歧种主要有小黄鱼、三疣梭子蟹、日本蟳等；C 组与 D 组的组间分歧种主要有三疣梭子蟹、鮸和凤鲚等。RDA 分析表明，水温是决定渔业生物群落结构变化的重要因素。

关键词：群落结构；聚类分析；优势种；江苏近海南部；相对重要性指数

Interannual changes in the community structure of fishery assemblage in the southern coastal waters of Jiangsu Province，China

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Abstract：Based on the data of trawl survey in the southern coastal waters of Jiangsu Province in two seasons from 2014 to 2018. Cluster, MDS, SIMPER and RDA were used to analyze the variation in the community structure of fishery assemblage and their relationship with environmental factors. The results showed that there are 114 fishery species in the survey area, belonging to 3 classes,17 orders, 59 families, and 94 genera. The main dominant species included Collichthys lucidus, Miichthys miiuy, Palaemon gravieri, Oratosquilla oratoria, Portunus trituberculatus. The results of Cluster and MDS showed that during the 5 survey years, station groups in spring cound be divided into Group A and B and the average dissimilarity was 65.49. Station groups in autumn cound be divided into Group C and D and the average dissimilarity was 55.33. SIMPER showed that the main discriminating species of Group A and B were Larimichthys polyactis, Portunus trituberculatus and Charybdis japonica. While they were Portunus trituberculatus, Miichthys miiuy and Coilia mystus in Group C and D. RDA showed that temperature was the major factor in the change of community structure of fishery assemblage.

Key words: community structure; cluster analysis; dominant species; southern coastal waters of Jiangsu Province; index of relative importance

东海大黄鱼生物学特征演变及修复前景分析

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摘要：摘要：根据 2013 年—2021 年的春秋两季（4 月、11 月）和 2020 年—2023 年四季的渔业资源调查所获得的大黄鱼样本，进行大黄鱼基础生物方面研究（主要研究大黄鱼的体长、体重关系，性腺成熟度和摄食等级等，根据耳石年龄鉴定和体长数据，利用 logistic 回归方程，研究大黄鱼的生长规律。结果如下。大黄鱼的体长范围为 53.6—255mm，平均体长 168.9mm。雌雄个体体长不存在显著差异（ANOVA , $P>0.05$）。体长与体重关系式为：（$R2=0.9897$）。雌雄比例为 1.65：1，雌性多于雄性。性腺成熟度范围为 II—VI 期,以 II 期为主。雌性个体初次性成熟体长($L50\%$)大约为 167.5mm。摄食等级以主要以 0 级为主，主食口虾蛄（Oratosquilla oratoria）、龙头鱼（Harpadon nehereus）等为主。

关键词：大黄鱼；生长；摄食；繁殖；舟山海域

Analysis of biological characteristics evolution and restoration prospect of large yellow croaker in the East China Sea

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Abstract：According to the spring and autumn of 2013-2021 (April, November) and 2020-2022 four seasons of fishery resources samples, Larimichthys crocea basic biological research (main study of Larimichthys crocea body length, weight relationship, gonad maturity and feeding grade, etc., according to the otolith age identification and body length data, using logistic regression equation, study the growth pattern of Larimichthys crocea. The results are as follows. The body length ranged from 53.6 to 255mm, with a mean body length of 168.9mm. There was no significant difference in body length between males and females (ANOVA, $P> 0.05$). The relationship between body length and body weight is: ($R2=0.9897$). The ratio of males and females was 1.65:1, with more females than males. The gonadal maturity ranged from stage II to stage VI, mainly from stage II. The sexual mature for the first time body length($L50\%$) of the females is approximately 167.5mm. The feeding grade is mainly 0, the staple food mantis Oratosquilla oratoria, Harpadon nehereus etc. Logistic Equation fits the body length growth curve, the equation is:, $L\infty$ body length is 367 ± 20mm. Through the comprehensive analysis of literature, the key problems of repairing large yellow croaker resources are studied. This study shows that the large yellow croaker in the East China Sea showed the gradual decrease in the length of primary sexual maturity, advanced sexual maturity, individual miniaturization and low age, and the staple food is benthic organisms. To realize the restoration of large yellow croaker resources, it is necessary to fully understand the causes of the decline; secondly, to grasp the biological characteristics of large yellow croaker resources; third, to grasp the selectivity of the habitat; fourth, to maintain or form the minimum spawning group.

Key words: Larimichthys crocea; Growth; Feeding; Reproduction; Zhoushan sea area

非经典生物操纵对大黄堡湿地缓冲区池塘水体富营养化的治理

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摘要：为改善大黄堡湿地缓冲区池塘水质和生物状况，在利用鲢、鳙滤食性鱼类直接摄食藻类的非经典生物操纵的基础上，组合投放有益藻类和刮食性鱼类细鳞斜颌鲴，为水环境保护、修复及合理运用提供参考。结果表明，监测期间共鉴定浮游植物 7 门 124 种（属），主要以绿藻门为主；浮游植物平均丰度为 14.74×107 ind./L，以绿藻门为主，且蓝藻门丰度下降了 99.11%；常见优势种为菱形藻、席藻、小球藻和蹄形藻等，优势种种类组成由最初的蓝藻为主变为以绿藻和硅藻为主；浮游植物群落结构多样性 H'、J 和 D 平均值分别为 2.59、0.61、1.54，调查湿地池塘水体处于轻污染水平。水体 pH、氧化还原电位、总氮和总磷与浮游植物优势种丰度变化有显著相关性（$P < 0.05$）。总氮、总磷、硝酸盐和磷酸盐分别下降了 42.65%、33.04%、90.22%和 40.27%，表明此调控方法可有效改善水质、控制蓝藻水华，重塑浮游生物群落结构。

关键词：湿地池塘；生物调控；水质；浮游植物；水生态环境监测；污染评价

Water eutrophication control in the pond of Dahuangpu Wetland buffer zone by using non-traditional biomanipulation

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Abstract： In order to improvement of the water quality and biological conditions in the pond of Dahuangpu Wetland buffer zone, based on the non- traditional biomanipulation using filter-feeding fishes of Silver carp and Bighead carp for direct algal feeding, combination of beneficial algae and mixing of scraper-feeding fish species, Xenocypris. During the monitoring period, a total of 124 species belonging to 7 phyla were identified, dominated by Chlorophyta species. The average abundance of phytoplankton was 14.74×107 ind./L, and also dominated by Chlorophyta species. Common dominant species were Nitzschia sp., Phormidium sp., Chlorella sp. and Krichneriella sp., The composition of dominant species changed from Cyanophyta to Chlorophyta and Bacillariophyta. The average values of phytoplankton diversity index (H'), evenness index (J) and richness index (D) were 2.59, 0.61 and 1.54, respectively. The water quality of the pond in the buffer zone was lightly polluted. The pH, redox potential and the content of total nitrogen and total phosphorus had significantly correlationship with the changes of phytoplankton community structure ($P < 0.05$). The contents of total nitrogen, total phosphorus, nitrate and phosphate were decreased by 42.65%, 33.04%, 90.22% and 40.27%, respectively, the species abundance of Cyanophyta decreased by 99.11%. It was shown that this control method can effectively improve water quality and control cyanobacterial blooms, reshaping plankton community structure.

Key words: Wetland pond; biomanipulation; Water quality; Phytoplankton; Water environment monitoring; Pollution evaluation

长江江豚人工饲养群体摄食及游泳行为声信号特征研究

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摘要：长江江豚为我国特有的一种小型齿鲸，拥有发出回声定位信号并获取其中探测信息的能力。为探究不同行为状态下长江江豚回声定位信号特征差异，通过筛选摄食及游泳状态下的声信号，对其声学参数统计分析，并运用模糊函数研究其分辨能力。结果显示，长江江豚在两种状态下回声定位信号的-10 dB持续时间、-3 dB带宽、重心频率及均方根带宽表现出显著差异(P<0.05,T-test)。长江江豚回声定位信号的距离分辨能力较强，达到了毫米级。本研究为长江江豚生物声学研究提供一定科学参考。

关键词：长江江豚；回声定位信号；行为状态；模糊函数

Acoustic signal characterization of feeding and swimming behaviors of captive Yangtze finless porpoise

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Abstract: The Yangtze finless porpoise (Neophocaena phocaenoides), a small toothed whale endemic to China, has the ability to emit echolocation signals and obtain detection information. In order to investigate the differences in echolocation signals of Yangtze finless porpoises in different behavioral states, we screened the acoustic signals in feeding and swimming states, analyzed their acoustic parameters statistically, and applied fuzzy functions to study their discriminative ability. The results showed that the echolocation signals of the Yangtze finless porpoise showed significant differences in the -10 dB duration, -3 dB bandwidth, center of gravity frequency and root-mean-square bandwidth between the two states (P<0.05, T-test). The echolocation signals of the Yangtze finless porpoise had a strong distance resolution of millimeters. The present study provides some scientific references for the bioacoustic study of the Yangtze finless porpoise.

Key words: Yangtze finless porpoise; Echolocation signal; Behavioral state; Ambiguity function

短期流速刺激对草鱼生化和转录反应的影响

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摘要：自 2011 年以来，三峡水库不断开展生态调度试验，以提高葛洲坝下四大家鱼的产卵量。因此，探索短期流速刺激对草鱼卵巢发育的影响，对于了解自然繁殖对生态流量的响应至关重要。我们对经过流水刺激和未经刺激的个体进行卵巢组织学分析和生化测定。结果显示，虽然短期流速刺激对草鱼卵巢的发育没有明显影响，但雌二醇、孕酮、促卵泡生成素和三碘甲状腺原氨酸的浓度升高。我们也对卵巢组织进行 RNA 测序，进一步探索了短期性流速刺激下草鱼的卵巢发育情况。与对照组相比，短期流速刺激下分别有 221 个基因上调，741 个基因下调。大部分差异表达基因富集在 ABC 转运体、细胞因子-细胞因子受体相互作用、细胞外基质-受体相互作用和类固醇激素生物合成等通路中。本研究结果揭示了短期流速刺激下草鱼卵巢发育的潜在调控基因和通路，为进一步制定生态调控策略提供了新的思路。

关键词：草鱼；流速；卵巢；激素；转录组

Effects of short-term water velocity stimulation on the biochemical and transcriptional responses of grass carp

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Abstract： Since 2011, ecological operation trials of the Three Gorges Reservoir (TGR) have been continuously conducted to improve the spawning quantity of the four major Chinese carp species below the Gezhouba Dam. In particular, exploring the effects of short-term water velocity stimulation on ovarian development in grass carp (Ctenopharyngodon idellus) is essential to understand the response of natural reproduction to ecological flows. We performed ovary histology analysis and biochemical assays among individuals with or without stimulation by running water. Although there were no obvious effects on the ovarian development characteristics of grass carp under short-term water velocity stimulation, estradiol, progesterone, follicle-stimulating hormone (FSH), and triiodothyronine (T3) concentrations were elevated. Then, we further explored the ovarian development of grass carp under short-term water velocity stimulation by RNA sequencing of ovarian tissues. In total, 221 and 741 genes were up- or downregulated under short-term water velocity stimulation, respectively, compared to the control group. The majority of differentially expressed genes (DEGs) were enriched in pathways including ABC transporters, cytokine-cytokine receptor interaction, ECM-receptor interaction, and steroid hormone biosynthesis. Important genes including gpr4, vtg1, C-type lectin, hsd17b1, cyp19a1a, cyp17a1, and rdh12 that are involved in ovarian development were regulated. Our results provide new insights and reveal potential regulatory genes and pathways involved in the ovarian development of grass carp under short-term water velocity stimulation, which may be beneficial when devising further ecological regulation strategies.

Key words: grass carp; water velocity; ovary; hormones; transcriptome

梯级水电开发对嘉陵江干流鱼类多样性和群落组成变化的影响

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摘要：河流生境连续性对鱼类多样性维持具有重要作用。长期以来，梯级开发打破了河流的连续性，导致了鱼类多样性格局产生了显著变化。持续有效的鱼类多样调查是评估鱼类多样性格局的重要手段。因此本研究于 2023 年 8 月对嘉陵江干流 20 个梯级江段进行了水生态调查，共采集 60 个环境 DNA 水体样本，检测出鱼类 98 种（不含未鉴定到种水平的 1 属），隶属于 7 目 20 科 74 属，其中包括国家级保护鱼类 5 种、长江上游特有鱼类 18 种及外来鱼类 11 种，鱼类组成与嘉陵江历史传统调查的鱼类组成相似。结合历史文献分析发现，嘉陵江干流鱼类趋于小型化，适应急流生境的鱼类和产漂流性卵的鱼类减少，表明梯级开发对嘉陵江干流鱼类多样性和群落组成产生了一定影响，地理区划分析还发现，梯级库区间以及上中下游间的鱼类种类组成和物种多样性总体上差异均较小。总体上，本研究揭示了嘉陵江鱼类多样性现状和分布格局，表明 eDNA 方法可作为嘉陵江鱼类多样性检测的有效工具。

关键词：环境 DNA；梯级水电；鱼类多样性；群落组成

Influence of the terraced hydropower development on change patterns of fish diversity and community assembly in the Jialing River main stream

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Abstract： River habitat continuity plays an important role in maintaining fish diversity. For a long time, terraced development has broken the continuity of the river, leading to significant changes in fish diversity patterns. Sustained and effective fish diversity surveys are an important means for assessing the patterns of fish diversity. Therefore, in August 2023, this study conducted a water ecological survey on 20 terraced river sections of Jialing River main stream, and a total of 60 environmental DNA water samples were collected, and 98 species of fishes (excluding one genus that was not identified to the species level) were detected, belonging to 74 genera of 7 orders, 20 families, including 5 species of nationally protected fishes, 18 species of fishes endemic to the upper reaches of the Yangtze River, and 11 species of alien fishes, and the composition of fishes was similar to that of the historical and traditional surveys of the Jialing River. Based on the analysis of historical literature, it was found that fishes in the mainstem of the Jialing River tended to be miniaturized, and fish adapted to flowing habitats and the fish producing floating eggs decreased, indicating that the cascade development had a certain impact on the diversity and community composition of the fish in the main stream of the Jialing River, and the geographical division analysis also found that the differences of fish species composition and species diversity between the cascade reservoir and the upper, middle and lower reaches were small in general. Overall, this study revealed the current status and distribution pattern of fish diversity in Jialing River, demonstrating that eDNA method can be used as an effective tool to detect fish diversity in Jialing River.

Key words: environment DNA；the terraced hydropower；fish diversity；community composition

大小鱼山附近海域生物多样性现状

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摘要：根据2022年春秋季以及2023年春季在舟山渔场大小鱼山附近海域开展的渔业资源调查获得的鱼类资料，研究了该海域的鱼类种类组成、优势种、生物多样性等群落结构特征。结果表明：（1）鱼类35种，隶属于9目、19科、26属；（2）不同站位鱼类多样性差异较大，且三个季节的多样性最高值和最低值分别出现在不同站位；（3）2022年春季鱼类群落相似性低于2022年秋季，但是高于2023年春季；2023年春季各群落代表性鱼类均不同，2022年春秋季个群落代表性鱼类略有重复；（4）三个季度的ABC曲线W统计值均为正，附近海域未受到明显外界干扰。

关键词：群落结构；多样性；舟山渔场

Status of biodiversity near Dayu Mount and Xiaoyu Mount

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Abstract: Based on the fish data obtained from the fishery resources survey in the spring of 2022 and in the spring of 2022 and the spring of 2023, the community structure characteristics such as fish species composition, dominant species and biodiversity in the sea area were studied. The results show that: (1) 35 species of fish belonging to 9 orders, 19 families and 26 genera; (2) the diversity of fish in different stations, and the highest and lowest diversity of the three seasons appear in different stations; (3) the similarity of fish communities in spring 2022 is lower than that in spring 2022 but higher than spring 2023; in spring 2023, with different representative fish in spring and autumn 2022; (4) ABC curve W statistics in three quarters are positive, and the nearby waters has no obvious external interference.

Key words: community structure; diversity; Zhoushan fishing ground

基于 eDNA 的长江流域重庆段鱼类多样性空间格局研究

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摘要：为了解成库后长江流域重庆段鱼类多样性现状及空间格局演变，本研究于 2022 年 5 月-6 月利用环境 DNA（eDNA）技术对江津至巫山 6 个干流断面和 8 个重要一级支流断面的鱼类多样性进行了调查，共检测到鱼类 107 种，隶属于 7 目 20 科 74 属，其中包括国家级保护鱼类 6 种，长江上游特有鱼类 17 种，以及外来鱼类 12 种。基于成库后不同时期鱼类多样性对比分析发现，外来鱼类现状相较于三峡水库试运行期间增多。不同生境偏好鱼类种类占比波动明显，喜流水鱼类现状相较于水库试运行期间减少，广适性鱼类增加。此外，支流生境的鱼类 Alpha 多样性指数普遍高于其邻近的干流江段。分组模型表明江津-涪陵江段平均 Alpha 多样性指数高于涪陵-巫山江段，组间的鱼类物种组成具有显著性差异。总体上，本研究揭示了长江流域重庆段鱼类多样性现状及格局演变，进一步验证了 eDNA 技术在鱼类多样性监测中的可行性和高效性，可作为传统调查方法的重要补充手段。

关键词：鱼类多样性；外来鱼类；环境 DNA；三峡库区

Study on the spatial pattern of fish diversity in the Chongqing section of the Yangtze River Basin Based on eDNA

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Abstract：In order to understand the current status and spatial pattern evolution of fish diversity in the Chongqing section of the Yangtze River Basin after the completion of the reservoir, this study used environmental DNA (eDNA) technology to investigate the fish diversity of 6 main stream sections and 8 important primary tributary sections from Jiangjin to Wushan from May to June 2022. A total of 107 species of fish were detected, belonging to 7 orders, 20 families, and 74 genera, including 6 species of national protected fish, 17 species of endemic fish in the upper reaches of the Yangtze River, and 12 species of exotic fish. Based on the comparative analysis of fish diversity at different stages after the completion of the reservoir, it was found that the current situation of foreign fish has increased compared to the trial operation period of the Three Gorges Reservoir. The proportion of fish species with different habitat preferences fluctuates significantly, and the current situation of rheophilic fish species decreases compared to the trial operation period of reservoirs, while the number of eurytopic fish species increases. In addition, the alpha diversity index of fish in tributary habitats is generally higher than that in their adjacent main river sections. The grouping model indicates that the average Alpha diversity index of the Jiangjin Fuling section is higher than that of the Fuling Wushan section, and there is a significant difference in fish species composition between groups. Overall, this study reveals the current status and pattern evolution of fish diversity in the Chongqing section of the Yangtze River Basin, further verifying the feasibility and efficiency of eDNA technology in fish diversity monitoring, and can serve as an important supplementary means to traditional survey methods.

