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目录

微波真空干燥扇贝(*Patinopecten yessoensis*)闭壳肌：传热传质的数值分析

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摘要：为了探究扇贝微波真空干燥特性，对扇贝在不同微波功率密度(1W/g、2W/g、3W/g、4W/g)干燥下的温度和含水率进行试验，得到扇贝微波干燥曲线以及干燥的最佳微波功率密度，建立了扇贝微波真空干燥动力学模型。将微波真空干燥扇贝的几何模型代入到 COMSOL Multiphysics 软件中，建立电磁场、固体传热和稀物质传递三场耦合模型，结果表明，微波真空干燥的最佳微波功率密度为 1 W/g，在这种条件下干燥的扇贝色泽浅黄诱人，质地致密，不结皮、不变形且收缩率小，蛋白质的保留率可达 79.53%， Page 模型可以更好的描述微波真空干燥扇贝闭壳肌的干燥特性。仿真结果表明，微波真空干燥的扇贝在物料边角处的样品温度高于物料中心处的样品温度，且单个扇贝中心处的样品温度最低。但含水率的分布与温度分布相反，电场的不均匀分布直接导致了温度的不均匀分布。

关键词：扇贝； 微波真空干燥；Comsol 仿真

Microwave-vacuum drying of scallop (*Patinopecten yessoensis*) adductor muscle: numerical analysis of heat and mass transfer

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Abstract： In order to explore the characteristics of scallop microwave vacuum drying, the temperature and moisture content of scallop under different microwave power densities (1W/g, 2W/g, 3W/g, 4W/g) were tested. The microwave drying curve and the ideal microwave power density of scallop drying were then obtained, and the kinetic model of scallop microwave vacuum drying was established. The three field coupling models of electromagnetic field, solid heat transfer, and dilute matter transfer were developed using the geometric model of microwave vacuum drying scallop that was entered into the COMSOL Multiphysics software. The findings indicated that 1 W/g was the optimal microwave power density for microwave vacuum drying. In this state, the scallop's dry hue was a pleasing pale yellow, and its texture was thick. The rate of protein retention can increase to 79.53%. The drying properties of microwave-vacuum-dried scallop closed shell muscle are better described by the page model. According to the simulation results, the sample temperature at a material's corner was higher than at its middle, and the sample temperature within a single scallop was the lowest. The distribution of water content, on the other hand, is the polar opposite of that of temperature, and an uneven distribution of the electric field immediately affects the distribution of temperature.

Key words: Scallop; Microwave vacuum drying; Comsol simulation

鲢鱼脱细胞鱼皮基质的制备及研究

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摘要：目前，脱细胞支架以哺乳动物组织为主，水生动物组织为原料的较少。鱼皮以其高胶原蛋白含量，低抗原性和优异的三维网状结构而受到广泛关注。本研究以产量大、易于人工养殖的淡水鱼-鲢鱼的鱼皮为原料，制备一种低 DNA 和内毒素的脱细胞鱼皮基质。鲢鱼皮(SCK)分别经胰蛋白酶/十二烷基硫酸钠（SDS）和 TritonX-100 处理后，DNA 降至 34.96±0.79ng/mg，内毒素去除率达 96.8%。鲢鱼脱细胞鱼皮基质（SC-AFSM）的孔隙率为 79.64±0.17%，有利于细胞浸润、增殖，细胞相对增殖率为 117.79%，创口愈合实验表明 SC-AFSM 的无不良急性促炎反应，与市售产品促组织修复效果一致。因此，SC-AFSM 在生物材料方面有巨大的应用潜力。

关键词：鲢鱼皮；脱细胞基； DNA 含量；内毒素；生物材料

Study on the preparation and properties of acellular matrix from the skin of silver carp (*Hypophthalmichthys molitrix*)

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Abstract： Acellular matrices are mainly composed of mammalian tissues, and few aquatic animal tissues have been employed as raw materials. China is the largest freshwater fish producer in the world, with silver carp being one of the main species. In this study, an acellular matrix with low DNA and endotoxin was prepared from the skin of silver carp. After treatment with trypsin/sodium dodecyl sulfate and Triton X-100 solutions, the DNA content in silver carp acellular fish skin matrix (SC-AFSM) reached 34.96±0.79 ng/mg, and the endotoxin removal rate was 96.8%. The porosity of SC-AFSM was 79.64%±0.17%, which is favorable for cell infiltration and proliferation. The relative cell proliferation rate of SC-AFSM extract was 117.79%±15.26%. The wound healing experiment showed that SC-AFSM had no adverse acute pro-inflammatory response, which had a similar effect as commercial products in promoting tissue repair. Therefore, SC-AFSM has great application potential in biomaterials.

Key words:： Silver carp skin; Acellular matrix; DNA content; Endotoxin, Biomaterials

鲢鱼加工副产物作为微生物培养基替代氮源的应用及机制研究

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摘要：我国鱼类产量大，2020 年达到 3521.02 万吨。鱼类在加工过程中会产生约占鱼体重量 50%的副产物，包括鱼头、鱼骨、内脏、鱼皮、鱼鳍、鱼鳞等。这些副产物多用于制成动物饲料或直接丢弃，产品附加值低，且带来了严重的环境污染问题。针对上述问题，利用鱼类加工副产物水解物替代微生物培养基中的氮源，研究其对微生物生长的影响。结果表明，木瓜蛋白酶 1h 水解物替代 MRS 培养基中 75%氮源时，嗜酸乳杆菌 NCFM 的生长得到显著提高；木瓜蛋白酶 2h 水解物替代 MRS 培养基中 75%氮源能够促进双歧杆菌 BB-12 的生长，且这一促进作用和水解物中含巯基氨基酸的含量及肽的疏水性存在正相关关系。这些研究为鱼类加工副产物的高值化利用提供了新的思路，具有重要的研究意义。

关键词：副产物；高值化利用；氮源

Silver carp (hypophthalmichthys molitrix) by-product hydrolysates: A new nitrogen source for probiotics

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Abstract： Appropriate utilization of silver carp by-product is critical for enhancing industry profit and sustainability of aquaculture. The nitrogen source in the microbial medium is expensive. This study explored the effect of the silver carp by-product hydrolysates on the growth of Bifidobacterium animalis ssp. lactis BB-12. Results suggested that papain recovered more nitrogen and < 1 kDa components from silver carp by-products than neutrase and alcalase. Papain-2h (by-products hydrolyzed by papain for 2 hrs) was more effective in promoting the growth of BB-12. The content of <1 kDa components, sulfhydryl-containing amino acids, and peptides composed of all the hydrophobic amino acids in hydrolysates was positively correlated to the growth of BB-12. BB-12 cultured by papain-2h substituted medium exhibited a thinner and shorter morphology at 4 hrs of cultivation. This study provided a novel strategy for reducing waste and converting by-products to a potential nitrogen source for probiotics

Key words: by-product; value-added utilization; nitrogen sources

香蜂草精油对海鲈鱼有水保活运输工艺的研究

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摘要：海鲈鱼是我国重要的海水鱼类养殖鱼类，但由于在保活运输中诱发的胁迫应激导致其存活率较低。本项目探究了香蜂草精油在模拟保活运输中对海鲈鱼鳃组织形态结构、肝组织损伤和免疫能力的影响。在模拟保活运输 72h 后，海鲈鱼运输存活率均为 96%。经 40 mg/L 香蜂草精油处理后的海鲈鱼比其他各处理组中海鲈鱼的鳃组织损伤程度小，糖酵解率、能量消耗、脂质过氧化和肝细胞凋亡水平均最低。体内葡萄糖、乳酸、热休克蛋白、过氧化氢酶、髓过氧化物酶、谷胱甘肽过氧化物酶、尿酸和尿素氮水平较低，总抗氧化能力较高，且海鲈鱼的抗氧化应激能力随着水体中 MOEO 的添加浓度而增强。在运输水体中添加香蜂草精油与 MS-222 和丁香酚有相似的镇定和麻醉效果，且在长途模拟保活运输水体中添加 40mg/L 香蜂草精油可以有效减缓保活运输对海鲈鱼的组织损伤 能量代谢和氧化应激反应。

关键词：海鲈鱼；胁迫应激；精油；保活运输

Essential oil from Melissa officinalis L. is effective in reducing handling and transport stress in sea bass (*Lateolabrax maculatus*)

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Abstract： Sea bass (*Lateolabrax maculatus*) is an important mariculture fish in our country, but its survival rate is low due to the stress induced in keep-live transportation. This project investigated the effects of lemon balm (Melissa officinalis L.) essential oil on gill morphology, liver tissue injury and immune ability of sea bass during simulated keep-live transport. After 72 hours of simulated keep-live transport, the transport survival rate of sea bass was about 96%. Compared with other treatment groups, sea bass treated with 40 mg/L lemon balm essential oil had less gill tissue damage, the lowest glycolysis rate, energy consumption, lipid peroxidation and hepatocyte apoptosis. The levels of glucose, lactic acid, heat shock protein, catalase, myeloperoxidase, glutathione peroxidase, uric acid and urea nitrogen in vivo were lower, and the total antioxidant capacity was higher. The antioxidant stress ability of sea bass increased with the addition concentration of lemon balm essential oil.

Key words: Sea bass; stress stress; essential oil; keep-live transport

不同灭菌方式对南极大磷虾酱料品质的影响

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摘要：通过 4 种常见的水产品杀菌方式对以南极磷虾为原料制备的海鲜酱料进行处理，并通过检测质构、流变、色差、微生物残留情况及风味等指标综合分析 4 种商业杀菌方式的优劣。旨在加快南极磷虾资源的高值化利用。

关键词：南极大磷虾酱料；杀菌方式；品质变化；流变质构

Effects of Different Sterilization Methods on Quality of Antarctic krill（Euphausia superba）sauce

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Abstract： The seafood sauce prepared from Antarctic krill was treated by four common aquatic product sterilisation methods. Quality and safety of the four commercial sterilisation methods were analysed by indicators of the texture, rheology, colour difference, microbial residues and flavor. The work aims to accelerate the utilization of Antarctic krill resources.

Key words: Antarctic krill; sterilization methods; sauce; quality changes; texture

pH 响应性玉米醇溶蛋白/碳量子点包埋褐藻多酚纳米粒子的生物活性研究

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摘要：研究了 zein-PTN-CQDs-FeIII 纳米粒子在体外条件下的褐藻多酚释放率，对 HT-29（人结肠癌细胞）细胞的毒性作用以及抗炎效果。通过研究 PTN、zein-PTN、zein-PTN-CQDs 和 zein-PTN-CQDs-FeIII纳米粒子悬浮液 15 h 内在不同 pH 条件（pH 为 7.4、6.2、5.0 和 4.0）下的体外释放可以发现 zein-PTN-CQDs-FeIII纳米粒子利用酸碱环境不同可以将 PTN 靶向递送和缓释。细胞噻唑蓝（MTT）毒性实验表明纳米粒子对 HT-29 细胞有明显的的毒性且毒性呈剂量依赖性。高浓度的 zein-PTN-CQDs-FeIII 纳米粒子会诱导细胞凋亡。为了进一步研究 zein-PTN-CQDs-FeIII 纳米粒子对 HT-29 细胞的毒性作用，利用荧光显微镜研究细胞凋亡图像，得到的结果与 MTT 毒性实验的结果一致。

关键词：褐藻多酚；pH 响应；结构表征；纳米递送；生物活性

BIOACTIVITY OF pH-RESPONSIVE ZEIN/CARBON QUANTUM DOTS Phlorotannins POLYPHENOL NANOPARTICLES

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Abstract: The polyphenol release rate of zein-PTN-CQDs-FeIII nanoparticles in vitro, the toxicity on HT-29 cells and anti-inflammatory effect are studied. PTN, zein-PTN, zein-PTN-CQDs and zein-PTN-CQDs-FeIII nanoparticles suspension are studied under different pH conditions for 15 h. It is found that zein-PTN-CQDs-FeIII nanoparticles can deliver and sustained-release PTN in different acid-base environments. Cell MTT toxicity experiment shows that the nanoparticles have obvious toxicity to HT-29 cells in a dose-dependent manner. In order to further study the toxicity of zein-PTN-CQDs-FeIII nanoparticles on HT-29 cells, apoptosis images are studied by fluorescence microscopy, and the results are consistent with those of MTT toxicity test.

Key words: Phlorotannins; pH-respensive; structural characterization; nanoparticles delivery; bioactivit

浅谈银鲳鱼文化

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摘要：中国传统文化博大精深、源远流长，鱼文化作为中华文化的重要组成部分，经历了不断流传、翻新与发展的历程。银鲳鱼作为众多鱼类中的一种，兼具文化传承与日常食用的双重作用，因此对银鲳鱼文化的研究具有重要的文化历史价值和现实意义。本文从“鲳鱼直进”的历史传说，“头小、口小、牙细”的奇特个性，流网、单拖和雷达网捕鲳鱼的方式及各类饮食文化四个方面介绍了银鲳鱼文化的起源与发展，并为鱼文化的传承提出了：在政府政策的支持下鼓励更多的有志之士参与、创造一个良好的社会传承环境、利用新媒体优势多加宣传以及开辟多元化的文化传承方式等建议，以期为弥补银鲳鱼文化的空缺，丰富鱼文化的内涵提供相应的经验借鉴。

关键词：银鲳；鱼文化；文化传承

Basic research on silver pomfret (Pampus argenteus) culture

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Abstract： Chinese traditional culture is profound and has a long history. As an important part of Chinese culture, fish culture has experienced the process of continuous dissemination, renovation and development. As one of the many fish, Basic research on silver pomfret (Pampus argenteus) culture has the dual role of cultural inheritance and daily consumption. Therefore, the study of P. argenteus culture has important cultural and historical value and practical significance. This paper introduces the origin and development of P. argenteus culture from four aspects : the historical legend of ' pomfret straight forward ', the peculiar personality of ' small head, small mouth and fine teeth ', the way of fishing pomfret by drift net, single trawl and radar net, and various dietary cultures. It also puts forward some suggestions for the inheritance of fish culture : encouraging more aspiring people to participate with the support of government policies, creating a good social inheritance environment, using the advantages of new media to increase publicity and opening up diversified cultural inheritance methods, in order to make up for the vacancy of P. argenteus culture and enrich the connotation of fish culture. Provide corresponding experience for reference.

Key words: silver pomfret (Pampus argenteus); fish culture；cultural inheritance

仿生蝠鲼移动诱捕装置的设计与实现

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摘要：随着海洋捕捞技术与渔业资源开发领域逐渐走向现代化、智能化，对水下捕捞装备的设计提出了新的要求，研制一种基于仿生蝠鲼的鱼群诱捕水下移动装置。以蝠鲼为研究对象，基于 NACA 翼型方程构建仿生蝠鲼的三维模型；运用计算流体力学方法从低阻性、低扰动性两个方面优化运动模型，通过结构设计实现光诱设备的挂载性，进而完成仿生蝠鲼鱼群诱捕装置；最后通过野外海水实验，验证仿生蝠鲼装置对趋光性鱼类具备较强诱捕能力的可行性和高效性。结果表明：（1）基于 NACA 翼型方程建立的仿生蝠鲼三维模型，形态阻力系数为 0.09，具有良好低阻性能，推进运动中对环境扰动低（2）试验过程中，鱼群可跟随仿生蝠鲼从网箱下方游至水面，验证了仿生机器蝠鲼与鱼群的环境共融，并实现了鱼群的跟随与诱捕。本研究为仿生蝠鲼的制作方法提供了一定的设计思路，为机器鱼在海洋捕捞现代化、智能化方向的应用提供了一定的借鉴意义和参考价值

关键词：海洋捕捞技术；仿生蝠鲼；鱼群诱捕；计算流体力学；运动模型；环境共融

Design and Implementation of Bionic Manta Mobility Trapping Device

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Abstract： With the development of marine fishing technology and fishery resources gradually moving towards modernization and intelligence, new requirements are put forward for the design of underwater fishing equipment. An underwater mobile device for fish trapping based on bionic manta ray is developed.The three-dimensional model of bionic manta ray was constructed based on NACA airfoil equation. The computational fluid dynamics method is used to optimize the motion model from two aspects of low resistance and low disturbance. The mountability of the light-induced equipment is realized through structural design, and then the bionic manta ray fish trapping device is completed. Finally, the feasibility and efficiency of the bionic manta ray device with strong trapping ability for phototactic fish were verified by field seawater experiments.The results show that : (1) The three-dimensional model of bionic manta ray based on NACA airfoil equation has a shape resistance coefficient of 0.09, which has good low resistance performance and low disturbance to the environment during propulsion movement. (2) During the test, the fish group can follow the bionic manta ray from the bottom of the cage to the water surface, which verifies the environmental communion between the bionic manta ray and the fish group, and realizes the following and trapping of the fish group.This study provides a certain design idea for the production method of bionic manta, and provides a certain reference value for the application of robotic fish in the direction of marine fishing modernization and intelligence.

Key words: Marine fishing technology; bionic manta; fish trapping; computational Fluid Dynamics; motion model; environmental communion

基于 VOF 模型的真空吸鱼泵抽吸过程参数影响分析

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摘要：真空吸鱼泵是水产养殖中用于活鱼起捕输送的一种重要工具，为探究真空吸鱼泵抽气压力、吸程及管道入口流速之间的关系，计算建立了 5 种不同吸程的真空吸鱼泵流道物理模型，应用瞬态 VOF 方法捕捉不同参数影响下的水气界面气液两相流变化，数值计算结果表明：同一抽气压力下，不同吸程管道的入口速度在 0.5 s 内迅速增大，之后波动减小，且入口平均速度偏差仅 3.4%，表明吸程对管道入口平均速度几乎无影响；管道内水抽吸至集鱼筒后，充满了大量水与气团组成的泡沫状气液混合体，不同吸程下的集鱼筒在 t=8s 时均已注满水；吸程为 2 m、3 m、4 m、5 m、6 m 的吸鱼泵抽吸过程的所需的临界抽气压力分别为-13 kPa、-14 kPa、-16 kPa、-20 kPa、-25 kPa，吸程与临界抽气压力关系拟合为多项式，可得出同一真空吸鱼泵在任意吸程条件下所需最大抽气负压值。

关键词：真空吸鱼泵；气液两相流；吸程；抽气压力；入口速度

Analysis of the influence of the pumping process parameters of the vacuum fish pump based on VOF model

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Abstract： The vacuum fish pump is an important tool for catching and conveying in aquaculture. In order to research the relationship among the pumping pressure, suction range and pipe inlet velocity of the vacuum fish pump, five different suction range geometric models of the vacuum fish pump were established. The transient Volume of Fluid method was used to capture the changes of gas-liquid two-phase flow at the water gas interface under the influence of different parameters. The numerical results are displayed: under the same pumping pressure, The inlet velocity of pipes with different suction ranges increases rapidly within 0.5 s, and then the fluctuation decreases, the average velocity deviation at the inlet of the pipeline is less than 3.4%, indicating that the average velocity at the inlet of the pipe is hardly affected by the suction head; After the water in the pipeline is pumped to the fish collecting tank, it is filled with a large amount of foam gas-liquid mixture composed of water an

Key words: Vacuum fish pump; Gas-liquid two-phase flow; Suction range; Critical pumping pressure;Inlet velocity

不规则波流下单点系泊‘六三型’网箱动力响应模拟研究

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摘要：为研究不规则波流联合作用条件下的单点系泊‘六三型’深水网箱响应特性，本研究建立了网箱水动力仿真计算模型并结合模型试验对仿真模型进行验证，基于所验证网箱模型，考虑网箱拟实际作业海域条件，从网箱运动响应、锚绳系泊受力以及浮架结构应力三个方面，通过响应时历曲线、与波高时历对比、谱密度统计等研究网箱各部件结构响应特性。结果表明：网箱升沉运动主要受波浪条件影响，在垂直方向与波面升高基本一致，网箱纵荡运动与海流关系密切，相对波面升高运动滞后效应显著；波流联合作用下低频载荷对网箱纵荡运动影响明显；波面升高与锚绳系泊张力和浮架应力密切相关，张力、应力峰值与波面峰值几乎在同一时刻出现，但浮架应力在满足波频响应趋势下表现出了高频响应特性；流速在低频范围对系泊张力和浮架应力谱密度影响显著，表现为随流速增加，系泊张力和浮架应力谱密度值增大。本研究可为单点系泊‘六三型’网箱优化设计及分析提供计算依据。

关键词：‘六三型’网箱；时域分析；谱密度；运动响应；系泊力

Research On Dynamic Response Simulation Of Single Point Mooring 'Six-Three Type' Net Cage Under Irregular Wave And Current

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Abstract： A single point mooring ‘Six-three type’ deepwater cage was designed to adapt to the complex and harsh sea conditions. According to the literature consulted, the current research on this cage is still relatively limited. To study the response characteristics of different components of a ‘Six-three type’ deepwater cage under irregular wave and current, the hydrodynamic numerical model of the cage was created firstly based on the advanced hydrodynamic analysis software OCRAFLEX in this work. In the model, the net twines and mooring lines were simulated by 3Dbouy element, while the floating collar was simulated by 6Dbouy element because the floating collar can resist bending deformation and its bending moment can not be ignored. The coupled time-domain analysis method was used in the numerical simulation. To verify the numerical model, the results from numerical model were compared with the physical model tank test data. It is found that the results agree well between the tests and numerical simulations. Based on the verified numerical model of the cage, with the considerations of the conditions of real sea where the cage would be placed in, the motion response of cage, the tension of mooring line and the stress of floating collar were studied from 3 aspects: the time-domain curve of response, comparison with wave surface elevation and energy spectral density statistics. It should be noted that there is a strong correlation between pitch motion and heave motion of the cage and the motion response in other directions is small, thus only heave and surge motion were considered in this study. The results show that the heave motion of the cage is mainly affected by the wave conditions and the current has little influence on it. In addition, heave motion is consistent with the elevation of the wave surface. The surge motion of the cage is closely related to the current and the delay effect is significant by comparing with wave surface elevation. The heave and surge motion of the cage are mainly affected by the wave frequency load and the high frequency load has little effect on these motions. Under the combined loads from irregular wave and current, the low-frequency load has an obvious influence on the surge motion of the cage. The tension of the mooring line and the stress of the floating collar are closely related to the elevation of wave surface. The peak values of mooring line tension and collar stress almost appear at the same time when the wave surface peak value was met.

However, the stress of the floating collar shows high-frequency response characteristics on the premise of meeting the wave frequency response trend. The current velocity has a significant impact on both the mooring line tension and floating collar stress, where their energy spectral density increase with the increase of current velocity. The energy spectral density of both mooring line tension and the floating collar stress are almost zero under high frequency load. This study can provide a research basis and technical reference for the optimal design and response analysis of a single point mooring‘Six-three type’cage.

Key words: ‘six-three type’ net cage; time domain analysis; spectral density; motion response,; mooring force.

基于 FFT 和 Morlet 小波分析的网目尺寸和渔获物对中层拖网网囊形态和振荡特性的影响

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摘要：为提高能源利用率和网囊选择性，有必要探究网囊水动力、形态和振荡特性。本试验对 3 顶不同网目尺寸的网囊进行水槽试验，通过 FFT 和 Morlet 小波变换获取网囊振荡特性，研究网目尺寸和渔获物对网囊水动力特性，形态和振荡特性的影响。结果显示：空网条件下，随着网目尺寸的减小，网囊阻力增加 6.6%–25.1%，网囊中部断面面积减小 14.9%–51.7%。另外，网囊阻力振荡频率为 0.33–0.42 Hz 且随着网目尺寸的增加而增加；其振荡功率随网目尺寸的增加而减小。当网囊存在渔获物时，网囊形态表现为中部收缩尾部膨胀，其中部断面(X=104 cm)面积为空网时的 15.1%。网囊尾部位置振荡频率为 0.30–0.46 Hz，且网囊阻力振荡频率和位置振荡频率相同。

关键词：网囊；振荡特性；阻力；网囊形态；低频

The profile and fluttering characteristics of codend with different mesh sizes and catch by FFT and Morlet wavelet methods

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Abstract: In order to improve the energy efficiency and prevent the probability of the fish escaping, it is essential to understand its hydrodynamic behavior, fluttering motions, and spatial form. This study investigates the impact of the mesh size and catch on hydrodynamic characteristics, net cross-section, and fluttering motions of the codend in the flume tank. Thus, three codends models were designed using polyethylene material with three different mesh sizes (60 mm, 80 mm, and 100 mm). A Fourier analysis via the Morlet wavelet analysis and the FFT method was done by watching the wavelet coefficient and power spectrum of the codend fluttering motions and time evolution of the drag forces. The results showed that at the empty stage, the decrease in mesh size led to an increase in drag force by 6.6%,25.1%, codend length by 2.6%,4.3%, and a decrease in cross-section area by 14.9%51.7% of codend. In addition, the time evolutions were oscillatory quasi-periodic and related to the low-frequency activity. The codend drag oscillation frequency is mainly 0.33–0.42 Hz and decreased with the mesh size, and the power spectrum and wavelet coefficient of drag force increased as the mesh size decreased. For the codend with catch, the shape of each codend is the front mesh closed, the rear contour bulged, the middle part of each codend is the most closed, and the cross-section area is about 15.1% of the empty codend (X=104 cm). The codend position oscillates frequency is 0.30–0.46 Hz in X and Z-directions. The drag oscillation frequency is mainly 0.30–0.46 Hz and synchronized with the position motion. In addition, the codend with a greater mesh size showed more stable behavior with a lower frequency and oscillatory motions compared to the codend with a small mesh size leading to a decrease in drag on this codend.

Key words: Codend; fluttering motions; drag; spatial form; low frequency

基于斑点检测和运动预测的鱼苗计数方法

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摘要：鱼苗计数作为鱼类养殖中的基础操作，在各方面都具有重要意义。本研究基于斑点检测算法和运动预测分析，提出了一种鱼苗在线精准且快速估算方法；无需大量数据训练、计算成本低。首先，通过结合高斯混合模型分离算法和斑点检测算法完成鱼苗的检测和定位；其次，采用分段函数构建了鱼苗的运动预测模型；继而，根据运动预测模型获得前后帧鱼苗之间的关联概率，并构建损失矩阵；最后采用全局优化方法实现前后帧鱼苗的关联，并通过实时判断新出现鱼苗实现了鱼苗高精度连续计数。通过采集的 52 个数据集（来自 2 种不同品种和规格的鱼苗、低帧率（10fps）采集）上进行测试分析，本方法对 2 种鱼苗的平均计数准确率均超过了 99%，准确率标准差小于 0.7%。

关键词：鱼苗计数； 斑点检测； 模型预测； 全局优化；实时

A Fingerlings Counting Method Based on Blob Detection and Motion Prediction

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Abstract： As a basic operation in fish farming, fingerlings counting is an important guide in most aspects. In this study, an accurate and fast online fingerlings estimation method based on Blob detection and motion prediction analysis was proposed. Firstly, the detection and localization of fingerlings are accomplished by combining Gaussian Mixture-based Background/Foreground Segmentation Algorithm(MOG) and Blob detection; secondly, the motion prediction model of fingerlings in the counting area is constructed by using the segmentation function; then, the association probability between the front and back frames of fingerlings is obtained according to the motion prediction model, and the loss matrix is constructed; finally, the global optimization method is used to realize the association between the front and back frames of fingerlings, and the new fingerlings are judged and counted in real-time, realizing the continuous counting of fingerlings with high accuracy. Through testing and analysis on 52 collected data sets (low frame rate (10 fps) acquisition), the average counting accuracy of this counting method for both species of fry exceeded 99%, and the standard deviation of counting accuracy was less than 0.7%.

Key words: Fingerlings Counting; Blob Detection; Motion Prediction; Global Optimization; Real-time

斜坡地形影响下多体浮式渔场平台的水动力及波浪场特性分析

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摘要：近岛礁海域离岸距离较远，风浪较小，已经成为发展水产养殖业的重点区域。然而，岛礁附近存在较为明显的地形变化，波浪遇到地形所产生的反射波会改变养殖区域波浪场，可能会对养殖设施造成一定的破坏。同时，关于养殖结构水动力特性的研究大多未考虑地形的影响。为填补这一研究空白，本文通过物理模型试验的方法，研究了多体浮式渔场平台在地形影响下的水动力特性及网箱内部的波浪场。结果表明，地形的存在显著地增大了迎浪侧网箱纵荡方向的低频漫漂，而其垂荡和纵摇运动并未产生明显变化；地形对网箱内部的波浪场产生了一定的影响，当入射波长等于网箱边长时，地形的存在加剧了迎浪侧网箱内部的波浪破碎，网箱内的波浪响应逐渐由波频向高频转移，背浪侧网箱内的波浪响应与入射波长呈正相关关系，当入射波长等于网箱边长的三倍时，背浪侧网箱内部的波浪响应最大。本文的研究结果为近岛礁海域养殖结构的设计与优化提供了参考。

关键词：斜坡地形；多体浮式渔场平台；物理模型试验；水动力特性；波浪场

Analysis of hydrodynamic and wave field characteristics of multi-body floating aquaculture platform under the influence of slope topography

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Abstract： The coastal area near the islands has become a key area for the development of aquaculture because of the long offshore distance and suitable wind and wave conditions. There is a relatively obvious topographic change near the islands, and the reflected waves generated by topography will change the wave field in the aquaculture area, which may cause the structural damage of the net cage. Meanwhile, most studies on the hydrodynamic characteristics of aquaculture structures do not consider the effect of topography. In order to bridge the gap, the hydrodynamic characteristics of multi-body floating aquaculture platform and the wave field inside the net cage under the influence of slope topography were studied via physical model test. The presence of the terrain significantly increases the low-frequency drift of the surge response of the cage on the weather side, and the heave and pitch motions do not change obviously. The topography has some effect on the wave field inside the cage. When the incident wavelength is equal to the length of the cage, the topography makes the wave breaking inside the cage more obvious, and the wave response gradually shifts from wave frequency to high frequency. The wave response inside the cage on the lee side is positively correlated with the incident wavelength. When the incident wavelength is three times the length of the cage, the wave response is the largest. The results of this paper provide a reference for the design and optimization of aquaculture structures near islands.

Key words: Slope topography; Multi-body floating aquaculture platform; Physical model test,; Hydrodynamic characteristics; Wave field.

基于 DPIV 技术草金幼鱼动力学研究

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摘要：鱼类巡游中其推进机理及推进性能的研究是鱼类行为学中研究热点，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（DPIV）和涡量矩定理，对摆动尾鳍流场进行测试，分析了草金幼鱼在转弯过程运动学和动力学变化。研究结果表明：草金幼鱼在转弯过程中，发生“C”型摆动，整个转弯过程根据尾鳍摆动方向的变化分为五个阶段，第一阶段鱼体释放能量于流体中，第二、三阶段鱼体尾部发生两次大幅度摆动，第四、五阶段鱼体摆动速度相对较大，发现草金幼鱼涡量呈余弦分布，且较小的尾涡结构更有利于鱼体的转弯。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设计提供参考依据，并为探究鱼类运动行为、鱼群机动行为提供一定的基础。

关键词：推进机理；草金幼鱼；数字粒子图像测速技术；尾鳍摆动；尾涡脱落；鱼类运动行为

Experimental study on dynamics of larval herbaceae based on DPIV technique

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Abstract: The research on propulsion mechanism and propulsion performance of fish cruising is a hot topic in fish behavior. In nature, most fish generate more speed and thrust through the fluctuation pattern of caudal fin. In this paper, digital particle image velocimetry (DPIV) and vorticity moment theorem were used to test the oscillating caudal fin flow field, and the kinematics and dynamics changes of juvenile brachyderma were analyzed during the turning process. The results show that: Grass Kim young fish in the process of turning, swing type "C", the whole process of turning according to the direction of the tail movements change is divided into five stages, the first phase of the fish body to release energy in the fluid, the second and third stage fish tail in two large swing, fourth and fifth stage fish swing speed is opposite bigger, found the grass gold larval vorticity cosine distribution, And the smaller tail vortex structure is more conducive to fish turning. The relevant research results provide a reference for the study of the movement mechanism of cyprinid fish and other fish and the design of underwater biomimetic models, and provide a certain basis for the study of fish movement behavior and fish mobility behavior.

Key words: propulsion mechanism; juvenile grasshopper; digital particle image velocimetry; caudal fin swing; trailing vortex shedding; locomotor behavior of fish

金枪鱼围网生态型人工集鱼装置漂流特性模型试验研究

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摘要：人工集鱼装置（FAD）的漂流速度与漂流轨迹影响着下方金枪鱼的随附行为，进而影响金枪鱼围网捕捞计划的制定。本研究基于弗劳德相似准则设计了 10 种 FAD 模型，通过循环动水槽对不同流速条件下各 FAD 漂流特性进行测试，并采用 t 检验对相同流速条件下 FAD 模型漂流时间的差异性进行两两配对比较。研究结果表明：在 5 种流速条件下 FAD4 平均漂流时间最短，FAD9 与 FAD10 的平均漂流时间最长且近乎一致；当筏体结构相同时，水下结构为单根棉绳与网束的 FAD 最慢且近乎一致；当水下结构相同时，筏体结构为竹筏的 FAD 漂流速度最慢。此外，除少数结果外（v=55 cm/s，FAD2 与 FAD3 和 v=35 cm/s，FAD9 与 FAD10），水下结构为单根棉绳与网束 FAD 的漂流速度差异不显著。建议在实际生产中制作筏体结构时可使用竹筏替代浮排，并采用等直径棉绳逐步替代网束，以实现非/低缠绕型 FAD 向天然/可降解 FAD 的快速过渡。

关键词：金枪鱼围网；人工集鱼装置；漂流特性；生态型人工集鱼装置

Model test on drifting characteristic of ecological fish aggregation devices (FAD) in tropical tuna purse seine fishery

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Abstract：The drift speed and trajectory of the fish aggregation device (FAD) affect the associative behavior of tunas, and thus affect the formulation of tuna purse seine fishing plans. In this study, 10 ecological FAD models of tuna purse seine were designed based on Froude's similarity criterion. The drifting characteristic of FAD models were tested under different flow rates in a dynamic tank, and the t-test was used for pairwise pairing to compare the drifting time differences of FAD models under the same flow rate. The results show that FAD 4 (double floats + cotton canvas) has the shortest average drifting time under the five flow rates, while FAD 9 (bamboo raft + single cotton rope) and FAD 10 (bamboo raft + netting bundle) have the longest and almost the same drifting time. With the same raft structure, the FAD equipped with single cotton rope and netting bundle submerged structure exhibited the lowest and almost the same drifting velocity. With the same submerged structure, the FAD equipped with bamboo raft exhibited the lowest drifting velocity. Moreover, except for a few results (v=55 cm/s, FAD 2(double floats + single cotton rope) ~ FAD 3 (double floats + netting bundle) and v=35 cm/s, FAD 9 ~ FAD 10), there was no significant difference in the drifting velocity between the FAD equipped with single cotton rope and netting bundle submerged structure. It is suggested that bamboo raft can be used to replace floats raft when making raft structures in actual production, and cotton ropes can also be used as submerged structure to gradually replace the same diameter netting bundle , so as to realize the rapid transition from NE-FAD to Bio-FAD.

Key words: tuna purse seine; fish aggregation devices; drifting characteristic; ecological FAD

一种智慧混合型漂浮式微藻反应器水动力特性研究

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摘要：漂浮式微藻反应器（FPBR）具有能源投入低和制造成本少等优势，满足微藻生物能源大规模生产的迫切需求。尽管漂浮反应器一般情况下可成功培养微藻，但存在波浪能量不稳定、混合不充分的问题，而高效的混合对于提高漂浮式反应器生产力至关重要。针对这一问题，在先前的研究基础上设计了一种混合装置，并结合自动控制原理实现了反应器的智慧混合。为验证该设计的合理性，本文通过CFD数值模拟技术研究了带有混合装置的反应器内部水动力特性，重点分析了反应器的混合特性、死区系数、能耗功率等关键参数。结果表明，混合装置运动行程越大，混合效果越好；在运动行程相等的条件下，混合装置匀速运动引起的混合效果比正弦变速运动更好，但能耗功率也相对更大；此外，混合装置运行引起的死区空间动态变化导致现有死区系数计算公式并不适用。研究结果为漂浮式微藻反应器设计及优化提供新思路，具有一定的科学意义。

关键词：微藻生物能源；漂浮式反应器；智慧混合；CFD；数值模拟

Numerical study on the inner hydrodynamic of a smart mixed floating photobioreactor

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Abstract： Floating bioreactor (FPBR) has the advantages of low energy consumption and manufacturing cost, which meet the urgent needs of large-scale production of microalgae biofuels. Although the floating reactor can successfully cultivate microalgae in general, there are still some problems of unstable wave energy and insufficient mixing, especially the efficient mixing is crucial to improve the productivity of the floating bioreactor. In order to solve this problem, a mixing device was designed based on the previous research, and the intelligent mixing of the bioreactor was realized by combining the automatic control principle. To validate the rationality of the design, the hydrodynamic characteristics of the bioreactor with mixing device are studied by using CFD technology, and the key parameters are analyzed such as mixing characteristics, dead zone coefficient and energy consumption power of the bioreactor. The results show that the larger the motion travel of the mixing device, the better the mixing. The mixing caused by uniform motion of the mixing device is better than that of sinusoidal variable motion under the condition of equal motion travel, but the energy consumption power is relatively larger. In addition, the dynamic change of dead zone space caused by the operation of the mixing device is unable to describe by the existing dead zone coefficient calculation formula. The results provide a new idea for the design and optimization of floating microalgae reactor, which has certain scientific significance.

Key words: Microalgae bioenergy; Floating bioreactor; Smart mixing; CFD; Numerical simulation

基于数值模拟方法的集鱼灯三维光场分布与最佳配置

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摘要：集鱼灯作为光诱渔船生产作业成本的重要部分，集鱼灯光照度在水下的有效水体体积是高效捕捞的重要基础。本文利用分布光度计进行 LED 集鱼灯光强分布，并利用数值模拟方法配置集鱼灯三维有效水体体积，并以 8154 型鱿钓渔船为例进行灯光配置的分析与探讨。结果表明，（1）LED 集鱼灯实测单灯平均功率为 130W，光通量为 1693lm，最大光强 907cd，光效达 12.99lm/W，光束角为 88.5，光束轴线偏离角 0.25；（2）照度在 0.01-10lx 之间的有效水体体积较为合适，在灯间距为 0.5m，水上高度为 6.5m 时，10lx 的等照度线在水深方向大概 16m 处，距离船水平方向 14m 处；0.01lx 的等照度线在水深方向大概 50m 处，距离船水平方向 80m 处，有效水体体积为 534090m3。研究为选择合适光强、光效最优的集鱼灯，并合理分配和优化光诱渔船集鱼灯配置，以提高捕捞效率降低生产作业成本提供一定的参考。

关键词：集鱼灯；有效水体体积；数值模拟；灯光配置；照度分布

Three-dimensional Light Field Distribution and Optimal Configuration of Fish-collecting Lamp Based on Numerical Simulation Method

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Abstract： Fish-collecting lamp is an important part of the production cost of light-induced fishing vessels. The effective water volume of fish-collecting lamp illumination under water is an important basis for efficient fishing. In this paper, the light intensity distribution of LED fishing light is carried out by using the distribution photometer, and the three-dimensional effective water volume of fishing light is configured by numerical simulation method. Taking the 8154 squid fishing vessel as an example, the light configuration is analyzed and discussed. The results show that : (1) The average power of LED fish-collecting lamp is 130W, the luminous flux is 1693lm, the maximum light intensity is 907cd, the luminous efficiency is 12.99lm / W, the beam angle is 88.5, and the deviation angle of beam axis is 0.25. (2) The effective volume of water body with illuminance between 0.01-10lx is suitable. When the lamp spacing is 0.5m and the water height is 6.5m, the 10lx isoluminal line is about 16m in the water depth direction and 14m away from the horizontal direction of the ship. The isoluminal line of 0.01 lx is about 50 m in the water depth direction and 80 m in the horizontal direction of the ship, and the effective water volume is 534,090 m3. The research provides a certain reference for selecting the fish-collecting lamp with appropriate light intensity and optimal light efficiency, and rationally allocating and optimizing the configuration of fish-collecting lamp of light-induced fishing vessels, so as to improve fishing efficiency and reduce production costs.

Key words: fish lamp; effective water volume; numerical simulation; Lighting configuration; illumination distribution

循环水养殖下单体大口黑鲈吞食声和咀嚼声特征提取与分类

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摘要：为提高水产养殖中投饲的精准度，节约工厂化养殖成本，采用被动声学技术对水产动物的摄食行为进行研究成为了近年来智能投饲热门研究方向。该研究针对大口黑鲈投饲后的摄食声，提出了一种将短时平均能量、平均梅尔倒谱系数、功率谱主峰值和主峰频率作为声学识别特征，使用支持向量机对大口黑鲈（*Micropterus salmoides*）的吞食声实现识别的方法。该研究采用被动声学信号采集装置获取鱼的吞食声信号，运用子空间语音增强法对声信号进行降噪，声像同步得到吞食声信号样本 564 个，咀嚼声信号样本 189 个。5-折交叉验证得到最优的核参数 c 为 0.5，g 为 0.0039。用支持向量机进行分类识别。测试结果表明特征融合后的识别模型准确率可达 96.15%，召回率达到 100%，f-分数达到 98.04%，精度达到 92.19%，较单一梅尔倒谱系数和结合短时能量识别效果更好。该研究对为以后研发真实养殖环境下鱼类声学智能投饲装置提供

关键词：大口黑鲈；被动声学；信号处理；声音识别；支持向量机；声学模型

Feature extraction and classification of swallowing and chewing sounds of single largemouth bass（Micropterus salmoides） under recirculating aquaculture

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Abstract： In order to improve the accuracy of feeding in aquaculture and save the cost of factory farming, the use of passive acoustic technology to study the feeding behavior of aquatic animals has become a popular research direction in intelligent feeding in recent years. Aiming at the feeding sound of largemouth bass after feeding, this study proposes a method that takes the short-term average energy, average Mel cepstral coefficient, main peak of power spectrum and main peak frequency as acoustic identification features, and uses support vector machine to identify largemouth bass. (*Micropterus salmoides*) swallowing sound to achieve recognition method. In this study, the passive acoustic signal acquisition device was used to obtain the fish's swallowing sound signal, and the subspace speech enhancement method was used to denoise the sound signal. 5-fold cross-validation obtained the optimal kernel parameters c of 0.5 and g of 0.0039. Classification and recognition with support vector machines. The test results show that the accuracy of the recognition model after feature fusion can reach 96.15%, the recall rate can reach 100%, the f-score can reach 98.04%, and the accuracy can reach 92.19%, which is better than the single Mel cepstral coefficient and combined short-term energy recognition effect. . This research provides a theoretical basis for the future development of acoustic intelligent feeding devices for fish in real breeding environments.

Key words: Micropterus salmoides; Passive acoustics; Signal processing; Voice recognition; Support vector machine; Acoustic model

基于双频识别声呐的养殖塘南美白对虾探测与初步分析

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摘要：虾类水下行为特征对虾类资源养殖具有重要的指导意义。为了实现高效、快速和准确的虾类资源监测，本文提出一种基于双频识别声呐 DIDSON 的池塘养殖南美白对虾探测与行为分析方法。在上海某养殖塘，利用 DIDSON 识别声呐采集 2h 南美白对虾声学图像数据，基于 Echoview 软件构建图像分析模型，开展白对虾目标识别与计数。实验结果发现，虾群呈现一定方向的规律性运动，在养殖塘八个采样点观测的虾群密度值，最大为 870 只/m^2，最小为 750 只/m^2，均值为 832 只/m^2。八个采样点单位时间内的虾群通量最大值为 58 只/min，最小值为 51 只/min。八个采样点的虾群密度和通量的变化较小，可以推断养殖塘内虾群以一定速度进行洄游。本文研究结果表明，DIDSON 识别声呐能够应用于浑浊养殖水体中虾类行为研究，能够为虾类资源评估和生活习性研究提供有效的方法支持。

关键词：南美白对虾；双频识别声呐；虾类行为特征；通量

Detection and preliminary analysis of Penaeus vannamei in culture ponds based on dual-frequency identification sonar

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Abstract： The underwater behavior characteristics of shrimp have important guiding significance for shrimp resource culture. In order to achieve efficient, fast and accurate monitoring of shrimp resources, this paper proposes a detection and behavior analysis method for pond culture of Penaeus vannamei in pond culture based on dual-frequency recognition sonar DIDSON. In a breeding pond in Shanghai, the DIDSON identification sonar was used to collect 2h of South American white shrimp acoustic image data, and an image analysis model was constructed based on Echoview software to identify and count targets of Penaeus vannamei. The experimental results showed that the shrimp population showed regular movement in a certain direction, and the density value of the shrimp population observed at the eight sampling points of the pond was 870 /m^2 at the maximum, the minimum was 750 /m^2, and the average value was 832 /m^2. The maximum throughput of shrimp populations per unit time at eight sampling points was 58 shrimps/min and the minimum value was 51 shrimps/min. The changes in shrimp population density and flux at the eight sampling points were small, and it can be inferred that shrimp populations in the culture pond migrate at a certain rate. The results of this paper show that DIDSON recognition sonar can be applied to the study of shrimp behavior in turbid cultured waters, and can provide effective method support for shrimp resource assessment and life habit research.