Key words: fish diversity; exotic fishes; environmental DNA; The Three Gorges Reservoir Area

基于血液转录组分析的长江江豚不同环境适应特征

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摘要：长江江豚(Neophocaena asiaeorientalis asiaeorientalis，YFP)是中国长江特有的一种小齿鲸，也是江豚属中唯一的淡水种群。为比较分析不同栖息环境下的长江江豚适应性变化，本研究采用 RNA-seq 技术对生活于半自然迁地水域和人工饲养水体的长江江豚血液组织进行测序分析，富集分析发现，差异表达基因主要富集在视觉、消化和免疫系统等相关通路。其中“趋化因子信号通路”和“B 细胞受体信号通路”等多个免疫系统相关关键通路在迁地保护长江江豚中被激活。视觉相关通路如“光转导通路”和“炎症介质对 TRP 通道的调节”等以及消化系统相关通路如“蛋白质的消化吸收”和“唾液分泌”等在人工饲养长江江豚中被激活。结果提示，长江江豚迁地群体可能通过增强机体免疫功能以适应半自然水域复杂的环境条件；基于水体透明度较高及规律摄食等人工饲养条件，长江江豚的视觉功能及蛋白质消化功能较迁地群体有所提高。本研究为评估长江江豚对多样生境的适应能力提供理论依据，为今后长江江豚的保护和生物学研究提供有益参考。

关键词：长江江豚；栖息环境；血液转录组；视觉；消化系统；免疫系统

Blood transcriptome analysis provides adaptive characteristic of ex-situ and captive Yangtze finless porpoises

(Neophocaena asiaeorientalis asiaeorientalis)

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Abstract： The Yangtze finless porpoise (Neophocaena asiaeorientalis asiaeorientalis, YFP) is a small-toothed whale endemic to the Yangtze River in China and is the only freshwater population in the genus Neophocaena. To compare and analyze the adaptive changes of YFPs between ex-situ and captive waters, we performed RNA sequencing of YFPs blood tissues for ex-situ and captive population. A total of 1,201 differentially expressed genes (DEGs) were identified, of which 423 were upregulated in ex-situ population and 778 were upregulated in captive population. Gene Enrichment analysis showed that DEGs were generally enriched for visual, digestive and immune system related pathways. Further analysis revealed that several key immune system pathways, such as chemokine signaling pathway and B cell receptor signal pathway, were activated in ex-situ population. In addition, key pathways related to vision, including phototransduction and inflammatory mediator regulation of TRP channels, as well as pathways related to the digestive system, such as protein digestion and absorption and salivary secretion, were activated in captive population. These results suggest that the ex-situ population may have adapted to the complex environmental conditions of semi-natural waters by enhancing their immune function; and that the visual function and protein digestion of YFPs have been improved compared to the ex-situ population based on the conditions of artificial feeding, such as higher transparency of the water and regular feeding. This study provides a theoretical basis for evaluating the adaptability of the YFPs to different environment and provide useful reference for the ex-situ and captive protection in the future.

Key words: Yangtze finless porpoise; environment; blood transcriptome; visual; digestive system; immune system

基于 citespace 分析的
气候变化对头足类种群动态影响研究进展

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摘要：以 Web of science 核心合集数据库为数据源，将气候变化对头足类种群动态影响研究相关文献利用 citespace 进行可视化比较分析，形成科学知识图谱。结果表明，1990-2020 年有头足类研究相关英文文章 4832 篇，其中与气候变化相关的文章有 101 篇，从 1997 年之后该领域的文章总体呈增长趋势。对选取文献进行主要研究机构、国家、作者、期刊、关键词、文献共被引等分析，以期为今后的研究者提供一个科学依据。经分析得到：主要研究机构有研究内容主要从气候变化、环境因子变化和头足类的生物学方面的变化进行；气候变化方面主要有厄尔尼诺等现象，环境因子方面主要有温度等，头足类生物学方面主要有生长、繁殖等；主要的研究范围有地中海海域、英吉利海峡、西北大西洋等；主要应用的模型有 GIS 模型等。总体而言，与气候变化相关的头足类研究领域的文章较少，但随着历年文章增长的趋势，可能成为今后与头足类相关的研究热点。

关键词：气候变化；头足类；citespace；知识图谱

Progress in the study of climate change impacts on cephalopod population dynamics based on citespace analysis

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Abstract：Using the Web of science core ensemble database as the data source, the literature related to the research on the impact of climate change on cephalopod population dynamics was visualized and compared and analyzed using citespace to form a scientific knowledge graph. The results showed that there were 4832 English articles related to cephalopod research from 1990 to 2020, among which 101 articles were related to climate change, and there was a general increasing trend of articles in this field from 1997 onwards. The selected literature was analyzed in terms of major research institutions, countries, authors, journals, keywords, and literature co-citation, in order to provide a scientific basis for future researchers. After analyzing the literature, we obtained the following results: the main research institutions have the research contents mainly from the changes of climate change, environmental factors and cephalopod biology; the main climate change phenomena are El Niño and other phenomena, the main environmental factors are temperature, etc., and the main cephalopod biology is growth and reproduction, etc.; the main research areas are the Mediterranean Sea, the English Channel, the northwestern Atlantic Ocean and so on; and the main applied models are the GIS model, etc. Generally speaking, there are fewer articles in the field of cephalopod research related to climate change, but with the increasing trend of articles over the years, this direction may become a hotspot for cephalopod-related research in the future.

Key words: Climate change; cephalopods; citespace; knowledge map

浙江省健跳港牡蛎礁的
幼体补充量和多样性变化

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摘要：本研究通过连续三年跟踪监测浙江省健跳港牡蛎礁海域的牡蛎幼体补充量，并分析了牡蛎的遗传多样性和幼体补充量的时空变化特征。结果显示，蛎江滩牡蛎礁中共出现有 6 种牡蛎，补充量中以熊本牡蛎占绝对优势，相对丰度达 95%以上。牡蛎补充量介于 0～44200 个/m2，月平均补充量为(7165±1246)个/m2。在牡蛎群落多样性分析中，熊本牡蛎的种群占比由 91.06%上升为 95.48%，近江牡蛎的占比由 3.37%下降为 1.56%，其他 3 种牡蛎仅在定性调查中发现。蛎江滩熊本牡蛎和近江牡蛎遗传多样性均较低，核酸多样性指数π分别为 0.01241 和 0.00237。结果表明：蛎江滩牡蛎礁中的牡蛎群落物种多样性显著下降。未来需进一步研究近江牡蛎及其他本地稀有牡蛎的性腺指数变化情况。

关键词：牡蛎礁；近江牡蛎；熊本牡蛎；多样性；补充量；

Changes in larval recruitment and diversity of oyster reefs in Jiantiao Harbor, Zhejiang Province

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Abstract： In this study, oyster larvae recruitment was monitored for three consecutive years in the oyster reef of Jianchao Port, Zhejiang Province, and the temporal and spatial variations of oyster genetic diversity and larval recruitment were analyzed. The results showed that there were 6 species of oysters on the oyster reef in the oyster marshland. Crassostrea ariakensis, C.sikamea, C. Anngulata, C. Hunkongensis, Talonostrea talonata and C.gigas. In addition, C.sikamea was the dominant species, with a relative abundance of more than 95%. Oyster supplementation ranged from 0 to 44200 oysters /m2, with an average monthly supplement of (7165±1246) oysters /m2. In the diversity analysis of oyster community, the proportion of C.sikamea increased from 91.06% to 95.48%, while that of C.ariakensis decreased from 3.37% to 1.56%. The other three species were only found in the qualitative survey. The genetic diversity of both oysters was low, with a nucleic acid diversity index π of 0.01241 and 0.00237, respectively. The results showed that:The species diversity of oyster community in oyster reef decreased significantly in oyster marshland. Further studies are needed to investigate the changes in gonadal index of C.ariakensis and other local rare oysters.

Key words: oyster reef； Crassostrea ariakensis； Crassostrea sikamea； Diversity； Amount of supplementation

黑水河短须裂腹鱼栖息地适宜性研究

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摘要：基于 2018-2019 年对黑水河短须裂腹鱼（Schizothorax wangchiachii）的渔获物数量及同时采集的溶解氧、水温、透明度、流速、水深、pH 值、盐度等相关环境因子数据进行分析，旨在评估黑水河短须裂腹鱼栖息地的适宜性。研究使用 Spearman 相关性分析确定与短须裂腹鱼相对资源密度值（RAI）呈极显著（$P < 0.01$）相关的环境因子。通过应用随机森林算法，确定各环境因子的权重，使用加权平均法计算鱼类栖息地适宜性指数(HSI)。结果表明：在所选取的 16 个环境因子中，水温、流速、水深、海拔、电导率和盐度与短须裂腹鱼相对资源密度值(RAI)之间存在极显著相关关系($P＜0.01$)，通过将短须裂腹鱼 RAI 值与各环境因子拟合，确定短须裂腹鱼最适栖息水温范围为 17.04 ℃~17.65 ℃，流速范围为 0.41 m/s ~0.50 m/s，水深范围为 35cm~60cm，海拔范围为 742 m

关键词：短须裂腹鱼；栖息地适宜性指数；随机森林；环境因子；加权平均法；黑水河

Investigation of Habitat Suitability for Schizothorax wangchiachii in the Heishui River

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Abstract： Based on the data collected from 2018 to 2019 regarding the catch of Schizothorax wangchiachii in the Heishui River, along with measurements of dissolved oxygen, water temperature, transparency, flow rate, water depth, pH value, and salinity, an analysis was conducted to assess the suitability of the habitat for S.wangchiachii in the Heishui River. Spearman correlation analysis was used to determine the significant environmental factors that were strongly correlated ($p < 0.01$) with the relative abundance index (RAI) of S. wangchiachii. By applying the random forest algorithm, the weights of each environmental factor were determined, and a habitat suitability index (HSI) for the fish species was calculated using the weighted average method. The results revealed that among the 14 selected environmental factors, water temperature, flow velocity, water depth, altitude, conductivity, and salinity exhibited a highly significant correlation with the RAI of S. wangchiachii ($P<0.01$). By fitting the RAI values with each environmental factor, the study determined the optimal water temperature range for S. wangchiachii to be between 17.04°C and 17.65°C, flow velocity range between 0.41 m/s and 0.50 m/s, water depth range between 35 cm and 60 cm, altitude range between 742 m and 826 m, conductivity range between 304 S/m and 309 S/m, and salinity distribution range between 0.14‰ and 0.16‰.The results of the random forest analysis revealed the following order of importance for the environmental factors: water depth > watertemperature > altitude > salinity > conductivity > flow velocity, with corresponding weights of 0.38, 0.20, 0.14, 0.13, 0.11, and 0.04, respectively. The HSI calculations showed that the habitat distribution of S. wangchiachii was mainly concentrated in the downstream area of the Heishui River. Only the S5 location had an HSI value greater than 0.7, while the HSI values for all locations upstream of Lao mu River Dam accounted for only 50% of the downstream values. The study also validated the results through measured data (R2=0.83), which showed a good fit, with the relative abundance values increasing with higher HSI values. This research provides a feasible method for assessing the habitat suitability of S. wangchiachii in the Heishui River, offering a scientific basis for relevant conservation and management decisions.

Key words: Schizothorax wangchiachii; Habitat suitability inde; Random forest; Environmental factors; Weighted average method; Hei shui river

梯级开发背景下乌江干流浮游生物多样性及其群落结构研究

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摘要：为探究乌江梯级开发背景下浮游生物多样性状况及群落结构特征，本研究于 2023 年 4 月在乌江干流各梯级库区设置 27 个采样断面进行水生态调查。经鉴定，乌江干流共分布有浮游植物 8 门 356 种，其中以绿藻门（Chlorophyta）为主，浮游植物平均生物密度和生物量为 53.9×104 个/L、0.974mg/L，浮游植物香农-威纳指数 H、Margalef-丰富度指数 R 和均匀性指数 J 平均值分别为 2.486、4.732 和 0.813。浮游动物有 4 门 170 种，轮虫（Keratella）为主，浮游动物平均生物密度和生物量为 0.048×104 个/L、0.453mg/L，浮游动物香农-威纳指数 H、Margalef-丰富度指数 R 和均匀性指数 J 平均值分别为 2.312、4.383 和 0.806。浮游植物多样性呈现下游小于中游，思林库区和彭水库区浮游植物群落结构稳定性较其他库区有明显下降，这可能与乌江下游流经城镇的人类活动有关。

关键词：浮游生物；群落结构；多样性；梯级开发；乌江

Study on the Diversity and Community Structure of Plankton in the Main Stream of the Wujiang River under the Background of Cascade Development

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Abstract：In order to explore the community structure characteristics and diversity status of plankton under the background of Wujiang cascade development, 27 sampling sections were set up in April 2023 in the Wujiang River for investigation. The results show that there are 8 phyla and 356 species of phytoplankton, dominated by the Chlorophyta phyla. The average value of density and biomass of phytoplankton are 53.9 ×104 cell/L and 0.974mg/L. The average values of the Shannon Weiner index H, Margalef richness index R, and evenness index J of phytoplankton are 2.486, 4.732, and 0.813, respectively. There are 4 phyla and 170 species of planktonic animals, dominated by Keratella plylum. The average value of density and biomass of planktonic animals are 0.048 ×104cell/L and 0.453mg/L. The average values of the Shannon Weiner index H, Margalef richness index R, and evenness index J of planktonic animals are 2.312, 4.383, and 0.806, respectively. The diversity of phytoplankton in the downstream is smaller than that in the middle reaches, and the stability of phytoplankton community structure in the Silin and Pengshui reservoirs has significantly decreased compared to other reservoirs. This may be related to human activities in the towns flowing through the lower reaches of the Wujiang River. The diversity of planktonic animals in the downstream is greater than that in the middle reaches, and there is a significant difference in dominant species among the reservoir areas.The research results provide scientific basis for the Wujiang River environmental governance and the fishery development .

Key words: plankton; Community structure; Diversity; Cascade Development; Wujiang

珠江草鱼资源保护研究进展

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摘要：珠江草鱼喜相对平整的地形栖息，主要以近岸植物为食，兼食贻贝、轮虫、哲水蚤、绿藻等。种群平均体长为 347.89mm，平均体质量为 986.87g，年龄结构以 1-3 龄为主，生长拐点年龄为 8.29，与历史比较发现草鱼呈现小型化，草鱼生长性能和繁殖力下降。捕捞调查结果发现近年珠江中下游草鱼资源呈一定增长趋势，资源量与气温和流量呈正相关。珠江草鱼繁殖期为 4-10 月，繁殖持续周期为 93±26 天，种群数量与流量和水文显著正相关，繁殖呈现产卵时间提前、繁殖周期缩短趋势。遗传多样性分析发现流域群体遗传分化程度较低，中游江段遗传多样性相对较高，珠江草鱼的遗传多样性显著高于长江草鱼，长江流域的大部分单倍型均与珠江流域的单倍型呈现共享的现象，表明珠江野外种群中存在大量长江流域的种质资源。针对珠江流域草鱼资源衰退情况，分析了其主要胁迫因素，并提出保护措施。研究结果可为珠江草鱼资源恢复和养护提供参考依据。

关键词：珠江，草鱼，种群结构，遗传多样性，保护

Research advances on Ctenopharyngodon idellus resource in the Pearl River

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Abstract： Grass carp is an important economic fish in China and one of the main fishery objects in the Pearl River. Due to the influence of wading activities, grass carp resources decline seriously, and the protection of grass carp resources in the Pearl River is urgent. In recent years, the current situation of grass carp resources in the Pearl River has been investigated. The main research progress is as follows. Grass carp are widely distributed in the Pearl River Basin, prefers to inhabit relatively flat terrain, mainly feed on nearshore plants, and also feed on mussels, rotifers, daphania, green algae and so on. The average body length of the population was 347.89mm, the average body mass was 986.87g, the age structure is mainly 1-3 years old, the growth was uniform growth type, and the growth turning point age was 8.29. Compared with the history, it was found that grass carp showed miniaturization, and the growth performance and fertility of grass carp decreased. The results of fishing survey show that grass carp resources in the middle and lower reaches of the Pearl River have a certain increasing trend in recent years, and the resources are positively correlated with temperature and discharge. Based on the long-term monitoring results, the breeding period of grass carp in the Pearl River was mainly from April to October, the peak period was concentrated in May to August, and the breeding duration was 93±26 days. The population number of juvenile grass carp was significantly positively correlated with the flow rate and hydrology, and the spawning time of grass carp was advanced and the breeding cycle was shortened. Genetic diversity analysis found that the population of grass carp in the Pearl River was higher than that in the Yangtze River Basin, and most of the haplotypes in the Yangtze River Basin are shared with the haplotypes in the Pearl River Basin, indicating that there were a lot of germplasm resources in the wild population of the Pearl River Basin. According to the decline of grass carp resources in the Pearl River Basin, the main stress factors were analyzed and protection measures were put forward. The research results can provide reference for the restoration and conservation of grass carp resources in the Pearl River.