Key words: Penaeus vannamei; Dual-frequency recognition sonar; Shrimp behavioral characteristics; circulation

集鱼灯在浑浊水体中的照度分布数值模拟分析

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摘要：水下集鱼灯是近海鲐鱼灯光围网和灯光敷网等光诱渔业的关键设施。本文采用数值模拟方法计算二极管 (Light emitting diode, LED)集鱼灯与金属卤化物(Metal halide, MH)集鱼灯在浑浊海洋水体中光场分布情况。采用集鱼灯光谱数据、光强分布数据和海水固有光学参数，基于蒙特卡罗模拟方法构建了新的光场传输数值计算模型。应用模型分析了海水的叶绿素浓度、散射作用类型和散射相位函数中非对称参量 g 的取值对 LED 集鱼灯与 MH 集鱼灯光场分布的影响。研究表明：（1）白光 LED 和白光 MH 集鱼灯在浑浊水体中的光场分布几乎相同；（2）海水中叶绿素浓度对光场分布有显著影响，而散射类型和非对称参量取值的影响相对较小；（3）本文提供的数值模型可准确计算浑浊水体中集鱼灯光场分布，弥补了传统模型不足，可为集鱼灯有效诱集光场范围估算及其合理应用提供参考。

关键词：水下集鱼灯；照度分布；叶绿素浓度

Numerical simulation on illumination distribution of underwater fishing lamp in turbid marine water

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Abstract： Underwater fishing lamp is the key facility in light-fishing industry such as the large light purse seine and light lift net fishery in coast waters. Numerical simulations were used to calculate the illumination distribution of light emitting diode fishing lamp (LED) and metal halide fishing lamp (MH) in turbid marine water. A new computing model of underwater illumination of fishing lamp was developed based on Monte Carlo method by using spectrum and luminous intensity of lamps and the inherent optical properties of seawater. In this paper, the effect of chlorophyll concentrations, scattering type in the marine water and the scattering asymmetry parameters on the illumination distribution of LED fishing lamp and MH fishing lamp were analyzed through simulation. Conclusions: (1) although the spectral composition of white LED and white MH fish lamp were different, their illumination distribution in turbid water were almost the same; (2)the chlorophyll concentration of marine water has an important impact on the spatial distribution of light field in water, while the scattering type of the marine water and the setting of scattering asymmetry parameter has a much smaller impact; (3)the numerical model provided in this paper could accurately calculate the illumination distribution of fish lamp in turbid water, making up for the shortcomings of the traditional model, and also this study supports the proper application of fishing lamp and estimation of effective capture range of fishing lamp in turbid marine water.

Key words: underwater fishing lamp; illumination distribution; chlorophyll concentration

南极磷虾拖网变水层调节桁杆水动力分析与试验

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摘要：目前南极磷虾的主要捕捞方法为桁杆拖网，捕捞船通过牵引纲拖曳安装了网具的桁杆进行扫海捕捞作业。由于南极磷虾种群具有集体活动的特点，虾群常集中出现于某些特定深度的海域。现有的捕捞方法需要通过修正牵引纲长度与船只航行速度来控制扫海深度，不具备自主调节捕捞深度的定位功能。针对这一问题，提出了一种安装于桁杆上的变水层调节装置，用于实现主动升潜调节功能，以跟踪南极磷虾种群所处水层的深度，实现精确捕捞。对所提出的变水层调节桁杆进行水动力有限元仿真分析计算以确立其最佳运行状态，并通过水槽试验模拟工作环境来验证其水动力特性。实验完成后，制造了中尺度桁杆样机，并在东海完成了初步海试。结果表明，变水层调节桁杆方案可行，其深度调节功能在扰流板攻角 17°时效果最佳。本研究验证了变水层调节桁杆的可行性，为大尺度变水层调节桁杆优化设计和样机测试提供理论与数据支持。

关键词：捕捞；桁杆拖网； 变水层；流体动力学；水槽实验

Hydrodynamic Simulation and Experiment of Depth Adjustable Beam Trawl for Euphausia Superba

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Abstract： The existing fishing method of krill needs to adjust the trawling depth by modifying the length of the trawl warp and the navigation speed of the vessel, which cannot adjust the trawling depth independently. To solve this problem, we proposed a depth variable device installed on the beam to adjust the trawling depth independently, aiming to track the depth where the shoal of Antarctic Krill is located for accurate fishing. Simulate the hydrodynamic feature of the proposed beam trawl device by numerical analysis and water channel experiment to design the wing's profile and determine the effective range of angle of attack. A sea trial of mid-size trawl prototype was tested in East Sea. The results showed that the depth variable trawl is available. The performance of device was best when angle of attack was 17°. This research verified the feasibility of the depth variable trawl, and provided theory and data for large-size trawl prototype's optimal design and test.

Key words: Fishing; trawl; depth variable; hydrodynamic; water channel experiment

温室太阳能热泵海带干燥机的设计：系统性能和干燥动力学

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摘要：针对海带干燥时间长、能耗高、效率低和品质差等问题，本文设计了一种新型温室型双蒸发器太阳能辅助热泵干燥系统（SHPD）。研究了海带太阳能辅助热泵干燥(S-HP)（100-700 W/m2）和热泵单独干燥（HP）（30、40 和 50℃）的系统性能、干燥动力学和品质的影响。随着干燥温度和太阳辐照量的增加，干燥时间缩短。S-HP 系统的 COP 和 SMER 分别为 3.590-6.810 和 1.660-3.725kg/kW·h，大约是使用相同干燥环境时 HP 的两倍。S-HP 和 HP 的 Deff 分别为 5.431×10-11~11.316×10-11m^2/s，1.037×10-11~1.611×10-11m^2/s，相同温度下额外的太阳辐射显著提高了 Deff。Page 模型能准确描述海带 S-HP 和 HP 下水分变化，误差小于 5%。干燥海带颜色鲜艳，表面析出甘露醇，风味浓郁。证明了设计的 S-HP 系统对海带干燥更为节能、高效。

关键词：太阳能干燥；热泵；设计；海带；系统性能；动力学

Design of greenhouse solar assisted heat pump dryer of kelp（Laminaria japonica）: System performance and drying kinetics

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Abstract： In this work, a new greenhouse type double evaporator solar assisted heat pump drying system (SHPD) was built to address the issues of prolonged drying times, high energy consumption, low efficiency, and poor quality of kelp. Kelp solar assisted heat pump drying (S-HP) (100-700 W/m2) and heat pump drying (HP) (30, 40, and 50 °C) were both examined for system performance, drying kinetics, and quality impact. With an increase in drying temperature and solar radiation, the drying time was reduced. The COP and SMER of the S-HP system were 3.590-6.810, and 1.660-3.725 kg/kW·h, respectively, roughly double that of HP when using the same drying circumstances. The Deff of S-HP and HP were 5.431×10-11~11.316×10-11m^2/s, and 1.037×10-11~1.611×10-11m^2/s, respectively. At the same temperature, additional sun irradiation greatly improves Deff. Page model could accurately represent the change in moisture ratio of S-HP and HP for kelp with an inaccuracy of less than 5%. The dried kelp had a vivid color with robust flavor, mannitol was precipitated on surface. The S-HP system was higher efficiency energy saving for drying kelp and can be suggested as an alternate technique for drying aquatic products.

Key words: solar drying; heat pump; design; kelp; system performance; kinetics

渔用高性能绳索材料的研究进展

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摘要：绳索是重要的渔具材料，在渔业生产中发挥了重要作用，其综合性能直接影响到渔业生产效率及安全。本文主要围绕超高分子量聚乙烯（ＵＨＭＷＰＥ）绳索、钢丝绳、碳纤维绳索的主要性能及改性研究进行综述，分析对比了三种渔用高性能绳索材料在断裂性能、抗腐蚀性能、抗蠕变性能等综合性能上的优缺点；介绍了它们在渔业领域的发展现状，为渔用绳索新材料的进一步研发及应用提供理论参考。此外，本文回顾了渔用高性能绳索材料前期研究方向及应用技术方面的重点与难点，建议今后加强其基础研究及产业化应用技术研究。

关键词：高性能绳索；渔具材料；ＵＨＭＷＰＥ绳索；钢丝绳；碳纤维绳索；深远海网箱

Research progress of high performance rope materials for fishery

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Abstract： Rope is an important fishing gear material and plays an important role in fishery production. Its comprehensive performance directly affects the efficiency and safety of fishery production. This paper mainly reviews the main properties and modification research of ultra-high molecular weight polyethylene (UHMWPE) ropes, steel wire ropes and carbon fiber ropes. The advantages and disadvantages of comprehensive performance, etc. are introduced; their development status in the field of fishery is introduced to provide theoretical reference for the further research and development and application of new fishing rope materials. In addition, this paper reviews the key points and difficulties in the preliminary research direction and application technology of high-performance rope materials for fishing, and proposes to strengthen its basic research and industrial application technology research in the future.

Key words: 高性能绳索；渔具材料；ＵＨＭＷＰＥ绳索；钢丝绳；碳纤维绳索；深远海网箱

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，围网船大部分时间用在寻找目标鱼群或人工漂流集鱼装置上。海鸟雷达是金枪鱼围网渔船常用的探测设备，因为海鸟作为海洋捕食者代表着潜在的捕鱼机会。虽然许多研究阐明了影响海鸟行为特征的原因，但现有文献对人工漂流集鱼装置（FADs）影响海鸟动态分布的研究不足。我们利用海鸟雷达捕捉船舶周围 16 海里范围内的海鸟群信息，计算海鸟回波的空间聚类。本研究采用广义加性混合模型（GAMM）研究基里巴斯海域海鸟动态分布与漂流人工集鱼装置之间的关系。该模型将 FADs 视为随机效应，将经纬度视为固定效应。结果表明:人工集鱼装置对海鸟的动态分布具有一定的影响。海鸟数量、海鸟面积和海鸟运动能力的随机效应分别为 2.14、14.60、-0.18。在漂流的人工集鱼装置周围海鸟群数量中位数为 35 簇（8~71 簇），比附近没有人工集鱼装置的鸟类数量更集中，中位数为 28（范围：2~93）；人工漂流集鱼装置附近聚集的海鸟面积中位数为 109.5KM^2（范围：23.3~224.6KM2），平均运动能力中位数 2.0（范围：0.6~3.8），没有人工集鱼装置的海鸟群面积的中位数 78.3 KM^2 (范围：3.8~275.3 KM^2），运动能力中位数 2.5（范围：0.6~6.3）。在 165°E 范围内，鸟类数量和鸟类面积均达到最大值，然后呈向东递减趋势。但是运动能力与经度变化趋势相反，运动能力的最小值出现在 165°E 附近，且向东增加。

关键词：海鸟雷达；人工集鱼装置；GAMM 模型

Application of seabird radar image identified method for analyzing effect of FADs on seabird

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Abstract：In tuna purse seine fishery, detecting object spend a lot of time by seiner. Seabird radar is very efficient for detecting because seabirds as marine predator standing for potential fishing opportunities. Although many studies elucidated the reason that affecting behavioral characteristics of seabirds, the available literature provides insufficient evidence on the drifting Fish Aggregating Devices (FADs) influencing seabirds’ dynamic. We used seabird radar to catch the information of seabirds’ groups within 16 Nm around the vessel and calculated a spatial clustering of the seabird-echoes. In this study, generalized additive mixed models is used to investigate the relationship between drifting FADs and seabird dynamic in Kiribati. The model treating FADs as a random effect and Lat, Lon as fixed effect. The findings indicate that FADs variables affect seabird behavior, random effect of seabird number, seabird aera and seabird ability are 2.14, 14.60, -0.18. The bird numerical characteristics of cluster around drifting FADs, with a median of 35(range 8～71) were more concentrated than those without FADs, with a median of 28(range 2～93); the bird cluster without FADs of area, with a median of 78.3(range 3.8～275.3) were more speared than those with FADs, with a median of 109.5(rang 23.3～224.6); the bird cluster with FADs of sport ability, with a median of 2.0(range0.6～3.8) were less athletic than bird cluster without FADs, with a median of 2.5(range 0.6～6.3). The range of 165° E, it has maximum of bird number and bird area, and then it has decrease trend as eastward. However, it has the opposite trend of bird sport ability and longitude in model 3, the minimum value of bird sport ability occurred around 165° E and increase to the east.

Key words:：Key word: seabird, FADs, seabird radar, gamm

基于四种机器学习模型识别单拖渔船航行特征的比较分析

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摘要：渔捞日志数据能够记录渔船的作业状态等信息，但由于渔捞日志数据存在误报、漏报等情况，导致其记录内容的准确性往往难以保证。渔船监控系统(VMS)能够实时监测和记录渔船的航行信息，因此使用 VMS 数据可提高识别渔船状态的准确度。若将 VMS 数据与渔捞日志相结合，建立两者之间的联系，可对渔船航行特征和作业行为等进行精准识别与分析。本研究在对 2012 年 9 月到 2013 年 1 月期间三艘单拖渔船的 VMS 数据和渔捞日志数据进行匹配后，从 VMS 数据中提取航速、航向、经度、纬度和时间作为特征值，并建立四种机器学习模型：随机森林(RF)，自适应提升(Adaboost)，K 最近邻(KNN)和梯度提升决策树(GBDT)，对渔船的航行特征进行预测，随后使用归一化混淆矩阵和 ROC 曲线对模型的预测性能进行了评估。结果表明，空间特征(经纬度)和时间特征的重要性高于航速和航向特征。通过比较四种模型的归一化混淆矩阵，发现 RF 模型对捕捞状态的预测性能最高，而 Adaboost 模型则对非捕捞状态的预测性能最高。根据 ROC 曲线判断，RF 模型和 Adaboost 模型的预测性能高于 KNN 模型和 GBDT 模型。该结果可以为判断渔船航行特征的相关研究提供理论依据，并有助于进一步分析渔船作业规律，服务渔业生产管理。

关键词：VMS；渔捞日志；单拖渔船；状态识别；机器学习

Identification of navigation characteristics of single otter trawl vessel based on four kinds of machine learning models

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Abstract: Fishing logbook can record the fishing behaviours and other information of fishing vessels. However, the accuracy of the recorded information is often difficult to guarantee due to the misreport and concealment. The fishing vessel monitoring system (VMS) can monitor and record the navigation information of fishing vessels in real time, and it may be used to improve the accuracy of identifying the state of fishing vessels. If the VMS data and fishing logbook are combined to establish their relationships, then the navigation characteristics and fishing behaviour of fishing vessels can be more accurately identified. In this paper, we firstly aim to propose a method for determining the state of VMS data points using fishing log data. Secondly, the relationship between VMS data and the different states of fishing vessels is further explored. Thirdly, the state of the fishing vessel is predicted using VMS data by building machine learning models. We extract the speed, heading, longitude, latitude, and time as features from the VMS data by matching the VMS and logbook data of three single otter trawl vessels from September 2012 to January 2013 and establish four machine learning models (Random Forest [RF], Adaptive Boosting [AdaBoost], K-Nearest Neighbour [KNN], and Gradient Boosting Decision Tree [GBDT]) to predict the behaviour of fishing vessels. The prediction performances of the models are evaluated by using normalised confusion matrix and receiver operator characteristic curve. Results show that the importance rankings of spatial (longitude and latitude) and time features are higher than those of speed and heading. The prediction performances of the RF and AdaBoost models are higher than those of the KNN and GBDT models. RF model shows the highest prediction performance for fishing state. Meanwhile, AdaBoost model exhibits the highest prediction performance for non-fishing state. The main contribution of the research is that it proposed a technical basis for judging the navigation characteristics of fishing vessels, which can enrich the algorithm for judging the behavior of fishing vessels based on VMS data, improve the prediction accuracy and can make the fishery management more scientific and efficient.

Key words: Vessel monitoring system (VMS); Fishing logbook; Single otter trawler; State identification; Machine learning

基于计算机视觉的茎柔鱼几何形态特征提取与分析

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摘要：茎柔鱼作为重要经济渔获物种类，计算机视觉技术对渔获物的形态特征测量与生产效率的提升具有重要意义。本文对茎柔鱼图像利用 Canny 算法提取形态轮廓，通过高斯滤波将形态周围噪声区域过滤得到形态轮廓优化图像；在灰度图像中，采用双阈值边缘检测的方法找到最佳轮廓图像；通过迭代扫描法得到边缘轮廓图像的像素坐标与各特征点二维坐标下的坐标值，以获得生物外形态参数值并将形态参数特征化。结果表明，通过计算机视觉技术对茎柔鱼的形态参数可实现自动测量；利用各特征点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进行特征的数值化。将计算机视觉应用于鱼类形态学的研究可以提高研究的高效性，同时也为后续的研究提供了新的实验思路和方法为资源量的评估提供参考方法。

关键词：茎柔鱼；特征点；计算机视觉；边缘检测；双阈值；迭代扫描法

Geometric feature extraction and analysis of Dosidicus gigas based on computer vision

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Abstract： As an important economic catch species, computer vision technology is important for morphological feature measurement and production efficiency of the catch. In this paper, the morphological contour is extracted by Canny algorithm, and the morphological contour optimized image is obtained by filtering the noisy area around the morphology through Gaussian filtering; the best contour image is found by double-threshold edge detection in grayscale image; the pixel coordinates of the edge contour image and the coordinate values of each feature point in two-dimensional coordinates are obtained by iterative scanning method to obtain the values of the biological exomorphological parameters and to characterize the morphological The results show that the best contour image is obtained by computer vision. The results show that the morphological parameters of the Dosidicus gigas can be automatically measured by computer vision technology; the values used to calculate the morphological parameters of the Dosidicus gigas can be obtained using the two-dimensional coordinates of each feature point; and the numerical characterization of the features can be performed based on the measurement results of the morphological parameters.

Key words: Dosidicus gigas; feature points; computer vision; edge detection; dual thresholding; iterative scanning method

养殖网衣清洗装置设计及试验研究

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摘要：针对进口网衣清洗装备价格昂贵，国产网衣清洗装备对海虹、牡蛎、藤壶等贝类附着物清洗不净的问题，本文设计了一种高压射流与机械转盘耦合的清洗装置。应用 Fluent 软件进行喷嘴射流仿真，基于 Design-Expert 软件进行出口角度、喉管长度、出口直径对空化强度的响应面分析，优化喷嘴结构参数，基于 LS-DYNA 软件进行了清洗装置破贝仿真研究，并通过正交实验研究了泵压、靶距、喷嘴夹角对清洗效果的影响规律。结果表明：各因素对喷嘴空化强度影响的主次顺序为出口角度＞喉管长度＞出口直径；出口角度与喉管长度的交互作用极显著影响喷嘴空化强度($P<0.01$)，喉管长度与出口直径的交互作用对喷嘴空化强度的影响次之（$P<0.06$）；经回归分析得到最优结构参数为出口角度 45°、喉管长度 3mm、出口直径 1.4mm，在此条件下，喷嘴空化体积分数达到 85%。明确了清洗装置破贝的最小打击力为 84.677±1.27N。各因素对清洗效果影响的主次顺序为泵压＞靶距＞喷嘴夹角，泵压与靶距的交互作用极显著影响清洗效果（$P<0.01$），泵压与喷嘴夹角的交互作用对清洗效果的影响次之（$P<0.05$）；经回归分析得到最优工作参数泵压为 20Mpa、靶距 25mm、喷嘴夹角 45°。研究表明：基于 Fluent 的有限体积仿真分析方法可用于高压射流与机械转盘耦合的清洗装置设计与参数优化,所设计的高压射流与机械转盘耦合的清洗装置可为网箱清洗机械化装备设计提供参考。

关键词：网箱清洗装置；喷嘴结构；冲蚀能力；参数优化

Design and experimental study of a farm netting cleaning device

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Abstract： In order to solve the problem that the netting cleaning equipment does not clean the attached shellfish such as sea rainbow and oyster, this paper designs a netting cleaning device coupled with a high pressure jet and mechanical turntable. Fluent software was applied for nozzle jet simulation, response surface analysis of each parameter based on Design-Expert software, and shell-breaking simulation study of the cleaning device based on LS-DYNA software. The results show that: the main order of influence of each parameter on the nozzle cavitation strength is exit angle > throat length > exit diameter, pump pressure > target distance > nozzle angle; the interaction between exit angle and throat length, pump pressure and target distance is very significant ($P < 0.01$), the interaction between pump pressure and nozzle angle, throat length and exit diameter is the second ($P < 0.05$); by regression analysis to obtain the optimal parameters for the exit angle 45°, throat length 3mm, outlet diameter 1.4mm, pump pressure 20Mpa, target distance 25mm, nozzle angle 47°, under this condition the nozzle cavitation volume fraction reached 85%. The study shows that the simulation method based on Fluent and LS-DYNA can be used to design and optimise the parameters of a cleaning device coupled with a high-pressure jet and a mechanical turntable.

Key words: net tank cleaning device; nozzle structure; erosion capacity; parameter optimization

大连地区裙带菜生物力学特性试验研究

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摘要：本文以大连地区裙带菜为研究对象，分析厚度、取样部位、加载速率对其力学特性的影响。通过拉伸、压缩、剪切和茎叶分离试验，测得裙带菜各部位的最大载荷、应力、应变和弹性模量等力学指标，用 SPSS 对裙带菜力学特性进行相关性分析。结果表明：随着厚度增加裙带菜茎叶抗拉强度、抗压强度、抗剪强度、茎叶分离力依次增加；随着加载速率增加裙带菜茎叶抗拉强度、抗压强度、抗剪强度和茎叶分离力依次降低；裙带菜各部位的茎叶最大抗拉力和最大剪切力虽有不同，但是抗拉强度和抗剪强度均处于同一水平，茎叶分离力从头部至尾部逐渐降低。裙带菜茎抗拉强度、抗压强度、抗剪强度均值依次为 2.27MPa、9.29MPa、2.58MPa，裙带菜叶抗拉强度、抗压强度、抗剪强度均值依次为 1.67MPa、8.35MPa、2.32MPa，茎叶分离力均值为 9.95N。此试验结果可为裙带菜茎叶分离设备研发提供设计依据。

关键词：裙带菜；力学特性；抗拉强度；抗剪强度；茎叶分离

Experimental investigation of the wakame's biomechanical characteristics in Dalian

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Abstract： In this study, wakame in Dalian examined the impact of thickness, sample location, and loading rate on its mechanical properties. The maximum load, stress, strain, and elastic modulus of each wakame portion were measured using tensile, compression, shear, and stem-leaf separation tests, and the mechanical properties of wakame were evaluated using SPSS. The findings demonstrate that as thickness is increased, wakame's tensile strength, compressive strength, shear strength, and stem-leaf separation force all increase. The wakame's tensile strength, compressive strength, shear strength, and stem-leaf separation force all increase as the loading rate rises; The separation force between the stem and leaf steadily decreases from the head to the tail, despite the fact that the maximum tensile force and maximum shear force of the stem and leaf in each portion of the wakame are different. Wakame stems had average tensile, compressive, and shear strengths of 2.27 MPa, 9.29 MPa, and 2.58 MPa; wakame leaves had average tensile, compressive, and shear strengths of 1.67 MPa, 8.35 MPa, and 2.32 MPa; and the average separation force of the stems and leaves was 9.95 N. The outcomes of this test may serve as the foundation for the construction of machinery for wakame stem and leaf separation.

Key words: Wakame; Mechanical properties; Tensile strength; Shear strength; Stem and leaf separation

装配柔性帆布的双翼性网板水动力特性水槽试验研究

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摘要：本研究通过水槽试验探究了装配 2 mm 厚尼龙帆布的双翼型网板的水动力特性。在展弦比为 2.0 和弯曲度为 15%的情况下，设计了 8 个不同双翼间距幅度 G/c（0.75、0.9、1.05）、交错角θ（30°、45°、60°）和柔性面积占比 fr（0、55%、65%、75%）的小尺寸结构物进行试验。结果表明：(1) 装配柔性帆布提升了双翼型网板的升力和稳定性。(2) 在 fr=55%时，结构的阻力降低了 1.9%。此外，在不同流速下，升力系数和阻力系数的变异系数分别为 2.69%和 2.28%，变化幅度小于柔性面积占比相对较大的结构。(3) 与其他试验结构相比，G/c=0.9、θ=45°、fr=55%的框架式柔性结构水动力性能表现最佳，在冲角为 18°~ 28°时，阻力比刚性双翼型网板降低了 5.72%，升力提高了 4.8%。因此，使用柔性帆布替换部分刚性结构的双翼型网板的方案对于中、浅层拖网作业是有效的。

关键词：框架式柔性结构；水动力特性；柔性面积占比；水槽试验

Hydrodynamic characteristics of the biplane-type otter board with the canvas through flume-tank experiment

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Abstract： Hydrodynamic characteristics of a biplane-type otter board, equipped with nylon canvas of 2 mm thickness was investigated through flume-tank experiment in this study. A series of predesigned structures with different gap-chord ratios G/c (0.75, 0.9, 1.05), stagger angles θ (30°, 45°, 60°), and proportions of flexible area fr (0, 55%, 65%, 75%), at an aspect ratio of 2.0 and a camber ratio of 15%, were carried out. Results: (1) The improvement of lift and stability for the biplane-type otter board was concluded. (2) At fr = 55%, the coefficient of variation of the lift and drag coefficient at different current velocities were 2.69% and 2.28%, respectively. (3) The frame-type flexible structure with the gap-chord ratio of 0.9 and a stagger angle of 45° and the proportion of the flexible area of 55%, performed best, and it was reduced by 5.72% in drag and increased by 4.8% in lift, compared with the rigid biplane-type otter board at the angles of attack from 18° to 28°.

Key words: Frame-type flexible structure; Hydrodynamic characteristics; Proportion of flexible area,; Flume-tank experiment

田内准则大尺度比对拖网模型试验的影响

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摘要：渔具模型试验是渔具水动力性能研究的重要手段，试验所使用准则及其换算关系是模型试验的核心问题。本研究以中层拖网作为原型网，采用田内准则，换算并制作三种不同大尺度比（4、6、8）的模型网，在静水槽中进行拖曳试验，并与原型网海上实测数据进行对比，分析田内准则大尺度比对拖网模型试验的影响；并使用田内修正公式对模型试验结果进行修正，比较修正前后不同大尺度比的模型网换算结果与实物网海上实测结果的偏差。结果显示：（1）三种大尺度比模型网的换算阻力值均大于实物网海上实测值，且随着大尺度比的增加，模型网换算阻力值与实测阻力值的偏差增大；在拖速 2.5 kn 时，4、6、8 三种大尺度比模型网的换算阻力值与实测阻力值偏差分别为 2.90%、9.93%、17.35%。（2）大尺度比变动对模型网换算的网口高度没有显著性影响（$P > 0.05$）。（3）试验网具的阻力系数随着雷诺数的增大而减小。

关键词：田内准则；大尺度比；修正公式；模型试验

Effects of large scale of Tauti’s law on model test

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Abstract： The model test of fishing gear is an important means to study the hydrodynamic performance, the law used in the test and its conversion relationship are the core issues of the model test. In this study, the mid-water trawl was used as the prototype net, and the Tauti’s laws was used as the model test law. Three model nets with different large-scale ratios (4, 6, 8) were designed and fabricated, and the tests were carried out in the tank of the East China Sea Fisheries Research Institute. Prototype nets are tested and data collected in the South China Sea. Use the Tauti’s correction law to correct the model test data, and compare the deviation between the model net of different scales before and after the correction and the experimental results of the actual physical net measured at sea. The results show that：(1) The converted resistance values of the three large-scale ratio model nets are all greater than the measured values of the physical net at sea; when the towing speed is 2.5 kn.

Key words: Tauti’s law; large scale ratio; correction formula; model test

基于 CFD 的养殖液舱内流场和固体污染物分布规律的研究

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摘要：水产养殖池内的流场特性可以直接影响养殖鱼类的行为和养殖池系统的自清洁性能，对福利化养殖至关重要。本研究关注了养殖工船系统中，养殖液舱内的水动力条件，并为提高养殖工船的养殖效能，设计了一种新型的养殖液舱结构——矩形单侧圆弧角养殖液舱。本研究基于数值模拟的方法，在数值模型验证的基础上，重点关注了液舱的几何结构和进水管到侧壁的水平距离对液舱内水动力参数的影响；并结合离散相模型（DPM），评估了流场特性对颗粒收集和排放规律的影响。研究表明，养殖液舱的几何结构和进水管的布设位置对液舱内的流场特征和固体颗粒的汇聚和排出规律都有很大影响。研究发现，1）较矩形液舱相比，矩形单侧圆弧角养殖液舱内的流场条件显著改善，其中η=0.2 和 0.3 的液舱更有利于均匀稳定流场的构建；2）将进水管适当的远离侧壁布设可以有效提高养殖系统的自清洁性能，其中δ=0.02－0.04 是进水管的优选布设区间。

关键词：循环水养殖系统（RAS）；水动力特性；自清洁性能；养殖液舱的结构；计算流体动力学（CFD）

Investigation of flow field and pollutant particle distribution in the aquaculture tank for fish farming based on computational fluid dynamics

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Abstract： Hydrodynamics is important for fish survival in the aquaculture tank systems, as it can directly affect the behaviour of farmed fish and the self-cleaning property of culture tank systems. The present study designs a new tank configuration, rectangular single-side arc angle tanks, to improve the performance of aquaculture vessels. The tank hydrodynamics was investigated by solving the Reynolds-Averaged Navier–Stokes (RANS) equations and combined with the discrete phase model (DPM) model to study particle motion. The velocity at the monitoring point and the discharge rate of particles from the tank were separately measured using Acoustic Doppler Velocimetry and the MATLAB image recognition method to validate the numerical model. We numerically tested the effect of culture tank configurations and the horizontal distance from the inlet pipe to the sidewall on hydrodynamics parameters, including velocity magnitude and uniformity, turbulence region and vortex distribution. Subsequently, to further understand the self-cleaning property of the culture tank systems for settleable particles, 300 cylindrical particles with a uniform size of 2.5 mm are tracked in the Lagrangian frame. Meanwhile, velocity distribution and pressure gradient have been employed to quantitatively evaluate the effects of hydrodynamics on the collection and discharge regularity of particles. Through CFD-assisted design verification, the tank configuration and the position of the inlet pipe layout have a considerable impact on the removal of particles from the tank and the energy to sustain the flow in the tank. Some key findings are found that 1) the hydrodynamics was improved significantly after rounding two right-angle edges in the rectangular culture tank, in which the configuration tanks of η=0.2 and η=0.3 could establish the strengthened rotational flow with better uniformity; 2) the inlet pipes proper far from the sidewall can enhance the self-cleaning property of the tank and the inlet pipe layout position of δ=0.02-0.04 is the preferred interval.

Key words: Recirculating aquaculture system (RAS); Hydrodynamics; Self-cleaning property; Tank configurations; Computational fluid dynamics (CFD)

展弦比对 P50-3 翼型网板水动力性能的数值模拟分析

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摘要：在拖网渔业中，网板是一种提高捕获效率的重要渔具，广泛应用于拖网渔船中。而对于翼型网板的水动力性能的数值研究有限。研究基于 NACA 翼型方程，针对 P50-3 翼型网板采用数值模拟方法研究了其水动力性能，分析了展弦比、冲角、网板周围流场分布等参数的影响。研究表明原尺寸网板的升力系数与升阻比呈先上升后下降的趋势，阻力系数随着冲角的变大持续上升，而展弦比λ=2.00 的网板在 22°时取得最大升力系数，表明临界冲角为 22°，在 5°时，升阻比取得最大值，最佳工作冲角为 15°。冲角在 40°时，该网板背部涡流完全分离。展弦比的增加，升阻比的最大值增加，而最大升力系数减小，临界冲角减小，失速提前发生。展弦比为 3.125 是 P50-3 翼型网板的最佳展弦比。研究结果将为竖式翼面型网板的结构设计和优化提供理论参考。

关键词：数值模拟；翼型网板；水动力特性；flume tank experiment；NACA 翼型

Numerical Simulation Analysis of Aspect Ratio on Hydrodynamic Performance of P50-3 Airfoil otter board

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Abstract： In trawling fishery, otter board is an important fishing gear to improve capture efficiency and is widely used in trawlers. The numerical study on the hydrodynamic performance of airfoil otter board is limited. Based on the NACA airfoil equation, the hydrodynamic performance of the P50-3 airfoil otter board was studied by numerical simulation method. The effects of aspect ratio, angle of attack and flow field distribution around the otter board were analyzed. The results show that the lift coefficient and lift-to-drag ratio of the original size otter board increase first and then decrease, and the drag coefficient continues to increase with the increase of the angle of attack. The otter board with aspect ratio λ = 2.00 achieves the maximum lift coefficient at 22 °, indicating that the critical angle of attack is 22 °.At 5 °, the lift-to-drag ratio reaches the maximum value, and the optimal working angle is 15 °. When the incidence angle is 40 °, the vortex in the back of the mesh plate is completely separated. With the increase of the aspect ratio, the maximum lift-drag ratio increases, the maximum lift coefficient decreases, the critical angle of attack decreases, and the stall occurs in advance. The aspect ratio of 3.125 is the best aspect ratio of P50-3 airfoil otter board. The research results will provide theoretical reference for the structural design and optimization of vertical wing type otter board.

Key words: Numerical simulation; airfoil net plate; hydrodynamic characteristics; flume tank experiment; NACA airfoil

仿生海鳗游动参数与鱼群互动关系的影响探究

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摘要：随着我国渔业现代化水平的逐步提升，对智能化渔业装备与设施提出了更高的要求。由于仿生机器鱼在养殖与捕捞中的环境共融性优势突出，研究通过建立仿生海鳗几何形态构造三维模型并优化其形态阻力；基于 Lighthill 理论建立仿生海鳗运动模型，利用数值模拟方法分析鳗鲡式游动行为不同摆动频率、摆动幅度下的水动力特性；最后通过野外水池实验，探究仿生海鳗不同摆动频率与摆动幅度下，其与鱼群间的互动与共融关系。结果表明：（1）基于 NACA 翼型模型的仿生海鳗具有明显的减阻机制，以降低作业功耗；（2）仿生海鳗体波$\lambda=0.7$时，具有较好的水动力特性；（3）仿生海鳗的游动参数是影响鱼群聚集与跟随的重要因素，且仿生海鳗体波$\lambda=0.7$时，能够最大化的吸引鱼群的聚集与跟随。研究为仿生海鳗的鱼群共融性控制提供了一定的基础，以提高目标鱼种的诱集，并为机器鱼在现代化、智能化渔业装备中的应用提供了新参考。

关键词：仿生海鳗；共融性；运动模型；数值模拟；诱集

Study on the influence of swimming parameters of biomimetic moray eel on interaction with fish

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Abstract: With the gradual improvement of China 's fishery modernization level, higher requirements are put forward for intelligent fishery equipment and facilities. Due to the prominent advantages of environmental communion of bionic robotic fish in breeding and fishing, the three-dimensional model of bionic eel geometry was established, and its morphological resistance was optimized. Based on Lighthill theory, the motion model of bionic sea eel was established, and the hydrodynamic characteristics of eel swimming behavior under different swing frequencies and swing amplitudes were analyzed by numerical simulation. Finally, through the field pool experiment, the interaction and communion relationship between the bionic eel and the fish group under different swing frequency and swing amplitude were explored. The results show that: (1) The bionic sea eel based on NACA airfoil model has obvious drag reduction mechanism to reduce operating power consumption. (2) When $\lambda = 0.7$, the bionic eel body wave has better hydrodynamic characteristics; (3) The swimming parameters of the bionic sea eel are important factors affecting the aggregation and following of the fish school, and when the bionic sea eel body wave $\lambda = 0.7$, the aggregation and following of the fish school can be maximized. The research provides a certain basis for the control of fish swarm communion of bionic eel, so as to improve the attraction of target fish species and provides a new reference for the application of robotic fish in modern and intelligent fishery equipment.

Key words: Biomimetic moray eel; Communion;Motion model; Numerical simulation; To trap

runx2b 基因在鱼类肌间刺形成过程中的作用

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摘要：为明确鱼类肌间刺形成的关键细胞群，我们首先利用单细胞转录组测序技术（scRNA-seq）明确了野生型斑马鱼肌肉组织（含肌间刺）的 18 个细胞 cluster，筛选到了与肌间刺形成相关的肌腱祖细胞 cluster，肌腱分化细胞 cluster，成熟肌腱细胞 cluster 和成骨细胞 cluster，单细胞拟时序分析结果表明肌间刺是由肌腱祖细胞分化为肌腱分化细胞，再分化为成骨细胞而形成的。根据基因在肌腱细胞分化为成骨细胞或成熟肌腱细胞轨迹上的表达模式，筛选了 10 个与肌间刺形成的关键基因，并在斑马鱼上运用 CRISPR-Cas9 基因编辑技术构建 10 个基因的突变体品系。最终，我们发现 runx2b 基因突变斑马鱼肌间刺完全缺失，且其他骨骼的形成、个体生长、肌肉脂肪酸和氨基酸组成成份等性状没有受到显著影响。

关键词：硬骨鱼；肌间刺；runx2b；scRNA

Single-cell transcriptomes and runx2b−/− mutants reveal the genetic signatures of intermuscular bone formation in zebrafish

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Abstract：Intermuscular bones (IBs) are mineralized spicules, present in the myosepta of many, but not all teleost species. IBs are often small and sharp, and they consequently limit how the fish can be processed, cause injury or trauma if lodged in consumers' throat or mouth and therefore affect the appeal of the fish to many consumers. The development of IBs in teleosts is still not fully understood and the molecular basis of IB development remains to be established. Here, the characteristics of IB tissue is evaluated based on single-cell transcriptomic in wild-type zebrafish. The analysis defined 18 distinct cell types. Differentiation trajectories showed that IBs are derived from tendons and that a core tendon-osteoblast cell lineage is related to IB formation. In particular, the functions of 10 candidate genes were evaluated via CRISPR-Cas9 mutants. Among those, runx2b−/− mutants completely lost IBs, while swimming performance, growth, and bone mineral density were not significantly different form runx2b+/+ zebrafish. Comparative scRNA-seq analysis in runx2b−/− and runx2b+/+ zebrafish revealed the role of osteoblasts in IB formation. In addition, differentially expressed genes were enriched in TGF-β/BMP pathway after runx2b deletion. This study provide evidence for a crucial role of runx2b regulation in IB formation. Genetic breeding can target runx2b regulation and generate strains of commercial fish species without IBs, which can improve the safe consumption and economic value of many farmed fish species.

Key words: teleosts; zebrafish; intermuscular bones; scRNA-seq; tendon-osteoblast cell lineage; runx2bge; netic breeding

红螯螯虾的性逆转相关基因筛选及验证

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摘要：红螯螯虾（*Cherax quadricarinatus*）同时存在多种类型的性逆转个体，是研究甲壳动物性逆转现象的理想模型。为研究红螯螯虾性逆转分子机制，课题组对红螯螯虾进行染色体水平基因组测序组装，获得基因组大小 5.23 Gb，共挂载 100 条染色体，重复序列高达 78.69%，注释 20,460 个编码基因；开展雌性与雄性的全基因组重测序，筛选性别相关分子标记；对比分析雌雄性腺与性逆转个体性腺的转录组数据，筛选得到 MAG（membrane-anchored AG-specific factor）显著差异表达，qRT-PCR 结果表明，随着红螯螯虾生长，MAG 与 IAG 的表达趋势相反，性腺组织免疫荧光结果表明 MAG 与 IAG 蛋白定位存在差异，酵母双杂交结果表明 MAG 与 IAG 无蛋白水平互作关系，通过 RNAi 技术下调 IAG 基因表达后，MAG 基因表达水平显著上调，下调 MAG 表达水平后，IAG 基因表达无变化。

关键词：性逆转；染色体水平基因组；性腺转录组；RNAi

Screening and functional verification of sex reversal related genes in Cherax quadricarinatus

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Abstract： Cherax quadricarinatus is an ideal model for studying the sex reversal mechanism in crustaceans due to its multiple sex composition. In order to study the molecular mechanism of sex reversal in Cherax quadricarinatus, the chromosome level genome was sequenced and assembled, a total of 5.23 Gb genome was obtained and anchored to 100 chromosomes, with 78.69% repeat sequences, and 20,460 coding genes were annotated. The whole genome resequencing of female and male was carried out to screen sex-related molecular markers. The transcriptome data of male female and intersex gonads were analyzed and screened, and MAG (membrane-anchored Ag-specific factor) showed significant differential expression. qRT-PCR analysis showed that the expression patterns of MAG and IAG during individual growth were opposite, and yeast two-hybrid proved that there was no protein level interaction between MAG and IAG. After knock down the expression of IAG gene by RNAi technology, the expression level of MAG gene was significantly up-regulated, while after knock down the expression of MAG gene, the expression level of IAG gene was unchanged.

Key words: Sex reversal; Chromosome level genome assembly; Gonadal transcriptome; RNAi

毛蚶 C1qdc2 基因的分子特征及免疫功能分析

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摘要：为探究 C1q domain-containing protein 2 基因（C1qdc2）在毛蚶免疫过程中所起的作用,利用 PCR 技术获得了毛蚶 C1qdc2 基因的 cDNA 序列，并完成序列分析和蛋白结构预测。采用实时定量 PCR 技术确定了 C1qdc2 基因在不同组织和弧菌刺激后的表达模式,结果显示，毛蚶 C1qdc2 基因在各组织中均有表达且明显表达差异(P<0.05 或 P<0.01),弧菌刺激后，毛蚶血细胞中 C1qdc2 基因的表达含量呈现出先升高后降低的趋势。敲降 C1qdc2 基因表达后, Vitellogenin、lysozyme、Dscam1、CD109、C1q2 显著或极显著下调表达, 而 C1q4、Complement C3、PPAF、C1qdc 的表达显著或极显著上调。结果表明, C1qdc2 基因与其它基因共同参与免疫调控，C1qdc2 基因在毛蚶的先天免疫防御中具有重要作用。

关键词：毛蚶; C1qdc2；分子特征；表达分析； RNA 干扰

Molecular Characteristics and Immune Function Analysis of C1qdc2 Gene in Scapharca subcrenata

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Abstract： To explore the role of C1q domain-containing protein 2 gene (C1qdc2) in the immune process of subcrenata subcrenata, the cDNA sequence of C1qdc2 gene of subcrenata subcrenata was obtained by PCR, and the sequence analysis and protein structure prediction were completed. Real-time quantitative PCR was used to determine the expression pattern of C1qdc2 gene in different tissues and after vibrio stimulation. The results showed that the expression of C1qdc2 gene in all tissues of Scapharca subcrenata was significantly different ($P<0.05$ or $P<0.01$). After vibrio stimulation, the expression of C1qdc2 gene in blood cells of Scapharca subcrenata increased at first and then decreased. The expression of Vitellogenin, lysozyme, Dscam1, CD109, C1q2 was significantly or extremely significantly down-regulated while the expression of C1q4, Complement C3, PPAF and C1qdc2 was significantly or extremely significantly up-regulated. The results showed that C1qdc2 gene and other genes were involved in immune regulation, and C1qdc2 gene played an important role in the innate immune defense of subcrenata subcrenata.

Key words: Scapharca subcrenata; C1qdc2; Molecular characteristics; Expression analysis; rnainterference

噁唑酰草胺对雌性黄鳝（Monopterus albus）下丘脑-垂体-性腺（HPG）轴的影响和轴上基因表达的改变对性逆转的可能影响

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摘要：噁唑酰草胺 (MET) 是一种广泛使用的除草剂，而目前 MET 对鱼类内分泌系统影响的研究有限。本研究将雌性黄鳝暴露在不同浓度 MET（0、0.2、0.4、0.6、0.8 mg/L）下 96 h 研究对黄鳝 HPG 轴和性逆转的影响。结果表明，高浓度的 MET 暴露会增加肝脏和血浆中的卵黄原蛋白水平，但血浆中的性激素水平不受 MET 暴露的影响。MET 暴露增加了脑中调控性激素生成基因（CYP19a1b，CYP17）的表达，但卵巢中与性激素分泌相关的基因（CYP19A1a、CYP17、FSHR、LHCGR、hsd11b2、3β-HSD）、性别调控基因 Dmrt1 和肝脏中雌激素受体基因（esr1、esr2a 和 esr2b) 的表达均被抑制。本研究首次揭示 MET 可能具有雌激素作用，对黄鳝的 HPG 轴基因的表达有抑制作用，MET 并不能促进黄鳝的性逆转，相反，黄鳝的雄性发生途径被抑制。

关键词：黄鳝；噁唑酰草胺；内分泌干扰；HPG 轴；性逆转

Effects of metamifop on the hypothalamic-pituitary-gonadal (HPG) axis of female rice field eels (Monopterus albus) and the possible effects of altered axis genes expression on sexual reversal

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Abstract： Metamifop (MET) is a widely used herbicide, but the research on the effect of MET on fish endocrine system is limited. In this study, female M. albus were exposed to different concentrations of MET (0, 0.2, 0.4, 0.6, 0.8mg/L) for 96h to study the effects on HPG axis and sex reversal of M. albus. The results showed that high concentrations of MET exposure increased the levels of vitellogenin in liver and plasma, but the levels of sex hormones in plasma were not affected by MET. The expression of genes (cyp19a1b, CYP17) regulating sex hormone production in the brain were increased, but genes (cyp19a1a, CYP17, FSHR, LHCGR, HSD11b2, 3β- HSD, Dmrt1) related to sex hormone secretion and sex regulatory in the ovary, estrogen receptor genes (esr1, esr2a and esr2b) in the liver were inhibited after MET exposure. This study revealed for the first time that MET may have estrogen effect and inhibit the expression of HPG axis genes in M。 albus. MET could not promote the sexual reversal of M. albus.

Key words: Monopterus albus; Metamifop; Endocrine disruption; HPG axis; Sexual reversal

脊尾白虾甲壳肽 Crustin2 基因的克隆、表达与功能研究

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摘要：为研究脊尾白虾(*Exopalaemon carinicauda*)甲壳肽 Crustin 的结构特征和功能，本研究从脊尾白虾中克隆得到一种新型甲壳肽 EcCrustin2 基因。研究结果表明 EcCrustin2 氨基酸序列具有典型的甲壳肽结构特征，包括 N 端的信号肽和 C 端的 WAP 结构域。系统发育分析结果显示 EcCrustin2 与 I 型甲壳肽聚集。组织表达结果显示 EcCrustin2 在血淋巴细胞中表达最高，通过 LPS、LTA、副溶血弧菌和金黄色葡萄球菌刺激后，EcCrustin2 的表达水平显著上调($p<0.05$)，在虾肝肠胞虫（EHP）感染脊尾白虾后也有诱导 EcCrustin2 表达的趋势。RNAi 结果显示，利用 siRNA 敲低 EcCrustin2 后，受副溶血弧菌攻击的虾死亡率上升。这些结果表明 EcCrustin2 参与了针对细菌和 EHP 感染的免疫反应。

关键词：抗菌肽；Crustin；脊尾白虾；基因表达

Characterization of a crustin-like peptide involved in shrimp immune response to bacterial and enterocytozoon hepatopenaei (EHP) infection in Exopalaemon carinicauda

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Abstract： Crustins represent one type of AMPs that are key components of the innate immune process of crustaceans. This study identified a novel crustin-like peptide, EcCrustin2, in *Exopalaemon carinicauda*. The deduced amino acid sequence of EcCrustin2 exhibited typical characteristics of crustins in crustacean, including one signal peptide at the N-terminus as well as a WAP domain at the C-terminus. Phylogenetic analysis revealed that the EcCrustin2 was first clustered with Type I crustins. Expression of EcCrustin2 was mainly detected in hemocytes, gill and stomach. The expression level of EcCrustin2 was also significantly up-regulated after being exposed to LPS, LTA, V. parahaemolyticus and S.aureus. EHP infection could also induce EcCrustin2 expression in E. carinicauda. Finally, knockdown of EcCrustin2 with siRNA increased the mortality of V. parahaemolyticus challenged shrimp. These results indicated that EcCrustin2 takes part in the immune response against bacteria and EHP infection.

Key words: Antimicrobial peptides; Crustin; Exopalaemon carinicauda; Gene expression

坛紫菜磷酸甘油酸激酶基因的克隆、表达及酶活性分析

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摘要：磷酸甘油酸激酶(*Phosphoglycerate kinase*，*PGK*)催化糖酵解，是生命体正常生理代谢的关键酶。为阐明 PGK 在潮间带海藻紫菜应答逆境中的调控作用，本研究通过全基因组筛查和 PCR 克隆的方法获得 2 条坛紫菜（*Neoporphyra haitanensis*）PGK 基因。其中，NhPGK1 序列全长 1355 bp,具有一个长度为 1251 bp 的基因开放阅读框，编码 416 个氨基酸；NhPGK2 序列全长 1538 bp，具有一个长度为 1374 bp 的基因开放阅读框，编码 457 个氨基酸。实时荧光定量 PCR(qRT-PCR)检测结果显示，2 条 NhPGK 基因均会受到高温及高光胁迫的显著诱导表达，基因表达模式基本一致，均呈现出上调表达。酶活及外源添加抑制剂测定结果进一步验证了 PGK 积极参与坛紫菜应答非生物胁迫的功能。综上所述，本研究为解析 PGK 调控紫菜适应潮间带环境中的能量代谢机制提供了理论参考。

关键词：紫菜；糖酵解；磷酸甘油酸激酶；非生物胁迫

Cloning , expression and enzyme activity analysis of the phosphoglycerate kinase gene from Neoporphyra haitanensis

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Abstract： *Phosphoglycerate kinase* (PGK) catalyzes glycolysis and is a key enzyme in the normal physiological metabolism of living organisms. In order to elucidate the regulatory role of PGK in the response to adversity in the intertidal seaweed *Neoporphyra haitanensis*, two PGK genes from *Neoporphyra haitanensis* were obtained by genome-wide screening and PCR cloning. The sequence of NhPGK1 was 1355 bp , with an open reading frame of 1251 bp, encoding 416 amino acids, and the sequence of NhPGK2 was 1538 bp , with an open reading frame of 1374 bp, encoding 457 amino acids. The results of quantitative real-time fluorescence PCR (qRT-PCR) showed that both NhPGK genes were significantly induced by high temperature and high light stress, and the gene expression patterns were basically the same, with both showing up-regulated expression. The results of enzyme activity and exogenous added inhibitor assays further validated the active participation of PGK in the response to abiotic stresses in *Neoporphyra haitanensis*. In conclusion, the present study provides a theoretical reference for resolving the mechanism of PGK regulation of energy metabolism in the adaptation of *Neoporphyra haitanensis* mays to intertidal environments.

Key words: Pyropia; glycolysis; phosphoglycerate kinase; abiotic stress

胶原蛋白解螺旋速率指标及相关因素的研究

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摘要：采用天狼星红法研究了牛、黑鱼、鲢鱼、鲈鱼、鳕鱼胶原蛋白的变性过程，定义了一种衡量胶原蛋白解螺旋速率的参数-K 值。通过 NCBI 数据库分析了各胶原蛋白 COL1A1 和 COL1A2 序列，分别比较了其亚基α1、α2 的氨基酸组成。研究发现，胶原蛋白的变性温度与 K 值大小、α1、α2 亚基氨基酸组成密切相关。从深海冷水鱼到陆地哺乳动物，胶原蛋白的变性温度逐渐上升，胶原蛋白变性过程中解螺旋的速率（K 值）逐渐下降，α1 和α2 中 Pro 的含量升高，相应地，Gly 和 Ser 的含量降低。K 值的提出，揭示了胶原蛋白解螺旋速率的差异，为胶原蛋白研究提供新的依据。

关键词：胶原蛋白；变性温度；天狼星红；解螺旋速率

Study on Collagen Unwinding Rate Index and Related Factors

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Abstract： The denaturation process of collagen in calf, snakehead, silver carp, bass and cod were studied using the Sirius Red method, and a parameter (K) to measure the rate of collagen unwinding was defined. The sequences of each collagen (COL1A1 and COL1A2) were analysed by the NCBI database, and the amino acid compositions of subunit α1 and α2 were compared. The study found that the denaturation temperature of collagen is closely related to the K value and the amino acid composition of α1 and α2 subunits. From deep-sea cold-water fish to terrestrial mammals, the denaturation temperature of collagen gradually increased, the rate of unwinding (K) during collagen denaturation gradually decreased, and the content of Pro in α1 and α2 increased. Correspondingly, the content of Gly and Ser decreased. The proposal of K revealed the difference of collagen unwinding rate and provided a new basis for collagen research.

Key words: collagen; denaturation temperature; Sirius Red; unwinding rate

乌苏里拟鲿 igf 基因克隆及其与生长性状关联分析

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摘要：本研究克隆了乌苏里拟鲿 igf1 和 igf2 基因序列，并分析了其多态位点与生长性状的关系。获得 igf1 基因全长 cDNA 1245 bp，其中开放阅读框（ORF）长 477 bp，编码 158 个氨基酸，igf1 基因部分 DNA 序列 10 922 bp，igf1 基因由 5 个外显子和 4 个内含子组成；获得 igf2 基因全长 cDNA 2008 bp，ORF 长 741 bp，编码 246 个氨基酸，igf2 基因 DNA 部分序列 3700 bp，igf2 基因由 4 个外显子和 3 个内含子组成。在 igf1 基因中共检测到 5 个 SNP 位点，其中 1 个位于外显子，4 个位于内含子；igf2 基因中共检测到 5 个 SNP 位点，其中 1 个位于外显子、4 个位于内含子。挑选 igf1 和 igf2 基因中位于外显子的 SNP 位点与 5 个生长性状进行了关联分析，但未检测到显著关联性。本研究所得结果将为乌苏里拟鲿 igf 基因的深入研究提供参考。

关键词：乌苏里拟鲿；igf1 基因；igf2 基因；单核苷酸多态性；生长；关联分析

Cloning and association analysis with growth traits of the igf gene in Pseudobagrus ussuriensis

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Abstract： In the present study, sequences of igf1 and igf2 genes were cloned for Pseudobagrus ussuriensis, and relationships between polymorphic sites of igf and growth traits were analyzed by association analysis. The cDNA length of the igf1 gene was 1245 bp, containing an open reading frame (ORF) of 477 bp which coding a peptide with 158 amino acids (aa), moreover, the DNA sequence of the igf1 gene with a length of 10 922 bp containing 5 exons and 4 introns was also obtained. The total cDNA length of the igf2 gene was 2008 bp with an ORF of 741 bp coding a peptide consisting 246 aa, and a 3700 bp DNA segment containing 5 exons and 4 introns was cloned. A total of five simple sequence polymorphism sites (SNPs) were identified in the igf1 gene with 1 in exon and 4 in introns. The number of identified SNPs in the igf2 gene was also 5 with 1 in exon and 4 in introns. The 2 SNPs in exons of igf1 and igf2 genes were selected and their associations with 5 growth traits were also analyzed, but no significant associations were detected. Nevertheless, the results obtained in this study will provide useful references for further studies of igf genes in P. ussuriensis.

Key words: Pseudobagrus ussuriensis; igf1 gene; igf2 gene; simple sequence polymorphism (SNP); growth; association analysis

三角帆蚌生长性状改良的基因组选择

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摘要：三角帆蚌是中国重要淡水珍珠养殖品种。目前，淡水珍珠养殖产业高产低值问题突出，研究重点已从提高产量转至提高珍珠品质。通过选择育种提高三角帆蚌的生长性能是提高珍珠品质的关键，基因组选择（GS）技术被认为是一种高效的选择育种方法。本研究对 764 只蚌(496 只为参考群体，268 只为育种群体)进行了基因测序（GBS）分型，共鉴定出 97090 个高质量 SNPs，基于全基因组 SNPs，三角帆蚌壳长、壳高、壳宽、壳重和体重的遗传力均属于中高等水平（0.36 ± 0.11 至 0.51 ± 0.10）。进一步，比较 5 种 GS 模型（GBLUP、BayesA、BayesB、BayesCπ和 BayesLASSO）和不同 SNP 数量（三种 SNP 筛选策略选择）对基因组估计育种值（GEBVs）预测能力（PA）的影响，建立了以 GBLUP 为 GS 模型，GWAS 为 SNP 筛选策略挑选 10000 个性状相关标记的最适 GS 方法，并应用于计算育种群体各个体的 GEBV 值。选择高生长 GEBVs 的个体作为快速生长群体（FS）的亲本，剩余群体作为对照群体（CS）亲本进行群体繁殖实验，结果表明，FS 的生长性能明显优于 CS，在武义和崇明两基地的养殖实验发现各生长性状分别提升了 5.74−28.77% 和 11.93%−54.58%。这些结果将有助于推进三角帆蚌 GS 技术的大规模商业化应用，并为其他水产养殖物种提供一种具有成本效益的 GS 策略。

关键词：基因组预测能力；生长性状；GBLUP；选择育种；三角帆蚌

Genomic selection for improvement of growth traits in triangle sail mussel (Hyriopsis cumingii)

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Abstract：The triangle sail mussel, Hyriopsis cumingii, is the most important aquaculture species for freshwater pearl production in China. However, one major problem of freshwater pearl mussel industry is the low profit despite high pearl yield, and the focus of current research has now switched from yield to the improvement of pearl quality. It is essential to enhance the quality of pearls by improving the growth performance of mussels and, to this end, genomic selection (GS) has been proved as a useful method for selective breeding. In the present study, 764 mussels (496 for reference population, 268 for selection candidates) were genotyped by sequencing (GBS) and a total of 97,090 single nucleotide polymorphisms (SNPs) were identified. Based on genome-wide SNPs, the heritability was estimated to be moderate to high for the following five growth traits: shell length, shell height, shell width, shell weight, and body weight (0.36 ± 0.11 to 0.51 ± 0.10). Then, the effects of five GS models (i.e., GBLUP, BayesA, BayesB, BayesCπ, and BayesLASSO) and different SNP numbers (selected using three SNP screening strategies) on the predictive ability (PA) of the genomic estimated breeding values (GEBVs) were compared. The GBLUP model containing 10,000 SNPs selected by GWAS strategy was established and was used to calculate GEBVs in selection candidates. The individuals with high GEBVs were then selected as broodstock for the fast-growth strain (FS), and the rest for control strains (CS). At last, encouraging results were detected that the FS performed significantly better than CS in terms of growth, with different traits increasing by 5.74−28.77% and 11.93%−54.58% at the WY and CM sites, respectively. These results may assist in the future large-scale commercial application of GS in H. cumingii and provide a cost-efficient GS strategy for other aquaculture species as well.

Key words: Genomic predictive ability; Growth trait; GBLUP; Selective breeding; Hyriopsis cumingii

mRNA-miRNA 的联合分析揭示了 miRNA 在急性氨氮胁迫下青蛤肝胰腺代谢中的调节作用

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摘要：在本研究中，对 miRNA mRNA 进行了综合分析，以揭示 miRNA 在急性氨氮暴露下青蛤代谢中的调节作用。以揭示 miRNA 在急性氨氮暴露下青蛤代谢中的调节作用。许多参与解毒和氨排泄的基因表达不同，表明氮的同化和利用被调整以适应氨暴露。青蛤必须改变其葡萄糖和脂质代谢以满足能量需求，以适应环境中的急性氨暴露。miRNA 可以通过调节急性氨氮胁迫期间靶基因的表达来调节青蛤的代谢，最终调整氮的同化和利用。

关键词：青蛤；代谢；miRNA； 分子应答；mRNA；氨氮

Combined analysis of mRNA–miRNA reveals the regulatory roles of miRNAs in the metabolism of clam Cyclina sinensis hepatopancreas during acute ammonia nitrogen stress

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Abstract： Integrated analysis of miRNA-mRNA was conducted to reveal the regulatory roles of miRNAs in the metabolism of C. sinensis exposed to acute ammonia nitrogen. Numerous genes involved in detoxification and ammonia excretion expressed differently indicate that nitrogen assimilation and utilization is adjusted to accommodate ammonia exposure. The clam has to alter their glucose and lipid metabolism to meet energy requirements to adapt acute ammonia exposure in the environment. Numerous mRNA–miRNA pairs were involved in metabolisms of carbohydrate, lipid and amino acid and miRNA can regulate the metabolism of C. sinensis by regulating the expression of target genes during acute ammonia nitrogen stress. The net result is that nitrogen assimilation and utilization is adjusted to accommodate ammonia exposure. The current study is helpful for further investigation into the ammonia nitrogen response mechanisms in mollusks.

Key words: clam; metabolism; miRNA; molecular response; mRNA; NH3

脊尾白虾精巢和卵巢差异转录组分析与验证

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摘要：脊尾白虾是我国重要的海水养殖虾类。雌性个体比雄性个体长得更快，因此挖掘脊尾白虾雌雄表达差异基因对于脊尾白虾育种具有重要意义。由于脊尾白虾基因组数据尚未发表，关于脊尾白虾雌雄差异表达信息相对匮乏。本研究中，我们通过对脊尾白虾尚未发育的精巢和卵巢进行了转录组测序，找到了20891个差异表达转录本，包括11709个上调表达的转录本和9182个下调表达转录本。同时我们也挖掘到可能与脊尾白虾精子发生和细胞周期相关的差异表达因子，并进一通过荧光定量PCR进行验证；通过GO富集和KEGG富集分析，我们找到了雌雄差异的前20个GOterm和KEGG富集在前20的通路；另外我们还获得了23个家族的表达因子，我们重点关注了foxj1b基因的表达，并且进一步通过原位杂交验证发现它可能跟脊尾白虾早期卵巢发育相关。

关键词：脊尾白虾；生殖；性腺；转录组；foxj1b

Comparative transcriptomic analysis and validation of the ovary and testis in the ridgetail white prawn (Exopalaemon carinicauda)

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Abstract： The ridgetail white prawn, Exopalaemon carinicauda is an important cultured seawater species in China. As female E.carinicauda grows faster than males, it is significant to search for the differentially expressed genes (DEGs) between males and females. However, there is no public available E.carinicauda genome data, and genes related to E. carinicauda sex differences are unclear. In this study, the transcriptome sequencing for ovary and testis tissues of E. carinicauda were conducted, and 20,891 DEGs were identified including 11,709 up-regulated DEGs and 9,182 downregulated DEGs. The functional categories related to meiosis and reproduction were enriched as well as the steroidogenesis KEGG pathway was clustered. Furthermore, the genes related to male reproduction and cell cycle were dug out which were verified by real-time PCR. In addition, two-color fluorescence in-situ hybridization result showed that foxj1b might play roles in ovary development during early stage. Therefore, our study provides clues for the study of reproductive-related gene function in E.carinicauda.

Key words: Exopalaemon carinicauda; reproduction; gonad; transcriptome; foxj1b

皮质醇对暗纹东方鲀原代肠上皮细胞氧化应激、细胞凋亡及脂代谢的影响

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摘要：为了探讨皮质醇对暗纹东方鲀原代肠上皮细胞氧化应激、细胞凋亡及脂代谢的影响，本研究利用了 qRT-PCR 检测氧化应激相关基因，细胞凋亡相关基因和脂代谢相关基因的表达情况，Annexin V-FITC/PI 测定凋亡指数，同时检测 TG、TC 和 NEFA 含量。结果显示：随皮质醇处理浓度的升高，氧化应激相关基因（SOD、CAT 和 GSH-Px）及促凋亡基因（Caspase-3、Caspase-7、Caspase-9、Bax 和 p53）表达量和凋亡指数均上升，抗凋亡基因 Bcl-2 表达量下降；脂肪合成相关基因（G6PD、6GPD、PPARγ、FAS 和 ACC）表达量下降，脂肪分解相关基因（HSL、PPARα、LPL 和 CPT-1）表达量上升；TG 和 TC 含量均降低，NEFA 含量升高。结果表明，皮质醇能够促进暗纹东方鲀原代肠上皮细胞的氧化应激和细胞凋亡，同时促进脂肪的分解并抑制脂肪的合成。

关键词：暗纹东方鲀；原代肠上皮细胞；皮质醇；细胞凋亡；脂代谢

Effects of cortisol on oxidative stress, apoptosis and lipid metabolism of primary cultured intestinal epithelial cells in Takifugu fasciatus

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Abstract： In order to investigate the effects of cortisol treatment on oxidative stress, apoptosis and lipid metabolism of primary cultured intestinal epithelial cells in Takifugu fasciatus, qRT-PCR was performed to detect the relative expression of oxidative stress-related genes, apoptosis-related genes and lipid metabolism-related genes, Annexin V-FITC/PI was performed to measure the apoptosis index, and the contents of TG, TC and NEFA were also measured. The results showed that, with the increase of cortisol treatment concentration, the expression of oxidative stress-related genes (SOD, CAT and GSH-Px), pro-apoptotic genes (Caspase-3, Caspase-7, Caspase-9, Bax and p53) and apoptotic index were increased, while the expression of anti-apoptotic gene Bcl-2 was decreased; the expression of lipid synthesis-related genes (G6PD, 6GPD, PPARγ, FAS and ACC) were decreased and lipolysis-related genes (HSL, PPARα, LPL and CPT-1) were increased; both TG and TC contents were decreased and NEFA content was increased. These results indicated that cortisol could promote oxidative stress, apoptosis, lipid decomposition and inhibit the lipid synthesis of intestinal epithelial cells in T. fasciatus.

Key words: Takifugu fasciatus; Intestinal epithelial cell; Cortical; Oxidative stress; Cell apoptosis

三角帆蚌基质蛋白基因 Hc-transgelin 的鉴定及其生物矿化功能解析

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摘要：三角帆蚌生物矿化是一个复杂的过程，受许多基质蛋白调控。本研究在三角帆蚌中发现了一个新的基质蛋白基因 Hc-transgelin。克隆得到 cDNA 全长为 1200 bp，包含 501 bp 的 ORF，编码 166 个氨基酸，包含一个保守的钙调蛋白同源结构域。荧光定量实验表明，Hc-transgelin 在外膜中表达量最高。原位杂交检测到 Hc-transgelin 在外套膜外褶边缘有阳性信号。RNA 干扰实验表明，当 Hc-transgelin 表达受到抑制时，珍珠层文石薄片的形状发生变化，晶体生长受到抑制，棱柱层有机鞘出现裂纹。壳层修复实验中，12 至 25 天珠层快速积累阶段 Hc-transgelin 表达量较高。这些结果表明，Hc-transgelin 可能参与了文石薄片的形成，并在贝壳棱柱层有机鞘的形成中发挥作用。本研究对 Hc-transgelin 的功能提供新的见解，有助于对贝壳形成研究提供分子依据。

关键词：三角帆蚌；生物矿化；基质蛋白；Hc-transgelin

Hc-transgelin is a novel matrix protein gene involved in the shell biomineralization of triangle sail mussel (Hyriopsis cumingii)

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Abstract： In Hyriopsis cumingii, shell biomineralization is a complicated process that involves multiple gene products. Shell matrix proteins are involved in the formation of the organic framework and play an important role in the regulation of calcium carbonate deposition. In this study, A new shell matrix protein gene Hc-transgelin was identified in H. cumingii. The full-length cDNA of Hc-transgelin was 1200 bp, including a 501 bp open reading frame, which encoded 166 amino acids. Hc-transgelin is rich in lysine, it accounts for 11.40% of the protein. The predicted transgelin protein contained a conserved calmodulin homologous domain. A tissue-specific expression assay indicated that Hc-transgelin exhibited significantly highest expression in the mantle. Furthermore, Hc-transgelin in situ hybridization detected positive signals at the edge of the mantle outer fold, where nacre and prismatic layer biomineralization occur. An RNA interference assay showed that the shape of aragonite flakes in nacre changed and their growth was inhibited, and cracks appeared in the prismatic layer organic sheath when the expression of Hc-transgelin was suppressed. In a shell repair assay, a higher expression of Hc-transgelin appeared from day 12 to day 25 when the nacre accumulated quickly. These findings indicate that Hc-transgelin may be involved in the formation of aragonite flakes in the nacre and play a role in the formation of the organic sheath in the prismatic layer of the shell. This study provides new insights into the role of the Hc-transgelin gene and also contributes to the molecular understanding of mollusk shell formation.

Key words: Hyriopsis cumingii; Biomineralization; Matrix protein; Hc-transgelin

暗纹东方鲀 HTR4 基因的分子特征及其生长相关 SNP 位点筛查

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摘要：为探究生长相关基因 5-羟色胺受体 4 在暗纹东方鲀中的分子结构、表达特征和功能。采用 RACE 技术克隆获得了暗纹东方鲀 HTR4 基因 cDNA 全长序列；分别分析了 HTR4 基因在暗纹东方鲀不同组织、卵巢 5 个不同发育时期的表达模式；同时筛查了 HTR4 编码区生长性状相关的 SNP 位点。暗纹东方鲀 HTR4 cDNA 全长 2302bp，开放阅读框长度为 1170bp，共编码 389 个氨基酸；氨基酸序列比对及系统进化树分析结果显示，暗纹东方鲀与红鳍东方鲀 HTR4 的一致性最高。荧光定量 PCR 结果表明 HTR4 基因在暗纹东方鲀 10 个不同组织中均有表达，在脑组织表达量最高，其次是中肠，在肌肉组织表达量最低；HTR4 基因在卵巢发育的 IV 时期 HTR4 表达量最高。通过测序筛选出一个同义突变 SNP 位点关联分析表明该位点与肥满度性状显著相关，该基因在暗纹东方鲀生长发育中发挥了重要作用，可为暗纹东方鲀生长性状新品种的选育提供分子标记。

关键词：暗纹东方鲀；5-羟色胺受体 4；基因克隆；单核苷酸多态性；生长性状

Molecular characterization of the HTR4 gene and screening of growth-related SNP loci in Takifugu fasciatus

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Abstract： In order to study the molecular structure, expression characteristics and function of the growth related gene—HTR4 in Takifugu fasciatus. The full-length cDNA sequence of HTR4 gene was cloned by RACE PCR technology, Quantitative real-time PCR technology was used to analyze the expression patterns of HTR4 in T. fasciatus different tissues and different developmental stages; Finally, Sanger sequencing was used to screen the SNP loci related to growth traits in the coding region of HTR4. The cDNA full-length sequence of HTR4 gene in largemouth bass was 2302 bp in lenfth, and a 1170 bp open reading frame encoding 389 amino acids， with 5 exons; The results of amino acid sequence alignment and phylogenetic tree analysis showed that the highest identity (99.53%) was found between T. fasciatus and Takifugu rubripes; the spatial structure of HTR4 protein showed that it was conserved in fish. The HTR4 gene was found expressed in ten different tissues. The expression level in brain tissue was the highest for T. fasciatus, then followed by midgut, and the lowest expression in muscle tissue; the HTR4 gene was expressed in five different developmental periods of the ovary, with the highest expression of HTR4 was found in the IV period of ovarian development. Screened by sequencing, a synonymous mutant SNP locus (c.1202 C>G) was found in exon 4 (+1202bp) of the HTR4 gene, and association analysis showed obvious correlated ($P < 0.05$) between the SNP loci and the trait of fatness in T. fasciatus， and individuals with CC genotype had higher fatness. The HTR4 gene plays an important role in the growth and development of T. fasciatus, which can be used as a candidate gene, and it can provide a basis for the molecular selection of new varieties of T. fasciatus for growth traits.

Key words: Takifugu fasciatus; 5-Hydroxytryptamine receptor 4; Gene cloning; Single nucleotide polymorphism; Growth traits

银鲳腹鳍发生相关基因 Hoxd9 调控作用的功能验证

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摘要：hoxd9 基因是 HOX 簇中起定位肢芽起始的关键基因，为研究银鲳 Hoxd9 基因与腹鳍缺失的关联性，本文采用 PCR 和 RACE 技术克隆了银鲳 hoxd9 基因的 cDNA 全长，利用体视显微镜和扫描电子显微镜对不同发育时期的银鲳进行形态学观察，并利用荧光原位杂交和免疫荧光技术在基因和蛋白层面分析了 Hoxd9 mRNA 和蛋白在不同发育时期的银鲳中的定位，最后利用 siRNA 敲降银鲳 hoxd9 基因，观察上下游基因的表达情况。结果表明：银鲳不同发育时期从胸鳍形成区到尾部的整个侧板中胚层均未出现细胞堆积未见腹鳍芽；银鲳 hoxd9 基因的 cDNA 全长为 1602bp ，但缺失 HOX 结构域；Hoxd9 mRNA 和蛋白均未在腹鳍形成区有明显的荧光信号；hoxd9 敲降后，Pitx1、Ffg8 及 Fgf10 表达量显著降低，综上所述，hoxd9 结构域的缺失导致蛋白翻译出现错误，从而在银鲳腹鳍定位阶段发生错误，导致腹鳍缺失。

关键词：银鲳；hoxd9 基因；结构域缺失；肢芽定位；进化；腹鳍缺失

Functional verification of the regulation function of Hoxd9 gene related to pelvic fin development in Pampus argenteus

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Abstract：The hoxd9 gene is a key gene in the HOX cluster for localizing limb bud initiation. To investigate the association between the Hoxd9 gene and ventral fin deficiency in Pampus argenteus, the full-length cDNA of the Pampus argenteus hoxd9 gene was cloned by PCR and RACE techniques, and morphological observations of silver pompano at different developmental stages were performed using stereomicroscopy and scanning electron microscopy. We also analyzed the localization of Hoxd9 mRNA and protein in Pampus argenteus at different developmental stages using fluorescence in situ hybridization and immunofluorescence techniques at the gene and protein levels, and finally knocked down the Pampus argenteus hoxd9 gene using siRNA to observe the expression of upstream and downstream genes. The results showed that the hoxd9 gene was 1602bp in length, but the HOX domain was missing in the hoxd9 gene. However, neither the mRNA nor the protein showed significant fluorescence signal in the ventral fin formation region; after hoxd9 knockdown, the expression of Pitx1, Ffg8 and Fgf10 were significantly reduced, In conclusion, the deletion of the hoxd9 structural domain led to errors in protein translation and thus in the ventral fin localization stage of Pampus argenteus, resulting in the absence of the ventral fin.

Key words: Pampus argenteus; hoxd9 gene; structural domain deletion; limb bud localization; evolution; ventral fin deletion

高碱度对虾鳃的影响：组织病理学改变和细胞特异性反应

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摘要：高碱度是影响水生动物在盐碱水环境生存的主要胁迫因子，然而关于甲壳动物鳃组织响应碱度胁迫的报道却很少。本研究首先评估了碱度胁迫对脊尾白虾体内稳态和鳃组织微观结构的影响，然后通过单细胞转录组测序（scRNA-seq）探讨了鳃细胞的异质性响应。结果表明，碱度胁迫下血淋巴渗透压和 pH 显著升高。与对照组相比，碱度胁迫后鳃柱细胞排列更对称，肾原细胞空泡更大。鳃组织 scRNA-seq 结果显示，碱度胁迫后柱细胞比例明显降低，肾原细胞比例明显增加。与离子转运，尤其是酸碱调节相关的差异表达基因，如 V(H+)- ATP 酶和碳酸酐酶，在支柱细胞中显著下调表达，而在肾原细胞中显著上调表达。此外，拟时分析表明，一些肾原细胞在碱度胁迫后开始行使离子转运功能。荧光原位杂交结果显示碱度胁迫后肾原细胞中碳酸酐酶的阳性信号明显增加。以上结果表明，虽然碱度胁迫抑制了鳃柱细胞的离子转运功能，但是肾原细胞在碱度适应中发挥了积极作用。

关键词：碱度胁迫；鳃；脊尾白虾；单细胞转录组测序；柱细胞；肾原细胞

Effect of high alkalinity on shrimp gills: histopathological alternations and cell specific responses

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Abstract: High alkalinity stress was considered as a major risk factor for aquatic animals surviving in saline-alkaline water. However, few information exists on the effects of alkalinity stress in crustacean species or how this stressor affects the gill. The present study evaluated the effect of alkalinity stress in Exopalaemon carinicauda to determine changes in homeostasis and gill microstructure, and explore the heterogeneity response of gill cells by single-cell RNA sequencing (scRNA-seq). It was shown that high alkalinity stress resulted in a remarkable increased in the hemolymph osmolality and pH. For the gills, the pillar cells showed more symmetrical arrangement and longer lateral flanges, and the nephrocytes showed larger vacuoles after alkalinity stress compared with the control group. ScRNA-seq results showed that alkalinity stress leaded to decreased proportion of pillar cells and increased proportion of nephrocytes significantly. The differentially expressed genes (DEGs) related to ion transport, especially acid-base regulation, such as V(H+)-ATPases and carbonic anhydrases, were down-regulated in pillar cells and up-regulated in nephrocytes. Furthermore, pseudotime analysis showed that some nephrocytes transformed to perform ion transport function in response to alkalinity exposure. Notedly, the positive signals of carbonic anhydrase were obviously observed in the nephrocytes after alkalinity stress. These results indicated that the alkalinity stress inhibited the ion transport function of pillar cells, but induced the active role of nephrocytes in alkalinity adaptation. Collectively, our results provided the new insight into the cellular and molecular mechanism behind the adverse effects of saline-alkaline water and the saline-alkaline adaption mechanism in crustaceans.

Key words: alkalinity stress; gills; Exopalaemon carinicauda; scRNA-seq; pillar cell; nephrocyte

氮磷营养调控坛紫菜品质及有机物释放的特征

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摘要：海水氮（N）、磷（P）日常和季节性的波动可引发藻类广泛的生理生化变化。本研究通过测定藻体DOM、POM释放量和生理生化指标，结合转录组和代谢组学，探讨了N、P营养调控重要经济海藻紫菜的品质机制及藻体释放有机物的特征。结果表明：N、P浓度的变化引起坛紫菜藻体内多种代谢协同调节，导致糖类、脂质和蛋白质等细胞成分重新分配。其中，高N、P培养下，藻体组织N、P含量增加，而C含量没有显著变化。进一步分析发现，坛紫菜主要通过增强氮代谢、卟啉代谢和氨基酸代谢提高叶绿素、藻胆蛋白和氨基酸含量；但高N促使更多的C骨架转移至氮代谢中用于合成更多的氨基酸，进而抑制藻体碳水化合物的积累。另一方面，高N、P环境促进藻体释放有机N、P，N、P限制促进藻体释放有机碳。本研究为深入解析坛紫菜品质的调控机制及其元素生物地球化学循环功能提供了新的思路。

关键词：坛紫菜；氮；磷；品质；有机物释放

Characteristics of nitrogen and phosphorus regulating the quality and organic matter release of Neoporphyra haitanensis

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Abstract: Daily and seasonal fluctuations of seawater nitrogen (N) and phosphorus (P) can trigger a wide range of physiological and biochemical changes in algae. In this study, we investigated the mechanisms of N and P nutrient regulation of the quality of the economically important seaweed Neoporphyra haitanensis and the characteristics of organic matter release from algae by measuring algal DOM and POM release and physiological and biochemical indicators, combined with transcriptome and metabolomics. On the one hand, the results showed that the changes in N and P concentrations caused a synergistic regulation of multiple metabolisms in N. haitanensis, resulting in the redistribution of cellular components such as sugars, lipids and proteins. The tissues N and P content increased under high N and P incubation, while the C content did not change significantly. Further analysis revealed that N. haitanensis increased chlorophyll, phycobiliprotein and amino acid content mainly by enhancing N metabolism, porphyrin metabolism and amino acid metabolism; however, high N prompted more C skeletons to be transferred to N metabolism for synthesizing more amino acids, which in turn inhibited the accumulation of carbohydrates. On the other hand, high N and P environment promotes the release of organic N and P, and N and P limitation promotes the release of organic C. This study provides new insight to deeply analyze the regulatory mechanism of the quality of N. haitanensis and its elemental biogeochemical cycle function.

Key words: Neoporphyra haitanensis; Nitrogen; Phosphorus; Quality; Release of organic matter

鲜味诱食剂对银鲳味觉刺激及食欲调节作用的研究

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摘要：银鲳（*Pampus argenteus*）是中国重要的经济水产物种，主要分布于东海北部与黄海南部。随着近几年银鲳养殖规模的突破，养殖过程中一些关键问题逐渐暴露出来。主要问题之一就是银鲳对商品饲料的适口性较差。海水鱼类对于鲜味氨基酸有较强的喜好，可将鲜味氨基酸类物质作为海水鱼诱食剂，并且在养殖过程中发现银鲳对海蜇（*Rhopilema esculentum*）具有强烈的嗜好。通过前期研究证明，银鲳对海蜇中的氨基酸存在嗅觉喜好，故推测以海蜇为代表的水母（*Scyphozoa*）中可能存在鲜味氨基酸吸引银鲳强烈的摄食行为。鉴于此，本论文首先利用石蜡切片及电镜观察对银鲳舌组织进行了研究。随后，从海蜇中筛选出了两种含量最高的鲜味氨基酸：L-谷氨酸和 L-天冬氨酸，以及两种已知能够增强鲜味的核苷酸：鸟嘌呤和次黄嘌呤，利用行为学统计筛选出最优浓度后两两组合形成四种复合物；在复合物最佳诱食浓度刺激下，对银鲳舌、肠道和大脑进行转录组测序，并进行 RT-qPCR 验证对其诱导银鲳鲜味传递及摄食生理机制进行初探。本论文探讨了银鲳摄食方式与其舌组织结构之间的关系，并对其在氨基酸和核苷酸复合物刺激下的行为学进行统计分析，筛选对银鲳具有强烈诱食能力的鲜味物质，对鲜味诱导下味觉系统和摄食相关基因的差异表达进行研究，为鱼类摄食机制提供理论数据，为后期高适口性饲料开发提供应用基础。

关键词：氨基酸；核苷酸；味蕾；鲜味受体；食欲因子

The effects of umami attractant on taste stimulation and appetite reaction in silver pomfret (Pampus agenteus)

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Abstract： According to the observation of the feeding behaviour of the silver pomfret (Pampus argenteus) when they were fed for the different kinds of fodders, two highest abundant umami amino acids were selected: L-glutamate and L-aspartate, and two nucleotides known to enhance umami: guanine and hypoxanthine, and behavioral statistics were used to select the second optimal concentration to form four complexeswe. In the behavioral study of four complex stimulation, the feeding effect was significantly different ($P < 0.05$) between GG (glutamate and guanine complex) and GI (glutamate and hypoxanthine complex), and compared with AG (aspartate and guanine complex) and AI (aspartate and hypoxanthine complex). Both GG and GI group were better than single amino acid stimulation and single nucleotide stimulation, but there was no significant difference. By transcriptome analysis of silver pompano tongue tissue under complex stimulation, we selected three genes(Sweet taste receptor A, Sweet taste receptor B and sensory perception of taste) associated with feeding.The RT-qPCR verification results found that all the three genes in each group were significantly upregulated ($P<0.05$) under complex stimulation, with the most significant GG group, followed by AI group. By transcriptome analysis of intestinal tissue under complex stimulation, an appetite-related feeding-promoting gene, ghrelin, was selected. Through quantitative verification, the Ghrelin genes in each group were up-regulated to varying degrees, including significantly in the GI group ($P<0.05$). By analysis of transcription of brain tissue under the stimulation of GI group, We screened out three genes(orexin receptor type 1, prepro-orexin precursor and POMC) related to appetite.The results of RT-qPCR found that both OXR1 and prepro-orexin were upregulated under GI group stimulation, in which prepro-orexin was significantly upregulated ($P<0.05$). Under stimulation, the POMC was significantly downregulated ($P<0.05$). Through these data, we recognized some effective compounds that could be supplied in silver pomfret diet, and the results improved our understanding of the mechanism of taste-related receptors regulating appetite in fish.

Key words: amino acid; nucleotide; taste buds; umami receptors; appetite factor

泥蚶低氧胁迫后血细胞转录组及耐低氧相关基因的筛选与分析

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摘要：泥蚶是一种比较特别的具有较强耐低氧能力的经济贝类，但目前其耐低氧分子调控机理尚不知。为探究泥蚶耐受低氧的分子调控机理，本研究对低氧胁迫下的泥蚶血细胞转录组中富集的信号通路及生物学过程进行分析，并初步筛选分析耐低氧基因。对低氧（DO=0.5mg/L）胁迫 6、24、72、120h 的泥蚶血细胞进行转录组测序（RNA-seq）并开展生物信息学分析，筛选出差异基因集，并用 qPCR 方法检测 DEGs 的表达量并与转录组比较。结果显示通路分析主要富集在胰岛素及胰腺分泌的信号通路、HIF-1 通路、钙信号相关通路和细胞凋亡相关通路。本研究推测胰腺分泌信号通路、钙信号通路及凋亡通路在泥蚶耐受低氧过程中发挥重要作用，与这些通路相关的 JUN、PIM-3、TRIM45、MR-1B、CCKR 在耐低氧过程中起到关键作用，可为以后贝类耐低氧的调控机理探究及耐低氧品系的分子选育提供参考。

关键词：泥蚶；耐低氧；血细胞；差异表达基因；转录组测序

Hemocyte transcriptome and Screening , analysis of genes related to hypoxia tolerance of Tegillarca granosa

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Abstract： Tegillarca granosa is a economic shellfish with strong hypoxic tolerance, but there is unclear on its molecular mechanism of hypoxic tolerance. To explore the molecular regulatory mechanism of its tolerance to hypoxia, in this study, the transcriptome and enriched signaling pathways and biological processes of T.gr Hemocytes under hypoxia stress were analyzed. and to screen hypoxia tolerance genes. The results showed pathway analysis was mainly enriched in Insulin and Pancreatic secretion signaling pathways, HIF-1 pathway, Calcium signaling pathway and Apoptosis pathway, This study speculated that the Pancreatic secretion signaling pathway, Calcium signaling pathway and Apoptosis pathway play a key role in the tolerance to hypoxia of hemocyte, JUN, PIM-3, TRIM45, MR-1B and and CCKR related to these pathways play a key role in the process of hypoxic tolerance, which can provide reference for the exploration of the regulation mechanism and molecular breeding strains of hypoxic tolerance.

Key words: Tegillarca granosa; hypoxia; Hemocyte; differentially expressed genes; RNA-seq

贝类低深度测序数据的基因型填充策略研究

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摘要：全基因组选择（GS）已成为水产领域加快群体遗传改良的主流方法，覆盖全基因组的高密度分子标记是实施 GS 的关键。全基因组重测序（WGS）能获得全基因组范围的遗传信息，但费用昂贵。近年来，低深度重测序与基因型填充的结合使低成本、高通量地获得全基因组范围内高密度的 SNPs 成为可能。然而，在海洋贝类中应用基因型填充的最优策略仍需进一步探索。本研究利用虾夷扇贝多群体来源的高深度测序数据构建了单倍型参考数据库，综合评估了群体大小、测序深度及最小等位基因频率等的影响，探究了贝类 lcGWS 数据的最优填充策略。发现测序深度达到 0.5x 时，即可获得接近全基因组水平的标记数目，且填充准确率可达 94.76%。提升位点置信度 GP 值可进一步提高填充准确率，并且使稀有等位基因的填充准确率也显著提升。本研究建立了针对贝类低深度重测序的基因型填充方法，可以为贝类经济性状的遗传解析及全基因组选择育种提供高通量低成本的分型策略。

关键词：海洋贝类；基因型填充；低深度全基因组测序

Assessment of genotype imputation performance on low coverage whole genome sequencing data for marine bivalves

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Abstract： Genomic selection (GS) has become the dominate methodology in breeding programs of the aquaculture species. The basic principle of GS is to predict the genomic breeding values of individuals for improved animal selection by the use of high-density single nucleotide polymorphisms (SNPs). Though WGS could provide the most comprehensive genotyping of the entire genome, it is not an ideal option for GS, because genotyping whole-genome SNPs still remain cost-prohibitive. In recent years, genotype imputation in cooperation with lcWGS is emerging as a cost-effective and high-throughput methods enabling screening variation across the entire genome. However, further exploration for the optimal genotype imputation strategy is still required for marine bivalves. In this study, high-coverage WGS data of Patinopecten yessoensis individuals from multiple populations were applied to construct the haplotype reference panel. To evaluate the imputation performance, we took several factors into accounts, including the reference population size, sequencing depth, minor allele frequency (MAF) and so on. The results indicated that 0.5× coverage can almost acquire the same number of SNPs as that of the whole genome level with high imputation accuracy (94.76%). In addition, the imputation accuracy can be further improved by increasing the imputation confidence (measured as GPs), and the accuracy for low and rare frequency variants (MAF < 0.1) can also be significantly improved. This study provided insight into the designing and executing of genotype imputation for lcWGS when applying in marine bivalves and offered high throughput and cost-efficient genotyping methods for genetic analysis of economic traits and implementation of GS in marine bivalves.