Key words: The Pearl River; Ctenopharyngodon idellus; Population structure; Genetic diversity; Conservation

长江上游珍稀特有鱼类国家级自然保护区干流段鱼类群落结构特征分析

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摘要：为探究“十年禁渔”前保护区干流段鱼类群落结构特征，基于该江段 2017—2019 年渔获物监测数据，对鱼类群落的种类组成、生物多样性、群落结构稳定性等特征进行分析。结果显示，本次调查共采集到鱼类 134 种，隶属于 7 目 21 科 83 属，其中长江上游特有鱼类有 27 种，外来物种有 12 种，分别占总种类数 20.15% 和 8.96%。等级聚类分析 (Cluster)显示，保护区干流段鱼类的群落类型基本可分为 3 组，宜宾、泸州与合江可以聚为一组，巴南、江津分别独立成组。优势种有 14 种，其中瓦氏黄颡鱼是整个江段的优势种。鱼类多样性分析，表明保护区干流鱼类物种丰富，群落分布均匀度较高。ABC 曲线分析结果显示，江津站鱼类群落结构稳定性相对较高，其余站点鱼类群落结构均受到中度干扰。本研究补充了保护区干流鱼类群落研究的基础数据，以期为该江段鱼类资源管理与“十年禁渔”生态评估提供科学依据。

关键词：群落结构；鱼类组成；生态类型；多样性；长江上游

Analysis on the characteristics of fish community structure in the main stream section of the National Nature Reserve for Rare and Endemic Fish in the upper reaches of the Yangtze River

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Abstract： The National Nature Reserve of Rare and Endemic Fish in the upper reaches of the Yangtze River is located in the lower reaches of Xiangjiaba Dam. With the impoundment of cascade hydropower stations in the lower reaches of Jinsha River and the implementation of the "ten-year fishing ban" policy, the fish community in the main stream of the reserve may change. In order to explore the characteristics of fish community structure in the main stream of the Reserve before the "ten-year fishing ban", based on the catch monitoring data from five sampling sites of this section from 2017 to 2019, the characteristics of fish species composition, ecological types, community similarity, species dominance, biodiversity and community structure stability were analyzed. The results showed that 134 fish species were collected in this investigation, belonging to 7 orders, 21 families and 83 genera, among which 27 species were endemic to the upper reaches of the Yangtze River and 12 species were exotic, accounting for 20.15% and 8.96% of the total species respectively. The fish community was dominated by demersal fish, sunken eggs and omnivorous fish. Cluster analysis and Nonmetric Multidimensional Scaling (NMDS) analysis showed that the fish community types of five sections in the main stream could be basically divided into three groups at a certain level of similarity, as Yibin, Luzhou and Hejiang sections formed one group,Jiangjin section and Banan section formed separate groups independently. There were 14 dominant species, among which Pelteobagrus vachelli was the dominant species in the whole area, with the highest dominance in Hejiang section where the IRI value was 27.00%. Shannon-Wiener index, Simpson index, Margalef index and Pielou index ranged from 2.725 to 3.306, 0.883 to 0.942, 5.833 to 8.811, 0.699 to 0.773, respectively. As a result, fish species diversity and the community distribution uniformity was high in the main stream of the reserve. The results of ABC curve analysis showed that the fish community structure in Jiangjin section was relatively stable, but moderately disturbed in the other section. This study could supplement the basic data of fish community information in the main stream of the nature reserve, and also provide theoretically scientific support for fish resource management and ecological evaluation of "ten-year fishing ban" in this section of the river.

Key words: community structure; fish composition; ecological type; diversity; the upper reaches of the Yangtze River

围栏大黄鱼养殖基地底质特征研究

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摘要：大黄鱼属肉食性鱼类，其成长阶段需喂食一定数量的生物饵料(一般为冰鲜饵料鱼)，养殖基地经过两个养殖周期后，底质环境呈现富营养化趋势。为了了解围网内外底质沉积物的变化情况，同时结合前期取得的水质等分析研判。结果可见，沉积物的石油烃、硫化物、有机碳、砷、汞、锅、铅、铜均符合类沉积物质量标准。而常见的持久性有机污染物中六六六，DDT，多氯联苯多环芳烃含量极低，多数低于检出限。酸碱度和氧化还原电位值均低于海区平均水平，显示出还原性的特征，硫化物、有机碳、总氨等指标均显示养殖区内明显的富集作用，无论从感官及试验结果均显示经过 2a 的养殖使用，区内的底质环境有恶化的趋势，硫化物有机碳、总氮为主要的污染物。

关键词：大黄鱼；围栏养殖；底质

Study on the Sediment Characteristics of Pseudosciaena Crocea Enclosure Culture Base

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Abstract： Pseudosciaena Crocea is a carnivorous fish that needs to be fed a certain amount of biological bait (usually ice fresh bait fish) during its growth stage. After two breeding cycles, the bottom environment of the breeding base shows a trend of eutrophication. In order to understand the changes in bottom sediment inside and outside the fence, and to analyze and judge based on the water quality obtained in the previous stage. The results show that the petroleum hydrocarbons, sulfides, organic carbon, arsenic, mercury, pot, lead, and copper in the sediment meet the quality standards for similar sediments. Among common persistent organic pollutants, the content of hexachlorocyclohexane, DDT, and polycyclic aromatic hydrocarbons in polychlorinated biphenyls is extremely low, most of which are below the detection limit. The acidity, alkalinity, and redox potential values are lower than the average level in the sea area, showing reducing characteristics. Indicators such as sulfides, organic carbon, and total ammonia all show significant enrichment in the aquaculture area. Both sensory and experimental results show that after 2 years of aquaculture use, the bottom environment in the area has a trend of deterioration, with sulfide organic carbon and total nitrogen as the main pollutants.

Key words: Pseudosciaena Crocea；Enclosure Culture；Sediment

第七专题：水产品加工与综合利用

基于 UHPLC–MS/MS 不同加工方式的刺参（Apostichopus japonicus）代谢组学研究

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摘要：研究采用液相色谱串联质谱法对中国大连新鲜、盐渍泡发前后和即食海参体壁中的代谢物进行检测分析。PLS-DA 将不同加方式刺参体壁代谢物区分开来。差异代谢物主要包括氨基酸、脂质和碳水化合物。与新鲜刺参相比，盐腌加工使 16 种氨基酸和 C16:1、C18:0、C18:2N6C、C20:4N6 显著下调（$P<0.05$）。高温炖煮和浸泡处理导致 C20:4、C16:0、C20:5N3（DPA）显著上调（$P<0.05$）。盐渍泡发前后的刺参相比，浸泡使 16 种氨基酸（$P<0.05$）减少，且 DHA、EPA 下降。与即食刺参相比，由于盐腌处理，盐渍泡发后海参的氨基酸含量高于即食海参，但 DHA 含量低于即食海参。脂肪酸和氨基酸定量分析进一步验证了这些结果。KEGG 分析表明，脂质、碳水化合物和氨基酸代谢与加工方式之间存在显著关联。

研究揭示了不同加工方式海参的化学组成和营养价值，有助于消费者对合适的刺参加工方式及产品的选择。

关键词：刺参；加工；代谢组学

UHPLC-MS/MS metabolomics analysis of sea cucumber (Apostichopus japonicus) processed using different methods

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Abstract：The sea cucumber (Apostichopus japonicus), belonging to the phylum Echinodermata and class Holothuroidea, has a history of over a thousand years as a premium seafood ingredient in China, cherished for its delicious taste and nutritional richness. However, fresh sea cucumbers are highly susceptible to autolysis due to the presence of autolytic enzymes. As a result, more than 80% of sea cucumbers are processed into dehydrated products for improved storage and shelf life. The impact of different processing methods on the nutritional composition of Apostichopus japonicus has become a significant concern for consumers when choosing sea cucumber products.

In this study, liquid chromatography-tandem mass spectrometry was employed to analyze the metabolites in the body wall of Apostichopus japonicus from Dalian, China, at various processing stages, including fresh, unsoaked salted, soaked salted, and instant sea cucumbers. Metabolite identification was conducted using partial least squares discriminant analysis (PLS-DA), and KEGG pathway enrichment analysis was carried out to delve into the relevance and impact of these metabolites. PLS-DA successfully distinguished the metabolites in the body wall of sea cucumbers processed by different methods, further elucidating the differences among these metabolites.

The identified differential metabolites primarily included amino acids, lipids, and carbohydrates. Compared to fresh sea cucumbers, salt curing resulted in a significant reduction ($P < 0.05$) in 16 amino acids (e.g., Asp, Thr, Gly) and fatty acids (e.g., C16:1, C18:0, C18:2N6C, C20:4N6). High-temperature cooking and soaking treatments led to a significant increase ($P < 0.05$) in fatty acids such as C20:4, C16:0, and C20:5N3 (DPA). In comparison between unsoaked salted and soaked salted sea cucumbers, soaking resulted in a decrease in 16 amino acids ($P < 0.05$) and a reduction in unsaturated fatty acids.

This research reveals the influence of different processing methods on the chemical composition and nutritional value of sea cucumbers, providing valuable insights for consumers to make informed choices regarding the processing method and sea cucumber products.

Key words: Apostichopus japonicus; sea cucumber processing; UHPLC-MS/MS

现代微生物加工技术在黄鱼鲞创新生产中对脂肪酸和蛋白质氧化的研究

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摘要：传统盐腌风干大黄鱼又名黄鱼鲞，风味独特，是主要的大黄鱼加工品。高盐度和依赖自然发酵造成的风味不稳定，已不能满足消费者对健康和风味品质的需求。降盐和风味品质提升是黄鱼鲞创新研发的主要思路。本研究应用现代微生物加工技术，接种源于风味发酵鱼和肉制品中的植物乳杆菌、酿酒酵母、木糖葡萄球菌、戊糖片球菌，利用食品栅栏保藏原理，成功开发了风味独特的低盐接种发酵黄鱼鲞创新产品。脂肪酸和氨基酸是主要风味前体物质，而发酵剂对其作用而增强风味的机理还不清楚。本研究以低盐接种发酵大黄鱼为试材，开展发酵剂对脂质氧化、蛋白质氧化、蛋白质含量和游离氨基酸的影响程度研究。结果表明，接种发酵降低了 TBARs 值，而促进了蛋白含量和游离氨基酸含量的增加，游离氨基酸中甜味、鲜味氨基酸和风味前体物质芳香族氨基酸含量增加，苦味氨基酸含量降低。结果表明发酵剂通过适度降低脂质和蛋白质氧化，促进风味氨基酸含量的提升而实现风味增强。

关键词：大黄鱼；风味品质；人工接种发酵；脂肪酸氧化；蛋白质氧化；游离氨基酸含量

Research on the oxidation of fatty acids and proteins in the innovative production of Huangyuxiang using modern microbial processing technology

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Abstract: Traditional salted and air dried large yellow croaker, also known as yellow croaker fry, has a unique flavor and is the main processed product of large yellow croaker. The instability of flavor caused by high salinity and dependence on natural fermentation can no longer meet consumers' needs for health and flavor quality. Reducing salt and improving flavor quality are the main ideas for innovative research and development of Huangyuxiang. This study applies modern microbial processing technology to inoculate Lactobacillus plantarum, Saccharomyces cerevisiae, Staphylococcus xylosus, and Streptococcus pentose from flavored fermented fish and meat products. By utilizing the principle of food barrier preservation, a unique low salt inoculated fermented Huangyuxiang innovative product has been successfully developed. Fatty acids and amino acids are the main flavor precursors, and the mechanism by which fermentation agents enhance flavor is still unclear. This study used low salt content and starter fermentation of large yellow croaker as the test material to investigate the effect of starters on lipid oxidation, protein oxidation, protein content, and free amino acids. The results showed that starters and fermentation reduced the TBARs value, while promoting an increase in protein content and free amino acid content. The content of sweet, fresh amino acids, and flavor precursor aromatic amino acids in free amino acids increased, while the content of bitter amino acids decreased. It indicate that the starters enhance the flavor by moderately reducing lipid and protein oxidation, promoting the increase of flavor amino acid content. The research results provide theoretical reference for improving the flavor quality of fermented large yellow croaker.

Key words: Large yellow croaker; Flavor quality; Artificial inoculation and fermentation; Fatty acid oxidation; Protein oxidation; Free amino acid content

代谢组和转录组整合分析揭示不同年龄中华鳖（Pelodiscus sinensis）肌肉代谢特征及基因调控机制

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摘要：中华鳖(Pelodiscus sinensis)作为中国传统的食疗佳品，肌肉中潜在的生物活性化合物的组成值得关注。消费者对中华鳖老鳖具有明显的消费偏好。本文选择 3 至 6 龄（M3 至 M6）中华鳖，分析其肌肉化合物组成特征及其动态变化的基因调控机制。在中华鳖肌肉中鉴定出 261 种代谢物，其中谷胱甘肽和鹅肌肽被认为是中华鳖肌肉潜在的活性成分，分别在 M5 和 M6 中含量最多。γ-亚麻酸、DHA、EPA、烟酰胺和泛酸在 M6 中含量最高。这些信息为消费者对老鳖的选择提供依据。呈味核苷酸 IMP、GMP 在 M3 中含量最多。与 M3 相比，M4 的胶原合成基因（col1a1、col1a2 和 col3a1）被抑制，游离氨基酸增加。糖原合成基因（hk 和 ugp2）下调和糖原分解基因（pgm2、pyg 和 pfk）上调导致 M5 中单糖增加。脂肪酸碳链延伸和去饱和增强（hacd1 和 scd1）使 M6 中富含高不饱和脂肪酸。

关键词：Pelodiscus sinensis；代谢物；LC-MS/MS；联合分析；肌肉品质

Integrated metabolome and transcriptome revealed the metabolite characteristics and genes regulation mechanism in muscle of different ages Chinese soft-shelled turtle (Pelodiscus sinensis)

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Abstract： The Chinese soft-shelled turtle (Pelodiscus sinensis) is an ancient luxury food that is favored for its high nutritional and medicinal value in East Asia. In pond culture, farmers tend to prolong the breeding period of P. sinensis for premium prices due to the aged preferences in customers. However, little information is available about the difference of meat quality and bioactive substances in P. sinensis muscle across age spectrum. In this study, metabolite profiles in P. sinensis from 3 to 6 years of age (from M3 to M6) were investigated to explore their chemical composition and potential physiologically active substances changes with age based on the LC-MS/MS. Subsequently, the integrating transcriptome and metabolome were used to reveal the dynamic change processes and gene-metabolite regulation mechanism with age in P. sinensis meat.

A total of 261 metabolites classified into 24 categories were identified in P. sinensis for the first time in this study. Among them, “Amino acids, peptides, and analogs”, “Fatty acids and conjugates”, “Organic acids and derivatives”, “Benzene and substituted derivatives”, and “Nucleotide metabolomics” were major metabolites classes in P. sinensis muscle, and conferred the basic flavor of its meat. The relative content of IMP and GMP were highest respectively in M3 and M4, while sweet constituents, including betaine, phenylacetic acid, aldohexose 6-phosphate, butanal, and isophorone were highest in M3 and decrease with age. 5 lipids molecules were enriched in the cluster of increase with age, and 2 were UFA (i.e., γ-linolenic acid and EPA). DHA, niacinamide and pantothenic acid were both abundant in M6 P. sinensis most. Non-essential pharmacological activity was focused in this study as well. Glutathione and anserine, known as antioxidant peptides, were identified as key metabolites with age and related to the medical function of P. sinensis.

Common enriched KEGG pathways between differential expression genes and metabolites were used for meat dynamic regulation mechanisms analysis of P. sinensis. Related nutrient metabolism in the top 10 corresponding pathways among groups were regarded as nutrient dynamic accumulation features with age. Overall, amino acid and protein metabolism, saccharides metabolism and unsaturated fatty acids metabolism were found the major nutrient accumulation characteristics severally from 3 to 4, 4 to 5, and 5 to 6 years of age in P. sinensis muscle. Compared with M3, collagen synthesis genes significantly down-regulated in M4, including col1a1, col1a2, and col3a1. Of all identified 16 amino acids, 12 of them were most abundant in M4 which might be the result of collagen synthetic inhibition. In the comparison of M5 and M4, the relative content of six-carbon sugars increased, D-fructose and D-Mannose-6-phosphate, through glycogen synthesis related genes down-regulated, such as hk and ugp2, with its decomposition related genes pygl up-regulated. 5 to 6 years of age was the biological synthesis process of UFA, HUFA (e.g., DHA and EPA) especially. acox1 and scp2 were responsible for the β-oxidase of fatty acids, while acot2 catalyzed hydrolysis acyl-coenzyme A into free fatty acids and CoA. hacd1 and scd1 respectively play the role of carbon chain elongation and desaturation in fatty acids. In M6, the acyl-CoA was blocked by downregulated acox1, scp2, and acot2 unless transforming into UFA or HUFA by upregulated hacd1 and scd1 compared to M5. Pearson correlation analysis was conducted based on metabolomic profiling and transcriptomic profiling data. Notably, several collagen genes were identified as key genes, including col1a1, col1a2, col6a2, and col3a1. col3a1 was significantly related to γ-glutamylcysteine content while col1a1, col1a2, and col6a2 were considered the key candidate genes that regulated arachidic acid accumulation.