Key words: marine bivalves; genotype imputation; lc-WGS

酪氨酸酶基因的克隆和鉴定为研究青蛤黑色素沉积提供了新的思路

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摘要：开展青蛤良种选育是当前重要的研究课题。利用青蛤壳色进行良种选育时，其壳色性状是否能够稳定遗传成为当前亟需解决的问题。本研究发现酪氨酸酶基因在青蛤贝壳内黑色素的形成过程中起到重要调控作用。研究通过 RACE-PCR 技术克隆获得了青蛤 tyr 基因的全长 cDNA，序列分析得到青蛤 tyr 基因的全长 cDNA 长度为 2993 bp，包含 112 bp 5’非编码区、2262 bp 开放阅读框和 619 bp 3'-UTR。tyr 基因共编码 753 个氨基酸，包含了 6 个外显子和 5 个内含子，其编码多肽链中含有一个酪氨酸酶典型特征功能结构域，酪氨酸酶共同中心结构域（Common central domain of tyrosinase），且该功能结构域在软体动物和脊椎动物中均较为保守。利用邻接法和最大似然法的系统进化分析发现，青蛤与软体动物组中的文蛤进化地位最为接近。qRT-PCR 技术分析得出，tyr 基因的 mRNA 在青蛤外套膜外缘高表达，与外套膜外缘中较高的黑色素含量结果较为一致，表明青蛤 tyr 基因参与了体内黑色素的合成。此外，tyr 基因的 mRNA 在青蛤鳃中高表达，推测其可能通过鳃组织参与自身的免疫应答反应，该推测有待后续进一步实验验证。

关键词：青蛤；Tyr；黑壳；黑色素

Cloning and identification of tyrosinase gene provides a new idea for the study of melanin deposition in Cyclina sinensis

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Abstract： It is an important research topic to carry out the selection and breeding of the improved species of Cyclina sinensis. When using the shell color of C. sinensis for the breeding of improved varieties, whether the shell color can be stably inherited has become an urgent problem to be solved at present.This study found that tyrosinase gene plays an important regulatory role in the formation of melanin in clam shell.The full-length cDNA of tyr gene was cloned by RACE-PCR.The full-length cDNA of tyr gene is 2993 bp, including a 112 bp 5 ' untranslated region(UTR), a 2262 bp open reading frame and a 619 bp 3 ' -UTR.The tyr gene encodes 753 amino acids, including 6 exons and 5 introns, and the encoded polypeptide chain contains a typical functional domain of tyrosinase, common central domain of tyrosinase.The phylogenetic analysis using neighbor-joining method and maximum likelihood method found that the evolutionary position of C. sinensis and Meretrix meretrix is the closest.The results of qRT-PCR showed that the mRNA of tyr gene was highly expressed in the outer edge of the mantle, which was consistent with the high melanin content in the outer edge of the mantle, indicating that the tyr gene was involved in the synthesis of melanin in the body.In addition, the mRNA of tyr gene was highly expressed in C. sinensis gills, suggesting that it may participate in the immune response through the gill tissue, which needs further experimental verification.

Key words: Cyclina sinensis; black shell; melanin; tyrosinase

盐胁迫下脯氨酸对缢蛏渗透调节的影响

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摘要：本文探究了高盐条件下缢蛏组织损伤程度及其脯氨酸对缢蛏渗透调节的影响。本研究将缢蛏置于高盐条件下进行 72 h 的胁迫实验。结果表明，高盐条件下缢蛏鳃组织和肝胰腺组织损坏严重于对照组，在 72h 其组织出现空泡化现象，形态排列不规则。同时检测高盐下缢蛏体内脯氨酸、牛磺酸、丙氨酸含量，对比发现高盐条件下三个渗透调节有机物含量明显高于对照组，且脯氨酸变化差异性最显著($P＜0.05$)。通过添加不同外源氨基酸（脯氨酸、牛磺酸、丙氨酸）检测不同时间点（0h，6h，12h，24h，48h，72h）缢蛏血清渗透压，结果表明添加外源脯氨酸条件下缢蛏血清渗透压与外界环境渗透压值更加接近。研究表明：脯氨酸对缢蛏在高盐条件下进行渗透调节有重要作用，可以有效帮助缢蛏调节渗透压平衡。本研究为进一步探究脯氨酸对缢蛏渗透调节的作用机制提供了理论参考。

关键词：缢蛏；高盐；脯氨酸；渗透调节；

Effect of proline on osmoregulation of Sinonovacula constricta under salt stress

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Abstract：In this paper, the degrees of tissue injury and the effects of proline on osmoregulation of razor clam Sinonovacula constricta under high salt were studied. Razor clam was exposed to high salt for 72 hours in this study. The results showed that under the high salt conditions , the damage of Gill tissue and hepatopancreas tissue was more serious than that in the control group. The tissue showed vacuolation and irregular morphological arrangement at 72 h. At the same time, the contents of proline, taurine and alanine in razor clam under high salinity were detected, respectively, significantly higher than those in the control group, and the change of proline was the most significant ($P < 0.05$). The serum osmotic pressure of razor clam was detected by adding different exogenous amino acids (proline, taurine and alanine) at different time points (0h, 6h, 12h, 12h, 48h, 72 h). The results showed that the serum osmotic pressure was closer to that of the external environment under the condition of adding exogenous proline. This study indicated that proline plays an important role in osmoregulation of razor clam under the high salt conditions and can effectively help razor clam adjust osmotic pressures balance. This study provides a theoretical reference for further exploring the mechanism of proline on osmoregulation of razor clam.

Key words: Sinonovacula contricta; high salinity; proline; osmoregulation

三角帆蚌谷胱甘肽硫转移酶 P1 基因克隆表达及对类胡萝卜素代谢的影响分析

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摘要：类胡萝卜素是重要的天然色素，谷胱甘肽硫转移酶 P1 是一种类胡萝卜素结合蛋白，在类胡萝卜素转运中发挥重要功能。为明确 HcGSTP1 在类胡萝卜素代谢中的功能，并探究该基因与三角帆蚌贝壳呈色的相关性，本实验对 HcGSTP1 进行了克隆、组织表达、原位杂交及干扰实验。结果表明 HcGSTP1 对三角帆蚌类胡萝卜素代谢有着重要的作用，为深入研究三角帆蚌类胡萝卜素代谢与贝壳和珍珠颜色形成机制提供了理论基础。

关键词：三角帆蚌；GSTP1 基因；类胡萝卜素代谢

Cloning and expression of glutathione sulfur transferase P1 gene in Hyriopsis cumingii and its effect on carotenoid metabolism

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Abstract： Carotenoids are important natural pigments. Previous studies have found that carotenoid metabolism is significantly correlated with shell color. Glutathione sulfur transferase P1, a carotenoid binding protein, plays an important role in carotenoid transport. In order to clarify the function of HcGSTP1 gene in carotenoid metabolism and explore the correlation between this gene and shell color, the total length of hyriopsis cumingii HcGSTP1 cDNA was cloned and identified, including 618bp ORF region, encoding 205 amino acids. It contains a GST-N-pi domain and a GST-C-Pi domain. The expression of HcGSTP1 gene in tissues of white and purple mussels was significantly higher than that in tissues of white mussels($P< 0.05$). In situ hybridization showed obvious positive signals of the gene in the outer fold, dorsal membrane region, peritoneal region, the junction between outer fold and middle fold, and part of middle fold of the mantle. After dsRNA interference chain injection, the expression of HcGSTP1 gene in the mantle significantly decreased, the interference rate reached 83.74%, and the TCC in the mantle decreased by 30.12% ($P<0.05$). Our results indicate that HcGSTP1 gene plays an important role in carotenoid metabolism in H. cumingii, which provides a theoretical basis for further study of carotenoid metabolism and the mechanism of shell and pearl color formation in H. cumingii.

Key words: Hyriopsis cumingii; GSTP1 gene; Carotenoid metabolism

黑鲷冷诱导 RNA 结合蛋白的基因克隆及其功能研究

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摘要：近年来，黑鲷在中国的水产养殖业中越来越受欢迎。然而，在遗传育种过程中产生的不耐低温和自然越冬期的低存活率是限制商业养殖发展的主要问题，其中的黑鲷低温响应机制仍是未知。冷诱导 RNA 结合蛋白（CIRBP）是在低温环境下生物机体响应的标志基因，但关于它在鱼类低温反应机制中的分子特征、表达和功能的信息很少。本研究成功地从黑鲷中克隆出 cirbp 基因的 cDNA 全长序列（1552bp），分别编码 182 个氨基酸的多肽。荧光实时定量 PCR 表明: cirbp 基因在黑鲷的肝脏中表达量最高，在冷应激和冷驯化条件下有不同的调控模式。RNA 干扰结果显示: 抑制黑鲷肝脏中 cirbp 基因的表达会导致黑鲷的肝脏在低温下的组织结构损伤和细胞凋亡现象加重。在细胞凋亡相关基因的研究中发现 cirbp 通过线粒体凋亡途径在低温下黑鲷的肝脏细胞凋亡中发挥重要作用。

关键词：黑鲷；cirbp 基因；基因克隆；RNA 干扰；低温胁迫；细胞凋亡

Identification and functional characterization of Cold-inducible RNA-binding protein gene in Acanthopagrus schlegelii

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Abstract： Black porgy has become more popular for aquaculture production in China in recent years. However, the low temperature intolerance that has resulted from the process of genetic breeding and low survival rate during that the natural overwintering period are the main problems limiting the development of commercial culture. The low temperature response mechanism is still not understood. Cold-induced RNA binding protein (CIRBP) plays a critical role in the maintenance of apoptosis. However, little information is available about its molecular characteristics, expression and function in low temperature response mechanism of fish. In this study, the complete cDNA sequences (1552 bp) of cirbp was successfully isolated from black porgy, encoding polypeptides of 182 amino acids respectively. Quantitative real-time PCR demonstrated that cirbp mRNA expression is high in the liver of black porgy and showed different regulatory modes under cold stress and cold acclimation. RNA interference results showed that inhibition of cirbp gene expression in liver of black porgy significantly affected the tissue structure and apoptosis in the liver of black porgy under low temperature. Results suggest that cirbp plays an important role in apoptosis of black porgy through the mitochondrial apoptosis pathway.

Key words: Acanthopagrus schlegelii; cirbp gene; Gene cloning; RNA interference; Low temperature stress; Apoptosis

银鲳野生群体和不同世代养殖群体的遗传多样性分析

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摘要：种内遗传多样性的丰富度对物种的生存至关重要，一个物种的遗传多样性越高即对外界遗传变化的潜在适应性就越强。本研究对银鲳的基因组数据开发验证了大量高度多态性的微卫星标记，并选择线粒体基因（CO1、Cytb、D-Loop、ND1）与微卫星标记作为分子标记，对野生银鲳群体以及不同世代的养殖银鲳群体(亲本、F1 代、F2 代)进行遗传多样性分析，以期为银鲳的种质资源评价与保护、资源的可持续发展与利用以及优良品种选育、商业化扩繁等提供基础资料。结果表明，（1）四个银鲳种群均具有较高的遗传变异；（2）共筛选出 15 对多态性高的微卫星引物，并基于其对银鲳种群的遗传多样性分析的结果还显示养殖银鲳种群并未出现种质退化现象。综上所述，本研究的分析结果说明目前银鲳养殖群体的养殖环境良好，其种苗来自遗传多样性丰富的亲鱼，养殖过程中尚未出现明显的近交衰退。同时，也意味着银鲳的养殖群体目前有着较强的环境适应能力、生长能力。

关键词：银鲳；遗传多样性；分子标记；微卫星开发

Genetic diversity analysis of wild and cultured Pampus argenteus populations

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Abstract： The richness of intra species genetic diversity is crucial to the survival of species. The higher the genetic diversity of a species, the stronger its potential adaptability to external genetic changes. In this study, a large number of highly polymorphic microsatellite markers were developed and verified based on the genomic data of Pampus argenteus , and mitochondrial genes (CO1, cytb, D-loop, ND1) and microsatellite markers were selected as molecular markers to analyze the genetic diversity of wild Pampus argenteus population and cultured Pampus argenteus populations of different generations (parents, F1 generation and F2 generation) in order to provide information for the evaluation and protection of germplasm resources of Pampus argenteus It provides basic information for sustainable development and utilization of resources, selection and breeding of excellent varieties, and commercial expansion. The results showed that: (1) the four populations of Pampus argenteus had high genetic variation; (2) A total of 15 pairs of microsatellite primers with high polymorphism were screened out, and the results of genetic diversity analysis on Pampus argenteus population also showed that there was no germplasm degradation in cultured Pampus argenteus population. To sum up, the analysis results of this study show that the breeding environment of Pampus argenteus breeding population is good at present, and its seedlings are from parents with rich genetic diversity. There has not been obvious inbreeding decline in the breeding process. At the same time, it also means that the breeding population of Pampus argenteus has strong environmental adaptability, growth ability and evolutionary potential.

Key words: Pampus argenteus, genetic diversity, molecular markers, microsatellite development

瓦氏雅罗鱼 *slc26* 基因家族的鉴定、表达与进化分析

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摘要：为探究瓦氏雅罗鱼 *slc26* 基因家族在 Cl^-、HCO_3^-等阴离子转运的作用机制，本研究基于瓦氏雅罗鱼基因组及转录组数据，结合生物信息学方法对 *slc26* 家族进行了基因鉴定、表达及进化分析。利用同源比对的方法，从瓦氏雅罗鱼基因组中共鉴定到 10 个 slc26 基因家族成员，分布在瓦氏雅罗鱼的 6 条染色体上，分别命名为 *slc26a1*、*slc26a2*、*slc26a3.1*、*slc26a3.2*、*slc26a4*、*slc26a5*、*slc26a6*、*slc26a6l*、*slc26a10 和 slc26a611*。系统发育和模体分析显示，*slc26a3.1*、*slc26a3.2* 和 *slc26a4* 同源性较高，*slc26a5*、*slc26a6* 和 *slc26a6l* 同源性较高，slc26a1、slc26a2 和 slc26a10 同源性较高，而 slc26a11 与其他 9 个基因的同源性相对较低，单独聚类；RNA-seq 和实时荧光定量分析显示，$NaHCO_3$ 碱度胁迫下瓦氏雅罗鱼 slc26 家族不同成员呈现出一定的组织表达特异性，即 *slc26a3.1*、*slc26a3.2* 和 *slc26a4* 在肠组织高表达，*slc26a5*、*slc26a6* 和 *slc26a6l* 在鳃和脑组织高表达，*slc26a1*、*slc26a10* 和 *slc26a11* 在肾组织高表达，*slc26a2* 在肝脏高表达，亲缘关系与表达结果基本一致。基于基因组重测序数据，统计了 slc26 基因在瓦氏雅罗鱼碱水种群（23 尾）和淡水种群（15 尾）的 SNPs 位点，基于 Fst top 10%，筛选出 12 个共享的潜在候选 SNPs，进一步基因型性状关联分析鉴定出 5 个 SNPs 位点在碱水种群和淡水种群存在显著的遗传分化($P<0.05$)。本研究结果将为瓦氏雅罗鱼酸碱调控机制的深入解析提供一定的科学依据。

关键词：瓦氏雅罗鱼；盐碱水；slc26 基因家族；离子转运；适应性进化

Identification, evolution and expression pattern of slc26 gene family in Leuciscus waleckii

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Abstract：To investigate the mechanism of the role of the *slc26* gene family in the transport of anions such as Cl- and HCO_3^- in Leuciscus waleckii, based on the genome and transcriptome data of expression and evolution analysis. A total of 10 members of the slc26 gene family were identified from the genome of L. waleckii, which were distributed on 6 chromosomes. Phylogenetic and modal analyses showed that *slc26a3.1, slc26a3.2* and *slc26a*4 were highly expressed in intestinal tissues, *slc26a5, slc26a6* and slc26a6l were highly expressed in gill and brain tissues, *slc26a1*, *slc26a10* and *slc26a11* were highly expressed in kidney tissues, slc26a2 was highly expressed in liver, and the affinities were generally consistent with the expression results. Based on the genome resequencing data, the SNPs loci for the slc26 gene were counted in the alkaline (23) and freshwater (15) populations of L. waleckii, and 12 shared potential candidate SNPs were screened based on the Fst top 10%, the further genotypic trait association analysis identified five SNPs loci with significant genetic differentiation in the alkaline and freshwater populations ($P< 0.05$). The results of this study will provide some scientific basis for the in-depth analysis of the acid-base regulatory mechanism in L. waleckii.

Key words: Leuciscus waleckii; alkali-saline water; slc26 gene family; ion transport; adaptive evolution

基于线粒体自噬研究纳米铜和硫酸铜对中华绒螯蟹肝胰腺的影响

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摘要：为探究中华绒螯蟹（*Eriocheir Sinensis*）在纳米铜和硫酸铜暴露下肝胰腺线粒体的自噬机制。本研究通过组织病理学观察，ROS 含量检测、线粒体膜电位（MMP）和氧化应激酶活测定，同时运用荧光定量 PCR 和免疫印迹等方法，系统检测中华绒螯蟹肝胰腺氧化应激水平、线粒体自噬程度及自噬相关基因和蛋白的表达变化。研究结果发现，50μg/L 硫酸铜组和 10μg/L 纳米铜组肝小管扩张出现空泡化现象，500μg/L 硫酸铜组肝小管大量解体，肝小管间隙和管腔中可观察到破碎的组织。500μg/L 硫酸铜组 SOD 活性显著抑制，CAT，GSH-Px 活性显著上升，MDA 含量显著上升，ROS 升高，MMP 去极化，线粒体受损。暴露 21 天后，线粒体自噬因子 BNIP3L 表达随浓度升高而上升，诱发细胞凋亡。结果表明，铜暴露诱导中华绒螯蟹肝胰腺过氧化并产生组织病变，ROS 富集导致线粒体损伤，激活 BNIP3L 介导的线粒体自噬通路。

关键词：中华绒螯蟹；纳米铜；硫酸铜；氧化应激；线粒体自噬

Effects of nano-copper and copper sulfate on the hepatopancreas of Eriocheir Sinensis based on mitophagy

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Abstract：In order to explore the mitophagy of hepatopancreatic mitochondria in *Eriocheir Sinensis* under the exposure of nano-copper and copper sulfate. In this study, histopathological observation, ROS content detection, mitochondrial membrane potential (MMP) assay, oxidative stress kinase activity measurement, real-time quantitative PCR and Western blotting and other technical methods were used to systematically detected the level of oxidative stress, the degree of mitophagy and the expression changes of autophagy-related genes and proteins in the hepatopancreas of Eriocheir Sinensis. The results of the study found that 50 μg/L copper sulfate group and 10 μg/L nano-copper group showed vacuolation in the dilation of hepatic tubules, massive disintegration of hepatic tubules in 500μg/L copper sulfate group and broken tissues were observed in the hepatic tubule space and lumen. The SOD activity was significantly inhibited ($P<0.05$), CAT and GSH-Px activities were significantly increased ($P<0.05$), MDA content was significantly increased ($P<0.05$), ROS increased, MMP depolarized, and mitochondria were damaged in the 500μg/L copper sulfate group. After 21 days of exposure, the expression of mitophagy factor BNIP3L increased with increasing concentrations, and induced apoptosis. The results showed that copper exposure induced peroxidation and tissue lesions in the hepatopancreas of Eriocheir sinensis, and ROS enrichment led to mitochondrial damage and activation of BNIP3L-mediated mitophagy pathway.

Key words: Eriocheir Sinensis; nano-copper; copper sulfate; oxidative stress; mitophagy

银鲳侧囊组织结构发育及其关键调控基因筛选研究

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摘要：为探究银鲳特殊消化道结构侧囊的组织结构特征，发育过程及其关键调控基因，本研究通过光镜和电镜技术对其形态结构进行观察及发育时期划分。结果显示，侧囊由粘膜、粘膜下层、肌层和浆膜组成。囊内的乳突结构中紧密排列的胶原纤维层包裹多孔内腔，腔内富含脂肪细胞。放射状基底由几丁质和胶原纤维构成。结合 1~60dph 侧囊发育过程形态学及组织学变化特点，将发育时期分为原基形成期（3~5dph），快速发育期（20~25dph），成熟前期(40~45dph)，成熟后期(50~60dph)四个时期。通过 1，6，20，40 和 60dph 的侧囊进行转录组分析，获得 26345 个差异基因。通路注释结果显示发育早期富集到蛋白质消化和吸收，细胞粘附等相关通路。发育后期富集补体和凝血级联，I 型糖尿病，EB 病毒等疾病相关通路，推测侧囊可能在免疫方面发挥作用。综上，本研究明确了侧囊结构特征及发育过程，也为侧囊发育机制研究奠定基础。

关键词：银鲳；侧囊；结构；发育；转录组

Morphology, histological structure characteristics and comparative transcriptome studies on pharyngeal sac development in farmed silvery pomfret (Pampus argenteus)

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Abstract： To study the structural characteristics, development process and key regulatory genes of pharyngeal sac Pampus argenteus, we used light and electron microscopy techniques to investigate the morphological and histological structures. The results showed that the pharyngeal sac was composed of mucosa, submucosa, muscularis and serosa. The porous cavity of papillaes were filled with fat cells and wraped tightly arranged collagen fibers. Stellate bases were composed of chitin and collagen fibers. The development stage was divided into four stages: primordium formation stage (3~5dph), rapid development stage (20~25dph), early maturity stage (40~45dph), and late maturity stage (50~60dph).
1, 6, 20, 40 and 60 dph of pharyngeal sac transcriptomes and 26345 differential genes were obtained. Pathway annotation results showed that protein digestion and absorption, cell adhesion molecules and other related pathways were enriched in early development. Meanwhile, complement and coagulation cascades, type I diabetes mellitus and Epstein−Barr virus infection were enriched, indicated that pharyngeal sac may play a role in immune function. In conclusion, this study clarified the structural characteristics and development process of pharyngeal sac, and offered a substantial contribution to the the gene expression during pharyngeal sac development.

Key words: Pampus argenteus; pharyngeal sac; structural characteristic; development; transcriptome

七彩神仙鱼催乳素受体基因的克隆及在亲代抚育行为中的表达

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摘要：催乳素(PRL)在调节哺乳动物亲代抚育行为中发挥重要作用，但在鱼类中相关报道较少。七彩神仙鱼可以利用表皮黏膜分泌粘液来喂养孵化出膜的子代，然而目前对七彩神仙鱼催乳素在其亲代抚育行为的功能研究较少。本文采用生物信息学技术鉴定分析了七彩神仙鱼PRLR(SaPRLR)分子的结构和进化关系，利用转录组学分析了该分子在抚育期间的表达模式。七彩神仙鱼中3种催乳素受体基因亚型为SaPRLR1、SaPRLR2和SaPRLR3；SaPRLR2与高等动物具有较高一致性，SaPRLR1/SaPRLR2与低等动物具有较高一致性。SaPRLR2基因全长克隆和其在成体组织中的mRNA表达结果显示，SaPRLR2在肾脏、鳃和肠等渗透调节组织中的存在与已知PRL在硬骨鱼中介导水盐平衡的作用相一致。再者，与非繁殖期鱼相比，繁殖期鱼皮肤中PRLR mRNA表达水平上调，表明PRL激素信号可能在亲代抚育过程中促进粘液生产。

关键词：七彩神仙鱼；催乳素；亲代抚育

Cloning of prolactin receptor gene and its expression in parental care of discus fish(Symphysodon aequifasciata)

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Abstract： Prolactin (PRL) plays an important role in the regulation of parental care behavior in mammals, but there are few related reports in fish. Discus fish (Symphysodon aequifasciata) can use the epidermal mucosa to secrete mucus to feed the hatched membrane offspring. However, there are few studies on the function of PRL in the parental care behavior of discus fish. In this study, the structure and evolutionary relationship of PRLR(SaPRLR) molecule were identified and analyzed by bioinformatics technique, and the expression pattern of SaPRLR molecule during rearing was analyzed by transcriptomics. SaPRLR1, SaPRLR2 and SaPRLR3 were three PRL receptor gene subtypes in discus fish. SaPRLR2 presented a high consistency with higher animals, and SaPRLR1/SaPRLR2 presented a high consistency with lower animals. The full-length cloning of SaPRLR2 gene and its mRNA expression in adult tissues showed that SaPRLR2's presence in osmoregulatory tissues such as kidney, gills and intestine was consistent with the known role of PRL in mediating water-salt balance in teleost fish. Furthermore, PRLR mRNA expression levels were upregulated in the skin of breeding discus compared with non-breeding fish, suggesting that PRL hormone signaling might promote mucus production during parental care.

Key words: Discus fish; Prolactin; Parental care

不同光周期处理对银鲳性腺发育的影响

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摘要：为了探究光周期对银鲳性腺发育的影响，于 2021 年 3 月对其进行光周期处理实验。实验设三组光周期，处理 60 天。结果显示雌性在长光周期诱导下具有较高的 GSI 和 HSI，卵巢成熟度更好，实验结束时雌激素（E2）处于高水平，LH 和 E2 以及 MT 的变化趋势一致，基因 foxl2、cyp19a1、kiss、gpr54、gnrh2 和 fsh 以及 lh 在长光周期处理下表达量更高。雄性在对照组光周期条件下具有较高的 GSI 和 HSI，精巢成熟度更好，实验结束时雄激素（T）、芳香化酶、MT 和 Kisspeptin 处于高水平且显著高于其他两组，基因 sox9a 和 gnrh3 在对照组中表达量更高。其中 foxl2、cyp19a1、gpr54、gnrh2、fsh 和 lh 在雌性中高表达，雄性中低表达。综合而言，延长光周期有利于银鲳的卵巢发育和成熟，精巢的发育与成熟在对照组光周期条件下更有优势。

关键词：光周期；银鲳；性腺发育；性类固醇激素；基因表达

Effects of different photoperiod treatments on gonad development of silver pomfret (Pampus argenteus)

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Abstract：In order to explore the effect of photoperiod on gonad development of silver pomfret.Three sets of photoperiods were set up in the experiment. After 60 days of treatment. The results showed that females had higher GSI and HSI, and the ovarian maturity was better under the induction of long photoperiod. At the end of the experiment, estrogen (E2) was at a high level, and the changes of LH and E2 and MT were consistent. The expression levels of genes foxl2, cyp19a1, kiss, gpr54, gnrh2, fsh and lh were higher under the treatment of long photoperiod. Under the control group photoperiod condition, the male had higher GSI and HSI, and the testis maturity was better. At the end of the experiment, androgen (T), aromatase, MT and Kisspeptin were at a high level and significantly higher than those of the other two groups, and the expression levels of genes sox9a and gnrh3 were higher in the control group. Generally speaking, prolonging the photoperiod is beneficial to the ovarian development and maturation of silver pomfret, and the development and maturation of testis were more advantageous in the control group under photoperiod condition.

Key words: Silver pomfret (Pampus argenteus), Photoperiod, Gonad development, Sex steroid hormones, Gene expression

许氏平鲉蛋白激酶 B(SsAkt)基因的克隆及表达分析

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摘要：蛋白激酶 B(PKB/Akt)是一种重要的细胞信号转导分子，在细胞存活与代谢、免疫调控与防御等多种生物过程中发挥重要作用。为研究 Akt 在许氏平鲉（*Sebastes schlegelii*）应答细菌胁迫过程中的作用，本研究基于前期转录组数据，克隆了许氏平鲉 SsAkt 基因的编码区序列，分析了其编码氨基酸序列的进化特征，预测了其氨基酸序列的三级结构，并研究了其时空表达特征和响应细菌胁迫的表达规律。研究表明，SsAkt 响应了外源微生物对许氏平鲉的刺激，在抵御外源微生物免疫应答过程中发挥重要作用。研究结果为许氏平鲉的免疫机理研究奠定了基础。

关键词：许氏平鲉；蛋白激酶 B；Akt；基因克隆；表达分析

Cloning and Expression Analysis of SsAkt in *Sebastes schlegelii*

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Abstract： Protein kinase B (PKB/Akt) is an important cell signal transduction molecule that plays an important role in various biological processes such as cell survival and metabolism, immune regulation and defense. In order to study the role of Akt in the response of *Sebastes schlegelii* to bacterial stress, this study cloned the coding region sequence of the SsAkt gene of *Sebastes schlegelii* based on the previous transcriptome data, and analyzed the evolutionary characteristics of the encoded amino acid sequence. We predicted the tertiary structure of its amino acid sequence, and studied its spatiotemporal expression characteristics and expression rules in response to bacterial stress. Studies have shown that SsAkt plays an important role in the process of resisting the immune response of exogenous microorganisms in response to the stimulation of exogenous microorganisms. The research results lay a foundation for the study of the immune mechanism of *Sebastes schlegelii*.

Key words: Sebastes schlegelii; Protein Kinase B; Akt; Gene cloning; Expression analysis

低氧胁迫和恢复对中华绒螯蟹肠道组织的影响

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摘要：目前甲壳动物肠道组织的环境胁迫研究已成为国内外研究热点，为探究低氧胁迫和恢复对中华绒螯蟹肠道组织的影响，本研究运用酶活测定、H&E 染色、qRT-PCR、TUNEL 检测以及 16S rRNA 测序技术等方法，分析低氧胁迫(3.0±0.1 mg/L)和恢复下(7.0±0.5 mg/L)中华绒螯蟹肠道氧化应激指标、组织结构形态、细胞凋亡以及微生物组成变化。结果显示:低氧胁迫下肠道抗氧化酶活性(SOD、CAT)、能量代谢酶活性(LDH)、丙二醛和乳酸含量显著升高；肠道组织受损现象逐渐加剧；肠道组织细胞凋亡程度随着低氧时间的延长而加剧，凋亡相关基因表达量显著升高，bcl-2 基因的表达量则减少；肠道微生物相对丰度降低。恢复溶氧后氧化应激反应仍维持在较高水平；缺氧引起的生理变化并未得到明显改善；肠道菌群数量有所增加。本研究结果可为解析低氧和恢复下中华绒螯蟹肠道组织内环境稳态调控机制提供一定的理论依据。

关键词：中华绒螯蟹；低氧胁迫；氧化应激；细胞凋亡；肠道微生物

Effects of hypoxia stress on intestinal microbiota of Chinese Mitten crab (*Eriocheir sinensis*)

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Abstract： At present, environmental stress in crustacean intestinal tissue has become a research hotspot at home and abroad. In order to explore the effects of hypoxia stress and recovery on intestinal tissue of Chinese mitten crab, enzyme activity assay, H&E staining, qRT-PCR, TUNEL detection and 16S rRNA sequencing technology were used in this study. The changes of intestinal oxidative stress indexes, tissue structure and morphology, cell apoptosis and microbial composition in Chinese Mitten crab under hypoxia stress (3.0±0.1mg/L) and recovery (7.0±0.5mg/L) were analyzed. The results showed that the activities of antioxidant enzymes (SOD, CAT), activities of energy metabolizing enzymes (LDH), contents of malondialdehyde and lactic acid were significantly increased under hypoxia stress. The damage of intestinal tissue was gradually aggravated. The degree of apoptosis in intestinal tissue was aggravated with the prolongation of hypoxia time, and the expression of apoptosis-related genes was significantly increased, while the expression of Bcl-2 gene was decreased. The relative abundance of gut microbes decreased. The oxidative stress response remained at a high level after the recovery of dissolved oxygen. The physiological changes caused by hypoxia were not obviously improved. The gut microbiota has increased. The results of this study may provide a theoretical basis for analyzing the regulatory mechanism of homeostasis in intestinal tissues of Chinese mitten crab under hypoxia and recovery.

Key words: Chinese mitten crab; Hypoxia stress; Oxidative stress; Apoptosis; Gut microbes

高温胁迫下黑龙江茴鱼幼鱼肝脏组织结构变化及转录组表达特征

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摘要：为探究急性高温胁迫下黑龙江茴鱼 *Thymallus arcticus grubei* 的响应机制，本研究采用组织病理学和高通量 RNA-seq 测序技术分析高温组（17℃）和对照组（11℃）在不同养殖时间条件下（1、6、12、24 及 48 h）黑龙江茴鱼肝脏组织结构变化及转录组表达特征。结果表明：17℃养殖高温胁迫下，黑龙江茴鱼肝脏组织结构出现明显的病理损伤，于胁迫 12 h 后肝脏组织出现不同程度的核萎缩变形及空泡化现象，且在胁迫 48 h 肝脏细胞损伤最为严重，甚至出现细胞溶解现象。转录组测序共获得 214.44 G 的有效数据，平均 GC 含量为 49.45 %，Q 30 碱基分布在 93.48~96.06 %。筛选到差异表达基因数（DEGs）共 9144 个，且 DEGs 数量随温度胁迫时间的延长呈先升高后下降的趋势。于胁迫 24 h 时差异基因数量最多有 7148 个，其中 3653 个上调，3495 个下调；胁迫 1 h 时差异基因数量最少有 602 个，其中 180 个上调，422 个下调。KEGG 通路富集分析发现，差异表达基因主要富集到的通路与能量代谢及免疫应激有关，主要为糖酵解/糖异生、乙醛酸和二羧酸代谢、内质网中的蛋白加工、细胞吞噬及 AMPK 和 P53 等通路，且随着胁迫时间的延长富集到能量代谢相关通路的差异基因显著下调表达，而富集到免疫应激相关途径的基因显著上调表达（$P<0.05$）。随机选择 6 个 DEGs 进行实时荧光定量 PCR 验证，基因表达变化趋势与转录组数据一致。研究表明，温度为 17℃的条件下，黑龙江茴鱼幼鱼肝脏组织在 12 h 后出现不同程度的应激损伤，且在转录组水平出现代谢受阻和免疫应激增强现象，本试验结果为深入研究黑龙江茴鱼高温胁迫响应的分子调控机制提供基础数据。

关键词：黑龙江茴鱼；高温胁迫；肝脏；转录组；组织病理

Effects of high temperature stress on transcriptome expression characteristics and tissue structure of thymellus arcticus grubei juvenile fish

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Abstract：In order to explore the response mechanism of *Thymallus arcticus grubei* under acute high temperature stress, this study used histopathology and high-throughput RNA seq sequencing technology to analyze the changes of liver tissue structure and transcriptome expression characteristics of Thymallus arcticus grubei in high temperature group (17 ℃) and control group (11 ℃) under different cultivation time conditions (1, 6, 12, 24 and 48 h). The results showed that under 17 ℃ high temperature stress, the liver tissue structure of Thymallus arcticus grubei obvious pathological damage. After 12 hours of stress, the liver tissue showed varying degrees of nuclear atrophy, deformation and vacuolization, and at 48 hours of stress, the liver cells were most severely damaged, even cell dissolution. A total of 214.44G of valid data were obtained by transcriptome sequencing, with an average GC content of 49.45% and a Q 30 base distribution of 93.48~96.06%. The number of differentially expressed genes (DEGs) was 9144, and the number of DEGs increased first and then decreased with the extension of temperature stress time. At 24 h of stress, there were 7148 differential genes at most, of which 3653 were up-regulated and 3495 were down regulated; At least 602 differential genes were found at 1 h stress, 180 of which were up-regulated and 422 were down regulated. The enrichment analysis of KEGG pathway showed that the pathways enriched by differentially expressed genes were mainly related to energy metabolism and immune stress, mainly including glycolysis/gluconeogenesis, glyoxylic acid and dicarboxylic acid metabolism, protein processing in endoplasmic reticulum, cell phagocytosis, AMPK and P53, and the differentially expressed genes enriched to energy metabolism related pathways were significantly down regulated with the extension of stress time, However, genes enriched in immune stress related pathways were significantly up-regulated ($P<0.05$). Six DEGs were randomly selected for real-time fluorescent quantitative PCR validation, and the trend of gene expression was consistent with the transcriptome data. The study showed that under the condition of 17 ℃, the liver tissue of Thymallus arcticus grubei appeared different degrees of stress damage after 12 hours, and the metabolism was blocked and the immune stress was enhanced at the transcriptome level. The results of this experiment provided basic data for in-depth study of the molecular regulation mechanism of the response of Thymallus arcticus grubei to high temperature stress.

Key words: Thymallus arcticus grubei; High temperature stress; liver; Transcriptome; Histopathology

温度变化对黑鲷 5 个群体抗氧化和免疫相关酶活的影响

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摘要：为探究温度变化对黑鲷 3 个选育系（XY1、XY2、XY3）、杂交鲷（HF2，黑鲷♀×真鲷♂杂交子二代）与野生群体子一代（YS）等的影响差异，实验设置降温组（17℃、13℃、℃ 9 及 5℃）和升温组（26℃、30℃、34℃及 38℃），温度处理 12 h 后，分别记录存活率、取样测定肝脏组织的总超氧化物歧化酶（T-SOD）、过氧化氢酶（CAT）、碱性磷酸酶（AKP）以及溶菌酶（LZM）等活性。结果得出，黑鲷各品系在 5℃~34℃范围内存活率高于 84.1%，38℃时存活率为 7.8%（YS）~16.9%（HF2）；温度下降过程中，XY1、XY2 和 YS 等 3 个品系的 4 种酶活性均在 9℃达到最高值，而 XY3 和 HF2 两品系的 T-SOD 和 AKP 活性随温度降低而持续升高；随着水温上升，5 个品系的 T-SOD、CAT 和 AKP 等酶活先升后降，除 YS 外的 4 个品系 LZM 活性随温度升高持续上升，水温升至 38℃后，XY3 的 T-SOD 活性显著高于其余 4 个品系（$P＜0.05$），HF2 的 CAT 活性显著高于 XY1、XY2（$P＜0.05$）。研究结果表明，温度变化对黑鲷不同品系的存活率、抗氧化及免疫相关酶活性的影响效果不同，其中 XY3 与 HF2 两个品系表现较好。

关键词：黑鲷；温度胁迫；抗氧化酶；；免疫因子

Effects of temperature changes on antioxidant and immune-related enzyme activities in five populations of Acanthopagrus schlegelii

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Abstract： In order to study the different effects of temperature stress on five populations of Acanthopagrus schlegelii, the experiment was performed with rising temperature group (26℃ (control group), 30℃, 34 ℃ and 38℃) and cooling temperature group (17℃ (control group), 13℃, 9℃ and 5℃). The activities of antioxidant enzymes and immune-related factors of fish liver were measured at different temperature. The results showed that the enzymes activities of T-SOD, CAT, AKP and LZM in the three populations of XY1, XY2 and YS increased first and then declined with the dropping of temperature, and the activities of T-SOD and AKP increased continuously with the decrease of the temperature of the two populations of XY3 and HF2; At 5℃, the CAT and LZM activities of five populations decreased, the CAT activities of XY3 and HF2 were significantly higher than YS ($P<0.05$), and the LZM activity of HF2 was significantly higher than that of the other four groups ($P<0.05$). The activities of T-SOD, CAT and AKP increased first and then decreased with the increase of temperature in five populations, and the activities of LZM continued to increase with the increase of temperature except YS populations; At 38℃, the T-SOD activity of XY3 was significantly higher than that of the other four groups ($P<0.05$), the CAT activity of HF2 was significantly higher than that of XY1 and XY2 ($P<0.05$). The above results showed that temperature change had different effects on the survival rate, antioxidant and immune-related enzyme activities of different populations of Acanthopagrus schlegelii, and the two populations of XY3 and HF2 showed better performance.

Key words: Temperature stress; Acanthopagrus schlegelii; Antioxidant enzymes; Immune enzyme

环境 DNA 技术研究进展及其在长江流域中的应用前景分析

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摘要：长江流域巨大的渔业资源优势与丰富的生物多样性，维持着生态系统的稳定发展，但由于各种因素影响，资源急剧衰退为了更好地推进长江流域绿色健康发展，恢复鱼类资源，拯救濒危动物栖息地；探究分析环境 DNA 技术的研究进展及其在长江流域的应用，以此总结分析环境 DNA 技术应用于长江流域生态监测，鱼类资源调查等。本文首先综述了环境 DNA 定义、发展史、研究方法与优劣势；然后分析探讨了该技术在长江流域的应用前景；最后对环境 DNA 技术应用潜力进行了展望。

关键词：环境 DNA；长江流域；应用前景

Research progress of environmental DNA technology and its application in the Yangtze River Basin

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Abstract： The huge advantages of fishery resources and rich biodiversity in the Yangtze River Basin maintain the stable development of the ecosystem, but due to various factors, the resources decline sharply. In order to better promote the green and healthy development of the Yangtze River Basin, restore the fish resources and save the habitat of endangered animals, this paper explores the research progress of environmental DNA technology and its application in the Yangtze River Basin Environmental DNA analysis technology has been applied to ecological monitoring and fish resources investigation in the Yangtze River Basin. In this paper, the definition, development history, research methods, advantages and disadvantages of environmental DNA were summarized firstly. Then, the application prospect of environmental DNA technology in the Yangtze River Basin was analyzed and discussed. Finally, the application potential of environmental DNA technology was prospected.

Key words: Environmental DNA; Yangtze River Basin; application analysis

中国对虾基因组组装及性染色体探究

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摘要：中国对虾是我国最具代表性的商业养殖对虾之一，获得高质量的基因组序列对重要经济性状的遗传机制解析至关重要。本研究利用 PacBio 平台对一尾雄性“黄海 1 号”中国对虾进行测序，并采用 Hi-C 技术进行挂载，得到的基因组大小为 1.47 Gb, contig N50 为 472.84 Kb，锚定在 43 条染色体上，scaffold N50 为 36.87 Mb，预测蛋白编码基因 25026 个。中国对虾基因组中与免疫相关的基因家族显著收缩，导致该物种抗病力较弱。与野生群体相比，选育群体在与代谢、光传导和神经系统相关的基因上检测到选择信号，证明驯化过程中中国对虾的生长、视觉和行为受到了人工选择。首次在中国对虾基因组中定位到了性染色体，判断中国对虾属于雌性异配型性别决定机制（ZW 型）。中国对虾性染色体的形成仍处于初级阶段，Z 染色体和 W 染色体的分化程度较低，大量雄性特异表达基因在 Z 染色体分化区域聚集。组装了 W 染色体特异性聚集。组装了 W 染色体特异性序列，并进行分子验证，筛选出中国对虾遗传性别鉴定的分子标记，为中国对虾性别控制技术研发奠定了基础。

关键词：甲壳动物；中国对虾；基因组；性染色体；分子标记

Improved genome assembly and sex chromosome research of Chinese shrimp Fenneropenaeus chinensis

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Abstract： Fenneropenaeus chinensis is a commercially cultured shrimp in China. A high-quality reference genome is necessary to determine the molecular mechanisms underlying important biological phenomena. In the present study, a chromosome-level genome assembly of the Chinese shrimp F. chinensis was performed. Muscle of a male shrimp was sequenced using PacBio platform, and assembled by Hi-C technology. The assembled F. chinensis genome was 1.47 Gb with contig N50 of 472.84 Kb, and was anchored to 43 pseudochromosomes, with scaffold N50 of 36.87 Mb. In total, 25,026 protein-coding genes were predicted. The contracted gene families of F. chinensis were associated with virus infection process, resulting in a weak disease resistance of this species. Furthermore, the selection signature analysis identified genes associated with metabolism, phototransduction, and nervous system in cultured shrimps when compared with wild population, indicating targeted, artificial selection of growth, vision, and behavior during domestication. We located the candidate sex chromosome in the genome of F. chinensis and preliminarily verified the female heterogametic (ZW) sex determination mechanism of F. chinensis based on resequencing data. However, sex chromosome formation in F. chinensis is halted at the primary stage, the differentiation of the Z and W chromosome is limited. According to the RNA-seq data, many male-biased expression genes were observed to accumulate in the Z-specific region, which could further intensify the divergency between the Z and W chromosomes. We also assembled female-specific (W chromosome-specific) sequences, which could be used as molecular markers to identify the sex of F. chinensis.