In conclusion, tasty compounds relative content highest in M3 (IMP and sweet substances) and M4 (GMP and free amino acid). Nutritional and bioactive substances, such as unsaturated fatty acids (γ-linolenic acid, DHA, and EPA), vitamins (B3 and B5) and pharmacoactive antioxidant peptides (anserine) showed the highest level in M6. From M3 to M4, collagen synthesis (col1a1, col1a2, and col3a1) were inhibited while FAA increased. Compared with M4, glycogen synthesis genes down-regulated (hk and ugp2) with glycogenolysis genes up-regulated (pgm2, pyg, and pfk) caused monosaccharides increasing in M5. Fatty acid carbon chain elongation (hacd1) and desaturated (scd1) enhancing promoted fatty acids highly unsaturated in M6. In addition, the accumulation of arachidic acid may be associated with col1a1, col1a2, and col6a2. These results provide customers with a basis for the proper choice of different-aged individuals and present available information for breed improvement of P. sinensis.

Key words: Pelodiscus sinensis; metabolite; LC-MS/MS; transcriptome; meat quality

第八专题：休闲渔业与渔文化

饲料中甲基睾酮含量对阿里雌鱼生长及体色的影响

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摘要：为探索甲基睾酮对阿里雌鱼生长及体色的影响，将初始体质量为(5.78±1.05)g 的阿里雌鱼 450 尾鱼随机分为 5 组，每组 3 个平行，每个平行 30 尾鱼，分别投喂含甲基睾酮 0、4、8、12、16 mg/kg5 个浓度梯度的饲料，观察 8 周增色时间和 4 周停药期鱼的生长及体色变化情况。结果显示，不同浓度的甲基睾酮对阿里雌鱼的成活率没有影响，均为 100%; 12mg/kg 的甲基睾酮处理组的体质量显著高于其他各组（$p<0.05$）；12mg/kg 与 16mg/kg 甲基睾酮浓度组增色效果差异不显著（$P>0.05$）,但显著高于其他各组（$P<0.05$）；增色后的阿里雌鱼体色在后 4 周停药期中，体色呈现先增艳，后又缓慢减弱现象，但仍维持在体色较艳的程度。表明外源甲基睾酮对阿里雌鱼具有适应性反应，增色后的阿里雌鱼体色能够稳定 4 周以上，甲基睾酮适宜添加量为 12mg/kg。

关键词：甲基睾酮；阿里；雌鱼；增色

Effects of methyltestosterone on growth and body pigmentation of female Sciaenochromis fryeri

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Abstract：In order to study on the effects of Methyltestosterone on growth and bodycolour in Female Sciaenochromis fryeri.Four hundred and fifty fisheswith initial body weight of (5.78±1.05)g were randomly divided into 5 groups and fed five containing methyltestosterone tested diets(0、4、8、12、16mg/kg， w/w) respectively for 8 weeks,and then all fishes were fed the control diet for 4weeks.Growth performance and body pigmentation of female Sciaenochromis fryeri were determined every 2 weeks during the 12 weeks experimental period. The results showed that the average survival rate of each group of female Sciaenochromisfryeri was 100%，the average weight of 12mg/kg group fish was significantly higher than other groups($P<0.05$).There was no significantly diffence in body pigmentation beween12 mg/kg group and 16 mg/kggroup（$P>0.05$）,but were remarkable higher than other groups($P<0.05$).After enhancing the colouration of female Sciaenochromisfryerifor 8 weeks，the fish colour of all groups were all raised somewhat， and then decreased slightly,the fishcolour was remained at stable level constantly.Which showed that the methyltestosterone had adaptive reaction to female Sciaenochromisfryeri，and the optimal recipe was methyltestosterone 12mg/kg.

Key words: Methyltestosterone; Sciaenochromis fryeri; female; body pigmentation

福建省休闲渔业空间分布及影响因素

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摘要：[目的]研究福建省休闲渔业空间分布及影响因素，有助于优化资源配置，减少重复建设和资源浪费，合理规划各区域休闲渔业。[方法]以福建省 243 个“水乡渔村”为研究对象，借助 ArcGIS10.8 空间分析工具，综合运用最近邻指数、核密度估计、聚类和异常值分析、灰色关联分析对福建省休闲渔业空间分布特征和影响因素进行探讨。[结果]福建省休闲渔业整体呈聚集分布，部分区域离散分布，形成“闽东北聚集，闽西南散落”的分布格局；旅游资源、道路交通、地区经济以及渔业基础都对福建省休闲渔业的空间分布有显著影响，其中 A 级景区数量影响最大。休闲渔业分布与交通区位有良好的空间耦合关系。“水乡渔村”主要分布在交通主干道 15km 的缓冲半径内，随着与交通干线距离的增加，数量急剧下降。[结论]旅游资源和交通条件是影响福建省休闲渔业空间分布的主要因素；虽然不同地区经济水平存在较大差异，但经济欠发达地区也依托优渥的景区资源。

关键词：休闲渔业；水乡渔村；空间分布；福建省；空间分析

SPATIAL DISTRIBUTION AND INFLUENCING FACTORS OF RECREATIONAL FISHERIES IN FUJIAN PROVINCE

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Abstract： Recreational fisheries play a key role in promoting sustainable development of fisheries and rural revitalization. Spatial distribution patterns and influencing factors analysis of recreational fishery could help to optimize resource allocation and avoid repetitive construction, however, only few studies on some coastal provinces are available nowadays. 243 recreational fishery demonstration bases from 8 prefecture-level cities were used as research object in present study, the average nearest neighbor, Thiessen-Polygon, nuclear density estimation, local Molan index and gray correlation analysis were used to analyze the spatial distribution characteristics and the influencing factors of recreational fisheries in Fujian Province. The overall spatial distribution of recreational fishery in Fujian is clustered, while, in some areas, it is scattered, forming a distribution pattern of "clustering in northeast and scattering in southwest ". Tourism resources, traffic conditions, regional economy and fundamentals of fisheries all significantly correlated with the spatial distribution of recreational fishery in Fujian. The number of A-class scenic spots showed the maximum associated coefficient K value among all the total 11 secondary factors investigated in present study, and the distribution of recreational fishery in Fujian demonstrate a good spatial coupling relationship with the traffic location and tourism, respectively. In addition, the recreational fishery demonstration bases are mainly distributed within the 15km buffer radius of the main traffic routes, and the number of it decreases sharply with increasing distance from the main traffic routes. In conclusion, tourism and traffic conditions are the main factors influencing the spatial distribution of recreational fisheries in Fujian. Although there are large differences in the economic levels of different regions, the recreational fisheries of less developed regions still developed well depending upon the excellent tourism resources. The fundamentals of fisheries play a certain role in promoting the development of recreational fishery in Fujian, but there is still much room for further development. In general, the abundant tourism resources, convenient transportation, solid fundamentals of economic and fisheries jointly form the distribution patterns of recreational fisheries in Fujian.

Key words: Recreational fisheries; Spatial distribution; Influencing factor; Fujian Province

锦鲤产业打造渔业转型升级高地，

锦鲤文化助力乡村全面振兴

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摘要：农业农村部已经将休闲渔业定义为五大重点支柱产业之一，观赏鱼则是休闲渔业的重要组成部分，锦鲤又是非常受欢迎的重要观赏鱼品种。现在以食用为目的的水产养殖渔业出现过剩的现象，而国家对环保的要求也越来越严格，全国渔业也面临转型升级，锦鲤作为观赏鱼是非常符合渔业转型升级方向。狠抓新旧动能转换重要契机，提托锦鲤养殖产业基础，将锦鲤文化产业与休闲渔业、旅游服务业融合开展，构建锦鲤全产业链，全力打造锦鲤文旅。

关键词：休闲渔业；锦鲤产业；渔业转型升级；锦鲤文化

Koi industry to build a highland for fishery transformation and upgrading , Koi culture to boost the overall rural revitalization

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Abstract： The Ministry of Agriculture and Rural Affairs has defined recreational fishery as one of the five key pillar industries. Ornamental fish is an important part of recreational fishery, and Koi is also a very popular and important species of ornamental fish. There is now a surplus of aquaculture fishery for food, and the country's requirement for environmental protection is becoming more and more stringent. The fishery industry is also facing transformation and upgrading, Koi as ornamental fish is extremely in line with the direction. Pay close attention to the important opportunity of the transformation of new and old kinetic energy, tito Koi breeding industry foundation, integrate Koi cultural industry with recreational fishery and tourism service industry, construct the whole industrial chain of Koi and strive to create Koi cultural tourism.

Key words: recreational fishery; Koi industry; fishery transformation and upgrading; Koi culture

渔文化视野下传统渔业乡镇休闲渔业发展对策探究——以浙江省石浦镇为例

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摘要：渔文化是人类历史发展过程中以渔民为代表的人群生存模式的综合反映,形成于渔民这类群体对鱼类的生存需求,并在渔业耕牧的历史传承中,具有广泛性、动态性和整体性的特征，并具有较为浓郁的地方民俗特色。浙江省石浦镇历经千年渔村文化和渔业生产活动，是典型的传统渔业重镇,随着近海渔业资源的逐步衰竭，以及现代经济和生活方式的冲击，迫切需要进行渔业的转型升级，发展休闲渔业是其重要的选择之一。经资料查阅和实地调查表明,石浦镇的渔文化历史悠久、文化底蕴深厚，充分研判该地区的资源、经济、社会和人文特点,做好文旅策划,重视文化承延续,发掘渔文化的内涵要素和市场潜力，将有助于石浦镇休闲渔业产业的快速发展。

关键词：渔文化；休闲渔业；发展对策；石浦镇

Research on the development countermeasures of leisure fishery in traditional fishing towns from the perspective of fishing culture -- A case study of Shipu Town, Zhejiang Province

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Abstract： Fishing culture is a comprehensive reflection of the survival mode of the population represented by fishermen in the process of human history development. It is formed from the survival needs of fishermen such groups for fish, and has extensive, dynamic and integrated characteristics in the historical inheritance of fishery farming and animal husbandry, and has relatively strong local folk characteristics. After thousands of years of fishing village culture and fishery production activities, Shipu Town of Zhejiang Province is a typical traditional fishing town. With the gradual depletion of offshore fishery resources and the impact of modern economy and lifestyle, it is urgent to transform and upgrade the fishery industry, and the development of recreational fishery is one of its important choices. The data review and field investigation show that the fishing culture of Shipu town has a long history and profound cultural heritage. Fully studying and determining the resources, economy, society and humanistic characteristics of the region, doing a good job in cultural tourism planning, paying attention to the continuation of culture, and exploring the connotation elements and market potential of fishing culture will help the rapid development of leisure fishery industry in Shipu Town.

Key words: Fishing culture; Recreational fisheries; Development countermeasures; Shipu Town

第九专题：现代渔业设施装备与信息化

结构参数对立式曲面 V 型网板水动力性能的影响研究

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摘要：为研究结构型式及尺寸对立式曲面 V 型网板水动力性能的影响机理，本文基于计算流体力学方法，建立立式曲面 V 型网板三维数值模型计算分析其水动力性能，并通过设计制作缩比模型开展动水槽实验验证数值结果的有效性。在此基础上开展导流板角度、导流板拱度的结构参数对立式曲面 V 型网板水动力性能的影响规律研究，进而探究最优化的结构设计方案。研究结果发现：两块导流板角度、拱度均会对立式曲面 V 型网板的水动力性能产生不同程度的影响。若从提高网板扩张效果考虑，将导流板 A 角度设置为 40°、导流板 B 角度设置为 30°，或将导流板 A、B 拱度均设置为 18%，均可在一定范围内将立式曲面 V 型网板的最大升力系数提高到最大值；而从网板综合性能考虑，将导流板 A 角度设置为 25°、导流板 B 角度设置为 30°，或将导流板 A 拱度设置为 6%、导流板 B 拱度设置为 9%，均可在一定范围内将网板最大升阻比可提高至最大值。

关键词：立式曲面；V 型网板；水动力性能；结构参数

Effect of structural parameters on the hydrodynamic performance of vertical curved V-Type otter board

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Abstract：In order to study the influence mechanism of structural type and size on the hydrodynamic performance of vertical curved V-Type otter board, based on the computational fluid dynamics method, a three-dimensional numerical model of vertical curved V-Type otter board is established to calculate and analyze its hydrodynamic performance, and the validity of the numerical simulation results is verified by designing and constructing a scaled model for dynamic flume experiments. On this basis, the influence of the structural parameters of the deflector angle and the camber of the deflector on the hydrodynamic performance of the vertical curved V-Type otter board is studied, and then the optimal structural design scheme is explored. The results show that the angle and camber of the two deflectors will have different degrees of influence on the hydrodynamic performance of the vertical curved V-Type otter board. If the angle of guide plate A is set to 40 °, the angle of guide plate B is set to 30 °, or the camber of guide plate A and B is set to 18 %, the maximum lift coefficient of vertical curved V-type otter board can be increased to the maximum value within a certain range. Considering the comprehensive performance of the otter board, the angle of the guide plate A is set to 25 °, the angle of the guide plate B is set to 30 °, or the camber of the guide plate A is set to 6 %, and the camber of the guide plate B is set to 9 %, the lift-to-drag ratio of the otter board can be increased to its maximum value.

Key words: Vertical curved; V-Type otter board; Hydrodynamic characteristics; Structural parameters

基于流固耦合算法的拖网网板模型材料对水动力试验的影响研究

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摘要：摘要：拖网网板的水动力模型试验结果会因加工方式、结构简化等各种因素出现不同程度的试验偏差。为探究网板模型加工材料对水动力试验的影响机理，选取双开缝矩形曲面网板为研究对象，基于流固耦合算法结合动水槽模型试验，分析三种 3D 打印材料（ABS，PP，PVC）网板模型与传统钢质网板模型的结构响应差异及其对水动力试验的影响规律。结果显示：采用传统金属材料（结构钢）与非金属材料（ABS）加工的网板模型在结构响应及水动力性能方面均具有显著差异，且随冲角的增加，网板模型的总变形量增加，进而导致升/阻力系数差异也进一步增加；PVC 材料因其弹性模量较大、刚性较强，结构响应与金属材料较为接近，因而对水动力试验结果影响较小。基于上述结果，设计网板水动力模型试验时，可选用 PVC 作为 3D 打印材料，在保证模型精度的同时减小模型材料对水动力试验结果精度的影响。本文旨在为拖网网板水动力模型试验的设计与开展提供理论参考。

关键词：关键词：拖网网板；流固耦合；数值模拟；模型试验；影响机理

Study on the influence of trawl net plate model material on hydrodynamic test based on fluid-structure interaction algorithm

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Abstract： Abstract: The hydrodynamic model test results of trawl mesh panels will have different degrees of test deviation due to various factors such as processing mode and structural simplification. In order to explore the influence mechanism of mesh model processing materials on hydrodynamic test, the double-slit rectangular curved mesh plate was selected as the research object, and the structural response difference between the three 3D printing materials (ABS, PP, PVC) mesh model and the traditional steel mesh model was analyzed based on the fluid-structure interaction algorithm combined with the moving sink model test. The results show that the mesh model processed by traditional metal materials (structural steel) and non-metallic materials (ABS) has significant differences in structural response and hydrodynamic properties, and the total deformation of the mesh model increases with the increase of the impact angle, which in turn leads to the further increase of the lift/drag coefficient difference. PVC materials have little influence on the hydrodynamic test results due to their large modulus of elasticity, strong rigidity, and close structural response to metal materials. Based on the above results, PVC can be selected as the 3D printing material when designing the hydrodynamic model test of the mesh plate, which can reduce the influence of the model material on the accuracy of the hydrodynamic test results while ensuring the accuracy of the model. This paper aims to provide a theoretical reference for the design and development of hydrodynamic model tests of trawl panels.

Key words: Keywords: trawl board; fluid-structure interaction; numerical simulation; model testing; Mechanism of influence

自推进鱼群的水动力相互作用和尾流动力学分析

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摘要：自然界中，鱼类常以群体的形式进行摄食、生殖及洄游等。但鱼类的群体游动规模较大，对鱼类游动进行简单队列的编队便于更好的理解集群游动时的水动力性能和机理。本文采用 CFD 方法对鱼类在不同队列间距下串列队列、并列队列及矩形队列模式的自主游动进行了数值研究。对不同队列模式和队列间距下鱼类个体游动能力和水动力性能及尾迹动力学进行了综合分析。结果发现，队列模式对鱼类集群游动有不同影响，串列队列中鱼类游动速度得到提升；并列队列中鱼类游动速度较单条鱼减少；矩形队列中鱼类游动速度各不相同。队列间距对鱼类游动产生影响，串列队列中鱼类游动速度随间距增大而减小；并列队列中鱼类游动速度随间距增大而增大；矩形队列中随间距增大，各条鱼游动速度越接近单条鱼游动速度。通过对鱼类尾迹动力学进行分析，发现鱼类游动时游动能力产生差异的原因可能在于，鱼类可以利用周围鱼类所产生的尾迹来增强自身贴体压力区的低压区以改善其水动力性能。

关键词：自主游动；推进性能；数值模拟；鱼群

Hydrodynamic interactions and wake dynamics analysis of self-propelled schooling

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Abstract： In nature, fish often feed, reproduce, and migrate in groups. However, the swimming scale of schooling is relatively large, and a simple queue formation of fish swimming can facilitate a better understanding of the hydrodynamic performance and mechanism of group swimming. This article uses the CFD method to numerically study the autonomous swimming of fish in series, parallel, and rectangular queue modes with different queue spacing. A comprehensive analysis was conducted on the swimming ability, hydrodynamic performance, and wake dynamics of individual fish under different queue modes and queue spacing. The results showed that the queue mode had different effects on the swimming speed of fish clusters, and the swimming speed of fish in the tandem queue was improved; The swimming speed of fish in parallel queues is reduced compared to a single fish; The swimming speed of fish in a rectangular queue varies. The distance between queues has an impact on fish swimming, and the swimming speed of fish in a tandem queue decreases with the increase of distance; The swimming speed of fish in parallel queues increases with the increase of spacing; As the spacing increases in a rectangular queue, the swimming speed of each fish becomes closer to that of a single fish. By analyzing the dynamics of fish wakes, it was found that the difference in swimming ability of fish may be due to the fact that fish can use the wakes generated by surrounding fish to enhance the low-pressure area of their own body pressure zone and improve their hydrodynamic performance.

Key words: Autonomous swimming; propulsion performance; numerical simulation; schooling

重力式深水网箱布局参数理论计算及影响因素分析研究

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摘要：网箱规划布局是海水养殖全链条中的关键一环，不仅涉及到养殖产出效益，更是影响设施安全的关键因素。重力式深水网箱在未来一定时期内仍是深远海养殖的主要设施类型，关于其规划布局大多依靠以往的工程经验积累，缺乏一定的理论依据支撑，本研究将重力式深水网箱布局分为“交叉式”布局和“无交叉”布局，从理论角度分别给出不同布局形式下网箱部分布局参数及相应的计算公式，并据此分析系泊缆根数、锚绳长度以及安全控制距离等不同布局参数对规划海域网箱海域利用率的影响，最后讨论了网箱布局型式并给出了网箱布局建议，研究可为深远海养殖中网箱规划布局提供理论借鉴与支撑。

关键词：网箱；HDPE；规划布局；理论分析；影响参数

Research on the theoretical calculation of HDPE circular gravity cage layout parameters and analysis of influencing factors

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Abstract: The layout design of net cages is a crucial part in the entire chain of mariculture. It not only involves the aquaculture output but also plays a critical role in ensuring the safety of facilities. The HDPE circular gravity deep-sea net cage will still be the main facility for deep-sea aquaculture in the foreseeable future. However, the layout design of these cages have largely relied on past engineering experience, lacking a certain theoretical basis. This study divided the layout of HDPE circular gravity net cages into ‘cross’ layout and ‘non-cross’ layout. From a theoretical perspective, it provided the layout parameters and corresponding calculation formulas for different cage layouts. Based on this, the study also analyzed the impact of different layout parameters such as the number of mooring lines, length of mooring lines and safety margin on the utilization rate of the planned sea area for net cages. Finally, some suggestions for net cage layout were provided by taking into account the current status of net cage aquaculture. This study can provide theoretical reference and support for the layout design of net cages in deep-sea aquaculture.

Key words: Net cages; HDPE; Layout design; Theoretical analysis; Influence parameters

基于 EDEM 的养殖蛤仔底质对采捕犁的阻力仿真研究分析

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摘要：针对目前浅海蛤仔采捕装置导致产品含砂率高、破碎率大等问题，设计一种新型的浅海蛤仔采捕犁利用水平直元线法，参照犁体相关技术参数并结合采捕情况，设计一种采捕犁适用于浅海蛤仔采捕作业。实测蛤仔养殖底质含水量 57.41%、土壤堆积角 44.75°，标定土壤颗粒间 JKR 表面能 8.11 (J·m-2)、弹性恢复系数 0.43、滚动摩擦系数 0.01、静摩擦系数 0.45。建立仿真试验土壤颗粒床，以阻力为评价指标；使用单因素试验设计方法开展显著性筛选试验，得到与阻力相关指标耕宽、犁铧安装角、切土角显著性因素的范围；利用 Design-Expert 软件进行分析，以阻力大小为响应指标，对 3 因素进行 Box-Behnken 试验设计，得到 192.0mm 耕宽、37.805°犁铧安装角、25.843°切土角最佳设计参数。现场试验结果表明采捕犁可以实现开采蛤仔并减阻的效果，并为解决生态型浅海蛤仔采捕提供参考。

关键词：蛤仔养殖底质；采捕犁；单因素实验；响应面实验；阻力

Simulation study and analysis of EDEM-based resistance of cultured clam substrate to harvesting ploughs

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Abstract： Aiming at the current shallow sea clam harvesting devices that lead to high sand content and large crushing rate, a new type of shallow sea clam harvesting plough is designed to be suitable for shallow sea clam harvesting operations by using the horizontal direct line method, referring to the relevant technical parameters of the plough and combining with the harvesting situation. The water content of the clam breeding substrate was measured to be 57.41%, the soil accumulation angle was 44.75°, and the JKR surface energy between soil particles was calibrated to be 8.11 (J-m-2), the elastic recovery coefficient to be 0.43, the coefficient of rolling friction to be 0.01, and the coefficient of static friction to be 0.45. The soil particle bed for the simulation test was established, and the resistance was taken as the index of the evaluation; a one-way experimental design was used to carry out a significance screening test to obtain the results for the resistance. The range of significance factors of ploughing width, ploughshare mounting angle and soil cutting angle related to resistance was obtained. Using Design-Expert software for analysis, Box-Behnken experimental design was carried out on three factors with resistance as the response indicator, and the best design parameters of 192.0mm ploughing width, 37.805° ploughshare mounting angle and 25.843° soil cutting angle were obtained. The results of the field test showed that the harvesting plough can achieve the effect of clam mining and drag reduction, and provide a reference for solving the ecological shallow sea clam harvesting.

Key words: Clam culture substrate; harvesting and trapping plough; one-way experiment; response surface experiment; resistance

随机波浪与随机边界变形联合作用下网衣的动力特性研究

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摘要：开展深远海养殖是海水养殖产业发展的必然趋势。在深远海波浪更大、海流更急，对养殖网箱的安全有更严格的要求。本研究采用集中质量法模拟大面积网衣的三维非线性运动，采用势流理论刻画外界随机波浪场，基于 Morison 公式和 Screen 模型计算网衣受到的水动力载荷，详细分析了随机波浪和随机边界变形联合作用下网衣的动力响应特性。研究表明：网箱框架结构的随机弹性变形将使网衣的运动响应变得更加复杂，频率更加丰富，网线张力变大，更容易发生破坏。

关键词：随机波浪；随机边界变形；网衣动力响应；网衣破坏。

Dynamic responses of a flexible net excited by irregular waves and irregular boundary deformations

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Abstract： In the industry of marine aquaculture, it is inevitable to perform aquaculture in the deep and far sea. However, in those areas, the waves are bigger and the currents are faster. The aquaculture cages should be built more reliable and more safety. In this study, the nonlinear vibrations of a large-area flexible net are simulated with the lumped-mass method in three dimensions. The irregular waves are described with the potential flow theory. The hydrodynamic forces exerting on the flexible net are solved based on the Morison's equation and the Screen model. The dynamic response characteristics of the flexible net under the combined excitations of irregular waves and irregular boundary deformations are investigated in detail. The results demonstrate that when the frames of the aquaculture cage deform irregularly with time, the vibrations of the flexible net will become more complex, the vibration frequencies will become more, and the dynamic tensions of the net twines will become larger which is prone to failure.

Key words: Irregular waves; Irregular boundary deformations; Dynamic responses of the net; Net broken

基于金枪鱼围网海鸟雷达图像识别技术探究

人工集鱼装置对海鸟分布的影响

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摘要：在金枪鱼围网渔业中，侦察阶段占据了大部分的作业时间。雷达是探测海鸟的一种非常有效的方法。海鸟作为海洋捕食者，它们总是在寻找捕鱼机会。虽然有许多关于海鸟行为特征的研究，但现有文献对漂流的集鱼装置（Drift Fish Aggregation Devices, DFADs）如何影响海鸟的行为动态提供的证据不足。在本文中，我们利用渔船的雷达收集了距离渔船 29.632 公里内的海鸟群信息，并计算了海鸟回声的空间聚类。广义加性混合模型（Generalized Additive Mixed Model，GAMM）被用来研究 DFADs 和海鸟动态之间的关系。该模型将 DFADs 作为随机效应，纬度/经度作为固定效应。研究结果表明，DFADs 变量影响海鸟行为。对海鸟数量、海鸟面积和海鸟能力的随机效应分别为 2.14、14.60 和-0.18。

我们提出了一种雷达图像海鸟回声识别方法，可以计算出海鸟的数量、海鸟的面积和海鸟的活动水平。然后，我们比较了计算出来的雷达图像信息。DFADs 周围的鸟群数量平均为 28 只（范围 2-93），比没有 DFADs 的区域更集中，平均为 35 只（范围 8-71）。没有附近 DFADs 的鸟类集群，平均数量为 78.3 只（范围 3.8-275.3），覆盖总面积为 78.3 平方公里（范围 3.8-275.3 平方公里），比有 DFADs 的鸟类集群更稀疏，后者覆盖总面积平均为 109.5 平方公里（范围 23.3-224.6 平方公里）。附近有 DFADs 的鸟类集群的平均活动水平为 2.0（范围 0.6-3.8），比没有 DFADs 的鸟类集群的活动水平低，后者的平均活动水平为 2.5（范围 0.6-6.3）。我们还发现海鸟的分布和行为与经度和纬度之间存在一些关联。经度 165°E 的鸟群数量最多，鸟类居住的面积也最大，但这些都向东减少。然而，模型 3 显示了鸟类活动水平与经度之间的相反关系；鸟类活动水平的最低值出现在东经 165°附近，并向东增加。

关键词：海鸟，人工漂流集鱼装置，雷达，广义加性混合模型

Application of seabird radar image identified method for analyzing effect of FADs on seabird

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Abstract： In the tuna purse seine fishery, seiners spend a considerable amount of time detecting objects such as seabirds. Radar is a very efficient method for detecting seabirds. As marine predators, they are always looking for fishing opportunities. Although many studies exist on the behavioral characteristics of seabirds, the available literature provides insufficient evidence on how drifting Fish Aggregating Devices (DDFADs) influence seabirds' behavioral dynamics. In this study, we used a fishing vessel's radar to collect information on seabird groups within 29.632 km of the vessel and calculated a spatial clustering of the seabird-echoes. Generalized additive mixed models were used to investigate the relationship between drifting DFADs and seabird dynamic in the Republic of Kiribati.

The model treated DFADs as a random effect and latitude/longitude as fixed effect. The findings indicate that DFADs variables affected seabird behavior. The random effects on seabird number, seabird area, and seabird ability were 2.14, 14.60, and −0.18, respectively.

We present a radar image seabird identification method that can calculate the number of seabirds, the area of seabirds, and the activity level of seabirds. Then, we compared the radar image information that was calculated. The number of bird clusters around drifting DFADs had a mean of 28 (range 2–93) and were more concentrated than in areas without DFADs, which had a mean of 35 (range 8–71). The bird clusters without nearby DFADs, with a mean population of 78.3 birds (range 3.8–275.3) and covering a total area of 78.3 km2 (range 3.8–275.3 km2), were sparser than those with DFADs, which covered a mean total area of 109.5 km2 (range 23.3–224.6 km2). Bird clusters with nearby DFADs had a mean activity level of 2.0 (range 0.6–3.8) and were less active than bird clusters without DFADs, which had a mean activity level of 2.5 (range 0.6–6.3). We also found some correlations between the distribution and behavior of seabirds and the latitude and longitude. The longitude of 165°E had the highest number of bird clusters and the greatest amount of area inhabited by birds, but these decreased to the east. However, model 3 showed the opposite relationship between bird activity level and longitude; the minimum value of bird activity level occurred around 165°E and increased to the east.

Key words: seabird; FADs; seabird radar; gamm

立式双曲面网板水动力性能优化研究

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摘要：为研究结构型式及尺寸对立式双曲面网板水动力性能的影响机理，基于计算流体力学方法，建立立式双曲面网板三维数值模型，计算分析其水动力性能，并通过设计制作缩比模型开展动水槽试验，验证数值结果的有效性。在此基础上开展曲面板弯曲度、弯曲度位置、支撑板间距等不同结构参数对立式双曲面网板水动力性能的影响规律研究，进而探究最优化的结构设计方案。研究结果表明：曲面板弯曲度的同步改变和单一改变均会对立式双曲面网板的水动力性能产生不同程度的影响。如果只考虑扩张效果，曲面板 A、B 的弯曲度均设置为 20%左右，或曲面板 A 弯曲度设置为 15%、曲面板 B 弯曲度设置为 25%左右，均可在一定范围内将立式双曲面网板的最大升力系数提高到最大值。当曲面板弯曲度位置同步设置为 50%时，网板升力系数可达到最大值，而当曲面板弯曲度位置同步设置为 20%时，最大升阻比达到峰值，支撑板间距对立式双曲面网板水动力性能的影响不明显。

关键词：立式双曲面网板；水动力性能；数值模拟；水槽试验；结构参数

Research on Hydrodynamic Performance Optimization of Vertical Hyperboloid Mesh Board

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Abstract： In order to study the influence mechanism of structure type and size on the hydrodynamic performance of vertical hyperboloid mesh board, a three-dimensional numerical model was established based on computational fluid dynamics method, and its hydrodynamic performance was calculated and analyzed. The dynamic flume test was carried out by designing and making the scaled model, and the validity of the numerical results was verified. On this basis, the influence of different structural parameters such as curvature, curvature position and support plate spacing on the hydrodynamic performance of vertical hyperboloid mesh plates is studied, and then the optimal structural design scheme is explored. The results show that both the simultaneous change and the single change of the curvature of the curved plate will have different degrees of influence on the hydrodynamic performance of the vertical hyperboloid plate. If only the expansion effect is considered, the bending degree of curved board A and B is set to about 20%, or the bending degree of curved board A is set to 15%, and the bending degree of curved board B is set to about 25%, the maximum lift coefficient of vertical hyperboloid mesh board can be increased to the maximum within a certain range. When the bending degree of the curved plate is set to 50%, the lift coefficient of the mesh plate can reach the maximum value, and when the bending degree of the curved plate is set to 20%, the maximum lift-drag ratio reaches the peak value. The influence of the support plate spacing on the hydrodynamic performance of the vertical hyperboloid mesh plate is not obvious.

Key words: Vertical hyperboloid net board; Hydrodynamic performance; Numerical simulation; Water tank test; Structural parameter

基于动态模型的矩形曲面网板水动力及稳定性研究

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摘要：随着数值模拟方法的迭代和更新，动网格目前广泛应用在解决动态模型数值模拟等问题上。此方法可以获取研究对象在流场中连续变化下的物理量。区别于前人对静止网板模型的研究，本文采用动网格的方法结合动态网板模型对矩形曲面网板冲角及倾角发生连续偏转时的水动力及稳定性进行了研究。研究结果显示：1）动网格数值模型计算得到的升阻力系数与动水槽模型试验结果匹配较好，可以较为准确地计算网板水动力及稳定性。2）在不发生倾斜时，网板在 12°冲角下存在最大升阻比 2.68。3）连续内倾时，Cpc（翼展方向压力中心系数）随倾角增大而减小，Cpb（翼弦方向压力中心系数）基本保持不变，网板压力中心下移。4）连续外倾时，Cpb 和 Cpc 随倾角增大而增大，网板压力中心上移。5）前倾时 Cpb 随倾角增大而减小，Cpc 增大，后倾时 Cpb 随倾角增大而增大，Cpc 减小。研究表明，网板在发生倾斜时时水动力性能及稳定性整体呈降低趋势。

关键词：矩形网板；动网格；水动力性能；稳定性

Research on Hydrodynamic Performance and Stability of Rectangular Otter Board based on Dynamic Mesh

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Abstract： Research on Hydrodynamic Performance and Stability of Rectangular Otter Board based on Dynamic Mesh. With the iteration and updating of numerical simulation methods, Dynamic Mesh are currently widely used to solve problems such as dynamic model numerical simulation. This method can obtain the physical quantities of the research object under continuous changes in the flow field.Different from the previous studies on static board model, this paper adopts the dynamic mesh method combined with dynamic board model to investigate the hydrodynamic and stability of rectangular otter board when the angle of attack and heel angle undergoes continuous deflection.The results of the study show: 1)The lift coefficient and drag coefficient calculated by the Dynamic Mesh Numerical Model matches well with the test results of the flume tank experiment, which provide Dynamic Mesh can calculate the hydrodynamic performances and stability of the otter board accurately. 2)The maximum lift-drag ratio of the otter board is 2.68 at the 12 attack angle with no inclination. 3)During continuously tilting inward, Cpc decreases with the increase of heel angle, while Cpb remains basically unchanged, and the pressure center of the board moves down.4)During continuously tilting outward, Cpb and Cpc increase with the increase of heel angle, and the pressure center of the board moves up. 5)When the board tilts forward continuously, Cpb decreases and Cpc increases, while when the board tilts backward continuously, Cpb increases and Cpc decreases.The research shows that the hydrodynamic performance and stability of the board tend to decrease when it is tilted.