Key words: Crustacea; Fenneropenaeus chinensis; genome; sex chromosome; molecular marker

马口鱼仔稚鱼发育观察及饥饿不可逆点确定

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摘要：为研究马口鱼仔稚鱼发育特点及确定其饥饿不可逆点（PNR），对马口鱼仔鱼进行持续显微观察和饥饿再投喂试验，结果表明：水温 21~26℃，仔鱼卵黄囊发育方程：V= -0.0001d3 + 0.0071d2-0.1483d + 0.9085（R^2= 0.9693）；1~43 日龄池塘仔稚鱼生长发育方程：L=1.0913d-0.7778（R^2= 0.9248）。马口鱼初孵仔鱼身体透明，全长 5.13±0.16 ㎜；5 日龄，卵黄囊呈棒状；6 日龄，胸鳍鳍条形成；9 日龄，鳔初步形成；10 日龄，肠道内可见食物；11 日龄，卵黄囊几乎消失;18 日龄，鳔两室, 各鳍发育完成；27 日龄，鳞片出现，进入稚鱼期；43 日龄，鳞片完全，进入幼鱼期。水温 21.5±1℃,10 日龄饥饿组仔鱼开口率 55.56%，11 日龄达最高值 88%，12～13 日龄到达 PNR，14 日饥饿组仔鱼全部死亡。本文的研究为马口鱼的鱼苗培育提供了基础资料。

关键词：马口鱼；仔稚鱼；早期发育；饥饿；不可逆点

Observation on the development of Opsariichthys bidens larvae and determination of the irreversible point of starvation

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Abstract： In order to study the biological characteristics of early development of Opsariichthys bidens larvae and determine the irreversible point of starvation (PNR), Continuous microscopic observation and starvation refeeding test on Opsariichthys bidens larvae ，The results showed that the water temperature was 21-26℃, Developmental equations of the yolk sac of the larvae：V= -0.0001d3 + 0.0071d2- 0.1483d + 0.9085（R^2= 0.9693）；and the yolk sac development equation of larvae was 1-43 days old：L=1.0913d-0.7778（R^2= 0.9248）。The newly hatched larvae are transparent and full-length，Full length5.13±0.16 ㎜;The yolk sac of 5-day-old larvae is rod-shaped; 6-day-old larvae, pectoral fins formed; 9-day-old larvae, swim bladder initially formed; 10-day-old larvae, food can be seen in intestines; 11-day-old larvae, yolk sac almost disappeared;18-day-old larvae have two chambers, and the development of each fin is nearly completed; On the 27th day, scales began to appear and entered the juvenile stage; 43-day-old juvenile fish, with full length and complete scales, enter the juvenile stage.The water temperature was 21.5±1℃, the opening rate of 10-day-old larvae was 55.56%, and the highest value was 88% at 11-day-old, reaching PNR at 12-13 days old, and all the larvae in the 14-day-old hungry group died. The research in this paper provides basic information for the fry breeding of Opsariichthys bidens。

Key words: Mackerel; larva; early development; irreversible point of starvation

弧菌感染下 AP-1 介导的 IL-17D 表达对泥蚶生理变化的影响

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摘要：泥蚶（*Tegillarca granosa*）是一种具有较高经济价值的滩涂贝类，泥蚶促炎因子白介素-17D（TgIL-17D）参与了弧菌感染后的免疫与炎症反应。TgIL-17D 的 cDNA 序列全长 1587bp，开放阅读框 594bp，编码 197 个氨基酸。TgIL-17D 与贻贝的同源相似性最高，且在 6 种泥蚶组织中均有表达，其中鳃的表达水平较高。TgIL-17D 启动子内含有多个 TgAP-1 蛋白结合位点。TgAP-1 表达下调，降低了 TgIL-17D 的表达水平。而弧菌感染则增加了 TgAP-1 和 TgIL-17D 的表达。TgIL-17D 参与了泥蚶抗弧菌病的先天免疫反应，TgAP-1 在 TgIL-17D 的表达调控中发挥了重要的作用，通过敲降 TgAP-1 可减弱 TgIL-17D 带来的炎症反应和组织损伤，下调 TgIL-17D 的表达可有效阻止泥蚶在弧菌感染后的大规模应激死亡。

关键词：泥蚶；IL-17D；AP-1；炎症反应；弧菌感染

Interleukin-17D mediates Vibrio harveyi infection-related changes in Tegillarca granosa though activation of activator protein-1 in vivo

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Abstract： Blood clam (*Tegillarca granosa*) is a kind of beach shellfish with high economic value. Interleukin-17D, a proinflammatory factor of clam, was involved in the immune and inflammatory response after Vibrio infection. The cDNA sequence of TgIL-17D is full-length 1587 bp with ORF 594 bp, which encodes 197 amino acids. The homologous similarity between TgIL-17D and mussel was the highest, and the expression level of gill was higher. There were several TgAP-1 protein binding sites in the TgIL-17D promoter. Down-regulation of TgAP-1 can reduce the expression level of TgIL-17D, while Vibrio infection increased the expression of TgAP-1 and TgIL-17D. TgIL-17D participated in the innate immune response of clams against Vibrio disease. TgAP-1 played an important role in the regulation of TgIL-17D expression. By knocking down TgAP-1, it can reduce the inflammatory reaction and tissue damage. Down-regulate of TgIL-17D can effectively prevent large-scale stress death of clams after Vibrio infection.

Key words: Tegillarca granosa; IL-17D; AP-1; Inflammation; Vibrio infection

活饵与饲料投喂下鳜胃 ghrelin 的表达变化比较

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摘要：本研究探究了饲料和活饵投喂下鳜摄食前后胃饥饿素 ghrelin 的调控作用。诱食试验模拟鳜进食前看到食物但不能摄食现象，进食试验模拟鳜正常摄食现象。结果表明：鳜 preproghrelin 基因含有 4 个外显子和 3 个内含子，属于II型基因型。Ghrelin 阳性细胞位于胃腺中。诱食试验中，活饵组胃 ghrelin mRNA 和蛋白表达水平均显著升高；而饲料组 ghrelin 基因 mRNA 和蛋白表达水平未发生显著变化，且显著低于活饵组。进食试验中，活饵组进食后 0h，胃 ghrelin mRNA 和蛋白表达水平显著上升，进食后 2h 下降至摄食前水平；饲料组进食后 0h 至胃排空 ghrelin mRNA 表达水平未出现显著变化，蛋白水平呈波动变化。综上，鳜胃 ghrelin 细胞位于胃腺位置，参与调节摄食活动，进食前上升，进食后下降，而饲料投喂下 ghrelin 对摄食调节作用明显减弱。

关键词：鳜；胃饥饿素；饲料投喂；活饵投喂

Comparison on ghrelin expression in stomach of mandarin fish (Siniperca chuatsi) under different diets feeding

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Abstract： We detected the changes of ghrelin gene and protein expression in the stomach after induced and fed. The attraction test simulates the sighting of food before feeding but the inability to feed, while the feeding test simulates the normal feeding of mandarin fish.The results show that the preproghrelin gene contains 4 exons and 3 introns and belongs to type II.Immunohistochemistry revealed ghrelin-production cells located in the gastric glands. In the attraction test, ghrelin mRNA and protein expression levels were significantly higher in the live-bait group; whereas ghrelin expression levels did not change significantly in the compound food group and were significantly lower than in the live-bait group. In the feeding test, ghrelin mRNA and protein levels in the live-bait group increased significantly at 0h and decreased to normal levels at 2h after feeding, while the compound feed group showes no significant change in mRNA level, and fluctuations in protein expression.

Key words: Siniperca chuatsi; ghrelin; live bait; compound food

三角帆蚌纤维蛋白 Hc-fibrillin 的克隆鉴定及在贝壳矿化作用机制研究

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摘要：Fibrillin 是形成微纤维骨架的关键分子，参与结构形成和信息传递的生物网络，在多种生物过程中发挥着重要作用，包括高等动物成骨细胞分化。然而，其在无脊椎动物的生物矿化功能的研究较少。本研究获得了三角帆蚌 *Hc-fibrillin* 的全长，并研究了其在贝壳形成中的作用机制。*Hc-fibrillin* 全长为 1952bp，ORF 为 1389bp，编码了 462 个氨基酸，其中包含 8 个 EGF-CA 结构域。通过氨基酸比对和进化树分析发现，*Hc-fibrillin* 与厚壳贻贝同源性较高，为 44.32%，并且亲缘关系更近。*Hc-fibrillin* 在外套膜和鳃中高表达，表明其在钙离子吸收和转运过程中发挥着重要的作用。在贝壳修复实验中，*Hc-fibrillin* 在破壳后的第 16-25 天表达量显著增加。当 *Hc-fibrillin* 被沉默时，珍珠层中的文石小片由正常状态下的六边形逐渐变圆，而棱柱层中碳酸钙晶体表面变得更加粗糙，大小差异明显，晶体之间的有机基质呈现骨架化，表明其在生物矿化中发挥着重要的作用。体外碳酸钙结晶试验表明，*Hc-fibrillin* 多肽可以诱导方解石变为球文石，这可能是三角帆蚌产生低光泽珍珠的原因。该研究结果为三角帆蚌的生物矿化提供了新的认识，并为珍珠品质的改善奠定了理论基础。

关键词：三角帆蚌；生物矿化；基质蛋白；*Hc-fibrillin*

Molecular cloning and functional characterization of *Hc-fibrillin* in shell biomineralisation of the triangle sail mussel *Hyriopsis cumingii*

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Abstract： Fibrillin (FBNs) are key relay molecules that form the skeleton of microfibrils, which integrate a biological network of structural and guidance information, play an important role in a variety of physiological processes, including osteoblast differentiation in higher animals. However, its biomineral function in invertebrates remains poorly understanding. In this study, a full-length cDNA of Hc-fibrillin from the triangle sail mussel Hyriopsis cumingii was obtained, and its function in shell formation was investigated. The full-length cDNA of *Hc-fibrillin* was 1952 bp with an open reading frame (ORF) of 1389 bp encoding apolypeptide of 462 amino acids, including eight EGF-CA domains. We also found high homology of *Hc-fibrillin* with *M.coruscus*, accounting for 44.32%, consistent to the most closed phylogeny with M. coruscus. The tissue expression pattern showed that *Hc-fibrilli*n was expressed in all tested tissues, highly in the mantle and gill, suggesting its role in absorption and transport of calcium ion. In the shell repaired assay, there was a significantly higher expression of *Hc-fibrillin* in shell repair group from day 16 to day 25. After Hc-fibrillin was silenced, the shape of aragonite flakes in the pearl layer gradually changed to round, while the surface of the calcium carbonate crystals in the prismatic layer got rougher with great size differencr, and the organic matrix between the crystals appeared skeletonized, indicating the important function in biomineralization. In vitro calcium carbonate crystallization assay showed that in spite of calcite, fibrillin peptide can also induce calcium carbonate crystals to vaterite, probably suggesting the reason of low-luster pearl produced by freshwater mussels. The results provide new insights about the biomineralization in freshwater molluscs and lay a theoretical basic for pearl quality improvement.

Key words: Hyriopsis cumingii; Biomineralization; Matrix protein; Hc-fibrillin

高温与低盐胁迫诱导半滑舌鳎产生不同的性逆转效应

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摘要：全球变暖在过去的几十年对海洋环境造成了深远的影响，这不仅给人类社会带来了巨大的挑战，同时也让不同地域的海洋生态系统面临着威胁。在众的不断变化的环境因子中，温度和盐度即在变化最显著且对海洋生物影响最大的因子之列，因此，温度、盐度胁迫下有机体的遗传变化以及生物学响应亟待深入研究。在本研究中，我们人工设置了高温胁迫（29℃）、低盐胁迫（20 ppt）以及对照条件（自然海水温度、盐度）养殖性别决定期半滑舌鳎，一种同时具有遗传型与环境型性别决定系统的硬骨鱼，来探究不同环境胁迫因子对半滑舌鳎性别决定和性腺分化的影响。在研究过程中，我们对三组半滑舌鳎的生长性状进行了统计，结果显示在 75 dpf 之前，高温组个体大小及生长速度显著小于对照组，而低盐组则显著大于对照组；75 dpf 之后高温组和低盐组的个体大小和生长速度均显著小于对照组。同时我们通过组织学观察的方法追踪了性别决定期半滑舌鳎性腺分化过程；并在成鱼期比较了高温、低盐胁迫对半滑舌鳎性腺分化的组织学影响，结果显示高温胁迫会造成半滑舌鳎伪雄鱼性腺发育和生殖细胞增殖分化的滞缓现象，同时通过表型性别和遗传性别的比较分析我们发现高温胁迫提高了伪雄率，而低盐胁迫减少了性逆转比率。接下来我们构建了各组 55 dpf 及 100 dpf 半滑舌鳎性腺转录组文库来进一步分析比较各组性腺的转录谱差异，在组装后共计 76 个转录组文库的 Q20 均大 97.28，Q3 大 92.8，共获得了 534.03G 数据。差异分析以及 GO/KEGG 富集分析筛选出了大量的参与高温和低盐胁迫诱导不同性逆转效应的基因、条目和通路，同时我们发现 HPI 轴和 HPG 轴的互作在上述效应中发挥至关重要的作用。最后通过 WGCNA 分析，我们在高温胁迫和对照以及低盐和对照构建的基因共表达网络中均筛选出了相同的关键 hub 基因：*hspb8-like*。

关键词：高温；低盐；性别决定；性腺分化；半滑舌鳎

High temperature and low salinity stress induce distinct masculinization effect in Cynoglossus

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Abstract： In this study, the effect of chronic high temperature and low salinity stress on teleosts' sex differentiation was investigated using Cynoglossus semilaevis. The comparative experiment was conducted employing artificially simulated seawater of 29 ℃(HT group), 20 ppt (LS group) and ambient sea water (CT group) to cultivate juveniles C. semilaevis. Throughout the experiment, the growth performances were documented and compared. Adopting histological observation, the gonadal differentiation status was tracked, results showed that high temperature caused intensive masculinization effect whereas low salinity stress could reduce the sex reversal rate. A total of 76 libraries from 55 and 100 dpf gonads were constructed with a data size of 534.03 G. Differential analysis and GO/KEGG enrichment showed that the crosstalk between HPI and HPG axis played crucial roles in above effect. The WGCNA was proceeded subsequently and a collective hub gene: *hspb8-like* was screened in co-expression networks constructed using data from both HT_VS_CT group and LS_VS_ CT group.

Key words: High temperature; low salinity; sex determination; gonadal differentiation; Cynoglossus semilaevis

标记密度对大黄鱼白鳃病基因组选择预测准确性的影响

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摘要：白鳃病是影响大鱼养殖业的主要病害之一，因为病原体尚未确定，也没有有效的治疗方法。 幸运的是，选择性育种可以提高对白鳃病的抵抗力。在当前的研究中，构建了一个包含2,083 个样本和 10,201,978 个 SNP 的数据集。 白鳃病的遗传力估计值为 0.33。 我们尝试了两种不同的策略来评估不同标记密度对大黄鱼白鳃抗病性预测准确性的影响。 结果表明，30 K SNP 的标记密度可以达到与使用整个数据集相似的精度，并且随着 MAF 的增加，标记密度逐渐降低。 在具有相对密切遗传关系的种群中，低标记密度将是确保大黄鱼白鳃病基因组选择精度高的一种经济有效的方法。

关键词：大黄鱼；遗传力；白鳃病；标记密度；基因组选择

The impact of maker density on genomic prediction accuracy in Larimichthys crocea

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Abstract： White gill disease is one of the major diseases affecting the Larimichthys crocea industry because the pathogen has not been determined and there is no effective treatment. Fortunately, selective breeding can improve resistance to white gill diseases.In the current study, a dataset containing 2,083 samples and 10,201,978 SNPs was constructed. The heritability estimate for white gill disease was 0.33. We tried two different strategies to evaluated the effect of different marker densities on the prediction accuracy of the white gill disease resistance in L. crocea. Our results showed that the marker density of 30 K SNP can achieve accuracy similar to that of using the entire dataset,and the marker density was progressively decreased by increasing MAF. In populations with relatively close genetic relationships, low marker density would be a cost-effective method to ensure high genome selection accuracy for white gill diseases in L. crocea.

Key words: Larimichthys crocea; Heritability; White gill disease; Marker destiny; Genomic selection

光照强度对红螯螯虾幼虾影响的研究

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摘要：为了研究光照强度对红螯螯虾幼虾的影响，本研究进行了实验，结果表明：1.光照强度20lux组成活率较高；2.光照强度20 lux、200 lux和0 lux这3组生长速度较快；3. 0lux和20lux组具有较高的分散度，其他光照组幼虾总是聚集在一起或在2-3天内分散；4. 0lux和20lux组的抗氧化能力更高，20lux组的免疫能力更高；5. 0lux和20lux组的单胺类物质含量较低；6. 0lux或20lux组α-AMY或EcR基因表达量较高。综上所述，光照强度控制20lux时，幼虾具有较高的存活率、生长率、分散度、生理代谢、免疫能力和α-AMY基因的表达。因此，在实际生产过程中，幼虾中间培育的最适光照强度为20lux。

关键词：红螯螯虾；幼虾；光照强度

A study on the effects of light intensity on juveniles of the red claw crayfish Cherax quadricarinatus

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Abstract： To study the effect of light intensity on red claw crayfish juveniles, experiments were carried out in this study. The results showed the following. 1) The 20 lux group had the highest survival rate. 2) The growth rates of the 20 lux, 200 lux and 0 lux groups were faster. 3) The 0 lux and 20 lux groups had higher dispersion, while other groups were always clustered or dispersed within 2-3 days. 4) Antioxidant capacities in the 0 lux and 20 lux groups were higher, and immune capacity in the 20 lux group was higher. 5) Monoamine contents were lower in the 0 lux and 20 lux groups. 6) α-AMY or EcR expression in the 20 lux or 0 lux group was higher. In conclusion, when the light intensity was controlled at 20 lux, the juveniles had a high survival rate, growth rate, dispersion, antioxidant capacity, immune capacity and expression of α-AMY. We considered in actual production, it could be necessary to control 20 lux light intensity during the intermediate cultivation period of juveniles.

Key words: Cherax quadricarinatus; red claw crayfish; juveniles; light intensity

间歇低氧条件下大口黑鲈代谢反应为探究其低氧适应机制提供新思路

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摘要：在机体代谢过程中，分子氧是一种必需的底物，氧水平失衡会破坏生物体内的稳态。近年来，低氧预适应在提高运动能力和耐低氧能力方面的积极作用已成为研究热点。在本研究中，我们探讨了间歇性低氧暴露（每天 1 小时或 3 小时）对大口鲈耐低氧能力的影响。结果表明：（1）间歇性低氧暴露显著降低了大口鲈的 LOEcrit（失去体平衡的临界 O2 张力）值，其耐低氧能力显著增强。（2） 与 HH1 组（每天暴露于低氧条件下 1 小时）相比，HH3 组（每天低氧暴露 3 小时）大口黑鲈肝脏中的氧化应激水平降低。（3） 间歇性低氧暴露条件下大口黑鲈乳酸含量显著降低，肝脏糖异生过程显著增强。（4） 间歇性低氧暴露促进大口黑鲈肝脏脂质动员和脂肪酸氧化。总之，本研究结果表明，IHE 可以通过调节大口黑鲈的能量代谢来提高其耐低氧能力，其结果也为解决大口黑鲈在集约化水产养殖中重要胁迫因素—低氧，提供了新的见解。

关键词：间歇低氧暴露；大口黑鲈；代谢反应；转录组分析

Metabolic response provides insights into the mechanism of adaption to hypoxia in largemouth bass (Micropterus salmoides) under intermittent hypoxic conditions

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Abstract: In metabolism, molecular oxygen is a necessary substrate. Oxygen imbalances are linked to a variety of circumstances in the organism's homeostasis. Recently, the positive effects of hypoxia treatment in improving exercise ability and hypoxia tolerance have become a research focus. We explored the effects of intermittent hypoxia exposure (IHE, for one hour or three hours per day) on the hypoxia tolerance of largemouth bass in this study. The results showed that (1) IHE significantly reduced the LOEcrit (the critical O2 tension for loss of equilibrium) value of largemouth bass, indicating that its hypoxia tolerance was enhanced. (2) The level of oxidative stress in the liver decreased in the HH3 group (exposed to a hypoxic condition for 3 h per day) compared to HH1 group (exposed to a hypoxic condition for 1 h per day). (3) IHE reduced the content of lactic acid and enhanced the process of gluconeogenesis in the liver. (4) The whole transcriptome sequencing results showed that differentially expressed mRNA were mainly enriched in PPAR, fatty acid metabolism and fatty acid degradation signaling pathways. According to the analysis of biochemical indexes, IHE promoted the gluconeogenesis, lactic acid metabolism and fatty acid oxidation in largemouth bass liver. The research results show that IHE can improve the ability to tolerate hypoxia by regulating the ability of largemouth bass to remove anaerobic metabolic by-products and the choice of metabolic substrates. The results also provide new insights to solve the important stress factor (hypoxia) of largemouth bass in intensive aquaculture.

Key words: Intermittent; hypoxiaLargemouth; bassMetabolic; responseTranscriptome

点带石斑 gsdf/Gsdf 在双向性转变过程中的调控机制

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摘要：点带石斑为先雌后雄的硬骨鱼类，雌鱼经雄激素处理后转变成雄鱼，但停止处理后会再次性逆转为雌性，稳定雄性石斑具有一定的商业性需求。gsdf 是 TGF-β超家族一员并仅存在于鱼类中，主要表达于性腺中的生殖体细胞并参与雄性性别决定或性别分化，因此本研究拟探讨 gsdf 是否参与点带石斑之性转变与性逆转。qPCR 结果表明，gsdf 在精巢表达量高于卵巢，雄激素撤除后性逆转过程中高表达。原位杂交和免疫组织化学染色结果表明，在性转变过程中，gsdf/Gsdf 表达在精巢的 Sertoli cell 和卵巢卵原细胞周边的生殖体细胞中，在性逆转过程中，gsdf/Gsdf 表达在精原细胞周边的生殖体细胞中。此外，rGsdf 在体外卵巢组织培养中降低了卵原细胞的细胞新生，对性别相关基因表达没有影响。因此，Gsdf 信号抑制早期生殖细胞新生，此外，我们推测 Gsdf 信号与早期生殖腺分化有关，但不具性别的专一性。

关键词：gsdf；石斑；性转变；性别分化

The characteristics and expression profile of gonadal soma-derived factor (gsdf/Gsdf) during androgen-induced reversible sex change in the protogynous orange-spotted grouper, Epinephelus coioides

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Abstract：Gonadal soma-derived factor (gsdf) is a teleost- and gonad-specific growth factor involved in gonadal differentiation and early germline cell development. In protogynous grouper, the androgen-induced precocious male phase is transient, and a reversible sex change occurs after chemical withdrawal. Our results showed that the expression of gsdf was higher in the MT-induced male than in the control female. Conversely, high gsdf expression was also found in the transient phase of reversible induced male-to-female sex change. Furthermore, gsdf/Gsdf was expressed in the Sertoli cells surrounding the spermatogonia and the somatic cells surrounding the oogonia. gsdf/Gsdf expression was also found in the somatic cells surrounding the spermatogonia-like cells in the transient phase of induced male-to-female sex change. Moreover, the proliferation activities of the oogonia were decreased by rGsdf in in vitro ovarian tissue culture. Taken together, our data suggest that Gsdf signaling is related to the arrest of proliferation activity in early-stage germline cells but is not directly related to sexual phase determination.

Key words: gsdf, grouper; sex change; sex differentiation

重金属铜对日本沼虾呼吸功能的影响

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摘要：重金属铜作为一种重要的微量元素，具有很高的营养价值，是大多数生物体不可缺少的。然而对铜作用下甲壳动物的呼吸作用的研究是有限的。本研究结果表明铜胁迫会损害日本沼虾正常呼吸代谢活动，日本沼虾有氧呼吸和无氧呼吸均受到抑制，同时铜暴露还可能导致甲壳动物体内产生过量活性氧的产生，导致过多的铜离子进入日本沼虾体内,铜离子通过生物膜进入细胞，破坏细胞内离子平衡并诱发细胞毒性，对细胞结构和蛋白质的合成具有破坏作用，影响线粒体正常生理功能，造成组织损伤和细胞凋亡。本研究为含铜鱼药在日本沼虾实际养殖中的使用提供了安全浓度，为铜对日本沼虾的毒性机制提供了基础数据。

关键词：铜；呼吸；日本沼虾；线粒体

Impact of copper ions on respiratory function in the oriental river prawn (*Macrobrachium nipponense*)

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Abstract ： Heavy metal copper, as a vital trace element, has high nutritional value and is indispensable to most organisms. However, studies on the respiratory of crustaceans under copper are limited. Results in study showed that the copper can damage the normal respiratory and metabolic activities of M. nipponense, aerobic and anaerobic respiration are inhibited. At the same time, the copper can lead to oxidative stress and excess ROS, resulting in excessive Cu2+ entering M. nipponense through the gills. Then Cu2+ enter cells through biofilms, disrupt intracellular ion balance and induce cytotoxicity, disrupt cell structure and protein synthesis, affect the normal physiological function of mitochondria, and cause tissue damage and even apoptosis. This study provides the safety concentration for using copper-containing fish drugs in the actual culture of M. nipponense and provides basic data for the toxicity mechanism of copper to M. nipponense.

Key words: Copper; Respiratory; Macrobrachium nipponense; Mitochondrion

CHH 基因在红螯螯虾卵巢中的分子特征及表达分析

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摘要：甲壳动物高血糖激素家族神经激素是甲壳动物所特有的的神经多肽激素，高血糖激素家族神经激素共有下四个成员，分别包括高血糖激素（CHH）、蜕皮抑制激素（MIH）、性腺抑制激素（GIH），以及大鄂器官抑制激素（MIOH）,它们参与甲壳动物的各种生理活动。由于高血糖激素（CHH）在卵巢发育过程中的实际功能目前仍不清楚，我们主要对高血糖激素（CHH）在红螯螯虾卵巢发育过程中作用进行了探讨。在相关文献中提到高血糖激素（CHH）在不同种类中存在多型性现象，不同形式的 CHH 具有不同的功能，本文主要克隆了红螯螯虾 CHH 基因多种形式的一种-CHH1，通过 CHH1 在红螯螯虾卵巢中的分子特征及 RNA 干扰敲除 CHH1，显示 VTG-mRNA 和卵巢形态均出现异常特征。这些结果提示 CHH1 参与了卵巢发育，并通过调控 VTG 的表达而具有积极的调控作用，为进一步探讨甲壳动物卵巢发育的机制提供了新的见解。

关键词：红螯螯虾；CHH1；RNAi；表达水平；卵巢发育

Molecular characterization and expression analysis of CHH1 from Cherax quadricarinatus and its possible role in ovarian development

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Abstract： The crustacean hyperglycemic hormone (CHH) is a member of the CHH/MIH/GIH /MOIH neuropeptide family, and participated in a variety of physiological activities in crustaceans.They participate in various physiological activities of crustaceans. However, the actual functions of CHH in the processes of ovarian development were still not well defined. In the current study, we cloned and characterized CHH1 gene from the redclaw crayfish C. quadricarinatus. In the relevant literature, it is mentioned that hyperglycemia hormone (CHH) has polymorphism in different types, and different forms of CHH have different functions. This paper mainly cloned a variety of forms of CHH gene in Cherax quadricarinatus.The molecular characteristics of CHH1 in red crayfish ovary and knockdown of CHH1 by RNA interference suggest that CHH1 is involved in ovarian development and has a positive regulatory effect by regulating the expression of VTG.

Key words: Cherax quadricarinatus; CHH1. RNAi；expression level; ovarian development

脊尾白虾 uhrf1 基因在卵巢发育中的功能研究

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摘要：脊尾白虾具有很高的繁殖能力，一年可繁殖多达 3-4 代的虾类，为探讨影响脊尾白虾性腺发育的遗传因子，本研究在克隆脊尾白虾 uhrf1 基因（Ec-uhrf1）基础上，对其在卵巢发育中的功能进行了探索。脊尾白虾 uhrf1 基因开放阅读框 2286bp,共编码 761aa，拥有 UBL，TTD，PHD，SRA，RING finger 等多个基因组甲基化、组蛋白识别、染色质修饰相关结构域。通过系统进化分析，Ec-Uhrf1 氨基酸序列与凡纳滨对虾（*Litopenaeus Vannamei*）Uhrf1 相似性最高，与同为甲壳纲凡纳滨对虾和斑节对虾（*Penaeus monodon*）聚为一支。荧光定量 PCR 结果显示，uhrf1 在脊尾白虾卵巢组织中的表达量最高，且显著高于其他组织（$P<0.05$）。另外，其在卵巢发育 I-IV期逐渐上升，在IV期表达量最高且显著高于其他时期（$P<0.05$）。

关键词：脊尾白虾；uhrf1；表达分析；RNA 干扰；原位杂交

Study on the function of uhrf1 gene during ovarian development in Exopalaemon carinicauda

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Abstract: Ridgetail white prawn with high reproductive capacity can reproduce up to 3-4 generations a year. In order to explore the genetic factors affecting the gonadal development of ridgetail white prawn, the function of uhrf1 gene (Ec-uhrf1) in ovarian development was explored on the basis of cloning.The open reading frame of uhrf1 gene is 2286bp, encoding 761aa in total. uhrf1 has UBL, TTD, PhD, SRA, ring finger domains that are associated with genome methylation, histone recognition and chromatin modification.According to the phylogenetic analysis, the amino acid sequence of Ec-uhrf1 has the highest similarity with that of *Litopenaeus vannamei* uhrf1, and it is a branch of *Penaeus monodon* and *Litopenaeus vannamei*. The results of real-time quantitative PCR showed that the expression level of uhrf1 was the highest in ridgetail white prawn ovarian tissue, and was significantly higher than that in other tissues ($P<0.05$). In addition, it gradually increased in stages I-IV of ovarian development,

Key words: Exopalaemon carinicauda; uhrf1; RNA interference; In situ hybridization; Expression analysis

大黄鱼抗内脏白点病基因组选择育种进展

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摘要：大黄鱼是我国东南沿海最重要的海洋经济鱼类之一。然而，大黄鱼产业的可持续发展受到各种疾病问题的制约，特别是由变形假单胞菌引起的内脏白结节病（VWND）。基因组驱动的现代育种技术已被证明是解决这些问题的有效方法。本研究利用标准化的表型测量体系，构建了抗 VWND 的参考群体和候选群体，并使用简化基因组和育种芯片对所有的个体进行基因分型。基于基因组选择（GS）育种技术，使用最适合的 GS 模型计算候选群体的估计育种值（GEBV），培育出了抗 VWND 的后代。同时，全基因组关联分析 （GWAS）结果进一步支持了抗病性状存在微效多基因的遗传结构（h2~0.3），并且定位到了与 VWND 抗性显著相关的 SNP 位点。后代抗性测评结果表明，抗性品系的感染后成活率相比技术对照品系提升 18.67-27.77%。目前工作中，我们开发了机器学习和深度学习的图像采集技术采集感染程度性状，对遗传和分子机制的共同调控机制进行了研究。

关键词：基因组选择；表型测量；全基因组关联分析；机器学习；深度学习；分子机制

Breeding progress for visceral white-nodules disease resistance based on genome selection technology in large yellow croaker

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Abstract： Large yellow croaker is one of the most important marine economic fish in the southeast coast of China. However, the sustainable development of large yellow coraker industry is constrained by various disease problems, especially for the visceral white-nodules disease (VWND) that caused by Pseudomonas plecoglossicida. Genome-driven modern breeding techniques have been proved to be efficient ways to solve these problems. In this study, reference and candidate populations for VWND resistance were constructed using standardized phenotypic measurement system.Based on genomic selection (GS) breeding technology, the GEBV of candidate populations was calculated using the most suitable GS model, and VWND resistant offspring were bred. Meanwhile, the results of GWAS further supported the genetic structure of micro-effect polygenes (h2~0.3). The evaluation results of the offspring showed that the survival rate of RS increased by 18.67-27.77% compared with the TCS after VWND infection.

Key words: Genomic selection; Phenotypic measurement; GWAS, Machine learning; Deep learning; Molecular mechanism

日本沼虾(*Macrobrachiumnipponense*)环氧合酶(COX)基因的鉴定及其在卵巢发育和排卵中的作用

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摘要：前列腺素（PGs）与甲壳动物的卵巢发育和排卵相关，环氧合酶（COX）是合成 PGs 的限速酶。本研究克隆出了日本沼虾（*Macrobrachium nipponense*）的 COX（MnCOX）基因，并采用荧光定量 PCR（QPCR）、荧光原位杂交（FISH）、RNA 干扰（RNAi）、花生四烯酸（AA）和地塞米松（DEX）给药方法，研究了该基因对日本沼虾卵巢发育和排卵的作用。结果显示：MnCOX cDNA 全长 3238 bp，编码 615 个氨基酸；MnCOX 基因在Ⅴ期卵巢中表达量最高，其 mRNA 分布于卵原和卵母细胞的细胞质中；MnCOX 基因沉默导致卵黄蛋白原（Vg）和卵黄蛋白原受体（Vgr）基因表达量下降，卵母细胞发育延迟，日本沼虾性腺指数、产卵率和排卵数降低；AA 给药提高了日本沼虾的产卵率，DEX 给药降低了其产卵率和排卵数。结果证明 MnCOX 在日本沼虾卵巢发育和排卵过程中起重要的调节作用。

关键词：日本沼虾；环氧合酶；RNA 干扰；卵巢发育；排卵

Identification of cyclooxygenase (COX) gene from the oriental river prawn Macrobrachium nipponense and its roles in ovarian development and ovulation

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Abstract： Cyclooxygenase (COX) is the rate-limiting enzyme in synthesis of prostaglandins (PGs) which are involved in ovarian development and ovulation in female crustaceans. In this study, a complementary DNA (cDNA) of COX in *Macrobrachium nipponense* (MnCOX) was isolated, and its role in ovarian development and ovulation was investigated using quantitative real-time PCR (qPCR), fluorescence in situ hybridization (FISH), RNA interference (RNAi) and arachidonic acid (AA) and dexamethasone (DEX) administrations. The results showed that the complete cDNA of MnCOX is 3238 base pairs (bps) and contains an 1848 bp open reading frame (ORF) encoding 615 amino acids (aas). The richest MnCOX transcript of nine tissues was found in the gill, followed by the ovary and intestine. In six ovarian development stages, MnCOX transcript was the richest in the stage Ⅴ ovary. FISH showed that MnCOX transcript was present in the cytoplasm of oogonia and oocytes in I-Ⅵ stage ovaries. RNAi-mediated knockdown of MnCOX led to the decreases in expression levels of vitellogenin (Vg) and vitellogenin receptor (Vgr) genes and the gonadsomatic index (GSI) of prawn. Moreover, the oocyte development was delayed, as well as the oviposition rate and the number of eggs ovulated were reduced after MnCOX knockdown. AA administration increased the expression of MnCOX and the oviposition rate of prawn, while had no effect on the number of eggs ovulated. However, DEX administration decreased the expression of MnCOX, the oviposition rate and the number of eggs ovulated of prawn. This investigation illustrates an important regulatory role of MnCOX in the ovarian development and ovulation of M. nipponense.

Keywords: Macrobrachium nipponense; Cyclooxygenase; Gene expression; RNA interference; Ovarian development; Ovulation

黄鳝受噁唑酰草胺的急性毒性影响机体的免疫，抗氧化及免疫损伤

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摘要：本研究目的在于探讨在噁唑酰草胺影响下，通过免疫损伤指标，观察分析黄鳝机体是否会受到损伤，以及机体本身，会产生怎样的免疫，抗氧化来应对噁唑酰草胺的胁迫。在研究得出 96h LC50 后，将黄鳝暴露于 LC50 内设置的 4 个浓度梯度中，分别为 0.2mg/L，0.4mg/L，0.6mg/L，0.8mg/L，并以 0mg/L 为对照组，经过 96h 急性胁迫后，采集血淋巴及肝脏样本，测定免疫、抗氧化及应激损伤相关酶活性。研究结果表明，各浓度下 MET 对血淋巴中 WBC 有极显著影响（$P<0.01$），各浓度下 MET 在肝脏中对 AKP、SOD 无显著影响（$P>0.05$），对 ACP、CAT、MDA 有显著影响（$P<0.05$），对 GPX、ROS 有极显著影响（$P<0.01$）。研究结果表明，随着 MET 浓度升高，免疫及抗氧化相关酶活性显著低于对照组，对机体造成氧化损伤。

关键词：黄鳝；噁唑酰草胺；免疫；抗氧化

Effects of acute toxicity of metamifop on immunity, antioxidation and immune injury of Monopterus albus

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Abstract: The purpose of this study is to explore whether the rice field eel will be damaged under the influence of MET, through the immune injury index, observe and analyze whether the rice field eel will be damaged, and itself, what kind of immunity and antioxidant will be produced to cope with the stress of MET. After 96 h LC50 was obtained, the rice field eel was exposed to four concentration gradients set within LC50, which were 0.2mg / L, 0.4mg / L, 0.6mg / L, 0.8mg / L, and 0mg / L was used as the control group. After 96 h acute stress, hemolymph and liver samples were collected to determine the activities of immune, antioxidant and stress-related enzymes. The results showed that MET had a significant effect on WBC ($P<0.05$), ACP, CAT and MDA ($P<0.05$), GPX and ROS ($P<0.01$). The results showed that with the increase of MET concentration, the activities of immune and antioxidant related enzymes were significantly lower than those of the control group, causing oxidative damage.

Key words: Monopterus albus; MET; Immune; Antioxidant

小黄鱼经济性状相关位点挖掘及新种质创制研究金进展

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摘要：小黄鱼是我国传统四大海产之一，具有重要的经济价值，其人工繁殖和养殖关键技术于2015年成功突破后，已成为新兴养殖对象。研究团队利用高通量测序技术成功解析小黄鱼基因组序列，获得大小680M、contigN50高达25.99M的高质量小黄鱼基因组，以此为基础，利用QTL定位和GWAS分析方法挖掘生长、耐高温、营养品质等重要经济性状相关功能位点和基因，分别筛选出生长性状相关位点5个、耐高温性状相关位点25个和、营养品质性状相关位点65个，研究结果为开发SNP芯片进行基因组选择育种奠定了重要基础。同时，研究团队在2代群体选育的基础上，通过构建大规模全同胞和半同胞家系，利用REML和BLUP方法进行生长性状的遗传评估，筛选优良亲本繁殖后代，经过2代家系选育，培育出快速生长小黄鱼新品系，8月龄时生长速度较未选育群体提高25.6%，研究成果对于新品种培育和养殖业快速发展具有重要促进作用。

关键词：小黄鱼；经济性状；基因组；新品种培育

Progress in excavating relevant loci of economic traits and selective breeding of Larimichthys polyactis

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Abstract： Larimichthys polyactis, is one of the traditional "Four major seafood" in China and has important economic value. We successfully analyzed the genome sequence of L. polyactis using high-throughput sequencing technology, and obtained a high-quality genome with a size of 678.6 M and a contig N50 of 25.99M. On this basis, 5, 25 and 65 locus related to economic traits of growth, high-temperature tolerance and nutritional quality were screened by QTL mapping and GWAS analysis, respectively, which laid an important foundation for the development of SNP chip for genome selection breeding. In addition, on the basis of 2-generation population selection, large-scale families were constructed to carry out genetic evaluation of growth traits and screen excellent parents for breeding offspring. After 2-generations of family selection breeding, a fast-growing strain of was obtained. The growth rate of which at 8 months of age was increased by 25.6%.

Key words: Larimichthys polyactis; Economic trait; Genome; Selective breeding

转录组分析揭示了余氯对青蛤免疫的影响

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摘要：为了探究余氯急性胁迫下青蛤（*Cyclina sinensiss*）肝胰腺免疫基因的差异表达，本研究通过高通量测序技术，分析青蛤余氯急性胁迫组（20 mg/L、50 mg/L、100 mg/L）和对照组某些基因的差异表达，并对差异基因进行生物信息学分析，进一步采用实时荧光定量 PCR（RT-qPCR）对关键差异表达基因进行验证。通过本研究，发现余氯急性胁迫显著改变了与信号转导、微生物凝集、细胞凋亡、模式识别蛋白/受体和蛋白质编码相关的免疫相关分子的表达水平。综上所述，本研究为了解余氯急性胁迫对青蛤免疫功能的分子机制的影响提供了有价值的信息。

关键词：余氯；青蛤；转录组；免疫

Transcriptome analysis reveals the effect of residual chlorine on immunity in the Cyclina sinensis

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Abstract：In order to investigate the differential expression of hepatopancreatic immune genes in green clams (*Cyclina sinensis*) under acute residual chlorine stress, this study analysed the differential expression of certain genes in the hepatopancreatic groups (20 mg/L, 50 mg/L, 100 mg/L) and the control group by high-throughput sequencing. The differentially expressed genes were further validated by real-time fluorescence quantitative PCR (RT-qPCR). In this study, it was found that acute stress with residual chlorine significantly altered the expression levels of immune-related molecules associated with signal transduction, microbial agglutination, apoptosis, pattern recognition proteins/receptors and protein coding. Taken together, this study provides valuable information for understanding the effects of acute residual chlorine stress on the molecular mechanisms of immune function in Cyclina sinensis.

Key words:：Residual chlorine; *Cyclina sinensis*; Transcriptome; Immunity

缢蛏两个群体对高盐的耐受性比较分析

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摘要：探讨缢蛏早期发育阶段的高盐耐受性，本文对比了高盐对缢蛏两个群体（新品种“申浙一号”群体：SZSC、自然群体：ZRSC）幼虫和稚贝的影响。幼虫生长试验设置了 6 个盐度梯度（12、16、20、24、28 和 32），稚贝试验分为高盐（32）养殖以及不同盐度下（20、24、28 和 32）摄食率试验。结果表明，随着盐度上升，两个群体幼虫的生长速率、存活率及变态率均先上升再下降，各盐度组 SZSC 幼虫壳长、壳高日增长量均显著高于 ZRSC（$P<0.05$）。稚贝在高盐养殖下，SZSC 的存活率以及壳长、壳高、壳宽和体质量特定生长率均显著高于 ZRSC，同时摄食试验表明，盐度 24、28 和 32 组 SZSC 的摄食率显著高于 ZRSC。此外，在半致死盐度试验中，SZSC 的半致死盐度高达 34.64，显著高于 ZRSC。研究表明，SZSC 对高盐耐受力更强，各项评价指标均优于 ZRSC，本研究进一步为缢蛏耐高盐选育提供了参考依据。

关键词：缢蛏；幼虫；高盐；生长发育；摄食率

Comparative analysis of high salt tolerance traits among two populations of Sinonovacula constricta

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Abstract： To explore the high salt tolerance in the early developmental stage of razor calm Sinonovacula constricta. In this paper, the effects of high salinity on the larvae and juveniles of razor calm were studied, including the new variety "Shenzhe No.1" population(SZSC), and the natural population(ZRSC).The larval growth test was performed at different salinities (12, 16, 20, 24, 28 and 32).The test of juveniles was divided into high salt (32) culture and feeding test under different salinity (20, 24, 28 and 32). The results showed that the growth rate, survival rate and metamorphosis rate of larvae of the two populations increased at first and then decreased with the increase of salinity. The daily growth of shell length and shell height of SZSC larvae at each salinity were significantly higher than that of ZRSC ($P<0.05$). The survival rate and specific growth rates of shell length, shell height, shell width and body mass of SZSC in high salt group were significantly higher than those of ZRSC ($P<0.05$). The feeding test showed that the feeding rate of SZSC was significantly higher than that of ZRSC at 24, 28 and 32 salinity ($P<0.05$). In addition , the semi-lethal salinity of SZSC was 34.64, which was significantly higher than that of ZRSC ($P<0.05$). In summary, all the evaluation indicators of SZSC are better than ZRSC under high salt condition. This study further provides reference for the breeding of Sinonovacula constricta under high salt.

Key words: Sinonovacula contricta; larvae,high salinity; growth and development; feeding rate

青蛤 dmrt1 和 foxl2 的克隆表达及 E2 响应

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摘要：青蛤（*Cyclina sinensis*）是我国重要的养殖经济贝类之一，目前有关其性别决定及分化的研究较少。本研究采用 RACE 技术克隆青蛤 dmrt1 和 foxl2 基因的 cDNA 全长。通过分析 dmrt1 和 foxl2 在青蛤不同胚胎发育时期、不同组织、不同性腺发育阶段及不同月龄幼贝中的表达差异，发现 dmrt1 的表达呈现性别二态性；两个基因在性腺不同发育时期的表达水平与性腺发育呈正相关；不同组织中，foxl2 在斧足的表达量最高，说明 foxl2 在青蛤神经发育及组织分化中发挥作用。将青蛤浸泡在含有不同浓度雌二醇的海水中 21 天，荧光定量显示性腺中 dmrt1 和 foxl2 的表达水平都在 5ug/L 中最高；组织学观察到随着 E2 浓度增高，卵径变大。这些结果表明 dmrt1 和 foxl2 在青蛤的性腺发育和性别分化中起重要作用，有助于贝类性别分化的分子机制的研究。

关键词：青蛤；Dmrt1； Foxl2；序列分析；荧光定量 PCR；17β-雌二醇

Cloning and expression of dmrt1 and foxl2 and response to estrogen in clam *Cyclina sinensis*

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Abstract： The clam *Cyclina sinensis* is one of the important economical aquaculture shellfish in China. There are few studies on C. sinensis sex determination and differentiation at present. In this study, full-length cDNAs of dmrt1 and foxl2 were cloned from the gonadal tissues of C. sinensis by RACE. Analysis of the expression differences of dmrt1 and foxl2 in different embryonic development periods, different tissues, different gonadal development stages and different month-old juvenile clams revealed that the expression of dmrt1 showed sexually dimorphic expression. Expression levels of them at different periods of gonad development were positively correlated with gonad development. Dmrt2 expression peaked in the foot in different tissues, indicating that foxl2 plays a role in neural development and tissue differentiation in C. sinensis. Clams were exposed to 17β-Estradiol (E2: nominal concentration: 0 μg/L, 5 μg/L and 50 μg/L) for 21 days. RT-qPCR showed that the expression levels of dmrt1 and foxl2 in the gonads were highest in 5ug/L, and histologically, it was observed that the oocytes diameters became larger with increasing E2 concentration. These results suggest that dmrt1 and foxl2 play an important role in gonadal development and sex differentiation in C. sinensis and contribute to the study of the molecular mechanism of sex differentiation in shellfish.