Key words: Rectangular Otter Board; Dynamci Mesh; Hydrodynamic Performance; Stability

南极磷虾探测浮标研制与投放试验

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摘要：渔探浮标是商业捕捞和资源探测的重要工具。南大洋海洋环境特殊，对浮标结构和性能有一定要求。本文设计了一种南极磷虾探测漂流浮标，包括数据采集、通讯、供电和自持四个部分。数据采集部分包括 1 个换能器，2 个温度传感器和 1 个 GPS 模块，可通过 83kHz 和 200kHz 主动声呐探测虾群，探测距离 1~250m，分辨率 160 层；温度传感器分别采集气温和海表温；GPS 可实时获取浮标位置信息。通讯部分主要是 1 个铱星通讯模块。供电部分主要是 1 个锂电池电池组和 1 个太阳能电池板。自持部分用于保障设备正常运行，包括单向气阀等针对南极环境设置的结构。浮标投放试验由我国“深蓝”号南极磷虾船执行，投放地点位于南奥克尼群岛西侧海域，48.2 区。浮标正常工作 7 天后，于西格尼岛沿岸离线，期间采集的数据通过铱星通讯的方式发送至上海，并通过 PC 端软件可视化。试验结果表明，南极磷虾探测浮标具备技术可行性，对后续设备改进和投放有指导作用。

关键词：南极磷虾；渔探仪；漂流浮标；卫星通讯

Drifting Buoy for Antarctic Krill Detection

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Abstract： Fish finder is one of the important tools for commercial fishery and resource assessment. Considering the extreme environment of the Antarctic Ocean, the buoy demands specially modify. This paper introduces a drifting buoy for Antarctic krill detection, which consists of data acquisition module, communication module, powering module, and supporting module. Data acquisition module included a transmitting and receiving integrated transducer, 2 temperature sensors, and a GPS component. Transducer can detect krill shoals by 83kHz or 200kHz active sonar, with a 160 layers resolution in 0~250m detecting range. The temperature sensors can measure the air temperature and sea surface temperature separately. The GPS component can locate the buoy. Communication module was mainly an Iridium satellite communication component. Powering module included a Lithium battery pack and a solar powering panel. Supporting module mainly for protecting the buoy from the extreme environment, including single valve and some other structures. The experiment of buoy was conducted by the Antarctic krill Vessel “Sheng Lan”. The buoy was released at west of South Orkney Islands, Subarea 48.2. After more than 7 days’ work, the buoy finally offline at the coast of Signy Island. The data collected during experiment was sent back to Shanghai, and visualized by software on PC. The experiment showed that the buoy was technically feasible, and the result was instructive.

Key words: Antarctic krill; Fish finder; Drifting buoy; Satellite communication

回声测深仪中假底的识别与剔除

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摘要：为了避免回声测深仪成像中出现回声假底，影响测深仪的准确性与可靠性，本文利用“深蓝号”南极磷虾船与“蓝海 201”科考船检测到的回声测深仪数据，结合回声测深仪成像原理，研究了假底形成的原因，并根据其形成原因将假底分为三种类型，对每一种假底出现的深度进行了推导计算与实验验证。在判断出假底准确位置的基础上，本文通过一系列算法 将假底信号剔除。实验结果表明，本文剔除的计算假底公式计算结果与实际情况相符，90%以上数据的计算结果与实际误差小于 1%，99%以上数据误差小于 5%。而对假底信号剔除结果表明，当假底位置判断准确，假底信号均能得到较好的处理，处理后的假底信号与海水回声信号相近，不会影响目标鱼类以及其它目标物的判断。

关键词：回声测深仪；假底信号；深度计算；剔除假底

Identification and elimination of false-bottom in echosounder

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Abstract：In order to avoid the occurrence of echo false-bottoms in the imaging of the echosounder, which affects the accuracy and reliability of the echosounder, this article uses the echosounder data from the "Deep Blue" Antarctic krill ship and the "Blue Sea 201" scientific research ship, and combines the imaging principle of the echosounder to study the reasons for the formation of false-bottoms. According to the reasons for their formation, false-bottoms are divided into three types, and the depth at which each type of false-bottom appears is derived and calculated, and experimentally verified. On the basis of determining the accurate position of the false-bottom, this article uses a series of algorithms to eliminate the false-bottom signal. The experimental results show that the calculation results of the false-bottom formula excluded in this article are consistent with the actual situation, with an error of less than 1% for more than 90% of the data and less than 5% for more than 99% of the data. The results of remove false-bottom signals indicate that when the position of the false-bottom is accurately determined, the false-bottom signals can be well processed. The processed false-bottom signals are similar to the seawater echo signals and will not affect the judgment of the target fish or other target objects.

Key words: echosounder; false-bottom signal; depth calculation; remove false-bottom

鲐鱼目标强度实验测量与理论模型的比较

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摘要：鲐鱼是西北太平洋的重要经济和生态物种。声学测量数据由配备 Simrad EK 80 宽带科学回声测深仪的“松航”号科考船采集，用于估算渔业资源储存量。然而，迄今为止，对西北地区重要鱼类声学特性的研究还很少，这给渔业资源的量化和分类带来了巨大的挑战。因此，我们的研究利用实验测量和理论反向散射模型分析了鲐鱼的个体目标强度（TS），以研究鲐鱼的宽带频率响应以及不同方法之间的差异。从西北太平洋捕获的鲐鱼样本用海水冷冻，然后转移到实验室缓慢解冻。实验测量采用系绳法在消声淡水池中使用宽带回声测深仪进行，频率范围为 45-95 kHz 频段和 160-260 kHz 频段。声学数据采用 Echoview 13.0 基于单目标检测宽带方法进行处理。然后拍摄 X 射线照片以获得每个样品的形态参数以用于模型计算。我们报告了鲐鱼的 TS 和 TL 之间的关系，并比较了实验测量与理论反向散射模型方法之间的差异。

关键词：目标强度；鲐鱼；实验测量；理论模型

Comparison of Target Strength of Chub Mackerel (Scomber japonicus) from Ex-Situ Measurements and a Theoretical Model

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Abstract： Chub mackerel (Scomber japonicus) is a key economic and ecological species in the Northwest Pacific Ocean. Acoustic measurement data were collected by the scientific research vessel "Songhang" equipped with a Simrad EK 80 broadband scientific echosounder to estimate the fishery resource storage. However, so far, there are still few studies on the acoustic properties of important fish species in the Northwest, which brings great challenges to the quantification and classification of fishery resources. Therefore, our study analyzed the target strength (TS) of Chub mackerel individuals using ex-situ measurements and a theoretical backscattering model, to investigate the broadband frequency response of Chub mackerel and the differences between different methods.

Chub mackerel samples captured from the Northwest Pacific Ocean were frozen using seawater and transferred to the laboratory to slowly thaw. The ex-situ measurements were conducted by tether method in an anechoic freshwater tank (11m * 7m * 6m) by using calibrated broadband echosounders (Simrad EK80), with a frequency range of 45-95 kHz band and 160-260 kHz band. The measured tilt angles ranged from -90° to 90° by 5° steps, -90° means the fish side aspect is vertical with the incident wave, and 0° means the fish head is toward the transducer face. Acoustic data was processed by Echoview 13.0 based on the single target detection wideband method. Then X-ray photos were taken to get the Morphological parameters of each sample for model calculations.

We reported the relationship between the TS and TL for Chub mackerel and compared the differences between ex-situ measurements and the theoretical backscattering model method. Our results could provide basic data to evaluate the distribution and abundance of Chub mackerel using fishery acoustic technology.

Key words: Target strength; Chub mackerel; Ex-situ measurements; Theoretical Model

基于茎柔鱼几何形态的卷积神经网络特征提取与分析

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摘要：茎柔鱼作为我国远洋渔业的重要经济渔获物种类，其几何形态特征对研究茎柔鱼生长、种类、生活史和三维形态建模具有重要意义，而传统的手动测量方法通常耗时，且软体生物外形态特征的自动化获取较为困难。本文对茎柔鱼样本拍照获取图像进行校正，基于卷积神经网络架构提取图像中的敏感区域并获得图像特征。利用边缘轮廓图像提取图像像素坐标，以获得生物外形态参数值并将鱼体形态参数特征化。研究结果表明，通过卷积神经网络对茎柔鱼的形态参数指标可实现自动测量；利用各个特征的二维坐标可以得到用于计算茎柔鱼形态参数的值；根据形态参数的测量结果可以得到茎柔鱼头部的 4 个几何形态特征点、胴体的 4 个几何形态特征点、尾部 5 个几何形态特征点以及触腕 8 个几何形态特征点。将卷积神经网络应用于鱼类形态学的研究可以提供新的实验思路，为资源量的评估提供参考方法。

关键词：茎柔鱼；外形态；卷积神经网络；深度学习；形态参数特征化

Convolutional Neural Network Feature Extraction and Analysis Based on the Geometric Morphology of Dosidicus gigas

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Abstract： Dosidicus gigas, commonly known as the Giant Squid, holds significant economic importance in China's distant-water fisheries. Understanding its geometric characteristics is crucial for research on growth, classification, life history, and 3D morphological modeling. Traditional manual measurement methods are often time-consuming, and obtaining automated measurements of soft-bodied biological external morphological features presents challenges. In this study, we corrected images of Dosidicus gigas specimens and applied a convolutional neural network architecture to extract sensitive regions and capture image features. Pixel coordinates were derived from edge contour images to obtain biological external morphological parameter values and characterize the squid's body shape parameters.Research findings demonstrate that automated measurement of morphological parameters for Dosidicus gigas can be achieved using convolutional neural networks. The utilization of 2D coordinates of various features allows the calculation of morphological parameter values. Measurement results yield four geometric characteristic points for the head, four for the body, five for the tail, and eight for the tentacles of Dosidicus gigas. The application of convolutional neural networks in fish morphology research offers innovative experimental approaches and provides a reference method for resource assessment.

Key words: Dosidicus gigas; external morphology; convolutional neural network; deep learning; morphological parameter characterization

上升流循环水扇贝幼体培育系统研究

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摘要：针对现有扇贝育苗池培育密度低，人工换水劳动强度大的问题，设计了一种上升流循环水扇贝幼体培育装置。为使扇贝幼体均匀分布于培育装置，应用 EDEM-Fluent 耦合仿真进行上升流扇贝幼体运动仿真，基于 Design-Expert 软件进行培养锥底部锥角（θ）、培养锥柱高/锥高(n)和入口流速(v)对培养锥内 D 形虫轴向和径向分布变异系数的响应面分析，优化培养锥结构参数，进行样机验证试验并优化入口导流板角度(c)和培育密度(τ)。结果表明：各因素对 D 形虫分布变异系数影响的主次顺序为θ>v>n>c>τ；θn 和 cn 的交互作用极显著影响 D 形虫分布变异系数（P<0.01），vn 的交互作用对 D 形虫分布变异系数的影响次之（P<0.05）；经回归分析得到最优参数组合为θ=108.97°、n=1.8、v=0.19m/s、c=60.94°、τ=11 个/毫升。该研究可为上升流循环水扇贝幼体培育装置设计提供重要参考。

关键词：上升流循环水系统；扇贝幼体培育；分布均匀度；CFD-DEM；导流板

Design and Experiment of an Upflow Circulating Water Scallop Hatchery System

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Abstract：In order to solve the problems of low cultivation density and high labor intensity of manual water change in the existing scallop nursery pond, a larval cultivation device for scallop larvae in upwelling circulating water was designed. The EDEM-Fluent coupling simulation was used to simulate the movement of upwelling scallop larvae in order to distribute the larvae evenly in the cultivation device. Based on the Design-Expert software's response surface analysis, the effects of cone angle (θ), culture cylinder height/cone height (n), and inlet flow rate (v) on the coefficient of variation of the axial and radial distribution of D-shaped insects in the culture cone were analyzed, the structural parameters of the culture cone were optimized, the prototype verification test was conducted, and the angle of the inlet deflector (c) and the cultivation density (τ) were optimized. The findings indicated that θ>v>n>c>τ was the sequence in which each factor had an influence on the D-shaped worm distribution's coefficient of variation.The coefficient of variation of D-shaped parasites was significantly impacted by the interaction between θn and cn (P<0.01), and then by the interaction between vn and the coefficient of variation (P<0.05). The optimal combination of parameters was θ=108.97°, n=1.8, v=0.19m/s, c=60.94°, τ=11/ml, under these conditions, the simulated value of the coefficient of variation of the axial distribution of D-shaped insects was 34.40%, the measured value of the larval breeding device was 38.04%, and the relative error between the simulated value and the measured value was 10.58%. This study can provide an important reference for the design of larvae cultivation devices for scallop larvae in upwell-flowing circulating water.

Key words: Upwelling circulating water system; Scallop larval culture; Uniformity of distribution; CFD-DEM； Deflectors

基于 VMS 的东海拖网渔船分布变化及相关因素分析

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摘要：全球气候变暖导致了鱼类分布的变化，但对于是否因此影响到了渔业活动的分布，我们仍然知之甚少。为了解渔业活动近年来的变化并分析影响因素，我们以浙江象山拖网作业为例，使用其 2015 至 2022 年的船舶监测系统（VMS）数据统计得到捕捞努力量，并结合海面温度，风力强度，渔业资源采样调查结果等数据分析了浙江象山拖网渔船在中国东海的努力量分布变化。本研究利用重心法和经验正交函数分析了努力量的空间变化，以评估努力量的时空变化，分析表明，拖网作业的捕捞努力量在东海区域整体呈减少趋势，经度方向上表现出明显的向近岸靠拢的趋势，纬度方向上仅虾拖类作业向北移动。利用 CCM 和 S-Map 方法针对努力量分布与各因素之间的关系展开分析，分析表明，SST 对鱼拖努力量分布变异程度基本不产生影响；渔业资源因素也仅在鱼类资源对鱼拖的努力量分布变异程度上表现出一定强度的影响。相比之下，鱼拖努力量强度对分布变异程度的影响力更强。

关键词：船舶监测系统；捕捞努力量；经验动态建模；渔业资源

Analysis of changes in trawler distribution and related factors in the East China Sea based on VMS

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Abstract： Global warming has led to changes in fish distribution, but we still know little about whether this has affected the distribution of fishing activities. In order to understand the changes in fishing activities in recent years and analyze the influencing factors, we analyzed the changes in the distribution of fishing effort of Zhejiang Xiangshan trawlers in the East China Sea by taking its trawling operation as an example, using its Vessel Monitoring System (VMS) data from 2015 to 2022 to statistically obtain the fishing effort, and combining it with the data on sea surface temperature (SST), wind strength, and the results of the survey of fishery resources sampling. In this study, the spatial variation of effort was analyzed using the center of gravity method and empirical orthogonal function to assess the spatial and temporal variation of effort, and the analysis showed that the fishing effort of trawling operations showed an overall decreasing trend in the East China Sea region, and showed a clear tendency to move closer to the inshore in the longitude direction, and only shrimp trawling operations moved to the north in the latitude direction. CCM and S-Map methods were used to analyze the relationship between effort distribution and various factors, and the analysis showed that SST basically had no effect on the degree of variability in the distribution of fish trawl effort, and the fishery resource factors only showed a certain intensity of influence on the degree of variability in the distribution of fish trawl effort in terms of fish resources. In contrast, the strength of effort of fish trawls had a stronger influence on the degree of distributional variability.

Key words: VMS, fishing effort; EDM; fishery resources

空化射流式网箱网衣清洗装备关键部件设计及试验研究

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摘要：针对我国深远海大型网箱养殖网衣清洗装备缺乏难题，基于高压射流空化原理，本文研制出了一种双体深水网箱网衣清洗装备。利用在网箱养殖海域制作的网衣污损生物挂板开展淹没环境下的清洗装备冲击实验，探究不同工况下的喷嘴孔径、喷嘴与转盘夹角（喷嘴轴线与分流转盘盘面所呈角度）、靶距对清洗装备污损生物清洁率的影响。结果表明：（1）网衣挂板污损生物去除率受靶距、喷嘴孔径、喷嘴与转盘夹角等多因素影响，实验参数范围内网衣清洗装备污损生物去除率为 30.26 %~72.55%；（2）喷嘴孔径为 1.0 mm，喷嘴与转盘夹角为 60°，靶距为 0 cm 时网衣挂板污损生物去除率最大，靶距对网衣挂板污损生物去除率的影响最为显著，喷嘴与转盘夹角次之，喷嘴孔径影响最小。（3）贝类污损生物在网衣清洗装备空化射流冲击作用下主要以壳体破碎的形式脱落，清洗后仍有部分物质残留，主要残留物为具有较强吸附力的贝类软质足丝盘。研究结果进一步优化了水

关键词：网箱养殖；网衣清洗；结构参数；试验研究

Design and experimental research on key components of net cleaning equipment for deep-water cage

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Abstract: In response to the lack of cleaning equipment for large-scale net cage aquaculture in China, a net cleaning equipment for deep-water cage aquaculture has been developed based on the principle of high-pressure jet cavitation. Conduct impact experiments on cleaning equipment in submerged environments using net clothing fouling biological hanging plates made in cage aquaculture waters, to explore the effects of nozzle aperture, nozzle to rotary angle (angle between nozzle axis and diversion rotary plate surface), and target distance on the cleaning rate of fouling organisms in cleaning equipment under different working conditions. The results show that: (1) The biological removal rate of fouling on the net clothing hanging board is influenced by multiple factors such as target distance, nozzle aperture, and the angle between the nozzle and the rotary table. Within the experimental parameter range, the biological removal rate of fouling on the net clothing cleaning equipment is 30.26%~72.55%; (2) When the nozzle aperture is 1.0 mm, the angle between the nozzle and the turntable is 60 °, and the target distance is 0 cm, the removal rate of fouling organisms on the mesh hanging plate is the highest. The effect of target distance on the removal rate of fouling organisms on the mesh hanging plate is the most significant, followed by the angle between the nozzle and the turntable, and the effect of nozzle aperture is the smallest. (3) Under the impact of cavitation jet from net clothing cleaning equipment, shellfish fouling organisms mainly fall off in the form of shell fragmentation. After cleaning, there are still some residual substances, and the main residue is soft shellfish foot silk discs with strong adsorption power. The research results further optimized the parameter ratio of underwater cleaning equipment, providing theoretical support for the design of mesh cleaning equipment.