Key words: *Cyclina sinensis*; Dmrt1; Foxl2; sequence analysis; RT-qPCR; 17β-Estradiol

黄壳和黑壳河蚬的比较转录组学分析

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摘要：河蚬(*Corbicula Fluminea*，C.fluminea)，从属于软体动物门、瓣鳃纲、真瓣鳃目、异齿亚目、蚬科、蚬属。河蚬原产于亚洲，然后传播到北美、南美洲和欧洲，是一种重要的生态和经济双壳类动物。在本研究中，我们对河蚬两种壳色（黄色和黑色）进行了转录组测序，并通过RNA 序列和时间过程 qPCR 分析研究了与着色相关的特异性基因的差异表达模式。从转录组中获得 29283 个单基因，其中 24174 个被注释，包括 289 个的显著上调基因和 286 个显著下调基因（log2 (fold change) | ≥2 and qvalue<0.05）。黑色素生成途径在贝壳色素沉着过程中起着重要作用，并与表面图案的形成密切相关。我们推测流体剪切应力和动脉粥样硬化途径可能与贝类的颜色形成有关。本研究揭示了河蚬的着色和着色机制，并分析了黄色和黑色河蚬在免疫和代谢方面可能存在的差异。

关键词：河蚬；贝壳颜色；转录组分析；黑色素

Comparative transcriptomic analysis of yellow-shelled and black-shelled *Corbicula Fluminea*

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Abstract ： Comparative transcriptomic analysis of yellow-shelled and black-shelled *Corbicula Fluminea* River clams belong to the phylum Mollusca, class Petromorpha, order True Petromorpha, suborder Heterodontidae, family Clamidae, and genus Clam. C. fluminea are native to Asia and then spread to North America, South America and Europe, and are an ecologically and economically important bivalve. In this study, we sequenced the transcriptome of two shell colors (yellow and black) of river clams and investigated the differential expression patterns of specific genes associated with coloration by RNA sequence and time-course qPCR analysis. 29283 single genes were obtained from the transcriptome, of which 24174 were annotated, including 289 significantly up-regulated genes and 286 significantly down-regulated genes (log2 (fold change) | ≥2 and qvalue<0.05). The melanogenic pathway plays an important role in the process of shell pigmentation and is closely associated with the formation of surface patterns. We hypothesize that fluid shear stress and atherosclerotic pathways may be related to the color formation in shellfish. This study reveals the coloration and coloration mechanisms of river clams and analyzes possible immunological and metabolic differences between yellow and black C. fluminea.

Key words: *Corbicula Fluminea*; shell coloration; transcriptome analysis; melanin

中西太平洋金枪鱼围网渔获组成的比较分析

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摘要：金枪鱼围网渔业作业方式按集群类型可分为4类，鲣鱼、黄鳍金枪鱼、大眼金枪鱼为主要捕捞对象。本研究利用中西太平洋1984-2020年围网渔业数据，对中国、中国台湾、美国、西班牙围网船队下不同鱼种的作业方式、渔获率、空间分布进行分析，研究表明：160°E热带东部地区投网数相对更多；鲣鱼与大眼金枪鱼的CPUE之间存在显著的弱相关关系；黄鳍金枪鱼与大眼金枪鱼CPUE之间存在显著的弱相关关系；对不同作业方式的季CPUE进行单因素方差分析，存在显著性差异（$P= 0.00124<0.05$）；不同船队的CPUE不存在显著性差异。研究结果为围网渔业金枪鱼的科学养护与管理提供参考依据。

关键词：中西太平洋；金枪鱼围网；CPUE；集群

Comparative analysis of the catch composition of Western and Central Pacific tuna purse seine

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Abstract： According to the cluster type, the tuna purse Seine fishery can be divided into four categories. Bonito tuna, yellowfin tuna and bigeye tuna are the main fishing objects. Using the Seine fishery data from 1984 to 2020 in the Central and Western Pacific Ocean, this study analyzed the operation mode, catch rate and spatial distribution of different species under the Seine fleets of China, Taiwan, the United States and Spain. The results showed that the number of cast nets was relatively higher in the tropical eastern region at 160°E. There was a weak correlation between CPUE of Bonito and bigeye tuna. There was a weak correlation between CPUE and bigeye tuna. One-way analysis of variance (ANOVA) was performed for seasonal CPUE with different operating modes, and significant differences were found (*P= 0.00124< 0.05*); There was no significant difference in CPUE among different fleets. The results provide a reference for the scientific conservation and management of tuna in purse Seine .

Key words: Western and Central Pacific; Tuna purse seine; CPUE; Cluster

中国沿岸小型渔业特征及管理策略改进研究：以浙江省嵊泗县为例

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摘要：小型渔业为中国水产品供给、就业及维护社会稳定诸多方面作出了重大但难以计算的贡献。然而，小型渔业的差异性、脆弱性和复杂性问题没有引起社会的充分关注，其特征及管理策略研究十分有限。本文以嵊泗县为例，利用政府公开数据和渔民问卷调查、半结构访谈的数据，分析了嵊泗县小型渔业的特征，梳理了现行的浙江省、舟山市和嵊泗县小型渔业管理政策分析了其存在的问题并提出改进策略。我们的研究结果显示，嵊泗县小型渔业的现行制度主要采用投入控制措施，仅对降低捕捞强度和恢复近岸资源有促进作用而没有充分考虑小型渔业的社会经济特征。我们建议，应通过定量和定性指征的结合完善小型渔业的界定依据，细化小型渔业渔民、渔具、渔场的准入条件；提升小型渔业组织化程度，加强其自身能力建设及外界支持，同时探索和改进治理模式，完善职能部门间的协同机制，协调各利益方共同参与解决小型渔业的治理问题。

关键词：小型渔业；特征；管理策略；中国；嵊泗县

Characteristics of Small-Scale Coastal Fisheries in China and Suggested Improvements in Management Strategies: A Case Study from Shengsi County in Zhejiang Province

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Abstract：The small-scale fisheries (SSF) in China have made significant contributions to the supply of aquatic products, employment, and social stability. However, its complexity, dynamicity and vulnerability have not yet received sufficient attention either from the government or from the society. There are limited research on its characteristics and management strategies. We select Shengsi County, a community with traditional fishing activities, in Zhejiang Province as a case study to analyze, review, and examine the SSF' characteristics and current policies, based on government open data and information collected by questionnaires and semi-structured interviews. Our study shows that the current system of SSF in Shengsi County mainly adopts input control measures, which only contributes to fishing capacity control and restoration of inshore resources, yet lack of due consideration on the socioeconomic characteristics of SSF.

Key words: small scale fishery; characteristics; management strategies; China; Shengsi County

基于熵值法的中国水产养殖业绿色发展评价研究

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摘要：推进水产养殖业绿色发展是保护水域生态环境、推进水产养殖业高质量发展的重要举措。本文在系统阐释水产养殖业绿色发展内涵的基础上，构建了包含养殖资源、养殖环境、养殖技术、渔业管控和高效发展五个维度 27 个指标的水产养殖业绿色发展水平指标评价体系，并对 2012—2020 年间全国及 11 个水产养殖业主产省份的水产养殖业绿色发展水平进行评估。结果显示，在全国层面，我国水产养殖业绿色发展水平在考察期间实现平稳增长，但增速缓慢，发展水平不高；省域层面，各省份水产养殖业绿色发展水平差距较大，水产养殖业绿色发展较好的“领先型”省份多集中在东部沿海地区。研究认为，为提升我国水产养殖业绿色发展水平，应强化对渔业资源的保护和管理，完善绿色养殖补贴政策；加强水产养殖业生产监管和管理服务水平；鼓励渔业科技创新，创新科技成果转化推广形式；因地制宜发挥地域特色优势，加大渔业主产区的绿色生产投入。

关键词：水产养殖业；绿色发展；评价指标体系；熵值法

Evaluation of green development of aquaculture in China based on entropy method

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Abstract： Green development of aquaculture is an important measure to implement the new development concept, protect the ecological environment of water areas and implement the strategy of Rural Revitalization. It is also an inevitable choice to optimize the layout of fishery industry, deal with the contradiction between the upgrading of aquatic product consumption and traditional aquaculture production, and promote the transformation and upgrading of aquaculture. On the basis of systematically explaining the connotation of green development of aquaculture, this paper constructs an evaluation index system of green development level of aquaculture in China, which includes 27 indicators in five dimensions of aquaculture resources, aquaculture environment, aquaculture technology, fishery management and control and efficient development, and evaluates the green development level of aquaculture in China and 11 major aquaculture producing provinces from 2012 to 2020.

Key words: Aquaculture; Green development; Evaluation index system; Entropy method

远洋渔业集鱼灯实验室测评认证进度计划与管理研究

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摘要：远洋渔业中集鱼灯产品检测市场需求量大、种类繁多，但集鱼灯质量检测的规范化和标准化有待提升，本文对于集鱼灯实验室的检测能力的规范化和标准化进行研究。针对现有的集鱼灯检测指标与项目，对集鱼灯检测能力进行自我能力评价，其次寻求第三方实验室检测项目能力评估，然后申请实验室检测国家能力认可，最后申请国际检测能力的认可。以国家远洋渔业工程技术研究中心集鱼灯测评实验室认证为例，对该实验室的光强分布、光通量、光束角的检测能力进行自我能力评价；寻求第三方进行检测能力的评估；申请实验室检测中国计量认证；申请中国合格评定国家认可委员会的认可。资质认证对于提高集鱼灯实验室在业内的认可度、促进集鱼灯产品优化设计及应用具有关键作用，对于集鱼灯优化、提高捕捞生产效率具有一定推进作用。

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 progress plan and management of the evaluation and certification of the pelagic fishing lamp laboratory

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Abstract：There is a large market demand and a wide variety of fishing lamp products in the ocean fishery industry,However, the standardization and standardization of the quality inspection of fishing lamps need to be improved，this paper studies the standardization and standardization of the detection capabilities of fishing Lamp Laboratory.For the existing fishing lamp detection indicators and projects,Self-assessment of the detection ability of fishing lamps,Second, seek third-party laboratory testing project capability assessment,Then apply for national competence accreditation for laboratory testing,Finally apply for the recognition of international testing capabilities.Take the National Ocean Fishery Engineering Technology Research Center Fishing Lamp Evaluation Laboratory Certification as an example.Self-evaluation of the laboratory's ability to detect light intensity distribution, luminous flux,and beam angle,Seek third-party assessment of detection capabilities,Apply for Laboratory Testing China Metrology Certification.Apply for accreditation from China National Accreditation Service for Conformity Assessment,Qualification certification plays a key role in improving the recognition of Fishing Lamp Laboratory in the industry and promoting the optimal design and application of Fishing Lamp products. It has a certain role in promoting the optimization of fishing lamp and improving the efficiency of fishing production.

Key words: Pelagic fishing; Fishing lamp; Quality Inspection; Standardization; Testing ability; Certification

国内外水生野生保护动物研究现状及热点分析

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摘要：摘要:水生野生保护动物是水生生态系统中的重要组成部分。文章利用 CiteSpace 文献可视化软件分析了 Web of Science（WoS）核心数据库和中国知网（CNKI）全文数据库中 2001—2020 年水生野生保护动物相关的文献，对年度发文量、合作机构、国家合作和关键词聚类进行知识图谱分析。研究发现：近 20 年共发表外文文献 634 篇，发文量总体呈上升趋势，中文文献 128 篇，总体呈水平波动趋势；国外发文量最多的机构是美国鱼类及野生动植物管理局，研究机构间合作较为紧密，国内发文量最多的机构是青海省渔业环境监测站，研究机构间的合作分散；美国发文量占比为 58.20%，与其他国家交流最为密切，中国发文量占比仅为 3.31%，与国际合作关系不紧密；国外的研究热点主要是种群动态分布、栖息地利用和遗传多样性等，海洋与淡水物种均有研究；国内的研究热点主要是区域性保护措施，主要以淡水水生野生保护动物的研究为主，研究范围存在局限性。综合分析认为，我国应增进国内外研究机构间的交流与合作，重视海洋濒危水生野生动物的保护与研究，加强种群动态评估，开展国内对水生野生保护动物栖息地利用与遗传多样性分析的研究，从而实现水生野生保护动物种群的恢复。

关键词：水生野生保护动物；CiteSpace；知识图谱；可视化

Research status and hotspot analysis of aquatic wildlife protection at home and abroad

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Abstract： Protected aquatic wildlife is an important part of the aquatic ecosystems. This paper used CiteSpace document visualization software to analyze the literature on protected aquatic wildlife from 2001 to 2020 in the core database of Web of Science (WoS) and the full-text database of China National Knowledge Infrastructure (CNKI). This paper conducted the knowledge map analysis of annual publication volume, cooperative institutions,and keyword. The study found that a total of 634 foreign language papers were published in the past 20 years, with an upward trend in the number of publications, and 128 documents in Chinese showed a fluctuation trend; the organization with the largest number of foreign publications is the US Fish & Wildlife Service, with closer cooperation among research institutions, the organization with the largest number of domestic publications is the Qinghai Fishery Environmental Monitoring Station, with scattered cooperation among research institutions; foreign research hotspots are mainly population dynamic distribution, habitat use and genetic diversity and both marine and freshwater species have been studied; domestic research hotspots are mainly regional conservation measures, mainly focusing on the study of freshwater species. The comprehensive analysis suggests that China should enhance cooperation between domestic and foreign research institutions, attach importance to the research of marine endangered aquatic wildlife, strengthen the population dynamics assessment, and carry out domestic research on the habitat use and genetic diversity analysis of aquatic wildlife, so as to achieve the recovery of aquatic wildlife populations.

Key words: Aquatic wild protected animals; CiteSpace; Knowledge map; Visualization

浙江省渔业可持续发展研究评价

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摘要：根据浙江省 2011-2020 年渔业产值数据，运用偏离-份额分析模型和灰色关联分析法，分析浙江省渔业产业结构，以及产业内部结构和发展水平。结果表明：浙江省渔业近几年一直处于蓬勃发展的状态，渔业经济总产值和水产品总量不断提高。其中第一产业一直是强势产业，发展水平大于全国渔业的整体发展水平。第二产业产值近几年大幅度下降，第三产业目前产值占比较低，发展水平滞后，竞争力较弱。总体来看，产业结构正由“一二三”向“一三二”的产业形态演变，但短时间内难以有质的改变，处于一种较为均衡稳定的状态。建议稳定发展远洋渔业、大力发展海水养殖业、调整加工水产品结构、积极发展休闲渔业，以促进浙江省渔业产业结构调整和可持续发展。

关键词：渔业；产业结构；偏离-份额分析模型；灰色关联分析法；可持续发展

Evaluation of research on sustainable development of fisheries in Zhejiang province

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Abstract： According to the fishery output value data of Zhejiang Province from 2011 to 2020, the fishery industrial structure, internal structure and development level of Zhejiang Province are analyzed by using deviation-share analysis model and grey relational analysis method. The results show that the fishery in Zhejiang Province has been in a state of vigorous development in recent years, and the total output value of fishery economy and the total amount of aquatic products have been increasing. Among them, the primary industry has always been a strong industry, and its development level is higher than the overall development level of the national fishery. The output value of the secondary industry has declined significantly in recent years, the current output value of the tertiary industry is relatively low, the level of development lags behind, and the competitiveness is weak. Generally speaking, the industrial structure is evolving from "one, two, three" to "one, three, two", but it is difficult to change qualitatively in a short time, and it is in a relatively balanced and stable state. It is suggested that we should steadily develop offshore fishery, vigorously develop mariculture, adjust the structure of processed aquatic products, and actively develop leisure fishery, so as to promote the structural adjustment and sustainable development of fishery industry in Zhejiang Province.

Key words: fishery; industrial structure; shift-share analysis model; grey relational analysis; sustainable development

环境俘虏、资源依赖、农产品供应链结构与收益分配----以水产品供应链为例

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摘要：供应链支农是乡村产业振兴的重要方式。但现存的农产品供应链中，核心成员侵占小农户利益现象较为普遍，小农户弱势地位突出，获益较少，什么原因导致了这样不合理的分配格局？如何保护小农户利益？本文从协同治理理论出发，基于资源依赖理论，结构洞理论，俘虏理论以水产品供应链为例解构影响农产品供应链的不对称权力和不合理分配格局的关键因素，并运用 Stackelberg 模型、Nash 模型、Shapley-A-T 值等数理模型进行模型分析。结果表明：资源不平衡依赖、结构洞位置和环境俘虏是影响农产品供应链不合理分配格局的关键因素，即资源稀缺性强的供应链成员会获得更大的供应链权力和更多收益；占据结构洞位置的成员会获得信息、资源优势，得到一定供应链权力和收益；环境俘虏下，俘虏者成员会不断改善环境获取供应链权力，从而获得更多收益。“资源—依赖—权力”，“位置—资源—权力”，“环境—俘虏—权力”是影响供应链权力和收益分配的三条核心路径。小农户因其弱势，收益被不断侵占。基于此，本文通过四种协同治理机制即价值协调机制、优化结构机制、风险分担机制和监督控制机制去平衡资源依赖、限制环境俘虏和优化结构洞位置，打破“强者愈强”的马太效应。

关键词：农产品供应链；收益分配；协同治理；资源依赖；俘虏理论；结构洞理论

Environmental Capture, Resource Dependence, Agricultural Supply Chain Structure and Benefit Distribution---- Take the fish supply chain as an example

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Abstract： Supply chain support to agriculture is an important way to revitalize rural industries. However, in the existing supply chain of agricultural products, it is common for core members to encroach on the interests of small farmers, and small farmers are in a disadvantaged position and benefit less. How to protect the interests of small farmers from being damaged? This paper deconstructs the key factors affecting the asymmetric power pattern and unreasonable distribution of agricultural supply chain based on resource dependence theory, structural hole theory, and capturing theory from collaborative governance theory, and uses the mathematical and theoretical models such as Stackelberg model, Nash model, and Shapley value for model analysis. The results show that: resource imbalance dependence, structural hole position and environmental capturing are the key factors affecting the irrational distribution pattern of agricultural products supply chain, i.e., supply chain members with strong resource scarcity will get more supply chain power and more benefits; members occupying structural hole position will get information and resource advantages and get certain supply chain power and benefits; under environmental capturing, captors will continuously improve the environment to get supply chain power and thus gain more benefits. "Resource - dependency - power", "Location - resource --power" and "environment-captive-power" are the three lines that influence The three core paths of supply chain power and returns. Because of their vuses four types of collaborative governance mechanisms, namely, value coordination mechanism, optimal slnerability, smallholder farmers have their benefits continuously appropriated. Based on this, this paper utructure mechanism, risk sharing mechanism and supervision and control mechanism, to balance resource dependence, limit environmental capture and optimize structural hole position, and break the "strongest is stronger" Matthew effect.

Key words: Agricultural supply chain; Benefit distribution; Collaborative governance; Resource dependence; Captive theory; Structural hole theory

利用贝叶斯动态产量模型评估东、黄海日本鲭资源状况

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摘要：分布于东、黄海的日本鲭(*Scomber japonicus*)为我国主要经济鱼种之一，其资源现状和开发潜力日益受到重视。加强东、黄海日本鲭的资源评估研究是其科学管理与可持续利用的前提与基础。为此，本文基于 1979—2019 年中国福建、浙江、上海、江苏、山东、河北、天津及辽宁 6 省 2 市与日本、韩国的日本鲭捕捞产量以及相关文献的资源丰度指数数据，利用贝叶斯动态产量模型对日本鲭进行了资源评估。结果表明：由于 r 与 K 存在显著负相关关系，r 的先验分布影响模型的参数估计，给出合理的 r 先验有利于提高模型评估的质量；渔获量数据观测误差精度对模型参数估计及资源状态的判断具有重要影响；东、黄海日本鲭种群结构的划分仍存在争议，目前无法按种群分别进行资源评估，若按数据统计单元对日本鲭进行资源评估将不利于日本鲭资源的可持续利用；日本鲭有较大概率(大于 60%)被过度捕捞，总可捕捞量(Total Allowable Catch，TAC)低于 4.82×105 t 时，10 年后其未被过度捕捞的概率大于 60%。基于当前东、黄海日本鲭种群划分存在争议的现状及相应数据收集存在的困难，本文建议将东、黄海日本鲭作为同一个种群处理，以满足渔业资源评估模型的基本假设、提高该渔业资源的评估质量。而将渔获量控制在 4.82×105 t 以下则有利于该渔业资源的可持续利用。

关键词：东海；黄海；日本鲭；贝叶斯动态产量模型；资源评估

Assessment of the status of *Scomber japonicus* resource in the East China Sea and Yellow Sea using a Bayesian biomass dynamic model

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Abstract：Chub mackerel (*Scomber japonicus*) in the East China Sea and Yellow Seas is one of the major commercial pelagic species in China, and its resource status and exploitation potential are receiving increasing attention. Strengthening the stock assessment research is the premise and foundation of the scientific management and sustainable utilization of the chub mackerel. In this paper, a Bayesian biomass dynamics model was used to assess the chub mackerel. The catch data from 1979 to 2019 used in the assessment are from six provinces and two cities (i.e., Fujian, Zhejiang, Shanghai, Jiangsu, Shandong, Hebei, Tianjin and Liaoning) in China, Japan and Korea, and the abundance index data are from the references. Our results show that the prior distribution of r affects the parameter estimate of the model due to the strong negative correlation between r and K and a reasonable prior for r is helpful to improve the quality of the estimates of the model; the precision of the observation error of the catch data has an important impact on the estimates of the parameter and resource status; because the delineation of population structure of chub mackerel in the East China Sea and Yellow Seas is still controversial, it is not possible to conduct separate stock assessment for each stock and the stock assessment according to the data statistical units is not conducive to the chub mackerel sustainable utilization; chub mackerel has a high probability (>60%) of being overfished or being subject to overfishing; if the TAC (Total Allowable Catch) is below 4.82×105 t, a larger than 60% probability of the stock not being overfished and not undergoing overfishing after 10 years will be expected. Due to the current controversial status of the population classification of chub mackerel in the East China Sea and Yellow Sea and the difficulties in collecting corresponding data, we suggest that the stocks in the East China Sea and Yellow Sea betreated as a stock to meet the basic assumptions of the stock assessment model and to improve the quality of the stock assessment. It will be beneficial to the sustainable utilization of the chub mackerel if the catch is below 4.82×105 t.

Key words: East China Sea; Yellow Sea; *Scomber japonicus*; Bayesian biomass dynamics model; stock assessment

基于贝叶斯动态产量模型的东、黄海日本鲭资源评估研究

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摘要：为加强东、黄海日本鲭(*Scomber japonicus*)的资源评估研究，本文基于 1979—2019 年中国福建、浙江、上海、江苏、山东、河北、天津及辽宁 6 省 2 市与日本、韩国的日本鲭捕捞产量以及相关文献的资源丰度指数数据，利用贝叶斯动态产量模型对日本鲭进行了资源评估。结果表明：由于 r 与 K 存在显著负相关关系，r 的先验分布影响模型的参数估计，给出合理的 r 先验有利于提高模型评估的质量；渔获量数据观测误差精度对模型参数估计及资源状态的判断具有重要影响；东、黄海日本鲭种群结构的划分仍存在争议，目前无法按种群分别进行资源评估，若按数据统计单元对日本鲭进行资源评估将不利于日本鲭资源的可持续利用；日本鲭有较大概率(大于 60%)被过度捕捞，总可捕捞量(Total Allowable Catch，TAC)低于 4.82×105 t 时，10 年后其未被过度捕捞的概率大于 60%。

关键词：东海；黄海；日本鲭；贝叶斯动态产量模型；资源评估

Assessment of the status of *Scomber japonicus* resource in the East China Sea and Yellow Sea using a Bayesian biomass dynamic model

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Abstract: To strengthen the stock assessment research of the chub mackerel. In this paper, a Bayesian biomass dynamics model was used to assess the chub mackerel. The catch data from 1979 to 2019 used in the assessment are from six provinces and two cities in China, Japan and Korea, and the abundance index data are from the references. Our results show that the prior distribution of r affects the parameter estimate of the model ; the precision of the observation error of the catch data has an important impact on the estimates of the parameter and resource status; the delineation of population structure of chub mackerel in the East China Sea and Yellow Seas is still controversial; chub mackerel has a high probability (>60%) of being overfished or being subject to overfishing; if the TAC is below 4.82×105t, a larger than 60% probability of the stock not being overfished and not undergoing overfishing after 10 years will be expected.

Key words: East China Sea; Yellow Sea; *Scomber japonicas*; Bayesian biomass dynamics model; stock assessment

基于死亡率极限模拟的鲸目种群风险预测及其影响因素研究

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摘要：由于鲸目物种数据的获取具有较大的不确定性，通过模拟识别人为因素可能导致鲸目种群衰竭的死亡率水平，其中死亡率极限水平（根据《美国海洋哺乳动物保护法》称为潜在生物捕获量，PBR）通过最小种群估计（Nmin）、最大净生产率（Rmax）和恢复因子（Fr）的乘积获得，最终根据评估种群是否达管理目标即100年后种群是否恢复并保持或高于最大净生产力水平（MNPL）。本文通过拟议比较两种管理策略下，不同种群丰度100年间的变化趋势，并结合模拟数据中可能存在的偏差因子进行稳健性实验。结果表明，当鲸目物种丰度估计值的精度不高时，使用最佳丰度值（N50%）作为最小种群估计会导致管理策略的不保守性，因此使用最小丰度值（N2.5%）的管理策略将更具有优越性，在种群状态未知的条件下，Fr=0.5时足以保证不同鲸目种群状态达到管理目标，Rmax对于PBR的影响较小，在鲸目种群状态未知时可以采用默认值。此外，模拟的结果表明任何鲸目物种的死亡率水平大于参考点都可能导致种群处于耗竭或受威胁的状态。

关键词：生物参考点；鲸目动物；模拟

Risk prediction of cetacean population based on mortality limit simulation and its influencing factors

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Abstract： Considering the uncertainty of cetacean data, the mortality rate of cetacean population depletion caused by anthropic factors was determined by simulation. The limited mortality level (Potential Biological Removal, PBR) is obtained by multiplying the minimum population estimate of the stock (Nmin), the maximum theoretical or estimated net productivity rate of the stock at a small population size (Rmax) and a recovery coefficient (Fr). Finally, it is based on the evaluation of whether the population has reached the management objective and whether the population will recover and maintain or be higher than the maximum net productivity level (MNPL) after 100 years. In this paper, the change trend of different population abundance in 100 years under the two management strategies is compared, and the robustness trails carried out by combining the bias factors. The results show that when the accuracy of cetacean species abundance estimation is poor, using the best abundance value (Nmin=N50%)as the minimum population estimation will lead to the non-conservatism of the management strategy. Therefore, the management strategy of using the minimum abundance (Nmin=N2.5%) will be more advantageous. When the population state is unknown, Fr=0.5 is enough to ensure that different cetacean population can achieve the management goal, and Rmax has little influence on PBR, When the population state of cetaceans is unknown, the default value can be used. In addition, the simulation results show that the mortality level of any cetacean species is higher than the reference point, which may lead to the population being depleted or threatened.

Key words: Biological reference point; cetaceans; simulation

基于统计数据的江苏省海洋捕捞量结构及投入要素变化分析

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摘要：依据《中国渔业统计年鉴》中 2010—2020 年江苏省海洋捕捞相关生产数据，结合灰色关联理论，对江苏省“十二五” “十三五”时期海洋捕捞量结构和投入要素变化进行分析。研究结果为：（1）2010—2020 年，江苏省海洋捕捞总产量呈下降趋势；（2）江苏省海洋捕捞渔获物产量以鱼类和甲壳类为主；（3）江苏省海洋捕捞机动渔船和专业劳动力人口数量减少，海洋捕捞机动渔船总吨位整体趋于增长，主机功率则波动变化；（4）江苏省海洋捕捞产量与投入要素的关联度顺序为“海洋捕捞专业劳动力＞海洋捕捞机动渔船主机总功率＞海洋捕捞机动渔船数量＞海洋捕捞机动渔船总吨位”。江苏省海洋发展空间有所缩减，海洋资源状况发展后劲不足，海洋渔业发展管控力度有所加强，海洋渔业发展存在挑战, “十四五” 时期，江苏省需要不断规范海洋渔业行为，努力恢复渔业发展生态，实现海洋渔业转型升级，开创绿色向海经济新时代。

关键词：江苏省；海洋捕捞；投入要素；关联度；建议

Analysis of marine catch volume structure and input factor change in Jiangsu Province based on statistical data

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Abstract：Based on the production data of marine fishing in Jiangsu Province from 2010 to 2020 in China Fishery Statistical Yearbook and combined with the grey correlation theory, the structure of marine fishing volume and the change of input factors during the fishery development period of "12th and 13th Five-Year Plan" in Jiangsu Province were analyzed. The results were as follows :(1) from 2010 to 2020, the total marine fishing output in Jiangsu province showed a downward trend; (2) The yield structure of main marine catches in Jiangsu Province was dominated by fish and crustaceans; (3) The total tonnage of marine fishing vessels tended to increase, while the main engine power fluctuated with the decrease of the number of marine fishing vessels and professional labor population in Jiangsu Province. (4) The order of correlation between marine fishing output and input factors in Jiangsu Province is "marine fishing professional labor force > total power of marine fishing motor fishing vessels >

Key words: Jiangsu Province; marine fishing; input factors; correlation; advice

长江中游宜昌江段铜鱼资源量和种群特征

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摘要：为了解三峡水库蓄水后，长江中游宜昌江段铜鱼的种群动态变化特征，基于 2003~2005 年、2009~2011 年和 2017~2019 年在宜昌江段收集的 9120 尾铜鱼样本的基础生物学数据，运用 FISAT II 软件对种群参数和资源量进行估算。研究表明，三峡水库蓄水后，宜昌江段铜鱼仍为匀速生长型，资源数量增加明显，但生长速率减缓，存在小型化趋势。

关键词：铜鱼；种群参数；资源量；体长股分析；宜昌江段

Population growth characteristics and stock assessment of Coreius heterodon from Yichang reach of the middle Yangtze River

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Abstract： To reveal the changes in populations parameters and resources of Coreius heterodon, we collected 9120 specimens from Yichang reach, Yangtze River, between the Three Gorges Reservoir. The results showed that the body length ranged from 118 to 416 mm with the mean of (230.7±49.8) mm, and that the body weight ranged from 10 to 1000 g, with the mean of (195.8±123.6) g in 2003~2005; the body length ranged from 111 to 409 mm with the mean of (217.5±54.3) mm, and that the body weight ranged from 19 to 889 g, with the mean of (153.2±118.6) g in 2009~2011; the body length ranged from 107 to 380 mm with the mean of (267.2±34.1) mm, and that the body weight ranged from 16 to 816 g, with the mean of (250.3±84.2) g in 2017~2019. The growth index (b) values were 3.0151, 3.0319, and 2.9775, respectively; the limit body length ($L\infty$) were 535 mm, 530 mm, and 500 mm, respectively; the growth coefficient (k) value were 0.18, 0.14, and 0.15, which belongs to the medium-rate growth type; according to the length-structured virtual population analysis, the annual resources of C. heterodon are estimated to be 1,144,927, 1,890,899, and 2,103,556, respectively. C. heterodon in the Yichang reach had a type of uniform growth, and the number has increased significantly, but the growth rate slows down, and the populations tends to be miniaturized, after the Three Gorges Reservoir was impounded.

Key words: Coreius heterodon; population parameter; fishery resource; Yichang reach

基于体长频率数据的瓯江口刀鲚资源状况评估

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摘要：刀鲚（*Coilia nasus*）是瓯江口重要的经济鱼类之一。根据 2021 年 1 月—12 月采集的 1939 尾刀鲚全长、体长和体重等生物学信息，运用 ELEFAN I 估算其生长、死亡参数，并利用单位补充量渔获量模型评估资源的利用现状。结果表明，瓯江口刀鲚体长-体重关系的表达式为 W=1×10-6L3.2196（R2=0.9830），为正异速生长；von Bertalanffy 生长参数为渐近体长 L∞、生长速率 k、理论初始年龄 t0 分别为 355mm、0.42、－0.32a；总死亡系数 Z、自然死亡系数 M、捕捞死亡系数 F 分别为 1.17、0.42 和 0.75，开发率 E 为 0.64。YPR 模型估算结果显示，当前瓯江口刀鲚的开捕年龄接近最适值，但仍可适当增大。生物学参考点 F0.1 和 Fmax 的值分别为 0.35 和 0.69。刀鲚资源处于过度开发状态，应减小捕捞压力，以确保资源的可持续利用。

关键词：刀鲚；体长频率；资源保护；单位补充量渔获量；瓯江口

Assessment of the stock status of Coilia nasus in the Oujiang River Estuary based on length-frequency data

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Abstract： Based on the data collected in the Oujiang River Estuary in 2021, the population structure,length-weight relationship, growth and mortality of Coilia nasus were analyzed. A total of 1939 individuals were caught, from which the length-weight relationship were derived as W=1×10-6L3.2196, showing a positive allometric growth pattern. The growth parameters of von Bertalanffy formula estimated by ELEFAN I of FiSAT II were 355mm(L∞),0.42a-1(k) ,and -0.32a(t0). The total mortality Z estimated by length-converted catch curve was 1.17, while the natural mortality M and fishing mortality F were 0.42 and 0.75, respectively and the exploitation rate was 0.64. Beverton-Holt yield per recruitment model simulation showed that the body length at first capture was close to the optimum value. The biological reference points F0.1 and Fmax were 0.35 and 0.69,respectively. This study shows that C. nasus stock is over-exploited. Fishing pressure should be reduced to ensure sustainable use of the resource.

Key words: *Coilia nasus*; length frequency; resource conservation ; yield per recruitment; Oujiang River Estuary

大钦岛不同养殖年限深水网箱沉积物微生物群落结构分析

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摘要：为研究深水网箱养殖年限对沉积物微生物群落结构的影响，分别对大钦岛海域养殖 3、8、13、18 a 网箱以及非养殖区（DZ）表层沉积物（0~2 cm）进行 16S rDNA 高通量测序。结果显示，长年网箱养殖（13、18 a）区域沉积物菌群的丰富度和多样性均显著高于短期网箱养殖（3、8a）区域（*P<0.05*）。随着养殖年限的增加，网箱沉积物优势菌门变化显著（P<0.05），短期网箱养殖（3、8 a）和非养殖区（DZ）沉积物主要优势菌门为拟杆菌门（*Bacteroidot*a），变形菌门（*Proteobacteria*）、厚壁菌门（*Firmicutes*），长年网箱养殖（13、18 a）沉积物主要优势菌门为拟杆菌门，变形菌门、脱硫菌门（*Desulfobacterota*）。影响网箱养殖沉积物菌群结构的主导环境因子为 Hg、Cd、有机碳以及石油类。冰鲜野杂鱼的投喂可能是大钦岛长年网箱养殖区环境恶化的重要因素之一。

关键词：深水网箱；养殖年限；沉积物；微生物群落

Analysis of the microbial community structure of deep-water net tank sediments of Daqin Island at different culture years

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Abstract： To investigate the effect of deep-water net-pen culture years on the sediment microbial community structure, 16S rDNA high-throughput sequencing was performed on the surface sediments (0-2 cm) of 3, 8, 13 and 18 a net-pen culture and non-culture areas (DZ) in Dachin Island waters, respectively. The results showed that the abundance and diversity of sediment flora were significantly higher (*P<0.05*) in the long-term net box culture (13 and 18 a) than in the short-term net box culture (3 and 8 a). The dominant phylum in the net tank sediment changed significantly (P<0.05) as the number of years of culture increased. The dominant environmental factors affecting the sediment flora structure of net tank culture were Hg, Cd, organic carbon and petroleum species.The feeding of chilled wild fish may be an important factor in the environmental degradation of the perennial net tank culture area on Dachin Island.

Key words: deep-water nets; cuture years; sediment;microbial communities

芽孢杆菌和乳酸菌对斑点叉尾鮰肠道菌群及代谢组学的影响

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摘要：本试验旨在研究饲料中分别添加芽孢杆菌和乳酸菌两种益生菌对斑点叉尾鮰肠道微生物群落以及菌群代谢物的影响。选取体质量为（50±3）g 斑点叉尾鮰 360 尾，随机分为 3 组，分别为对照组（A），芽孢杆菌组（B）以及乳酸菌组（C），每组 3 个平行，养殖周期为 11 周。结果表明，饲料中添加芽孢杆菌和乳酸菌均可提高菌群 alpha 多样性，在门水平上，厚壁杆菌门／拟杆菌门线性降低，厚壁杆菌门丰度显著低于对照组($P<0.01$)，变形杆菌门($P<0.01$)、放线杆菌门($P<0.05$)相对丰度显著高于对照组；在属水平上，与对照组相比，伯克霍尔德菌属($P<0.01$)的相对丰度显著提高，而苏黎世杆菌属($P<0.01$)和伦布西亚属($P<0.05$)的相对丰度显著下降。不同分组之间进行差异代谢物分析，共获得 5-羟基吲哚乙酸、5-羟基-L-色氨酸、甲氧基吲哚乙酸、脱氢表雄甾酮、17α-羟基孕烯醇酮、磷酸胆碱、溶血磷脂酰胆碱等 25 个差异代谢物，涉及到 30 条代谢通路。综上，饲料中添加芽孢杆菌和乳酸菌在一定程度上可改善斑点叉尾鮰肠道微生物群落，增加群落多样性，根据差异代谢物和代谢通道，推测饲料中添加的益生菌主要通过氨基酸代谢、脂代谢等代谢影响其免疫、抗炎症等能力。

关键词：斑点叉尾鮰；芽孢杆菌；乳酸菌；肠道微生物；代谢组学

Effects of Bacillus and Lactobacillus on the intestinal flora and metabolomics of channel catfish

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Abstract： The aim of this experiment was to investigate the effects of two probiotics, Bacillus and Lactobacillus, respectively, on the intestinal microbial community and flora metabolites of channel catfish. A total of 360 channel catfish with a body weight of (50 ± 3) g were selected and randomly divided into 3 groups, and named as the control group, the Bacillus group and the Lactobacillus group. There were 3 parallels in each group, and the experiment lasted 11 weeks. The results showed that the addition of Bacillus and Lactobacillus to the feed could improve the alpha diversity of the intestinal flora. In the phylum level, the Firmicutes / Bacteroidetes was linear decreased; the abundance of Firmicutes was significantly lower than that of the control group ($P<0.01$), and the relative abundance of Proteobacteria ($P<0.01$) and Actinobacteria ($P<0.05$) was significantly higher than that of the control group. While in the genus level, the relative abundance of Burkholderia-Caballeronia-Paraburkholderia ($P<0.01$) was significantly increased, while the relative abundance of Turicibacter ($P<0.01$) and Romboutsia ($P<0.05$) were significantly decreased. The metabolite analysis between different groups obtained 25 differential metabolites such as 5-Hydroxyindoleacetic acid、5-Hydroxy-L-tryptophan、Methoxyindoleacetic acid、Dehydroepiandrosterone、17a-Hydroxypregnenolone、LPC(18:3)、LysoPC(20:2(11Z,14Z)),and 30 metabolic pathways were involved. In conclusion, Bacillus and Lactobacillus to the feed could improve the intestinal microbial community of channel catfish to a certain extent and increase the diversity of the community. According to the differential metabolites and metabolic paths, it was speculated that the probiotics added to the feed mainly affected their immunity and anti-inflammatory abilities through metabolisms such as amino acid metabolism and lipid metabolism.

Key words:： channel catfish; Bacillus; Lactobacillus; intestinal flora; metabolomics;

互花米草入侵对南通沿海滩涂生境微生物菌群结构及多样性的影响

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摘要：在南通沿海滩涂对贝类增养殖区和互花米草入侵区的水体及土壤中的微生物菌群结构及其多样性进行了分析。研究表明：两类区域的水体及土壤中优势细菌门均为变形菌门、厚壁菌门和拟杆菌门，但水体较土壤中的变形菌门占比更高，厚壁菌门占比更低；变形菌门的相对丰度总体较高, 但随着米草入侵程度加深，在水体及土壤中均呈现下降趋势；反映植被群落演替的厚壁菌门细菌，其丰度在土壤中随着米草入侵程度加深呈现增长趋势, 在水体中呈现下降趋势；α多样性分析显示，土壤中的菌群多样性会随着米草生长而显著下降（$p<0.05$），在水体中没有显著性差异。互花米草入侵改变了微生物菌群结构和多样性，减弱了湿地的固氮能力，对养分循环造成不利影响，破坏了滩涂的生态系统，并对增养殖贝类的生长造成不利影响。本研究结果可为滩涂湿地米草防控、生态服务功能提升以及贝类增养殖滩涂修复提供相关科学基础。

关键词：米草入侵；南通沿海滩涂；贝类生境；微生物菌群

Effects of invasion of Spartina alterniflora on the structure and diversity of microbial flora along the ecosystem of coastal tidals in Nantong

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Abstract：The structure and diversity of microbial flora in water and soil of the shellfish breeding area and Spartina alterniflora invasion area were analyzed in Nantong coastal tidals. The results showed that the dominant bacterial phyla were Proteobacteria, Firmicutes and Bacteroidetes, but the proportion of Proteobacteria in water was higher than that in soil, and the proportion of firmicutes was lower. The relative abundance of Proteobacteria was generally high, but with the deepening of invasion of S alterniflora, it showed a downward trend in water and soil, which weakened the nitrogen fixation ability of wetland and had adverse effects on nutrient cycling. The abundance of Firmicutes, which reflects the succession of vegetation community, increased with the degree of invasion of S alterniflora in soil, but decreased in water. α-diversity analysis showed that soil microbiota diversity decreased significantly with the growth of S alterniflora. ($p<0.05$), but there was no significant difference in water. The invasion of S alterniflora has changed the structure and diversity of microbial flora, weakened the nitrogen fixation ability of wetlands, adversely affected the nutrient cycle, damaged the ecosystem of tidals, and make a negative effect on the growth of cultured shellfish. This study can provide relevant scientific basis for preventing and controlling the growth of Spartina alterniflora in tidals, improving ecological service function and restorating the tidals of shellfish aquaculture.

Key words: invasion of Spartina alterniflora; Nantong coastal tidals; ecosystem of shellfish; microbial flora

新疆特克斯河斑重唇鱼胚胎发育和胚后发育观察

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摘要：为保护伊犁河水系特克斯河特有鱼类斑重唇鱼（*Distychus maculates*）种质资源，探究斑重唇鱼胚胎发育与胚后发育规律。2021 年 5 月，对斑重唇鱼开展人工繁殖，观察其胚胎发育和胚后发育过程，记录各发育阶段形态特征。水温 15.0 ~ 16.0 ℃条件下，斑重唇鱼胚胎发育历经受精、卵裂、囊胚、原肠胚、神经胚、器官形成和孵化出膜 7 个阶段，经过 2 969.830 ℃·h 破膜而出。斑重唇鱼成熟卵子淡黄色，卵径（2.75 ± 0.24）mm（*n = 20*），卵受精 35 min 后卵周隙最大，为（3.46 ± 0.16）mm（n = 20），其中卵黄约占体积的 3/5。胚后发育过程中，仔鱼全长（*LT，mm*）和出膜天数（*D*）关系式：LT = 0.50D + 9.15（R^2 = 0.90）；卵黄囊全长（*LY*）和出膜天数（*D*）关系式：LY = - 0.11D^2 + 7.61（R^2 = 0.76）；仔鱼全长（*LT*）和卵黄囊体积（*LP*）关系式：LT = - 2.35LP + 19.96（R^2 = 0.88）；卵黄囊全长（^{LY}）和卵黄囊体积（*LP*）关系式：LY = 0.49LP + 5.34（R^2 = 0.68）；卵黄囊体积（*LP*）和出膜天数（*D*）关系式：LP = 0.002D^2 - 0.24D + 4.67（R^2 = 0.98）。本研究通过特克斯河斑重唇鱼人工繁殖实验，观察其胚胎和胚后发育特征，丰富斑重唇鱼早期生活史资料，为特有鱼类苗种培育提供理论数据，进一步为种质资源保护和开发奠定基础。

关键词：特克斯河；斑重唇鱼；胚胎发育；胚后发育

Observation on Embryonic Development and Post-embryonic Development of Distychus maculates in Turks River, Xinjiang

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Abstract: *Distychus maculates*, an endemic fish of Turks River of the Yili River basin. In order to protect its resources, we carry out its artificial breeding to explore the embryonic development and post-embryonic development rule. In May 2021, artificial breeding was carried out on D. maculates, and the embryonic and post-embryonic development were observed and photographed with a dissecting microscope, and the morphological characteristics of each developmental stage were recorded. 30 and 10 embryos and early larvae were randomly selected each time, respectively. The biology data of embryo and larvae was measured with Image pro plus 6.0 software. Photoshop CS6 was used for image processing and the SPSS 16.0 software for data processing. K = NT, where K is accumulated temperature (℃·h), N is the time required for development to a certain stage (h), and T is the average water temperature at this stage (℃). Descriptive statistics was presented as mean ± standard error. In the water temperature of 15.0 - 16.0 ℃, the embryo development of the fish was divided into 7 key stages: fertilization, cleavage, blastocyst, gastrula, neuroembryo, organogenesis and membrane emergence, and broke the membrane after 2 969.830 ℃·h. The mature eggs of were pale yellow with a diameter of 2.75 ± 0.24 mm (n = 20). After 35 min of fertilization, the largest perioocyte gap was 3.46 ± 0.16 mm (n = 20), and the volume of yolk accounted for about 3/5. The relationship between the length of larval fish (L_T) and the days post hatching (D) was as follows: $L_T = 0.50D + 9.15$ ($R^2 = 0.90$); The relationship between the length of yolk-sac (L_Y) and the days of membrane emergence (D) was: $L_Y = - 0.11D^2 + 7.61$ ($R^2 = 0.76$); The relationship between larval length (L_T) and yolk-sac volume (L_P) was as follows: $L_T = - 2.35L_P + 19.96$ ($R^2 = 0.88$); The relationship between yolk-sac total length (L_Y) and yolk-sac volume (L_P) was as follows: $L_Y = 0.49L_P + 5.34$ ($R^2 = 0.68$); The relationship between yolk-sac volume (L_P) and membrane extraction days (D) was as follows: $L_P = 0.002D^2 - 0.24D + 4.67$ ($R^2 = 0.98$). The total length and volume of yolk sac decreased with the growth of body length. The yolk sac was consumed 15 days after membrane emergence. The whole length of larva increased with the days after film emergence. The whole length of larva increased significantly in yolk sac absorption stage. By studying the artificial reproduction experiment of D. maculates, this study explores its characteristics of embryo and post-embryonic development, to enrich its data of early life history, and provide a theoretical data for the breeding of unique fish seedlings, which further laid a foundation for the protection and development of germplasm resources.

Key words: Turks River; Distychus maculates; Embryonic development; Post-embryonic development

浙江近海曼氏无针乌贼季节分布特征

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摘要：为探究和补充浙江中北部近海曼氏无针乌贼生物学研究资料，本文根据2020年1月、4月、8月和11月在浙江中北部近海底拖网渔业调查数据，分析了该海域曼氏无针乌贼生物量资源密度的时空分布特征，采用广义相加模型（generalized additive model, GAM）研究了影响其时空分布的环境因子。结果表明，曼氏无针乌贼资源分布呈现明显的季节特征，4月和8月其分布在近岸海域，1月和11月向外海游动，与其他月份相比，4月资源量高于其他月份；模型拟合结果显示，该研究海域溶解氧、水深、海水底层温度、海水底层盐度以及浊度对曼氏无针乌贼资源分布影响显著。曼氏无针乌贼的出现在溶解氧6-8mg/l之间呈正效应，在水深20~60m范围内呈正效应，在底温15~20℃范围内呈正效应，在底盐30~35之间呈正效应，在浊度0~50之间呈正效应。

关键词：关键词；曼氏无针乌贼；资源密度；时空分布；环境因子；GAM模型

Seasonal DistributionCharacteristics of the Sepiella maindron in the Coastal Areas of Zhejiang

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Abstract: In order to explore and supplement the biological research data of the Sepiella maindroni in the coastal waters of Zhejiang,This article is based on the survey data of near-bottom trawling fisheries in Zhejiang in January, April, August and November 2020,The spatial and temporal distribution characteristics of the Sepiella maindroni biomass resource density in the sea area were analyzed,The environmental factors affecting its spatial and temporal distribution were studied using a generalized additive model (GAM).The results show that the resource distribution of Sepiella maindroni has obvious seasonal characteristics.It is distributed in nearshore waters in April and August, and swims to the sea in January and November,Compared with other months, resources in April are higher than other months;The model fitting results show that dissolved oxygen, water depth, bottom seawater temperature, bottom seawater salinity and turbidity have a significant impact on the distribution of Mansfield squid resources in the study area.The appearance of Sepiella maindroni has a positive effect in the dissolved oxygen range of 6-8mg/l, and has a positive effect in the water depth range of 20-60m,There is a positive effect in the range of bottom temperature 15~20℃, a positive effect in the range of bottom salt 30~35, and a positive effect in the turbidity range of 0~50.

Key words: Key words; Sepiella maindroni; resource density; spatiotemporal distribution；environmental factors; GAM

水产养殖中有益菌的研究进展

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摘要：微生物是海洋生物学研究的热点，利用生物防治来调控环境和治理病害已经成为当下水产养殖业可持续发展的最佳选择。目前从环境中所筛选出的多种益生菌应用在养殖中无毒无害，具有促进水产动物的健康生长、提高饲料利用率、平衡肠道菌群等优点，所以益生菌常被作为饲料添加剂投喂水产经济生物；同时一些益生菌产生的抗菌物质，对水产动物病害的预防和治理以及对养殖水体的调控提供新的方向。本文概述了在水产养殖过程中有益微生物在病害防治、生物的生长与免疫、饲料利用、有害藻防治等方面的作用，为益生菌与水产养殖之间的相互作用提供了理论基础。

关键词：水产养殖；益生菌；拮抗作用；微生态制剂

Research progress of beneficial bacteria in aquaculture

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Abstract： Microorganisms are the hot spot of marine biology research,and the use of biological control to regulate the environment and manage diseases has become the best choice for the sustainable development of aquaculture industry nowadays. At present, a variety of probiotics screened from the environment are applied in aquaculture non-toxic and harmless, with the advantages of promoting healthy growth of aquatic animals, improving feed utilization and balancing intestinal flora, so probiotics are used as feed additives fed to aquatic economic organisms; at the same time, some probiotics produce antibacterial substances, which provide new directions for the prevention and management of aquatic animal diseases and the regulation of aquaculture water bodies. This paper outlines the role of beneficial microorganisms in disease control, growth and immunity of organisms, feed utilization, and harmful algae control in aquaculture, providing a theoretical basis for probiotics and aquaculture.

Key words: Aquaculture; Probiotics; Antagonism; Microecological preparations

枸杞岛贻贝筏式养殖区大型底栖动物功能多样性及功能性状响应

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摘要：基于 9 个分类和功能多样性指数及 10 个功能性状，采用生物性状分析(BTA)研究大型底栖动物功能性状对枸杞岛贻贝筏式养殖区特殊生境环境因子的响应。同时采用广义线性模型(GLM)筛选出评价贻贝养殖区大型底栖动物功能多样性的关键指标，并通过广义可加模型(GAM)分析出影响该关键指标的环境因子。结果表明，季节更替是影响贻贝筏式养殖区大型底栖动物分类及功能多样性指数的主要变量。RDA 模型显示，6 种养殖压力源和 1 种自然环境因子显著影响大型底栖动物的功能多样性，方差分解分析(VPA)结果表明，养殖压力对功能多样性的影响显著大于自然变量。功能冗余指数是 GLM 模型中响应环境因子的关键指标。RLQ 分析表明，冬季大部分站位与其他三个季节明显分离，蒙特卡洛整体性检验表明，功能性状与所选环境因子间不存在整体显著相关性，第四角检验在应用调整后的 p 值也未观察到单个性状模态和单个环境因子之间的显著相关。

关键词：大型底栖动物；生物性状分析；功能多样性；贻贝养殖区；RLQ 和第四角分析；GAM 模型

Functional diversity and functional traits responses of macrobenthos in the mussel farm near Gouqi Island

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Abstract： Based on 9 taxonomic and functional diversity indices and 10 functional traits, biological trait analysis (BTA) was used to study the response of macrobenthos functional traits to special habitat environmental factors in the mussel farm near Gouqi island. The generalized linear model (GLM) was used to screen out the key index for evaluating the functional diversity of macrobenthos in the mussel farm, and the environmental factors affecting the key index were analyzed by the generalized additive model (GAM). The results showed that seasonal change was the main variable affecting the classification and functional diversity index of macrobenthos in mussel raft farming areas. The RDA model showed that six aquaculture stressors and one natural environment factor significantly affected the functional diversity of macrobenthos. The results of Variation partitioning analysis (VPA) showed that the effect of aquaculture stress on functional diversity was significantly greater than that of natural variables. The functional redundancy index is a key indicator of the response to environmental factors in the GLM model. RLQ analysis showed that most of the stations in winter were significantly separated from the other three seasons, Montel Carlo global test showed that there was no overall significant correlation between functional traits and selected environmental factors, and the fourth-corner test applied the adjusted-p also did not observe significant correlations between individual trait modalities and individual environmental factors.

Key words: Macrobenthos; Biological trait analysis; Functional diversity; Mussel farming area; RLQ and fourth-corner analysis; GAM model

非法捕捞生态损害补偿的量化及其影响因素

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摘要：本研究选取了中国江苏省近十年来规模最大的非法捕捞案件作为研究对象，来验证不同假设下的量化结果的差异。在本研究中，我们假设非法捕捞渔获全部由鳀鱼组成，计算结果表明不同因素的引入使量化结果发生了显著变化，损害的量化范围为 2.74×107 ~ 8.73×109 元。除经济因素和生态因素外，社会因素也是在量化非法捕捞所造成的海洋生态破坏的过程中必须要纳入考量的因素。本研究建议拟定修正系数，对非法捕捞所造成的生态损害的定量结果进行调整，以平衡生态修复的效果与责任方的实际支付能力。这一修正系数是非法捕捞的社会影响的综合反映，包括非法捕捞的持续时长和频次、渔获量的多少、以及涉案海域的功能分区等，用以差异化不同程度的非法捕捞所造成损害的定量结果。

关键词：海洋生态损害补偿；非法捕捞；海州湾；多物种放流；社会因素

Quantification of ecological damage from illegal fishing: more than economic and ecological factors

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Abstract: In recent years, the research on compensation for marine ecological damage has made great progress in China, but the research on illegal fishing as a source of damage lags behind the whole, and cannot match the huge number of illegal fishing cases. In this study, we selected a typical case from Jiangsu Province, China, which was the largest illegal fishing case in a decade. We hypothesized that illegal catches are composed entirely of anchovy Engraulis japonicus to verify the quantification results under different scenarios. The results show that the introduction of different factors significantly changes the quantification results, and the value of damage quantified ranged from 2.74×107 to 8.73×109 yuan. A quantitative method based on market value is the most convenient, but it overemphasizes the utilization value of Marine organisms to human beings and ignores the ecological value of species, and resulted in the lowest value of 2.74×107 yuan. An approach based on ecological restoration costs seems more reasonable, but the introduction of different ecological factors radiatively changes the final results, ranged from 7.99×107 to 8.73×109 yuan, which means that special attention should be paid to the selection of different ecological factors in the actual quantification process. Multi-species release was a resource reconstruction measure in line with Marine biodiversity, and the price and proportion of different species affect the final cost. But whether potential losses from illegal fishing need to be included in the calculations is debatable. Social factors are also necessary for the quantification of Marine ecological damage, although they are illusory compared to the first two factors. It is suggested to formulate a correction coefficient to adjust the quantitative results to balance the effect of ecological restoration with the ability of the responsible party to pay. The correction factor reflects the social impact of illegal fishing, including the duration and frequency of violations, the amount of the catch, and the functional zoning of the sea, and differentiates the quantitative results of illegal fishing with different levels of severity.

Key words: Compensation of marine ecological damage; illegal fishing; Haizhou Bay; multi-species release; social factors

海州湾毛虾稳产水域中浮游动物群落生态结构

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摘要：春夏季是中国毛虾（*Acetes chinensis*）洄游至近岸浅海孵化产卵、摄食和资源补充的重要时期，在此期间浮游动物的群落结构是影响中国毛虾资源补充的因素之一。本实验于 2021、2022 年 6~7 月分别在海州湾中国毛虾特许捕捞水域进行多航次浮游动物及相关因子调查，根据采集浮游动物样品的分析鉴定及环境因子的测试结果，对调查海域的浮游动物群落进行研究分析。结果表明，2021 年航次共鉴定出浮游动物分为 5 大类，其中桡足类最多有 11 种；其次为水母类、浮游幼虫类、枝角类各 2 种，毛颚类 1 种。2022 年航次共鉴定出浮游动物分为 7 大类，桡足类仍最多有 18 种；其次为浮游幼虫类 6 种，水母类 5 种，枝角类 2 种，毛颚类、多毛类和端足类各一种。本水域浮游动物群落结构较稳定，物种丰富度较高，个体分布较均匀。

关键词：浮游动物；群落结构；海州湾

Ecological structure of the zooplankton community in the stable waters of Acetes chinensis in Haizhou Bay

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Abstract： The zooplankton community structure is one of the factors influencing the replenishment of the *Acetes chinensis* during the spring and summer months when it migrates to shallow inshore waters for hatching and spawning, feeding and replenishment of resources. This experiment was conducted in June to July 2021 and 2022, respectively, to investigate the zooplankton and related factors on multiple cruises in the licensed fishing waters of Acetes chinensis in Haizhou Bay. The zooplankton community in the surveyed sea area was studied based on the analysis and identification of the collected zooplankton samples and the test results of environmental factors. it turned out that total 5 categories and 34 species were identified in 2021; the most group was Copepoda (10 species); there are Jellyfish class, Planktonic larvae, Cladocera and Chaetognatha on the rest. In 2022, total 7 categories and 34 species were identified and the most group was Copepoda (18 species); there were Planktonic larvae, Jellyfish class, Cladocera, Chaetognatha, Polychaeta and Amphipod on the rest. The structure of the zooplankton community in this water is relatively stable, with a relatively even distribution of individuals.

Key words: zooplankton; structure community; Haizhou Bay

浙江近岸海域大黄鱼的摄食生态研究

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摘要：本文基于 2020—2021 年拖网和刺网调查的大黄鱼样品，结合胃含物与稳定同位素研究大黄鱼的摄食习性。结果表明：胃含物分析结果显示大黄鱼主食鱼类、虾类、口足类、磷虾类、糠虾类和蟹类; 大黄鱼的摄食强度在夏季最大，春冬季最小，随体长增加而减小，不同季节和不同体长的大黄鱼胃饱满指数存在极显著差异($P<0.001$)；大黄鱼的δ13C 值范围为-21.1‰~-13.7‰，平均值为(-16.8±1.3)‰，最大差值为 7.5‰，δ15N 值范围为 7.4‰~13.2‰，平均值为(10.5±1.3)‰，最大差值为 5.9‰；稳定同位素分析结果显示，鱼类、虾类、口足类和蟹类对大黄鱼的营养贡献率较大；以厚壳贻贝为基线生物计算的大黄鱼平均营养级为 3.4, 不同季节的大黄鱼营养级没有显著性差异(P>0.05)，不同体长组的大黄鱼营养级存在极显著差异(P<0.001)。

关键词：大黄鱼；胃含物分析；稳定同位素；摄食生态；营养级

Study on feeding ecology of Larimichthys crocea in the Zhejiang coast area

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Abstract： In order to study the feeding ecology of Larimichthys crocea in the Zhejiang coast area, based on samples from trawler and gillnet research surveys from 2020 to 2021, combined with the stomach contents analysis and stable isotope analysis, the feeding habits were studied. The results of stomach contents analysis showed that the L. crocea mainly feeds on fish, Decapoda, Stomatopod, Euphausiacea, Mysidacea and crabs. The feeding intensity of L. crocea was maximum in summer and minimum in spring and winter, and decreased with the increase of body length. There were significant differences in stomach fullness index of L. crocea in different seasons and different body lengths (P<0.001). The δ13C values of L. crocea ranged from -21.1‰ to -13.7 ‰(-16.8±1.3), and the δ15N values ranged from 7.4‰ to 13.2 ‰(10.5±1.3‰). The results of stable isotope analysis showed that fish, shrimp, stomatopods and crabs contributed more to the nutrition of L. crocea. The average trophic level of L. crocea calculated with Mytilus coruscus as baseline was 3.4. There was no significant difference in trophic level of L. crocea in different seasons ($P>0.05$), but there was significant difference in trophic level of L. crocea in different body length groups ($P<0.001$).

Key words: Larimichthys crocea; stomach contents analysis; stable isotope; feeding ecology; trophic level.

盐度胁迫下曼氏无针乌贼的行为和生理响应

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摘要：盐度变化会引起头足类渗透调节和免疫应答等一系列生理应激反应，同时还会引发应激诱导的喷墨行为，最终可能导致其因渗透失衡出现大量死亡。结合头足类苗种繁育过程中因海水盐度波动出现摄食及行为异常等问题，本研究探究了盐度胁迫对曼氏无针乌贼行为活跃性、组织结构、渗透调节以及免疫应答的影响，明确了其对盐度变化的应激反应及适应能力。结果显示，在高盐胁迫下曼氏无针乌贼的行为活跃性显著增加，且倾向于绕水槽壁游动；与对照组相比，高盐组肌肉、鳃和肝脏组织结构呈现较严重的损伤；随着盐度的升高，鳃中 NKA 酶活性先降低后升高；33 PSU 组脑中皮质醇含量显著高于其他处理组；盐度升高或降低均会导致鳃和肝脏中 SOD、CAT 活性显著升高，MDA 含量显著增加，LZM 活性显著降低。综合分析认为，曼氏无针乌贼具有较好的耐低盐能力。在本研究设定的 15−33 PSU 盐度范围内，盐度变化会引起其免疫应答和渗透调节的改变。

关键词：曼氏无针乌贼；盐度胁迫；行为反应；组织结构；渗透调节；免疫应答

Behavioral and physiological responses of Sepiella japonica exposed to salinity changes

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Abstract： Changes in salinity may cause a series of physiological and behavioral stress responses in cephalopods, e.g. osmoregulation, immune responses, and stress-induced inking behavior, and can even lead to mass death due to osmotic stress. In the process of seedlings production of cephalopods, the behavior of broodstocks is highly affected by changes in salinity. To better understand the stress responses and the adaptability used by cephalopods to cope with salinity stress, this study investigated the effects of salinity changings on the behavioral activity, histopathology, osmoregulation and immune response of Sepiella japonica. The results showed that the behavioral activity of Sepiella japonica increased significantly under high salinity stress, and had obvious tendency to swim around the tank wall. Compared to the control group, the tissue structures of muscle, gill and liver in the high-salt groups showed more serious damage, and no significant change was found in the low-salt groups. With the increase of salinity, the activity of Na+/K+-ATPase in the gill decreased first and then increased. The cortisol in brain tissue in the 33 PSU groups was significantly higher than that of the other treatment groups. The increase or decrease of salinity could lead to the significant increase of activities of superoxide dismutase (SOD) and catalase (CAT) in gills and liver, the significant increase of content of malondialdehyde (MDA), and the significant decrease of activity of lysozyme (LZM). Based on these results, it can be concluded that the Sepiella japonica have good tolerance to low-salt conditions. The range of salinity used in this study (15−33 PSU) could cause immune responses and osmoregulation for Sepiella japonica.

Key words: Sepiella japonica; salinity stress; behavioral response; histopathology; osmoregulation; immune response

台风利奇马对海水贝塘浮游生物群落的影响

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摘要：为了揭示台风前后海水池塘贝类养殖过程中浮游生物群落结构的变化，对养殖水体环境基因组 DNA 中 16S 和 18S rRNA 基因进行了高通量测序和生物信息学分析。研究表明，台风扰动后，海水池塘浮游生物群落在短期内均发生了明显改变，原核生物改变大于真核生物，但随养殖过程进行，原核生物出现逐渐恢复的趋势。因此，在海水池塘贝类养殖中应对台风影响的重点措施应主要放在防止养殖生物对环境剧变产生应激，并适当补充用于环境调节的益生菌制剂，以弥补台风造成的菌相改变可能带来的生态功能缺失。

关键词：浮游生物；海水贝塘；高通量测序；16S rDNA；18S rDNA

Impact of Typhoon Lekima on plankton community in shellfish mariculture pond

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Abstract： In order to reveal the changes of plankton community structure during shellfish culture in seawater ponds before and after typhoon, 16S and 18S rRNA genes in the genomic DNA of aquaculture water environment were analyzed by high-throughput sequencing and bioinformatics.The results showed that after typhoon disturbance, the plankton community in seawater ponds changed significantly in a short period of time, and the change of prokaryotes was greater than that of eukaryotes, but the prokaryotes gradually recovered with the process of aquaculture.Therefore, the key measures to deal with the impact of typhoon in shellfish culture in seawater ponds should be mainly to prevent cultured organisms from causing stress to the drastic environmental changes, and to supply probiotics for environmental regulation appropriately, so as to make up for the loss of ecological functions possibly caused by the change of bacteria phase caused by typhoon.

Key words: plankton community; shellfish pond; High-throughput sequencing; 16S rRNA; 18S rRNA

定植密度和底质施肥对鳗草存活、生长和生理的影响

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摘要：海草床是近岸海域生产力极高的生态系统，具有极其重要的生态功能。本文以温带海域优势海草种类—鳗草为研究对象，在人工环境条件下，设置不同定植密度 [300(对照)、450、600、750 和 900 shoots/m^2] 和底质施肥量 [0(对照)、35、70、105 和 140 g/m^2]，探究了肥密互作对鳗草植株生长、扩繁和生理指标的影响。结果表明，合理肥密组合可有效促进植株的生长扩繁，其中植株分株频率高达 47.8%。综合植株生长存活指标，发现适宜的定植密度和施肥量分别为 501~530 shoots/m2 和 51~60 g/m^2。植株生理学指标的响应过程表明，定植密度和施肥对鳗草存活和扩繁的促进作用主要来自植株叶绿素含量的增加和非结构性碳水化合物的积累。研究结果明确了鳗草植株最优施肥量及定植密度，初步查明了鳗草植株应对肥密互作的生理响应过程，为建立海草植株高效扩繁理论和技术提供了重要的理论支撑。

关键词：定植密度；施肥；鳗草；生长；扩繁

The combined effect of planting density and sediment fertilization on survival, growth and physiology of eelgrass Zostera marina

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Abstract：We subjected shoots of Zostera marina to different combinations of planting density [300 (control), 450, 600, 750, 900 shoots m-2] and sediment fertilization [0 (control), 35, 70, 105, 140 g m-2] for 6 weeks under controlled conditions. We measured eelgrass responses in terms of survivorship, growth, productivity, leaf pigmentation and carbohydrate concentrations. Survival analysis combined with growth assessment suggested that the optimal ranges of planting density and sediment fertilization for the propagation of Z. marina shoots were 501 to 530 shoots m-2 and 51 to 60 g m-2, respectively. The promotion of survival and propagation of Z. marina that stemmed from planting density and sediment fertilization mainly depended on the increase of chlorophyll content and accumulation of non-structural carbohydrate. The results will provide data that could prove helpful in the development of efficient artificial propagation technology for Z. marina shoots.

Key words: planting density; sediment fertilization; Zostera marina, growth; propagation

八放珊瑚研究现状、问题与对策

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摘要：八放珊瑚广泛分布在近岸浅海到深海，以及热带、温带甚至寒带等高纬度海区，在维持海洋生态系统结构完整性和生物多样性方面发挥了重要作用。受气候变化和人类活动影响，八放珊瑚呈现不断衰退趋势，忽视海洋生态系统原生物种自然禀赋的现象明显，尤其是八放珊瑚可供头足类产卵附着的生态功能尚未引起足够重视。本文综合梳理了八放珊瑚的结构和分类、繁殖特性和生殖方式、影响生态因子和退化原因等研究现状和问题，提出针对性保护和修复八放珊瑚的对策与建议，以期为我国重要生态系统保护和修复重大工程的实施提供基础资料。

关键词：八放珊瑚；生态因子；退化原因；生殖方式；保护；修复

Research Status, Problems and Countermeasures of octocorals

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Abstract： Octocorals are widely distributed in shallow to deep coastal waters across tropical, temperate and even boreal zones and other high-latitude marine areas. Octocorals play an important role in maintaining the structural integrity and biodiversity of marine ecosystems. Due to the influence of climate change and human activities, octocorals show a trend of continuous decline. The phenomenon of neglecting the natural endowment of native species in marine ecosystems is noticeable, and especially the ecological function of octocorals for cephalopod spawning attachment has not yet received sufficient attention. In this paper, we have comprehensively reviewed the current status and problems of the structure and classification, reproductive characteristics and mode of reproduction, ecological factors and causes of degradation of octocorals, and proposed countermeasures and suggestions for the conservation and restoration of octocorals, in order to provide fundamental information for the implementation of major projects for the conservation and restoration of essential ecosystems in China.

Key words: Octocorals; ecological factors; causes of degeneration; reproductive mode; conservation; restoration

银色裂腹鱼线粒体基因组序列特征与系统进化分析

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摘要：银色裂腹鱼（*Schizothorax argentatus*）是我国裂腹鱼类中珍稀濒危品种之一。本研究采用高通量测序技术获得了银色裂腹鱼长度为 16580 bp 的线粒体基因组全序列。碱基组成分别为 A(30.25%)、G(17.28%)、C(27.20%)和 T(25.27%)，呈现明显的 AT 偏好性和反 G 偏倚。tRNA 基因中仅 tRNA-Ser(GCU) 因缺少 DHU 臂无而法形成典型的三叶草结构。银色裂腹鱼线粒体控制区包含了 3 个不同的结构域：终止序列区(ETAS)、中央保守区(CSB-F、CSB-E、CSB-D 和 CSB-B)和保守序列区(CSB1、CSB2 和 CSB3)，且在 CSB3 下游约 50 bp 处识别到鲤形目鱼类中普遍存在的保守序列片段 TT(AT)nGTG。基于 13 种裂腹鱼属鱼类线粒体基因组全序列构建的系统发育关系表明银色裂腹鱼分化时间较早，与其他类群亲缘关系较远。

关键词：银色裂腹鱼；线粒体基因组；序列分析；系统进化

Mitochondrial Genome Sequence Characteristics and Phylogenetic Analysis of Schizothorax argentatus

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Abstract： Schizothorax argentatus, only distributed in the Ili River basin in Xinjiang, is one of the rare and endangered species of schizothorax in China. It has high scientific and economic values. In this study, the complete mitochondrial genome sequence of S.argenteus with a length of 16580 bp was obtained by high-throughput sequencing. The gene composition and arrangement order were similar to those of typical vertebrates. it contained 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and a non-coding region (D-Loop). The nucleotide compositions were A (30.25 %), G (17.28 %), C (27.20 %) and T (25.27 %), respectively,showing obvious AT bias and anti-G bias. Among tRNA genes, only tRNA-Ser (GCU) could not form a typical cloverleaf structure due to the lack of DHU arm. The AT-skew and GC-skew values of the ND6 gene fluctuated the most, suggesting that the gene may experience different selection and mutation pressures from other genes. The mitochondrial control region of Schizothorax argenteus contains three different domains : termination sequence region (ETAS), central conserved region (CSB-F, CSB-E, CSB-D and CSB-B) and conserved sequence region (CSB1, CSB2 and CSB3). The conserved sequence fragment TT (AT) nGTG, which was ubiquitous in Cypriniformes, was identified at about 50 bp downstream of CSB3. Phylogenetic relationships based on the complete mitochondrial genome sequence of 13 Schizothorax species showed that S.argenteus differentiated earlier and had a distant relationship with other species, which may be closely related to the geographical location and hydrological environment of the waters where it lived.

Key words: Schizothorax argenteus; mitochondrial genome; sequence analysis; phylogenetics

锶元素对暗纹东方鲀幼鱼耳石的标记效果分析

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摘要：为探究锶标志技术应用于暗纹东方鲀的可行性，本研究利用 SrCl2·6H2O 对日龄为 166 d 左右的河豚进行 7 d 的浸泡实验。实验共设置 0 、12 、18 、36 、72 mg/L5 个浓度组。结果显示：（1）浸泡 7 d 后，除 72 mg/L 标记组外，其余各组存活率均为 100%，各标记组生长率均高于对照组，以 18 mg/L 标记组生长情况最佳。（2）浸泡 5 d 后，不同浓度组河豚耳石特定区域均可形成稳定的 Sr/Ca 峰值；结束浸泡后，Sr/Ca 值恢复至标记前水平，标记成功率为 100%。结合生长、存活情况和经济效益，建议今后对河豚进行锶标记时水体最适锶浓度为 18 mg/L，浸泡时间不少于 5 d。（3）探究 18 mg/L 标记组各组织中锶含量的变化。浸泡 7 d 后，肌肉、鳃、肝脏中的锶含量均显著升高（$P<0.05$），暂养 25 d 后与对照组无显著差异（$P>0.05$），为保证水产品安全，放流前应暂养至少 25d。

关键词：暗纹东方鲀；耳石；锶标记；元素分析；增殖放流；效果评估

Analysis of the effect of strontium on the marking of otoliths of juvenile dark oriental fish

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Abstract: In order to investigate the feasibility of strontium marking on otoliths of Takifugu obscurus, five different concentrations of strontium (0, 12, 18, 36 and 72 mg/L) were set up by SrCl2·6H2O to immerse T. obscurus (about 166 d post hatch) for 7 d, followed by rearing in non-additive water for 25 d. The results showed that: 1) After 7 d of immersion, the survival rate of all groups was 100% except for the 72 mg/L marked group, and the fertility of marked groups was higher than that of the control group, with the highest growth rate in 18 mg/L marked group; 2) After 5 d of immersion, stable Sr/Ca peaks could be obtained in specific areas of the otoliths in all marked groups, which can be remained after 25 d. Then, Sr/Ca gradually returned to pre-marking levels after the end of immersion, which showed the success rate of marking with strontium was 100%. In consideration of the growth, survival and economic benefits, it was suggested that the optimum strontium concentration was 18 mg/L for 5 d to mark T. obscurus in the future; 3) After 7 d of immersion, the strontium content in muscle, gill and liver increased significantly ($P<0.05$) in the 18 mg/L marked group. Fortunately there was no significant difference with the control group after 25 d of rearing in non-additive water ($P>0.05$), which shows that it is very necessary to keep at least 25 d before release to ensure the safety of aquatic products.

Key words: Takifugu obscurus; otolith; strontium marking; enhancement and release; stock assessment

两种蛇鳗线粒体基因组的比较分析：揭示蛇鳗科鱼类基因重排和系统发育关系

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摘要：蛇鳗科鱼类是鳗鲡目中数量和种类最多的，全世界有 300 多种有效物种。在已发表的蛇鳗科鱼类粒体基因组中都发现了基因重排事件，使得有必要对该类群的线粒体基因组特征和系统发育进化进行研究。本研究选择了艾氏蛇鳗和斑纹蛇鳗作为代表，基于 Illumina 高通量测序平台获得了两种蛇鳗 mtDNA 全序列。艾氏蛇鳗和斑纹蛇鳗的总长度分别为 17759 bp 和 17856 bp。与经典的线粒体基因顺序相比，ND6 和 tRNA - Glu (E)被移位到 tRNA - Thr (T)和 tRNA - Pro (P)之间，并且在 ND6 的上游有一个重复的控制区。基因重排可以用串联重复和随机丢失 (TDRL)模型来解释。基于 12 个蛋白编码基因(不含 ND6)构建的 ML 系统发育树表明，在鳗鲡目中，蛇鳗的遗传分化相对较晚。科蛇鳗科鱼类是单系起源，由于蛇鳗属不同物种之间的聚类关系比较混乱，因此该属可能是多系群的。

关键词：蛇鳗属；线粒体基因组

Comparative mitogenomic analysis of two snake eels reveals irregular gene rearrangement and phylogenetic implications of Ophichthidae

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Abstract： Family Ophichthidae has the largest number and the most various species in the order of Anguilliformes, and contains more than 300 valid species worldwide. Mitochondrial genome is the most commonly used inference target for phyletic analysis of fishes. It is generally known that the order of mitochondrial genes is highly conserved, but to date, along with the gradual increase of teleostean mtDNA sequences in the GenBank database, the gene rearrangement events have been identified in all the published complete mitogenomes of Ophichthidae species. This amusing finding makes it necessary to carry out studies on mitogenome characteristics and phylogenetic evolution of this fish group. Here, we chose Ophichthus evermanni and O. erabo as representatives and obtained the whole mtDNA sequences using the Illumina high-throughput sequencing platform. The total lengths of O. evermanni and O. erabo were 17,759 bp and 17,856 bp, respectively, containing 13 protein-coding genes, 2 ribosomal RNAs, 22 transfer RNA genes and two identical control regions. Comparing with the ancestral mitochondrial gene order, ND6 and tRNA-Glu (E) were translocated to the location between tRNA-Thr (T) and tRNA-Pro (P), and a duplicated control region was situated at the upstream of the ND6. The irregular gene rearrangement of could be explained by tandem duplication and random loss (TDRL) model appropriately. ML phylogenetic tree constructed based on 12 protein-coding genes (without ND6) demonstrated that the genetic divergent occurred in snake eels was relatively late among order Anguiliformes. Family Ophichthidae was monophyletic origin but genus Ophichthus might be multi-lineage because of the confused cluster relationships among different species.

Key words: Ophichthus; mitochondrial geno

热带河口幼鱼群落动态及其驱动因子研究——以海南万泉河口为例

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摘要：河口是鱼类重要的育幼场，在维持近海生态系统鱼类种群补充和生物多样性上具有显著的生态作用。热带河口具有复杂的生境，不同种类幼鱼对生境的偏好具有差异。为解析热带河口鱼幼鱼的动态格局特征和影响关键因素，以及对不同底质类型生境的偏好，以万泉河口为研究区域，分别在不同底质类型区域开展了周年季度调查。运用分子与形态学结合的方法共鉴定89个分类群，其中鉴定到种的有73种，隶属13目30科50属。万泉河口幼鱼的优势种为眶棘双边鱼、斑纹舌虾虎鱼、雷氏蜂巢虾虎鱼、齐氏罗非鱼和紫红笛鲷。洄游型的种类最多，其次为海洋型；半咸水型和淡水型占比较少。万泉河口幼鱼在5月和8月的多样性和丰度均比3月和11月高；沉水植物区和沙泥底质区具有较高的丰度；CCA结果显示, 温度、盐度和溶解氧是影响幼鱼群落结构的主要环境因子。通过以上结果分析表明万泉河口5月和8月是幼鱼育幼的关键时期，沉水植物区和沙泥底质区是幼鱼育幼的关键生境。

关键词：幼鱼；群落结构；底质类型；驱动因子；万泉河口

Spatiotemporal dynamics of juvenile fish in a tropical estuarine: example of the Wanquan river estuary

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Abstract： Estuaries are essential nursing grounds for fish and play a significant ecological role in maintaining fish population recruitment and biodiversity in offshore ecosystems. Tropical estuaries have complex habitats, and different species of juveniles have different habitat preferences. To analyze the dynamic pattern characteristics and key influencing factors of juvenile tropical estuarine fish, as well as the habitat preference of varying substrate types, Wanquan Estuary was used as the study area, and an annual, quarterly survey was carried out in different substrate types. A total of 89 taxa were identified by combining molecular and morphological methods, among which 73 species belonged to 13 orders, 30 families, and 50 genera. The dominant juvenile fish species in Wanquan Estuary were Ambassis gymnocephalus, Glossogobius olivaceus, Favonigobius reichei, Coptodon zillii, and tjanus argentimaculatus. The migratory type has the most species, followed by the marine type. brackish water type and freshwater type are less. The diversity and abundance of juvenile fish in Wanquan Estuary were higher in May and August than in March and November. High abundance was found in submerged plant areas and sediment areas. CCA results showed that temperature, salinity, and dissolved oxygen were the main environmental factors affecting the assemblage structure of juvenile fish. The above results show that May and August are the critical periods for juvenile nursing in the Wanquan estuary, and the submerged vegetation and sandy sediment areas are the critical habitats for juvenile nursing.

Key words: Juvenile fish; Assembage structure; Substrate type; influence factors; Wanquan river estuary

微塑料通过菌群-肠-脑轴影响鱼类捕食行为和生长

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摘要：微塑料作为一种新型污染物，其在水产养殖环境中对生物产生的毒性效应受到广泛关注。微塑料因为细小的尺寸容易被鱼类误食并在肠道中发生积累，在鱼鳃和皮肤组织处也发现了微塑料积累，进而对这些部位产生组织学变化和菌群紊乱。我们对鱼类肠道微生物群落和生理功能进行了进一步研究，发现微塑料暴露引起的肠道菌群改变，同时被抑制的消化能力和刺激的免疫反应也在鱼肠中被发现。结合神经行为学，我们发现微塑料通过肠脑轴介导影响鱼类的捕食行为，这样的机制主要体现在被干扰的肠道菌落和脑神经递质和相关基因表达。这些肠道生态效应在鱼体的生长表现中被放大，微塑料暴露后的鱼体生长明显减缓，氧化还原稳态和元素代谢周转标志物也受到显著干扰。微塑料在鱼类肠道内的积累改变了生物本身的肠道微生物群落模式，进而带来了肠道功能及其他生理活动的变化，这为人工干预微塑料抑制鱼类肠道微生态功能，保障水产养殖绿色健康发展提供了新的见解。

关键词：微塑料；肠脑轴；捕食；肠道生态

Microplastics affect fish predation behavior and growth through the microbiota-gut-brain axis

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Abstract： As a new type of pollutant, microplastics have been widely concerned about their toxic effects on organisms in aquaculture environment. Microplastics are easily ingested by fish because of their small size and accumulate in intestine. Microplastics accumulation has also been found in the gills and skin tissues of fish, resulting in histological changes and microbiota disorder in these parts. We further investigated gut microbiota and physiological functions of fish and found that alterations in gut microbiota caused by microplastics exposure, along with suppressed digestive capacity and stimulated immune responses, were also found in fish intestines. Combined with neuroethology, we found that microplastics influenced fish predation behavior through the gut-brain axis, which was mainly reflected in the disrupted intestinal colony and brain neurotransmitter and related gene expression. These intestinal ecological effects were amplified in the growth performance of fish, which was significantly slowed down after microplastics exposure, and REDOX homeostasis and element metabolic turnover markers were also significantly disturbed. The accumulation of microplastics in the intestinal tract of fish might change its microbial community pattern of organisms, and then bring about changes in intestinal function and other physiological activities, which provides new insights for artificial intervention of microplastics to inhibit the intestinal microecological function of fish and ensure the green and healthy development of aquaculture.

Key words: Microplastics; Gut-brain axis; Predation; Intestinal ecology

柴油水溶性组分对褐菖鲉稚鱼行为反应和胆碱酯酶活性的影响

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摘要：石油类污染是我国近岸海洋环境面临的主要污染类型之一，对近岸鱼类有着较强的致毒效应。行为变化是鱼类在逆境胁迫下的最直观体现，对石油类污染物标记有着良好的指示作用。本研究以我国东海区典型的近岸岩礁性鱼类褐菖鲉为研究对象，以近岸海水石油烃浓度本底调查为参考，探讨了不同浓度船用燃料油（0#柴油水溶性组分，DWSF）对褐菖鲉稚鱼行为活跃性、探索性及捕食能力的影响，并结合鳃的组织学变化与神经传递相关酶活性变化探究了石油类污染对褐菖鲉稚鱼的毒性效应。结果表明，当海水中 DWSF 浓度增加时，褐菖鲉稚鱼的探索性与活跃性呈现先增加后减弱的趋势。当 DWSF 浓度超过四类海水标准时（>0.30 mg/L）稚鱼的行为活跃性受到明显抑制，捕食能力显著降低；组织学观察发现，当 DWSF 浓度达到 0.45 mg/L 时，稚鱼的鳃组织会出现明显的病变和损伤，与神经传递相关的胆碱酯酶活性受到明显抑制，死亡率显著升高。综上可知，海水柴油污染能够引发褐菖鲉稚鱼的行为异常，显著降低其活饵捕食成功率，推断神经和呼吸系统功能受损可能是引发其行为异常的重要原因。为确保褐菖鲉等近岸岩礁性鱼类幼体的正常生长发育，海水中 DWSF 浓度应控制在 0.45 mg/L 以下。

关键词：褐菖鲉；行为；组织学；胆碱酯酶；死亡率

Effects of Water-soluble Fraction of Diesel Oil on the Behavioral Responses and Cholinesterase Activity of Post-larval Sebasticus marmoratus

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Abstract： Oil pollution is one of the main pollution types in the coastal areas of China, which has strong toxic effects on the marine fish inhabits in these areas. For fish under toxic stress, changes in behavior is one of the most obvious manifestations, which could be good indications for the marking of petroleum pollutants. Taking the background survey of petroleum hydrocarbon concentration in the offshore seawater areas of Zhoushan as a reference, this study investigated the effects of different concentrations of marine diesel oil (0#diesel oil water-soluble fraction, DWSF) on the activeness, exploratory behavior and predation ability of Sebasticus marmoratus, a typical rockfish inhabits in the coastal waters of East China Sea. Furthermore, we investigated the histological changes of gill tissues and enzyme activities related to neurotransmission to reveal the mechanisms under the toxic effect of marine diesel oil for S. marmoratus. The results showed that with the increase of the concentration of DWSF, the exploratory behavior and activeness of the post-larval S. marmoratus increased first and then decreased. It was noted that the fish behavioral activity was significantly inhibited and the predation ability decreased significantly when the concentration of DWSF exceeded the standard of inferior Class-V water quality (DWSF >0.30 mg/L). It can be observed that when the concentration of DWSF reached 0.45 mg/L, the gill tissue showed obvious lesions and damages, the activity of cholinesterase related to neurotransmission was significantly inhibited and the mortality rate increased significantly. Conclusively, the marine diesel oil can induce obvious abnormal behaviors, significantly reduce the success rate of the predation with live bait, and finally, resulting an increase in mortality of post-larval S. marmoratus. It can be inferred that the impaired nervous and respiratory system functions may play important roles for these abnormal behaviors. In order to ensure the normal growth and development of the larvae of S. marmoratus, and also other near-shore inhabiting rockfish, the concentration of DWSF in seawater should be controlled below 0.45 mg/L.

Key words: Sebasticus marmoratus; behavior; histology; cholinesterase; mortality rate

乌贼类产卵附着基的研究进展

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摘要：随着海洋自然保护地建设和人工增养殖技术研究不断推进，国内外专家学者对乌贼类产卵场修复、增养殖和不同产卵附着基的附卵效果进行了研究。本文根据乌贼类的产卵繁殖习性，通过天然附着基和人工附着基的对比分析，从相同点、不同点、内在联系和适用范围等 4 个角度对全球范围内近海常见经济乌贼类产卵附着基的类型和功能进行总结分析，论述了天然附着基和人工附着基在产卵场修复和人工增养殖中的实际应用，并对乌贼类产卵附着基的未来研究方向提出了几点思考，旨在为乌贼类的生境营造、增养殖以及渔业资源的可持续发展提出合理建议。

关键词：乌贼；附着基；产卵场；生态修复；可持续利用

Advances in studies on the ovipositing attachment substrate of cuttlefish

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Abstract： As the construction of marine nature reserves and research on artificial enrichment techniques continue to advance, experts and scholars from all over the world have conducted various studies on the restoration of spawning grounds, cuttlefish breeding and the effect of egg—attached substrates on different spawning attachment substrates. This paper summarizes and analyzes the types and functions of important economic cuttlefish spawning substrates from four perspectives: similarities, differences, internal relations and scope of application, based on the spawning and breeding habits of cuttlefish, through a comparative analysis of natural and artificial substrates. The practical applications of natural and artificial egg—attached substrates in spawning ground restoration and artificial enrichment are discussed, and several thoughts on the future research directions of cuttlefish spawning attachment substrates are presented, aiming to provide reasonable suggestions for cuttlefish habitat restoration, cuttlefish breeding and sustainable development of fishery resources.

Key words: cuttlefish; egg—attached substrate; spawning ground; ecological restoration; sustainable utilization

基于 Yolov7 的海面漂浮垃圾检测研究

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摘要：针对当前全球近海受海面漂浮垃圾污染严重，而传统漂浮垃圾清理方式费时费力等问题。本文提出一种基于 Yolov7 网络模型的海面漂浮垃圾检测方法，从岱山县近海等四个不同地区分别采集包括漂浮垃圾目标的图片共计 9762 张，然后用 LabelImg 对全部图片种的目标进行标记并按 8：2 的比例将全部图片划分为训练集与测试集。将划标注并划分好的图片文件放入本文所简历的 Yolov7 模型中进行训练，实验结果表明：本文所使用的 Yolov7 模型能够完成海面漂浮垃圾检测任务，且模型的 mAP 值高达 91.1%，准确率和召回率分别为 95.57%与 86.91%，此外模型的 F1 值为 90.27%，因此本模型在海面垃圾检测方面具有较高的能力，可以进行实际应用。

关键词：海面垃圾检测；Yolov7；LabelImg；mAP

Research on detection of floating garbage on sea surface based on Yolov7

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Abstract： In view of the current global coastal waters are seriously polluted by floating garbage on the sea surface, and the traditional methods of cleaning floating garbage are time-consuming and labor-intensive. This paper proposes a detection method for floating garbage on the sea surface based on the Yolov7 network model. A total of 9,762 pictures including floating garbage objects are collected from four different areas such as the offshore area of Daishan County. The ratio of : 2 divides all images into training set and test set. The marked and divided image files are put into the Yolov7 model resumed in this article for training. The experimental results show that the Yolov7 model used in this article can complete the task of detecting floating garbage on the sea surface, and the mAP value of the model is as high as 91.1%, with an accuracy rate of 91.1%. The recall rate and recall rate are 95.57% and 86.91% respectively, and the F1 value of the model is 90.27%, so this model has high ability in sea surface garbage detection and can be applied in practice.