Key words: Cage aquaculture; Net cleaning; Structural parameters; Experimental research

基于“浙岱渔 13461”鱿钓船集鱼灯配置优化策略研究

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摘要：鱿钓船的集鱼灯配置对捕捞效率和资源可持续性发展至关重要，因此在当前渔业环境中，寻找最佳配置以提高捕捞效率的同时减少对海洋生态系统的负面影响变得愈发重要。研究以"浙岱渔 13461"为例，基于灯光的各向特异性，采用将灯光离散化以及将海水网格化进行照度叠加计算的方法，对该船不同灯高、不同灯间距配置进行水中照度计算，实现水下光场分布可视化。结果表明，"浙岱渔 13461"鱿钓船的当前灯光配置在一定程度上具有合理性，但仍有改进的空间。通过对灯间距、灯高的参数优化，提高光诱渔业捕捞效率，水下光场的可视化分析进一步加强对灯光配置与水下环境的分析。水下光场的可视化分析旨在为今后灯光配置研究提供更具信息量的工具，用于平衡经济效益与环境可持续性。

关键词：集鱼灯配置；优化策略；水下照度；可视化分析

Optimal Configuration of Squid Jigging Vessel Fishing Lights: A Case Study of "Zhedaiyu 13461"

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Abstract： The configuration of fishing lights on squid jigging vessels plays a pivotal role in enhancing fishing efficiency and promoting sustainable resource development. Consequently, finding the most effective configuration to improve catch rates while mitigating adverse impacts on marine ecosystems has become increasingly crucial in the current fisheries environment. This study, using "Zhedaiyu 13461" as a case study, employs a method that utilizes the anisotropy of lighting. It involves discretizing the lighting and gridifying the seawater to calculate underwater illuminance for different configurations of light heights and light spacings, leading to the visualization of underwater light field distribution.The findings reveal that the current lighting configuration of "Zhedaiyu 13461" squid jigging vessel is reasonably practical to a certain extent, but there is still room for improvement. Optimizing parameters such as light spacings and light heights can significantly enhance the efficiency of light-attracting fishing and reduce resource wastage. Furthermore, the visualization analysis of the underwater light field further enhances the understanding of the relationship between lighting configuration and the underwater environment.The visualization analysis of the underwater light field is intended to provide a more informative tool for future studies on lighting configuration, enabling a balance between economic benefits and environmental sustainability.

Key words: Fishing light configuration; Optimization strategy; Underwater illuminance; Visualization analysis

仿海豚尾鳍诱导阻力对水动力性能影响的数值模拟研究

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摘要：摘要：海豚在水下优雅的运动姿态和高效的运动推进方式是水下航行器设计的重要灵感来源。而仿生海豚航行器的流体动力学性能在很大程度上受尾鳍诱导阻力影响。这项研究通过数值模拟来研究尾鳍诱导阻力对海豚模型整体水动力效率的影响情况。研究结果表明：流体动力学和尾鳍独特形态之间的相互作用。当流体穿过尾翼的跨度时，它会产生从压力到吸力侧的横向流动，从而引发尾涡。这些涡流产生向下指向的速度，从而减小有效攻角和随之产生的升力，深刻影响整体流体动力学性能。通过这一探索，该研究不仅分析了尾鳍诱导阻力对海豚整体水动力性能的影响，还强调了其在改进仿生设计以提高水环境中的水动力效率方面的关键作用。

关键词：仿生海豚；尾鳍推进；诱导阻力；水动力性能；尾涡；流体动力学；

A Numerical Simulation Study on the Impact of Biomimetic Dolphin Caudal Fin-Induced Drag on Hydrodynamic Performance

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Abstract： Dolphins' graceful underwater movements and efficient propulsion mechanisms serve as crucial inspiration for underwater vehicle design. The hydrodynamic performance of biomimetic dolphin-inspired vehicles is significantly influenced by tail fin-induced drag. This study employs numerical simulations to investigate the impact of tail fin-induced drag on the overall hydrodynamic efficiency of dolphin models. The research reveals the intricate interaction between fluid dynamics and the unique morphology of the tail fin. As fluid flows over the tail fin's span, it generates lateral flow from the pressure to the suction side, initiating tail vortices. These vortices induce downward-pointing velocities, reducing the effective angle of attack and, consequently, the generated lift, profoundly affecting the overall fluid dynamic performance. Through this exploration, the study not only analyzes the influence of tail fin-induced drag on dolphins' overall hydrodynamic performance but also emphasizes its pivotal role in enhancing hydrodynamic efficiency in aquatic environments through refined biomimetic designs.

Key words: Biomimetic Dolphins; Caudal Fin Propulsion; Induced Drag; Hydrodynamic Performance; Tail Vortices; Fluid Dynamics;

影响虹鳟穿越分级栅的因素及分级效果研究

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摘要：高密度水产养殖过程中由于对食物、空间等有限生活资源的竞争以及个体存在游泳、摄食等能力的差异，养殖鱼类会产生不同程度的种内竞争。长期在同一空间养殖的鱼类由于上述原因会产生大小异质性，需要通过定期分级，以减少大小个体的差异，实现养殖对象的健康生长。本研究通过实验探究虹鳟在网箱中的空间领域需求、食物引诱效果以及社群等级等因素对虹鳟主动穿越分级栅的影响，减缓摄食竞争强度，简化收捕操作，以实现养殖鱼获产量最大化、经济效益最大化。

关键词：分级；网箱装置；鱼类行为；社群等级

Research on the factors affecting rainbow trout （Oncorhynchus mykiss） crossing grading grid and grading effects

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Abstract：In the process of high density aquaculture, competitions for limited living resources such as food and space, as well as differences in individual swimming and feeding abilities, can lead to intraspecific competition in cultured fish. Fish raised in the same space for a long time may exhibit size heterogeneity due to the above reasons, and regular grading is necessary to reduce the differences in individual size and achieve healthy growth of the breeding fish. This study explores the impact of factors such as the spatial demand, food attraction effect, and social hierarchy of rainbow trout in cages on their actively crossing the grading grid, to weaken feeding competition intensity, simplify harvesting operations, maximize the output value of aquaculture fish and economic benefits.

Key words: fish grading; rainbow trout; cage device; fish behavior; social hierarchy

基于仿生蝠鲼鱼群观测装置的设计与实现

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摘要：鱼群观测是评估养殖池塘内鱼群生活状况的重要手段，为提升观测装置的环境共融性、稳定性，研究了一种基于仿生蝠鲼鱼群观测装置的设计与实现。该鱼群观测装置，结构设计受生物蝠鲼启发，基于计算机视觉技术对生物标本形态轮廓提取，建立鱼体展向形态模型；基于lighthill 理论建立展向运动学模型，结合鱼群观测系统、通信控制系统进行总体设计；设计动水槽试验和池塘试验，验证该装置的水动力性能和实际应用的可行性。结果与试验表明：（1）提取的展向轮廓与 NACA0013 对应的拟合优度最高且为 0.744，为样机设计奠定良好水动力性能基础（2）在工况 V=0.2m/s，f=1 Hz，A=40°下，空间内三维受力和力矩均发生振荡变化，揭示了蝠鲼型机器鱼运动过程的平稳性机理；（3）池塘试验中仿生机器蝠鲼装置表现共融性强，对鱼群扰动小，可实时传输水下图像，验证了仿生蝠鲼装置应用于水产养殖鱼群观测的可行性。研究结果为蝠鲼型仿生机器人鱼的设计和研究提供了参考依据，为养殖池鱼群观测设备提供了新的思路。

关键词：仿生蝠鲼；形态轮廓提取；动水槽试验；环境共融性；机器鱼；鱼群观测；

Design and Implementation of a Biomimetic Manta Ray Fish Observation Device

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Abstract：Fish observation is an important means to evaluate the living conditions of fish schools in aquaculture ponds. In order to improve the environmental compatibility and stability of the observation device, a design and implementation of a biomimetic manta ray fish observation device was studied. The structural design of the fish observation device is inspired by the biological manta ray, and based on computer vision technology, the morphological contour of the biological specimen is extracted to establish a fish body spanwise morphology model; Based on the lighthill theory, the spanwise Kinematics model is established, and the overall design is carried out in combination with the fish observation system and communication control system; Design dynamic water tank tests and pond tests to verify the hydrodynamic performance and feasibility of practical application of the device. The results and experiments indicate that: (1)The extracted spanwise contour has the highest goodness of fit corresponding to NACA0013 and is 0.744, laying a good foundation for the hydrodynamic performance of the prototype design;(2) At working conditions V=0.2 m/s, f=1 Hz, A=40 °, the three-dimensional forces and moments in space undergo oscillating changes, revealing the stationarity mechanism of the motion process of the manta ray type robotic fish; (3)In the pond experiment, the biomimetic robotic manta ray device showed strong compatibility, small disturbance to fish schools, and can transmit underwater images in real-time, verifying the feasibility of applying the biomimetic manta ray device to observe fish schools in aquaculture. The research results provide a reference basis for the design and research of manta ray biomimetic robotic fish, and provide new ideas for the observation equipment of fish schools in aquaculture ponds.

Key words: Biomimetic manta rays; Shape contour extraction; Dynamic water tank test; Pond test; Environmental compatibility; Observation of fish schools

纲索装配对网衣系统水动力学特性影响研究

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摘要：深远海大型养殖设施的网衣系统通常由大规格网衣和纲索组成，其安全性备受关注。其中，纲索在限制网衣变形以及承担网衣受力等方面发挥着至关重要的作用。为探究纲索装配对网衣系统水动力学特性的影响，本研究通过杆单元模型构建了网衣系统的数值模型，研究水流、波浪作用下纲索装配方案、预加张力施加、附着生物等因素对刚性网衣系统水动力学特性的影响。结果表明，纲索装配对刚性网衣系统的变形和受力分布有显著影响，随着纲索装配密度的增加，网衣系统变形和受力逐渐改善；当纲索布设间距达 2.5m 时（对应研究中网衣长度的八分之一），继续增加纲索布设密度对于限制网衣系统变形和改善受力的作用不明显；纲索预加张力的施加能够增加纲索抗变形能力，可以在一定程度上改善网衣变形和受力集中的问题。研究结果能够为深远海大型养殖装备上网衣系统纲索装配提供参考。

关键词：深远海养殖设施；网衣系统水动力；纲索装配；预加张力

Study on the influence of rib ropes on the hydrodynamic characteristics of rigid netting systems

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Abstract： The netting system of mariculture facilities, which consists of multiple net panels and rib ropes, plays a crucial role in providing living space for farmed fish. Therefore, its safety is of paramount concern. Rib ropes are instrumental in restraining net deformations and facilitating force transmission. To investigate the influence of rib ropes assembly on the hydrodynamic characteristics of netting systems, numerical simulation methods were employed to study the effects of rib ropes assembly schemes and pre-tensioning on the hydrodynamic characteristics of rigid net systems under the influence of current and wave. The results indicate that rib ropes assembly significantly influence the deformation and force distribution of rigid netting systems. With an increase in rib ropes assembly density, the deformation and force of the net system gradually improve. When the spacing between rib ropes installations reaches 2.5 m (corresponding to one-eighth of the net length in the study), further increasing the rib ropes installation density has a less noticeable effect on restraining net system deformation and improving force. The application of pre-tensioning in rib ropes increases their resistance to deformation, thereby enhancing the effect of reducing net deformation and force. These findings provide valuable insights for the design of rib ropes assemblies in netting systems for large-scale aquaculture facilities in deep-sea environments.

Key words: Deep-sea aquaculture facilities; Hydrodynamics of netting systems; rib rope; Pre-tensioning

通海口位置对舷侧开孔式养殖船养殖舱内水动力特性影响的数值分析

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摘要：舷侧开孔式养殖船是一种环境可持续的鱼类养殖解决方案，基于通海养殖舱，其可以充分利用海水并最大限度地降低鱼类逃逸的风险。本文采用计算流体动力学方法对在水头流和横流条件下的自交换水产养殖船进行了计算研究。在优化修剪网格上，使用隐式非定常二阶欧拉（有限体积）技术求解控制养殖舱内流体动力学的守恒方程。利用不确定性分析方法对实验值和预测值进行了评估，以验证当前数值模型的有效性。本研究探讨了在舷侧开孔式养殖工船近底部通海口位置对舱内水动力特性的影响机制。近底部通海口布设位置的优选布置有利于促进近底层和近顶层通海口之间的相互作用，从而显著增强了养殖舱内流场内的混合特性和流场均匀性。本研究的主要目的是为舷侧开孔式养殖工船的概念设计、建模和模拟分析奠定基础。

关键词：舷侧开孔式养殖工船；养殖舱；水动力特性；计算流体动力学

Influence of perforation placement on the hydrodynamics of a culture tank onboard a self-exchange aquaculture vessel

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Abstract： A self-exchange aquaculture vessel stands as an environmentally sustainable solution for fish farming, capitalizing on seawater utilization and minimizing the risk of fish escapes through the implementation of perforated culture tanks. This paper presents a computational study of self-exchange aquaculture vessels operating under both head current and beam current conditions, employing the Computational Fluid Dynamics (CFD) tool. The solution of conservation equations governing tank hydrodynamics is achieved using an implicit unsteady second-order Eulerian (finite volume) technique on optimized trimmed meshes. An evaluation of experimental and predicted values, based on the total resistance of the vessel model, was performed utilizing an uncertainty analysis method, thus affirming the validation of the present numerical model. This study delves into the impact of perforation placement near the bottom of self-exchange aquaculture vessels on flow field characteristics within the culture tank. The optimization of the layout of the near-bottom perforations fosters a seamless interaction between them and the crest layer perforations, resulting in a pronounced enhancement of mixing characteristics within the culture tank’s flow field, consequently promoting greater uniformity. The primary objective of this research is to establish a fundamental basis for the conceptual design, modeling, and simulation analysis of self-exchange aquaculture vessels. By offering valuable insights into the effects of perforation placement, the study contributes to the development of more efficient and environmentally friendly aquaculture practices.

Key words: Self-exchange aquaculture vessel; Culture tank; Hydrodynamics; Computational fluid dynamics (CFD)

第十专题：渔业经济、政策与管理

海南岛东部近岸海域两种延绳钓的渔获率研究

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摘要：本研究于 2022 年休渔期, 对海南岛东部近岸海域两种延绳钓进行了海上调查和上岸渔获调查, 统计了渔获率。研究结果包括：1.休渔期南海带鱼(Trichiurus nanhaiensis)总渔获率为 3.69%, 其中大规格南海带鱼（>350 g）的渔获率为 1.37%, 小规格南海带鱼（<350 g）的渔获率为 2.33%；星斑裸颊鲷(Lethrinus nebulosus)总的渔获率为 2.67％, 大规格星斑裸颊鲷（>500 g）的渔获率为 0.62％, 小规格星斑裸颊鲷（<500 g）的渔获率为 2.04％。2.星斑裸颊鲷总体渔获率较为稳定；3.影响渔获率的主要因素包括月相和副渔获物比例；4.南海带鱼渔业资源有衰退迹象；5.建议采取上岸渔获调查方法, 建立上岸渔获物统计体系, 实现渔获量化信息的采集和统计。本研究为解决海南岛延绳钓渔业管理提供科学依据。

关键词：延绳钓；渔获率；休渔期

Study on catch rates of two kinds of longline fishing in eastern coastal waters of Hainan Island

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Abstract： Longline fishing is the most important fishing gear for artisanal fisheries, and the coastal waters in the eastern part of Hainan Island mainly use bottom longline fishing and drifting longline fishing. In order to better understand the fishing patterns and characteristics, as well as their production characteristics, this study conducted a fishery resources survey and landing catch survey on two types of longline fishing in Tanmen Port, Qionghai City, Hainan Province during the fishing closed season of 2022, and calculated the catch rate. The research results include: 1. The total catch rate of Trichiurus nanhaiensis during the fishing season is 3.69%, with a catch rate of 1.37% for large T. nanhaiensis and 2.33% for small T. nanhaiensis; The total catch rate of Lethrinus nebulosus is 2.67%, the catch rate of the large L. nebulosus is 0.62%, and the catch rate of the small L. nebulosus is 2.04%. 2. The overall catch rate of the L. nebulosus is relatively stable; The main factors affecting the catch rate include lunar phase and the proportion of bycatch. There is no significant difference in relative drift longline fishing in different months, but the catch rate in bottom longline fishing is higher in the dark sky; The catch rate of bottom longline fishing is more affected by the proportion of bycatch than that of drift longline fishing; 4. There are signs of decline in the T. nanhaiensis fishery resources, with a significant decrease in the catch rate of large T. nanhaiensis compared to 2021, and a significant increase in small T. nanhaiensis; 5.It is recommended to adopt the method of shore catch investigation, establish a statistical system for shore catch, and achieve the collection and statistics of quantitative information on catch. This study provides a scientific basis for solving the management of longline fishing in Hainan Island.

Key words: longline fishing; catch rate; fishing closed season

浙江省水产种质资源保护、利用现状与研究

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摘要：加强水产种质资源的保护与利用，既是国家生物和遗传多样性安全的迫切需要，也是人们对优质健康水产品的需求。浙江水生生物多样性丰富。但受人为因素的影响，水产种质资源下降趋势未得到根本性好转，面临的形势依然严峻，如何加强水产种质资源保护与合理开发利用是浙江水产种业持续健康发展的关键。本文通过分析浙江水产种质资源现状、保护利用的成效及存在的问题，提出了相关建议，为推动水产种质资源保护与利用提供参考。

关键词：水产；种质资源；保护；利用

Study on the protection and use of aquatic germplasm resources in Zhejiang province

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Abstract：Strengthening the protection and use of aquatic germplasm resources is not only an urgent need for the safety of national biological and genetic diversity, but also a demand for high-quality and healthy aquatic products. Zhejiang is rich in aquatic biodiversity. However, due to human factors, aquatic germplasm reasources continue to decline. How to strengthen the protection and reasonable development and utilization of aquatic germplasm resources is the key to the sustainable and healthy development of Zhejiang's aquatic seed. Analyis the current situation, protection and use effectiveness, and existing problems of aquatic germplasm resources in Zhejiang, we put forward relevant suggestions to provide reference for promoting the protection and utilization of aquatic germplasm resources.

Key words: Aquaculture; Germplasm resource; Protect; Use

东太平洋不同海域环境因子对茎柔鱼分布的影响差异分析

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摘要：为探究东南太平洋不同海域环境因子对茎柔鱼栖息地分布的影响差异，本研究利用海表面温度、涡旋动能、海表面盐度、海表面高度、叶绿素浓度、混合层深度、溶解氧浓度七个海洋环境因子，结合东太平洋赤道海域、秘鲁外海与智利外海三个海域茎柔鱼渔业生产数据，利用最大熵模型探究不同海域夏、秋两个季节内茎柔鱼适栖息地分布情况以及探究环境因子对其影响的差异。结果显示，赤道夏季最适栖息地主要分布在 110°~120°W、1°N~3°S；秋季，主要分布在 97°~117°W、1.5°N~1.5°S，栖息地分布向东延伸。秘鲁外海夏季最适栖息地主要分布在 75°~86°W、15°~20°S；秋季，主要分布在 75°~84°W、15°~20°S，夏季到秋季最适宜栖息地整体向东南方向移动。智利外海夏季茎柔鱼最适栖息地主要分布 73°~85°W、20°~30°S；秋季，主要分布在 75°~85°W、20°~28°S 海域。

关键词：东太平洋；茎柔鱼；栖息地模拟；最大熵模型；环境影响

Differece of the effects of environmental factors on habitat distribution of Dosidicus gigas in different regions in the Eastern Pacific Ocean

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Abstract：Jumbo flying squid Dosidicus gigas is widely distributed in the Eastern Pacific Ocean. It has a short-lived life cycle and tends to extremely respond to environmental and climate variability. In order to investigate the difference of the effects of environmental factors on habitat distribution of Dosidicus gigas in different regions in the Eastern Pacific Ocean, the present study developed a habitat distribution model for this squid in summer and autumn in the equator, off Peru and Chile based on seven marine environmental factors including Sea Surface Temperature (SST), Eddy Kinetic Energy (EKE), Sea Surface Salinity (SSS), Sea Surface Height (SSH), Chlorophyll Concentration (Chl-a), Mixed Layer Depth (MLD), and Dissolved Oxygen Concentration (OXY). The fisheries data in the equatorial waters of the Pacific Ocean, the waters off Peru from 2016-2018, and the waters off Chile from 2015-2017 were used and obtained from National distant-water fisheries data center of China. This study used the maximum entropy model (MaxEnt) to investigate the distribution of suitable habitat for Dosidicus gigas and the differences in the effects of the environmental factors on it were examined in different seasons in different waters. The results showed that the AUC values of the maximum entropy model were higher than 0.8 in different seasons in different areas, and the actual fishing locations coincided with the range of suitable habitats fitted by the model. The distribution of optimal habitats in the three regions was as follows: in the equatorial waters in summer, the optimal habitats were mainly distributed within the ranges of 110°~120°W, 1°N~3°S; in autumn, the optimal habitats for Dosidicus gigas were mainly distributed within the ranges of 97°~117°W, 1.5°N~1.5°S, and the distribution of the suitable habitats was extended to the east from summer to autumn. In summer, the optimal habitats of Dosidicus gigas off Peru were mainly located in the range of

75°~86°W, 15°~20°S; in autumn, the optimal habitats of Dosidicus gigas were mainly located in the range of 75°~84°W, 15°~20°S, with the optimal habitats moving southeastward from summer to autumn. The optimal habitats of Dosidicus gigas in summer off Chile were mainly distributed in the range of 73°~85°W, 20°~30°S; in autumn, the optimal habitats were mainly distributed in the range of 75°~85°W, 20°~28°S, and the overall suitable habitats moved to the northeast from summer to autumn.

Key words: Eastern Pacific Ocean; Dosidicus gigas; habitat modelling; maximum entropy model; environmental impacts

利用三种模型对 1995–2020 年西北太平洋柔鱼进行 CPUE 标准化

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摘要：西北太平洋柔鱼(Ommastrephes bartramii)是一种具有重要经济价值的头足类动物。其短暂的寿命增加了其分布和丰度对环境条件直接影响的敏感性。单位努力量渔获量(CPUE)是鱼类丰度的重要指标，受包括环境变量在内的许多因素的影响。这些因素对 CPUE 的影响可能会改变 CPUE 与种群丰度之间的比例关系。因此，需要对 CPUE 进行标准化，以消除种群丰度以外因素的影响。本研究以西北太平洋柔鱼的捕捞数据为基础，采用广义加性模型(GAM)、随机森林模型(RF)和 XGBoost 模型(XGB)三种方法对柔鱼的 CPUE 进行标准化。结果表明:RF 模型和 XGB 模型确定的秋季群体(东部)和冬春群体(西部)丰度指数潜在影响的重要变量不同。标准化的 CPUE 比名义 CPUE 更稳定，但总体趋势基本相同。

关键词：西北太平洋柔鱼；CPUE 标准化；广义加性模型；随机森林模型；XGB 模型；西北太平洋；中国鱿鱼钓业

Standardized catch per unit effort (CPUE) of neon flying squid of the Chinese squid jigging fisheries in the Northwest Pacific Ocean from 1995 to 2020

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Abstract： The neon flying squid (Ommastrephes bartramii) in the Northwesst Pacific Ocean is an economically important cephalopod. Its short lifespan increases the susceptibility of the distribution and abundance to the direct impact of the environmental conditions. Catch per unit effort (CPUE) of species, a critical proxy for fish abundance, affected by many factors, including environmental variables. The impacts of these factors on CPUE may shift the assumed proportionality between observed CPUE and stock abundance. Thus, CPUE standardization is needed to remove the impacts of factors other than population abundance. In this study, Based on the fishing data in jigging fishery by Chinese squid jigging fisheries in the Northwest Pacific Ocean, We will standardize the CPUE for the neon flying squid, three methods are used to standardize CPUE, They are generalized additive models (GAM), Random Forest model (RF) and Xtreme Gradient Boosting model (XGB). Because the resource abundance of neon flying squid is highly susceptible to environmental factors,10 environmental factors that have a greater impact on the two populations of neon flying squid were selected by RF model and XGB model, respectively. Finally, the three models were used to standardize the winter-spring cohort (West) and autumn cohort (East) of neon flying squid, and the results showed that. Importance variables potentially affecting the abundance index of the autumn cohort (East) and the winter-spring cohort (West) confirmed by RF model and XGB model is different. The standardized CPUE is more stable than the nominal CPUE, but the overall trend is basically the same.

Key words: Ommastrephes bartramii; CPUE standardization; Generalized additive model; Random Forest model; XGB model; Northwestern Pacific Ocean; Chinese squid-jigging fishery

设计高性能生境适宜指数模型

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摘要：栖息地适宜性指数模型在野生动物管理中被广泛用于描述物种丰度与生态变量之间的关系并可能为栖息地保护和渔业管理提供科学依据，尤其是对于调查数据有限的物种。首先目前环境因素的可用信息正在快速增加，其权重组合呈现几何指数增长，模型的计算速度有待检验。其次栖息地建模中环境变量的权重很重要，尤其是对于分布不太清楚的物种。传统的加权方案如算术或几何平均，通常会导致栖息地的“梯度”分布模式。我们开发了新的方法，通过随机森林从众多环境因素中选择最重要的变量，并获得该变量的权重。这种方法节省了确定可变权重的时间，并使用多个模型选择标准来选择最佳拟合。我们使用西北太平洋柔鱼捕捞数据集和西南大西洋阿根廷滑柔鱼捕捞数据集中将我们的 HSI 与传统固定方法进行了比较。我们的 HSI 模型（RF）的整体性能优于两种传统的 HSI（AMM，GMM）加权方法。模型为我们发展鱿鱼空间动力学预测能力提供了重要工具

关键词：随机森林；生境适宜性指数模型；柔鱼；阿根廷滑柔鱼；西北太平洋；西南大西洋

Designing of high-performance habitat suitable index model

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Abstract： A habitat suitability index (HSI) model is widely used in wildlife management to describe the relations between species abundance and ecological variables and may provide a scientific basis for habitat protection and fishery management,especially for species with limited survey data.Firstly,At present, the available information of environmental factors is increasing rapidly, but the combination of weights presents geometric exponential growth, and the calculation speed of the model needs to be tested. Secondly,The weighting of environmental variables in habitat modelling is important, especially for species with a poorly understood distribution. Traditional weighting schemes, such as arithmetic or geometric mean, often cause “gradient” habitat distribution patterns. We develop a new method of selecting the most important variable from numerous environmental factors through random forests and obtaining the weight of that variable. This method saves time in determining variable weights and uses multiple model selection criteria to select the best fit. We compared our HSI with traditional fixed methods using the Northwest Pacific Ommastrephes bartramii fishing dataset (2005-2019) and the Southwest Atlantic Illex argentinus fishing dataset (2010-2019). The overall performance of our HSI model (RF_HSI) is superior to two traditional HSI(AMM_HSI, GMM_HSI) weighting methods. The proposed model provides an important tool in our efforts to develop forecasting capacity of squid spatial dynamics.

Key words: Random Forest; Habitat suitability index model; Ommastrephes bartramii; Illex argentinus; Northwest Pacific Ocean; Southwest Atlantic Ocean

确定基于机器学习的鱼类分布建模的最佳变量

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摘要：机器学习在鱼类分布建模中发挥着关键作用。 随着解释变量的增加，确定最佳变量变得至关重要。 我们提出了一种特征选择技术，即交叉验证的递归特征消除（RFECV），以确定太平洋黄鳍金枪鱼分布的最佳变量组合。 由 RFECV 驱动的四种基于树的模型：随机森林 (RF)、极限梯度提升 (XGBoost)、轻梯度提升机 (LightGBM) 和分类提升 (Catboost) 是使用综合渔业和生物/非生物数据开发的。 所有模型均认为海水温度 (Temp)、溶解氧浓度 (O2)、叶绿素 a 浓度 (Chl)、海盐度 (Sali) 和海面高度 (SSH) 等变量具有显着性。 这些模型根据各自的重要变量和渔业捕捞数据进行训练，预测了 1995 年至 2019 年黄鳍金枪鱼的时空分布。 所得结果可指导黄鳍金枪鱼的可持续利用，并为其他鱼类分布建模提供有价值的参考。

关键词：物种分布模型； 黄鳍金枪鱼； 特征选择； 基于树的模型

Identifying optimal variables for machine learning based fish distribution modeling

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Abstract： Machine learning has a pivotal role in fish distribution modeling. With increasing explanatory variables, identifying optimal ones has become crucial. We proposed a feature selection technique, Recursive Feature Elimination with Cross-Validation (RFECV), to determine optimal variables combinations for yellowfin tuna distribution in the Pacific Ocean. Four tree-based models, Random Forest (RF), eXtreme Gradient Boosting (XGBoost), Light Gradient Boosting Machine (LightGBM), and Categorical Boosting (Catboost), driven by RFECV, were developed using comprehensive fisheries and biotic/abiotic data. Variables including sea temperature (Temp), dissolved oxygen concentration (O2), Chlorophyll-a concentration (Chl), sea salinity (Sali), and sea surface height (SSH) were identified as significant by all models. These models, trained with respective significant variables and fisheries catch data, predicted yellowfin tuna spatiotemporal distribution from 1995-2019. The derived results can guide sustainable utilization of yellowfin tuna and provide valuable references for other fish species distribution modeling.

Key words: Species distribution models; Yellowfin tuna; Feature selection; tree-based model

东南太平洋鱿钓渔业的发展历程及管理

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摘要：鱿鱼一类重要的海洋生物，不仅在海洋生态系统中扮演着重要角色，而且在海洋渔业中占有重要的经济地位。鱿钓渔业是我国远洋渔业的重要组成部分，为维护我公海资权益、丰富国内市场供应作出了积极贡献。然而，长期以来，世界各国和地区对大洋性鱿鱼类的开发和利用，以及全球气候变化的加剧对鱿鱼类资源渔场的影响，使得远洋鱿钓渔业的可持续发展的风险加大。因此，为促进鱿鱼类资源的科学养护和可持续利用，实现我国远洋鱿钓渔业的可持续发展，采取科学的捕捞管理措施和合理的养护利用方式显得尤为重要。本文将结合东南太平洋鱿钓渔业的发展现状、发展趋势以及存在的问题等提出相关方面建议和对策，以推动我国远洋鱿钓渔业的高质量发展。

关键词：鱿钓渔业；发展现状；问题；对策

Development history and management of Chinese squid fishery in southeast Pacific

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Abstract： Squids, an important marine organisms, not only play an important role in the marine ecosystem, but also occupy an important economic position in marine fisheries. Squid jigging fishery is an important part of China's pelagic fishery, and has made positive contributions to safeguarding the rights and interests of our high seas and enriching the supply of the domestic market. However, for a long time, the development and use of oceanic squid species by countries and regions around the world, as well as the impact of the intensification of global climate change on squid resource fisheries, have increased the risks to the sustainable development of pelagic squid fisheries. Therefore, in order to promote the scientific conservation and sustainable use of squid resources and to achieve the sustainable development of China's pelagic squid fishery, it is particularly important to adopt scientific fishing management measures and reasonable conservation and use methods. In this paper, we will put forward relevant suggestions and countermeasures in the light of the current development status, development trend and problems of the squid fishery in the South-East Pacific Ocean, in order to promote the high-quality development of China's pelagic squid jigging fishery.

Key words: Squid fisheries; development status; problems; countermeasures

烟台市水产养殖现状分析及发展对策研究

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摘要：烟台市地处山东半岛北部，优越的自然环境孕育了丰富的渔业资源，是山东省重要的渔业养殖地区。为进一步掌握烟台市水产养殖现状，促进水产养殖业的可持续发展，本文基于2008-2021年《山东省渔业统计年鉴》及2021年烟台市第一次水产种质资源普查数据，运用物种多样性与聚类分析等方法，分析烟台市养殖物种组成与分布、养殖模式及养殖物种多样性特征。结果显示：2021年山东省共有养殖品种654种，其中烟台市共有养殖品种141种，隶属于38目55科75属。2008-2021年间，烟台市以海水养殖为主，海水养殖面积逐年增加；淡水养殖产量和面积逐渐减少。

关键词：烟台市；水产种质资源；物种组成；多样性分析；聚类分析

Status Analysis and Development Countermeasures of Aquaculture in Yantai City

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Abstract： Yantai City is located in the northern part of the Shandong Peninsula, and its superior natural environment has nurtured rich fishery resources. It is an important fishing and aquaculture area in Shandong Province. In order to further grasp the current situation of aquaculture in Yantai City and promote the sustainable development of the aquaculture industry, this article is based on the "Shandong Province Fisheries Statistical Yearbook" from 2008 to 2021 and the first survey of aquatic germplasm resources in Yantai City in 2021. Using methods such as species diversity and cluster analysis, the composition and distribution of aquaculture species, aquaculture patterns, and characteristics of aquaculture species diversity in Yantai City are analyzed. The results show that in 2021, there were a total of 654 species of aquaculture in Shandong Province, among which there were 141 species of aquaculture in Yantai City, belonging to 38 orders, 55 families, and 75 genera. From 2008 to 2021, Yantai City mainly focused on mariculture, with an increasing area of mariculture year by year; The production and area of freshwater aquaculture are gradually decreasing.

Key words: Yantai City; aquatic germplasm resources; species composition; diversity analysis; cluster analysis

集鱼灯测评实验室的认证进程与管理策略研究

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摘要：本研究旨在探讨集鱼灯测评实验室的认证进程与管理策略。随着远洋渔业的发展，集鱼灯作为一种重要的渔具装备，对于提高渔业效益和保护海洋生态环境具有重要意义。然而，目前对于集鱼灯测评实验室的认证进程和管理策略的研究还相对较少。本研究通过文献综述和实地调研，对集鱼灯测评实验室的认证流程和管理策略进行了深入分析和研究。研究结果表明，集鱼灯测评实验室的认证进程包括设备准备、实验设计、数据采集与分析等环节，而管理策略则涉及实验室人员培训、设备维护、数据管理等方面。本研究还提出了一些改进措施，包括加强认证标准的制定、优化实验室管理流程等，以提高集鱼灯测评实验室的认证效率和管理水平。本研究对于推动远洋渔业的可持续发展和提升集鱼灯测评实验室的认证质量具有一定的理论和实践意义。

关键词：远洋渔业；集鱼灯；质量检测；标准化；检测能力；资质认证

Research on the Certification Process and Management Strategies of Fish Aggregating Device Evaluation Laboratory

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Abstract： The aim of this study is to explore the certification process and management strategies of the Fish Aggregating Device (FAD) evaluation laboratory. With the development of offshore fisheries, FADs play a crucial role as important fishing equipment in improving fishery productivity and protecting marine ecosystems. However, research on the certification process and management strategies of FAD evaluation laboratories is relatively limited. This study conducted a comprehensive analysis and investigation of the certification process and management strategies of FAD evaluation laboratories through literature review and on-site research. The research findings indicate that the certification process of FAD evaluation laboratories involves equipment preparation, experimental design, data collection, and analysis, while management strategies encompass personnel training, equipment maintenance, and data management. Several improvement measures were proposed, including strengthening the formulation of certification standards and optimizing laboratory management processes, to enhance the certification efficiency and management level of FAD evaluation laboratories. This study has theoretical and practical significance in promoting the sustainable development of offshore fisheries and improving the certification quality of FAD evaluation laboratories.

Key words: Pelagic fishing ; FAD ; Quality Inspection ; Standardization ; Testing ability ; Certification

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