Key words: sea surface garbage detection; Yolov7; LabelImg; mAP

基于稳定同位素混合模型的东太平洋五种鲨鱼摄食的初步研究

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摘要：稳定同位素技术可以用于消费者营养溯源，以确定多种营养来源对消费者营养的贡献比重。本研究以中东太平洋海域兼捕的大青鲨、大眼长尾鲨、浅海长尾鲨、锤头双髻鲨和镰状真鲨为研究对象，利用 MixSIAR 贝叶斯混合模型计算了三种主要饵料类群对五种鲨鱼的贡献率，以确定各物种间的摄食差异。根据混合模型结果，头足类（如茎柔鱼、鱼钩乌贼等）可作为大眼长尾鲨、浅海长尾鲨、镰状真鲨和锤头双髻鲨的优势饵料群，大青鲨更喜好捕食小型硬骨鱼（如荧串光鱼，日本乌魴等）。大青鲨和大眼长尾鲨性别间无明显摄食差异，而其余三种鲨鱼性别间存在显著摄食差异。镰状真鲨和浅海长尾鲨在性成熟前后存在明显的摄食差异，性成熟后头足类所占其贡献比均增加。本研究有助于了解中东太平洋海域顶级捕食者所处食物网中的能量流动，为了解海洋生态系统营养结构以及保护海洋生物资源的提供基础资料和参考数据。

关键词：中东太平洋；稳定同位素；混合模型；贡献率; 大洋性鲨鱼

The preliminary research on the feeding of five pelagic shark species in the Eastern Pacific Ocean based on the stable isotopic mixing model

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Abstract：Based on stable isotope mixing model , SIA can be used for consumer nutrition traceability to determine the contribution of multiple sources of nutrition to the consumer. The proportional contribution of main prey group to the blue sharks (BSH), silky sharks (FAL) bigeye thresher sharks (BSH), hammerhead Sharks (SPZ) and pelagic thresher sharks (PTH) from the eastern central Pacific were calculated with MixSIAR to determine the interspecific feeding habit. According to the results of mixing models, cephalopods are the most important diet compositions of FAL, BTH, PTH and SPZ. BSH have a strong preference for small fishes. Both of BSH and BTH showed no significant differences in feeding between the sexes, and there are significant differences between the different sexes in feeding of the other three shark species.There was significant difference in feeding habits between sexual maturity stages for FAL and PTH, and the proportional contribution of cephalopods increased after maturity.

Key words: the Middle East Pacific; stable isotope; mixing model; proportional contribution; pelagic shark

禁捕初期长江安庆段仔稚鱼群聚特征

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摘要：长江安庆段是长江下游重要的鱼类栖息地之一，为了解该江段在禁捕初期仔稚鱼群落特征及与环境因子的关系，于 2021 年 4 月 18 日至 8 月 14 日针对长江安庆段进行了仔稚鱼逐日调查。研究表明，禁捕初期长江安庆段仔稚鱼种类数略少于 2020 年，优势种丰度明显增大；鱼类仍主要以小型鱼类为主，经济鱼类占比较少。

关键词：长江安庆段；禁捕初期；仔稚鱼；种类组成；丰度变化；环境因子

Clustering characteristics of larval and juvenile fish in Anqing section of the Yangtze River during the initial period of the fishing ban

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Abstract： The Anqing section of the Yangtze River is one of the important fishery resources in the lower reaches of the Yangtze River,In order to understand the community characteristics of larval and juvenile fish and their relationship with environmental factors during the initial period of the fishing ban,the daily survey was conducted on larval and juvenile fish in the Anqing section of the Yangtze River from April 18 to August 14, 2021.The results showed that in the Anqing section of the Yangtze River during the initial period of the fishing ban, the number of juvenile fish species was slightly less than that in 2020, and the abundance of dominant fish species increased significantly. Fish are still mainly small fish, economic fish accounted for less.

Key words: Anqing section of the Yangtze River; the initial period of the fishing ban; larval and juvenile fish; species composition; changes in abundance; Environmental factors

禁捕初期皖河仔稚鱼群聚特征

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摘要：长江安庆段是长江下游重要的鱼类栖息地之一，同时，皖河在此汇入长江，增加了安庆段对长江下游鱼类资源保护的重要性。于2022年3月28日至8月10日针对安庆皖河进行了仔稚鱼逐日调查。结果表明，共采集鱼类43种，隶属于7目10科43种，种类组成以鲤形目为主，鱼类仍主要以小型鱼类为主，经济鱼类占比较少。研究初步探明了安庆皖河仔稚鱼资源状况，以期为长江下游鱼类资源保护和管理提供数据支撑。

关键词：皖河流域；禁捕初期；仔稚鱼；种类组成；丰度变化

Characteristics of juvenile fish aggregation in Anhui River during the early period of prohibition

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Abstract： Anqing section of the Yangtze River is one of the important fish habitats in the lower reaches of the Yangtze River. At the same time, the Wanhe River joins the Yangtze River here, which increases the importance of the Anqing section for the conservation of fish resources in the lower reaches of the Yangtze River. The river merged into the Yangtze River here, which increased the importance of the Anqing section for the conservation of fish resources in the lower reaches of the Yangtze River. In order to understand the community characteristics of larvae and larvae and the relationship with environmental factors in the early period of fishing prohibition in this section. From March 28 to August 10, 2022, a daily survey of larvae and juveniles was conducted in the Anqing Wanhe River. The results showed that 115969 fishes were collected, belonging to 43 species of 7 orders, 10 families The species composition is mainly cypriniformes, the fish are still mainly small fish, economic fish account for a little. In order to provide data support for the conservation and management of fish resources in the lower reaches of the Yangtze River, this study preliminarily proved the status of juvenile fish resources in the Anqing Wanhe River.

Key words: Wan River Basin; the initial period of the fishing ban; larval and juvenile fish; species composition; changes in abundance

基于耳石不同切面的小黄鱼年龄鉴定及其生长方程年龄反演比较

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摘要：本文选取2018年4月采自黄海南部吕四渔场和2019年9月采自大沙渔场的45尾小黄鱼进行分析，对小黄鱼矢耳石开展年龄鉴定，并系统地归纳国内近30年来小黄鱼生长方程以其体长为生长参数进行年龄反演。结果表明，三个切面的年轮清晰度评分分别为纵切面最低(53.33%)、水平切面居中(66.67%)、横切面最高(73.33%)。通过比较纵切面、水平切面、横切面的年龄鉴定结果与19个生长方程的年龄反演结果，三个切面相似度较高的方程为Lt=366[1-e-0.11777(t+1.76429)]，相似度水平分别为纵切面53.33%、水平切面86.67%、横切面86.67%。以耳石为材料对小黄鱼进行年龄鉴定时，所选矢耳石切面以横切面为最佳、其次为水平切面；针对黄海海域小黄鱼群体，以体长为参数快速反演年龄时宜以生长方程Lt=366[1-e-0.11777(t+1.76429)]为优选。

关键词：小黄鱼；耳石；切面特征；年龄鉴定；年龄反演

Age identification for Larimichthys polyactis based on different sections of sagittal otolith and comparison with the result of age backward inferring from growth equation

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Abstract：To explore the accuracy of age identification by sagittal otolith and age backward inferring by growth equations for small yellow croaker (Larimichthys polyactis), we collected 45 individuals in the southern Yellow Sea to analysis three otolith sections, including the sagittal section, frontal section and transverse section of sagittal otolith. 15 individuals were caught in Apr. 2018 with stow net with double stakes in Lvsi fishing ground and 30 individuals in Sep. 2019 with stow net in Dasha fishing ground. And the von Bertalanffy growth equations of L. polyactis during recent 30 years in China were simultaneously summarized to age backward inferring based on fish body length. The results showed that the annual ring clarity was the lowest in the sagittal section (53.33%), higher in the frontal section (66.67%) and the highest in the transverse section (73.33%). The annual ring of the three sections became more distinct after acid etching. Comparing the age identification results for three otolith sections with the age inversion results from 19 growth equations, the von Bertalanffy growth equation Lt=366[1−e−0.11777(t+1.76429)] showed the highest similarity levels with 53.33 % for the sagittal section, 86.67 % for the frontal section and 86.67 % for the transverse section, respectively. This paper revealed that the optimization method proposed was the best with the transverse section and the second best with the frontal section for age identification of L. polyactis, and the growth equation Lt=366[1−e−0.11777(t+1.76429)] for age backward inferring for L. polyactis population in the Yellow Sea.

Key words: small yellow croaker; otolith; sectional features; age identification; age backward inferring

生长、摄食与母胚传递对镰状真鲨汞累积的影响

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摘要：镰状真鲨(*Carcharhinus falciformis*)是广泛分布于全球大洋中，由于过度捕捞等原因，其种群数量明显下降，被世界自然保护联盟(IUCN)列为“易危”物种。作为一种顶级捕食者，镰状真鲨可以积累大量的汞，对其种群生存构成潜在风险。本研究通过测定热带太平洋东部镰状真鲨肌肉、肝脏、真皮、红细胞和血浆中总汞含量，并测定δ15N 值，探讨多种因素对汞积累的影响。肌肉和肝脏汞含量较高，而真皮、红细胞和血浆汞含量较低。各组织中的汞含量随叉长增加而富集。镰状真鲨母体组织中汞元素可迁移至胚胎中，可能为母体排出汞的方式，同时也造成胚胎中汞含量较高。镰状真鲨五种组织中汞含量与δ15N 值的负相关关系表明其栖息地的变化。所有组织的汞含量之间存在较强的正相关性，表明利用肌肉和真皮组织的非致命取样技术可以有效地估计其他内部组织的汞含量，可为恢复鲨鱼资源及保护生态环境提供参考。

关键词：污染物；稳定同位素；多组织；生态毒理学；非致命取样

Effect of body size, feeding ecology and maternal transfer on mercury accumulation of vulnerable silky shark Carcharhinus falciformis in the eastern tropical Pacific

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Abstract: The silky shark *Carcharhinus falciformis* is a large pelagic species distributed in the global oceans and was recently listed as “Vulnerable” by the IUCN because of its decline in population due to overfishing. As an apex predator, the silky shark can accumulate elevated quantities of mercury, posing a potential risk to its remaining population. The highest total Hg concentrations (THg) were observed in muscle and liver rather than dermis, RBC and plasma. The THg in all tissue types were correlated with fork length and showed faster accumulation rates after maturity. Maternal transfer was observed in silky sharks. THg were negatively correlated with δ15N values for all tissues, indicating likely baseline variations in δ15N values that reflect changes in the foraging habitats. Strong correlations were observed among THg of all tissue types, indicating that nonlethal sampling of muscle and dermis tissue can be used effectively to quantify THg of other internal tissues.

Key words: contaminants; stable isotopes; multiple tissues; ecotoxicology; non-lethal sampling

西北太平洋桡足类稳定同位素特征及其影响因素

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摘要：浮游动物的碳、氮稳定同位素比值（δ13C 和δ15N）能够反映海洋环境的变动，常用于建立稳定同位素基线。本研究以 2019 年 3 月（春季）和 9 月（秋季）在西北太平洋采集的桡足类为对象，结合其形态特征和采样海域的环境因子，探讨桡足类的稳定同位素特征及其影响因素。结果显示，春季桡足类个体的形态特征（体长、面积和体积）均显著高于秋季，两个季节的δ15N 值与形态特征均呈显著正相关，而δ13C 值只在春季呈显著正相关，可能是因为秋季采样点与日本岛距离相近而具有相似的碳源。广义加性模型（GAM）分析显示，桡足类δ13C 和δ15N 值的季节性差异主要与叶绿素 a 浓度和 50 米海水层温度有关。本研究结果可为西北太平洋其他海洋生物的稳定同位素生态学研究提供基础资料。

关键词：西北太平洋；浮游动物；稳定同位素；形态特征；环境因子

Stable isotope signatures and driving factors of copepods from the northwest Pacific Ocean

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Abstract： We investigated the potential impacts of morphological characteristics of copepods and environmental factors of the studied areas on stable isotopic values. The results showed that the values of each morphological characteristic of copepods were significantly higher in specimens in spring than that of autumn, and the δ15N values were significantly positively correlated with morphological characteristics in both seasons. For δ13C values, however, only copepods in spring had a significant positive correlation with morphological characteristics, which might be due to the similar distances between sampling locations and Japan island in autumn with similar carbon sources. Results of the generalized additive model indicated that the seasonal variations of δ13C and δ15N values in copepods were mainly related to chlorophyll-a concentration and water temperature at 50 meters. These results provide the basic data for the further studies of the stable isotope ecology of other Marine organisms.

Key words: northwest pacific; zooplankton; stable isotope; morphological characteristics; environmental factors

江苏近海鮸胃含物初步分析

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摘要：鮸是江苏近海重要的经济鱼类之一。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,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春秋季主要的生物饵料，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（*C. stigmatias*）（*IRI%=6.65，Ip=13.83*）和凤鲚（*C. mystus*）（*IRI%=9.37,Ip=12.46*）。经过相似性分析，春秋季鮸食性组成相似性显著。

关键词：鮸；食性分析；胃含物

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.

Key words: Miichthys miiuy; food analysis; gastric contents; Jiangsu Costal Waters

草鱼单养和混养池塘的水质与生物组成特征

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摘要：为比较单养、混养草鱼养殖池塘的水质与生物组成特点，采取水质分析、环境 DNA 与传统鉴别方法对草鱼单养、混养(80:20)两类池塘进行分析。结果表明，混养池塘的水质优于单养池塘，混养池塘水体中总氮、硝态氮、氨氮、亚硝态氮的浓度比单养池塘分别低 10.15%、3.78%、5.07%、80.18%，总磷和活性磷的浓度分别低 27.14%和 56.26%；两类池塘中浮游植物均以绿藻门、蓝藻门、隐藻门为优势种，单养池塘中的藻类密度为 30×10^6 cells/L，低于混养池塘 104×10^6 cells/L；两类池塘中的浮游动物均以轮虫和原生动物为优势种，单养池塘中浮游动物密度高于混养池塘。在菌群组成方面，单养池塘水体中以厚壁菌门为优势类群，混养池塘水体中以变形菌门为优势类群。以上结果表明，草鱼混养有利于改善养殖池塘水质，增加浮游植物丰富度，改变养殖水体菌群的结构。本研究为构建高效池塘养殖模式提供了依据。

关键词：环境 DNA；草鱼池塘；物种组成；单养；混养

Water quality and characteristics of biological composition in monoculture and polyculture pond of grass carp

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Abstract： In order to compare the water quality and biological composition characteristics in monoculture and polyculture grass carp ponds, the water quality analysis, environmental DNA and traditional identification methods were adopted. The results showed, the water quality of polyculture pond was better. Chlorophyta, Cyanophyta and Cryptophyta were the dominant species of phytoplankton in ponds. The density of phytoplankton in monoculture pond was 30×10^6 cells/L, and was 104×10^6 cells/L in polyculture pond.The zooplankton had Rotifers and Protozoa as dominant species, the density of zooplankton in monocululture pond were higher. Firmicutes was predominant in monoculture pond, Proteobacteri was predominant in polyculture pond. The above conclusions indicated that polyculture is beneficial to improve the water quality, increase phytoplankton richness and change the structure of aquaculture water flora, which provides a basis for constructing an efficient pond culture model.

Key words: Environmental DNA; grass carp pond; species composition; monoculture pond; polyculture pond

中华白海豚声信号检测与分析

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摘要：本文设计了一种基于海豚声学特征的端点检测方法，根据海洋环境中噪声能量大且分布频率范围广，而 click 信号持续时间短、频率高特点，将采集到的海洋声音进行分帧，计算单帧信号短时能量、谱质心和谱质心二阶偏移率，当海豚发出 click 信号时，谱质心和能量相应发生突变，截取发生突变的信号实现端点检测。通过其他常见端点检测方法对比，结果表明此方法对中华白海豚 click 信号检测准确度更高，同时具有较强的抗干扰能力。使用该方法对广西三娘湾采集到的数据进行检测，发现该海域内的中华白海豚的回声定位信号是一种宽频高能量的信号，频率分布在 1K~140KHz，波峰持续时间为 10~30μs，单个完整 click 信号持续时间为 50~150μs。通过分时分布、天分布情况，分析中华白海豚发声习性结果表明中华白海豚发声行为比较稳定，夜里相比白天活动更为频繁，同时对异常值进行环境分析，结果表明中华白海豚活跃程度会受到温度影响。

关键词：中华白海豚；声信号特征；时频分析；回声定位信号

Acoustic signal detection and analysis of Sousa chinensis

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Abstract： This paper designs an endpoint detection method based on the acoustic characteristics of dolphins. According to the characteristics of large noise energy and wide distribution frequency range in the marine environment, short duration and high frequency of click signal, the collected marine sound is divided into frames, and the short-time energy, spectral centroid and second-order shift rate of spectral centroid of a single frame signal are calculated. When dolphins send click signals, the spectral centroid and energy change suddenly, Intercept the signal with mutation to realize endpoint detection. Compared with other common endpoint detection methods, the results show that this method has higher accuracy in detecting click signals of Sousa chinensis, and has strong anti-interference ability. Using this method to detect the data collected in Sanniang Bay, Guangxi, it is found that the echolocation signal of Sousa chinensis in this sea area is a broad-band high-energy sign

Key words: Sousa chinensis; Acoustic signal characteristics; Time frequency analysis; Echolocation signal

潮汐和昼夜节律对沙滩碎波带仔稚鱼群聚格局的影响研究

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摘要：沙滩碎波带是近海仔稚鱼重要的育幼生境。碎波带内分布有沟槽和沙洲等多种微生境类型，潮汐和地表径流带来的丰富营养物质，是仔稚鱼摄食、生长和躲避捕食的重要生境。碎波带作为陆海交错界面，受潮汐影响尤其显著。然而，目前有关碎波带仔稚鱼群聚对潮汐和昼夜节律的响应尚不清晰。基于以上研究背景，本研究在海南省文昌市高隆湾近岸研究了潮汐和昼夜节律对沙滩碎波带仔稚鱼群聚格局的影响。结果显示：1）采集到的 46 种鱼类中包含 16 种珊瑚礁-海草床鱼类、24 种红树林-河口鱼类和 6 种常见的近海鱼类。小潮阶段鱼类物种丰度和物种数显著高于大潮阶段。小潮阶段碎波带鱼类存在显著的昼夜分布规律，大潮阶段碎波带鱼类群聚主要受潮汐节律驱动。本研究结果表明，碎波带鱼类群落能够有效指示近岸典型生境的鱼类组成，在小潮阶段调查碎波带鱼类群落有助于提高近岸生态系统鱼类资源状况评估效率，为我国南海近海鱼类资源和典型生态系统的管理和保护提供科学支撑。

关键词：碎波带；潮汐；鱼类群聚；昼夜节律；生态类型；近海景观

Both tidal cycles and diel rhythms shape temporal fluctuations of fish assemblages in surf zones of sandy beach

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Abstract： We investigated fish assemblages in a surf zone of Gaolong Bay in China, a tropical sandy beach. The dynamics of the fish assemblages were examined during the neap tide and spring tide to understand the relationship among fish assemblages, tidal regimes, and diel rhythms. We collected a total of 46 species comprising 16 coral reef-seagrass species (CS), 24 mangrove-estuarine species (ME) and 6 common coastal species (CO). Fish abundance and richness were significantly higher during the neap tide than during spring tide. The dynamics of the fish assemblages were mainly shaped by the diurnal rhythms of fish movement during the neap tide and by the tidal cycle during the spring tide. Our results support the notion that surveys of fish assemblages during the neap tide could help us better assess the status of fish resources in coastal habitats.

Key words: Surf zones; tidal cycles; fish assemblages; diel activity patterns; ecotypes; coastal seascape

小球藻在海水养殖尾水中的生长状况及水质净化作用

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摘要：为了探索解决工厂化循环水养殖中存在的硝酸盐(NO_3^-)和磷酸盐($PO4^{3-}$)累积含量较高问题，实验调配了两种盐度(16 和 26)的海水养殖尾水。以空白组作对照，分别添加三种密度(1.0×10^6个/ml，*LD*；2.0×10^6个/ml，*MD*；3.0×10^6个/ml，*HD*)的小球藻（*Chlorella salina*），比较不同密度小球藻对养殖尾水中 NO_3^-、$PO4^{3-}$、总氮(TN)和总磷(*TP*)等的去除情况，并测定藻数目、藻干重、叶绿素 a 和 A750 等指标评价小球藻生长状况。结果显示：不同接种量小球藻能够充分利用尾水中 N、P 营养盐；在不同盐度条件下，各个藻密度组对 NO_3^-的去除率达到 91.79%以上，去除效果显著；不同藻密度组 $PO4^{3-}$去除率与初始藻数目显著正相关($P<0.05$)，即在两个盐度尾水中，*HD* 组均显示了最高的 $PO4^{3-}$去除率(分别为 71.10 和 79.42%)，经 6d 处理时间，实验组 *TN* 去除率均显著高于空白组($P<0.05$)，去除率均达到 85.18%以上，*HD* 组对两种盐度的尾水的 *TP* 去除率显著高于其他组($P<0.05$)，分别达到 71.09%和 78.79%；可将 *HD* 组作为海水养殖尾水处理的适宜密度。本研究为海水养殖尾水处理提供新的思路。

关键词：小球藻；盐度；接种密度；海水；水产养殖尾水

The growth status and purification effect of Chlorella salina in maricultural wastewater

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Abstract： In order to explore and solve the problem of high accumulation content of nitrate (NO_3^-) and phosphate ($PO4^{3-}$) in industrial recirculating aquaculture system, two kinds of salinities (16 and 26) were prepared in the experiment. The blank group was used as control, the removal of NO_3^-, $PO4^{3-}$, total nitrogen (*TN*) and total phosphorus (*TP*) in the wastewater was compared by adding three densities (1.0×10^6 cells/ml, LD; 2.0×10^6 cells/ml, *MD*; 3.0×10^6 cells/ml, *HD*) of Chlorella salina, and the growth of Chlorella was evaluated by measuring the number of algae, dry weight of algae, chlorophyll-a and A750. The results showed that different inoculum densities of Chlorella could make full use of N and P nutrients in wastewater. Under different salinity conditions, the NO_3^- removal rate of each algal density group reached more than 91.79%, and the removal effect was significant. $PO4^{3-}$ removal rate was positively correlated with the initial number of algae in different algal density groups ($P<0.05$), that is, the HD group showed the highest $PO4^{3-}$ removal rate (71.10 and 79.42%, respectively). After 6 days of treatment, the *TN* removal rate in the experimental group was significantly higher than that in the blank group ($P<0.05$), and the removal rate reached above 85.18%. The TP removal rates of the two salinities in *HD* group were significantly higher than those in other groups ($P<0.05$), reaching 71.09% and 78.79%, respectively. The *HD* group can be used as the suitable density for the treatment of mariculture wastewater. This study provides a new idea for the treatment of maricultural wastewater.

Key words: Chlorella salina; salinity; inoculation density; seawater; aquaculture wastewater

北太平洋东部金枪鱼延绳钓主要渔获物种类垂直分布

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摘要：掌握延绳钓渔获物的垂直分布特征有助于准确评估目标鱼种和兼捕鱼种分布，以降低兼捕率，为渔业管理及物种保护提供理论参考。本研究根据 2018 年 10 月至 11 月北太平洋东部我国金枪鱼延绳钓渔业数据，分析了主要钓获鱼种的垂直分布特征，结果显示，北太平洋东部延绳钓渔获种类共 16 种，其中，大眼金枪鱼、长鳍金枪鱼、黄鳍金枪鱼、斑点月鱼、沙氏刺鲅数量占比最多，总占比 98.38%；根据钓钩上浮率 10~30%修正，5 种主要渔获物深度分布范围为 54~287 m，鱼种间存在空间分布差异，其中大眼金枪鱼平均渔获深度最大，为 151~194 m，沙氏刺鲅最小，为 115~147m；5 种鱼类总体渔获频率较高的深度范围为 80~170 m。研究结果可为制定有效减少兼捕鱼种的管理措施提供科学依据。

关键词：北太平洋东部；延绳钓；兼捕；垂直分布

Vertical distribution of main species captured by tuna longline fishery in the eastern north Pacific

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Abstract：The objective of this study was to estimate depth distribution of pelagic species captured in a longline fishery and to evaluate the difference in depth distribution among species. We estimated depth distribution for 5 frequently captured species based on a Chinese longline fishing trip targeting bigeye tuna in the eastern north Pacific Ocean from October to November in 2018. Although other 3 species of the bycatch species were found to be distributed in water depths shallower than bigeye tuna , the rates of catch rates declined with increasing hook depths may be different. The depth distributions were found to be not significantly different between genders for all 5 species. There was no significant correlation between fish sizes and capture depths expect for bigeye tuna. The information derived from this study can play an important role in reducing bycatch in pelagic tuna longline fisheries in the eastern north Pacific Ocean.

Key words: eastern north Pacific; pelagic longline; bycatch; vertical distribution

禁捕前鄱阳湖鱼类群落多样性及环境影响因子

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摘要：为掌握全面禁捕前鄱阳湖鱼类群落特征，开展4个季度鱼类资源调查，并同步采集水环境样品。共采集鱼类67种，淡水定居型、杂食性、底层鱼类物种数最高。鱼类优势种有6种，第一优势种为似鳊。非度量多维尺度分析显示，空间上鱼类划分2个类群。冗余分析显示，总磷、叶绿素a和透明度是影响鱼类物种时空分布的关键环境因子。ABC曲线分析显示，鱼类群落受到严重干扰(W=-0.091)。本研究成果可为鄱阳湖禁渔效果评估提供本底资料。

关键词：长江禁捕；鄱阳湖；鱼类群落；环境影响因子；冗余分析

Fish community diversity and environmental influencing factors in Poyang Lake before the fishing ban

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Abstract: In order to grasp the characteristics of the fish community in Poyang Lake before the total ban on fishing, four quarters of fish resource surveys were carried out, and water environment samples were collected synchronously. A total of 67 species of fish were collected, and the number of freshwater sedentary, omnivorous and demersal fish species was the highest. There are 6 dominant species of fish, the first dominant species is the Pseudobrama simoni,. Nonmetric multidimensional scaling analysis shows that fish are spatially divided into 2 taxa. Redundancy analysis showed that total phosphorus, chlorophyll a and transparency were key environmental factors influencing the spatio-temporal distribution of fish species. ABC curve analysis showed that fish communities were severely disturbed (W=-0.091). The results of this research can provide background information for the evaluation of the effect of fishing ban in Poyang Lake.

Key words: Fishing ban in the Yangtze River; Poyang Lake; Fish community; Environmental influencing factors; Redundancy analysis

水生生物环境 DNA 监测数据分析中技术参数对分析结果的影响

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摘要：为了探讨环境 DNA 监测数据分析中技术参数的影响，在长江中游采集水样与渔获物，分析公共数据库与自建库之间的注释差异，研究不同的技术参数对分析结果的影响。结果显示：在对序列进行分析时，应当将 OTU 序列相似度设置≥99.9%，分类置信度设置为 90%时，数据分析结果更精确，且建立完善的长江鱼类 DNA 宏条形码数据库与国际公共数据库两者相结合使用，能使 eDNA 监测结果更加准确。

关键词：环境 DNA；长江中游；OTU 序列相似度；分类置信度

Influence of technical parameters on analysis results of DNA monitoring data of aquatic organisms

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Abstract： In order to explore the influence of technical parameters in the analysis of environmental DNA monitoring data, water samples and catches were collected in the middle reaches of the Yangtze River, and the annotation differences between the public database and the self-built database were analyzed to study the influence of different technical parameters on the analysis results. The results showed that the OTU sequence similarity should be set to ≥99.9%, and the classification confidence should be set to 90%, which would make the data analysis result more accurate. Moreover, the establishment of a complete macrobarcoding database of Yangtze River fish DNA combined with the international public database could make the eDNA monitoring result more accurate.

Key words: eDNA; The middle reach of the Yangtze River; OTU sequence similarity; classification confidence

北太平洋远东拟沙丁鱼渔场时空分布及其最适环境特征

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摘要：基于 2019—2020 年北太平洋灯光敷网渔业数据和海表温度（Sea surface temperature，SST）、叶绿素（Chlorophyll-a concentration，Chl-a）、海面高度（Sea surface height，SSH）等环境数据，采用空间叠加图、频次分析与经验累积分布函数、K-S 检验和 GAM 模型等 4 种方法分析了远东拟沙丁鱼（*Sardinops melanostictus*）渔场的单位捕捞努力量（Catch Per Unit Effort，CPUE）时空分布特征及与关键环境因子的相关关系。分析结果表明作业渔场重心分布范围为 147°~153°E、39°~43°N，在 4—8 月向东北方向移动，9—11 月则向西南方向折返。通过频次分析与经验累积分布函数分析中心渔场区域最适海表温度为 10.0~18.0 ℃，最适叶绿素浓度为 0..2~0.6 mg· m-3。

关键词：北太平洋公海；远东拟沙丁鱼；海洋环境因子；GAM 模型

Spatial and temporal distribution and optimum environmental characteristics of the sardinops melanostictus in the North Pacific Ocean

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Abstract： Sea surface Temperature (SST) and chlorophyll concentration in the North Pacific Ocean in 2019—2020 were analyzed based on the data of light net fertilization fisheries in the North Pacific Ocean in 2019 -- 2020.Chl-a), Sea surface height (SSH) and other environmental factors data,The spatial and temporal distribution characteristics of Catch Per Unit Effort (CPUE) and its relationship with key environmental factors of *Sardinops melanostictusfishery* in the Far East were analyzed by means of spatial superposition map, frequency analysis and empirical cumulative distribution function, K-S test and GAM model.The results show that the center of gravity of the fishery ranges from 147° to 153°E and 39° to 43°N, and moves to the northeast from April to August, and turns back to the southwest from September to November.According to frequency analysis and empirical cumulative distribution function, the optimal SST and chlorophyll concentration in the central fishing area are 10.0~18.0 ℃ and 0.

Key words: North Pacific high seas; Sardinops melanostictus; environmental factors; GAM

基于 GAM 模型的西北太平洋公海鲐鱼渔场与时空及环境因子的关系研究

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摘要：研究结合 2021 年西北太平洋开利号大型拖网渔船渔捞日志及该海域海洋环境数据，运用广义可加模型(GAM）建立了单位捕捞努力量渔获量 (CPUE) 对时空和环境因子的非线性响应模型，探究西北太平洋公海鲐鱼渔场分布变化与月份、经纬度等时空因子以及海表面温度、盐度、叶绿素浓度等环境因子的关系。 GAM 模型结果显示：月份、经度、海表面温度、海表面盐度与 CPUE 显著相关（$P<0.05$），从大到小进行排序依次为：月份>海表面盐度>海表面温度>经度。纬度、叶绿素浓度对 CPUE 的影响不显著（$P>0.05$）。鲐鱼适宜海表面温度为 12℃～14℃，适宜海表面盐度 32.5～33.5mmday−1，适宜叶绿素浓度为为 0.4~0.6 mg/m3。

关键词：鲐鱼；西北太平洋；环境因子；广义可加模型

Effects of spatiotemporal and environmental factors on the fishing ground of Scomber japonicus in the Northwest Pacific Ocean Sea based on the Generalized Additive Model

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Abstract： Research combined with 2021 northwest Pacific large trawlers fishing log and the Marine environment data, using the generalized additive model (GAM) established the Catch Per Unit Effort (CPUE) of space and space and environmental factors of nonlinear response model, to explore the northwest Pacific Sea Scomber japonicus fishery distribution changes and month, latitude and longitude factors and sea surface temperature, salinity, chlorophyll concentration and other environmental factors. The results showed that: month, longitude, sea surface temperature, and sea surface salinity were significantly correlated with cpue ($p<0.05$), ranking from large to small as: month> sea surface salinity> sea surface temperature> longitude. Latitude and chlorophyll concentration had no significant effect on cpue ($p>0.05$). The suitable SST of Scomber japonicus is 12℃ ~14℃, the suitable SSS is 32.5～33.5mmday−1, and the suitable chlorophyll concentration is 0.4~0.6 mg/m3.

Key words: Scomber japonicus; Northwest Pacific Ocean; environmental factor; generalized additive model

西北印度洋鸢乌贼渔场时空分布及其与环境因子的关系

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摘要：本研究基于西北印度洋 2017 年 1—3 月, 8—12 月鸢乌贼的渔捞日志数据，结合同期环境因子数据，运用渔场重心分析、地统计插值、GAM 模型分析，探究西北印度洋鸢乌贼渔场时空变动及其与海洋环境因子的关系。研究表明，2017 年 1—3 月, 8—12 月鸢乌贼渔场重心大多分布于海洋锋带附近，分布范围集中 13.6°N~17.2°N、58.3°E~ 62.2°E 海域，1—3 月渔场重心向西南迁移，8—11 月渔场重心往东北移动，12 月向西南折回。GAM 模型分析结果显示，西北印度洋鸢乌贼渔场最适 SST 范围是 25.5~27.0 ℃, 最适 Chl-a 浓度范围是 0.2~0.4 mg/m3, 月份是影响鸢乌贼单位捕捞努力渔获量的主要因子。研究结果对于了解该海域鸢乌贼资源变动规律、指导鸢乌贼资源科学生产具有重要意义。

关键词：西北印度洋；鸢乌贼；CPUE 时空分布；环境因子；GAM 模型

Temporal and spatial distribution of Sthenoteuthis oualaniensis fishing ground in the northwest Indian Ocean and its relationship with environmental factors

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Abstract： To study the spatial and temporal distribution of S. oualaniensis and its relationship with relevant environmental factors, we conducted fishing ground analyses, geostatistical interpolation, and generalized additive model analyses using environmental factors concentration, and logbook data from January to March and August to December in 2017. Our results indicate that: (1) S. oualaniensis fishing grounds are mainly distributed around the oceanic front; (2) the centers of gravity of S. oualaniensis fishing grounds range from 13.6°N to 17.2°N and from 58.3°E to 62.2°E, with migration occurring towards the southwest from January to March, then towards the northeast from August to November, and then towards the southwest in December; (3) S. oualaniensis prefers SST between 25.5–27.0 ℃ and Chl-a concentration 0.2–0.4 mg/m; (4) the catch per unit effort (CPUE) of S. oualaniensis varies significantly during the year. Our study contributes to understanding S. oualaniensis stock distribution and can be further applied for sustainable management in the Northwest Indian Ocean.

Key words: Northwest Indian Ocean; Sthenoteuthis oualaniensis; spatio-temporal distribution of CPUE; environmental factors; generalized additive model

基于框架测量法的东海海域两种方头鱼形态差异分析

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摘要：种类判别是渔业资源评估的基础，为了有效区分东海海域日本方头鱼和白方头鱼，根据 2021 年 8—10 月在 27°30′—30°00′ N、123°00′—126°30′ E 海域通过深水流网获取的 399 尾方头鱼样品（日本方头鱼 187 尾、白方头鱼 212 尾），利用框架测量法测得耳石形态的 28 个可量性状和鱼体形态的 55 个可量性状，并对其进行差异性分析和逐步判别分析（SDA）。差异性分析结果显示两种方头鱼的耳石形态在前端、后端、腹侧和背侧存在差异，鱼体形态差异分布在鱼的头部、躯干部和尾部；逐步判别分析结果显示基于耳石和鱼体形态参数的判别准确率分别为 85.1%和 94.0%，而基于两种形态参数的综合判别正确率达到 98.0%。研究表明利用耳石和鱼体形态特征均可对两种方头鱼进行有效判别，且结合多种形态特征参数进行判别将进一步提升判别的准确性。

关键词： 日本方头鱼； 白方头鱼； 框架测量法； 逐步判别分析

Morphological differences of two Branchiostegus in the East China Sea based on truss network

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Abstract： Population discrimination is the basis of fishery resource assessment. This study aims to effectively distinguish between Branchiostegus japonicus and Branchiostegus albus in the East China Sea. Based on 399 Branchiostegus samples（187 B. japonicus and 212 B. albus）collected by deep water drift net in 27°30′—30°00′ N、123°00′—126°30′ E from August to October 2021, we measured 28 morphometric characteristics of otolith and 55 morphometric characteristics of shape using truss network, and then further compared by determination and comparative analysis and stepwise discriminant analysis(SDA). We found that the otolith of the two Branchiostegus species was different in the anterior, posterior, ventral and dorsal sides, while the shape morphological differences were in the head, trunk and caudal areas. The results of the SDA showed that the discriminant accuracy based on otoliths and shape morphological parameters was 85.1% and 94.0%, respectively. The comprehensive discriminant accuracy was 98.0% based on the two morphological parameters. This study reveals that both otolith and shape morphology could effectively distinguish the two species of Branchiostegus, and incorporating various morphological parameters could further increase the discrimination accuracy.

Key words: Branchiostegus japonicus; Branchiostegus albus; truss network; stepwise discriminant analysis(SDA)

长江大保护背景下长江口北支邻近海域鳗鱼苗定置张网兼捕对江海洄游生物影响的初步研究

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摘要：2021 年长江大保护实施后，在长江口设置禁捕管理区，长江口北支鳗苗定置张网捕捞许可区域统一北移至 N31°41′36″以北。长江口是众多洄游性鱼类重要的栖息场所，为了研究长江口北支邻近海域鳗苗定置张网兼捕对江海洄游生物的影响,于 2022 年 2-4 月份，在长江口北支设置三个鳗鱼苗定置张网监测点，在每个月的大、小汛期间各连续监测 5 天，将每网渔获进行分析。结果发现，捕获日本鳗鲡苗 208 尾，需兼捕鱼、虾、蟹类 51 种 47196 尾，其中鱼类 30 种、虾类 15 种、蟹类 3 种、头足类 3 种，兼捕损伤率为 226.9；三个月大潮汛期间捕获的日本鳗鲡苗数量均大于小潮汛期间；共发现江海洄游生物 8 种，其中溯河洄游型生物 4 种，河口型生物 4 种，共计 2744 尾，平均体重 1.52g，兼捕损伤率为 13.19，占总兼捕量的 5.81%对比其他类渔获，长江口北支邻近海域鳗苗定置张网作业区域北移后其兼捕对江海洄游生物的影响较小。

关键词：鳗鱼苗；长江大保护；长江口北支；江海洄游性生物

A preliminary study on the effects of damage rate of fishes by-catch in elver nets in the adjacent areas of the North Branch of Changjiang Estuary on the migratory fishes of the Changjiang River under the background of the protection of the Changjiang River

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Abstract：After the implementation of the Changjiang River Protection in 2021, a marine sanctuary area set up at the Changjiang Estuary，and the area of the larval eels fishing permit area in the north of the Changjiang Estuary had be uniformly moved north to the north of N31°41′36".The Changjiang River Estuary is an important habitat for many migratory fishes,In order to study the impact of by catch in elver nets in the adjacent areas of the North Branch of the Changjiang Estuaryfrom February to April 2022, three monitoring stations were set up in the North Branch of the Changjiang Estuary, and each station was monitored for 5 consecutive days during the high and low tide of each month. The results showed that the capture of 208 Anguilla japonica required 47,196 fishing, shrimp and crab species, including 30 species of fish, 15 species of shrimp, 3 species of crabs and 3 species of cephalopods. The damage rate of fishes by-catch in elver nets was 226.9; the number of Anguilla japonica caught during the three-month high tide was greater than that during the low tide; a total of 8 species and 2744 tails of migratory fishes were found, with an average weight of 1.52g, and The damage rate of fishes by-catch in elver nets was 13.19, the impact of by catch in elver nets in the adjacent areas of the north branch of the Changjiang Estuary had a small impact on the Migratory organisms after the northward movement of the operation area.

Key words: Changjiang Estuary; Migratory fishes; Anguilla japonica; Damage rate of fishes by-catch in elver nets

回声探测浮标在金枪鱼围网渔业中的应用研究进展

周成 1,2,3,4，肖宇 1，万荣 1,2,3,4，许柳雄 1,2,3,4，王禹程 1，谢程兰 5，肖俞辰 1
1.上海海洋大学海洋科学学院；2.上海海洋大学，国家远洋渔业工程技术研究中心；3.上海海洋大学，大洋渔业资源可持续开发教育部重点实验室；4.上海海洋大学，农业农村部大洋渔业开发重点实验室；5.中国水产有限公司，

摘要：回声探测浮标能够为金枪鱼围网渔业远程持续地提供漂流人工集鱼装置（DFADs）的精确地理定位以及金枪鱼集群生物量的估计，有效减少围网船队搜索鱼群所产生的"碳足迹"和船队运营成本，从而提高船队的成功捕获率。除了在商业中的应用外，回声探测浮标有潜力作为观察远洋生物多样性的科学平台，为科学研究提供描述远洋鱼类活动模式的数据来源。本文介绍了 DFADs 的定义、类型和结构、生态影响及相关管理措施，以及回声探测浮标的发展沿革、种类和数据结构，并重点从金枪鱼随附鱼群生物量评估、鱼群随附行为和 DFADs 生态影响评估方面回顾了回声探测浮标在金枪鱼围网渔业中的应用。本文展望了回声探测浮标今后在技术上支持降低非目标物种和目标物种幼鱼死亡率的发展趋势，并从渔业资源可持续管理和海洋生物多样性保护方面讨论了利用浮标观测数据结合渔业数据进行资源评估。

关键词：回声探测浮标；漂流人工集鱼装置；金枪鱼围网；生物量评估；生态影响；金枪鱼行为

Research progress in application of echo-sounder buoys in tuna purse seine fishery

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Abstract： This paper firstly introduces the definition, type and structure, ecological impact and related management measures of DFADs, as well as the evolution, types and data structure of echo-sounder buoys. The application of echo-sounder buoys in tuna purse seine fishery was reviewed from the following three aspects: biomass assessment, fish association behavior and ecological impact posed by DFADs. To the end, this paper prospects the echo-sounder buoys on technical support in the future to reduce the target species and species, the development trend of the larval mortality from fishery resources and the sustainable management and marine biodiversity protection discussed combining fishery resources assessment data buoy observation data and to explore the climate change and human activities on the marine ecological influence the huge potential of the ecological system.

Key words: echo-sounder buoys; drifting fish aggregating devices; tuna purse seine; biomass estimation; ecological impact; tuna behavior

北太平洋柔鱼渔场变动及其与环境因子的关系

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摘要：柔鱼（*Ommastrephes bartrami*）是重要的大洋性经济头足类，其资源分布及渔场变动与环境关系密切。本文利用 2019 年 21 艘鱿钓船在北太平洋的生产统计数据和海表温度（SST）、叶绿素 a 浓度（Chl-a）等环境数据，运用渔场重心分析、聚类分析、GAM 模型分析等方法，探究了北太平洋柔鱼渔场变动及其与海洋环境因子的关系。结果显示，北太平洋柔鱼渔场的最适 SST 范围是 13~14℃，最适 Chl-a 范围是 0.6~0.8 mg/m3，5-11 月产量重心呈明显的西移趋势。研究认为北太平洋柔鱼渔场分布与 SST 关系密切，而 Chl-a 对柔鱼 CPUE 影响较小，渔场重心时空变化受 SST 和柔鱼洄游规律等因素的综合影响。

关键词：北太平洋；柔鱼；时空分布；环境因子；GAM 模型

Changes in Fishing Grounds of Ommastrephes bartrami in the North Pacific and its Relationship with Environmental Factors

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Abstract： *Ommastrephes bartrami* is an important economic oceanic cephalopod, and its resource distribution and changes in fishing grounds are closely related to the environment. Using the production statistics of my country’s squid fishing fleet in the North Pacific in 2019 and environmental data such as sea surface temperature (SST) and chlorophyll a (Chl-a), using methods such as fishery center of gravity analysis, cluster analysis, and GAM model analysis to explore the North The changes in fishing grounds of Pacific scorpionfish from May to November 2019 and its relationship with marine environmental factors. The results show that the fishing grounds of Squid in the North Pacific are concentrated in the sea areas of 39°N~43°N and 157°E~175°W; the optimal SST range of the fishing ground is 13~14℃, and the optimal Chl-a range is 0.6~0.8 mg/m3, the production center of gravity tends to move from southeast to northwest from May to November.This study believes that in May and June, the autumn populations in the west meridian waters were mainly harvested, the autumn populations in the Middle East waters were harvested in July, and the winter and spring populations were harvested in the central and western waters from August to November. The sea surface temperature has an important influence on the yield of soft fish, and Chl-a has a small effect on the yield of soft fish.

Key words: North Pacific Ocean; *Ommastrephes bartrami*; Spatial and temporal distribution; Environmental factors; GAM model

模拟渔获物对网囊水动力特性的影响研究

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摘要：网囊作为拖网系统的重要组成部分，其主要功能是聚集、选择和储存渔获物。渔获物的堆积会使网囊的结构发生改变，从而改变网囊水动力特性，进而影响网囊选择性和稳定性。为了更好的了解中层拖网网囊的水动力特性和囊内渔获物变化之间的关系，本研究利用循环动水槽试验，对存在不同渔获物的网囊模型在不同流速条件下的阻力、形态和振荡变化进行测试分析。该研究结果可为优化网囊结构、提高网囊水动力和形态特性，改善网囊选择性提供基础科学数据。

关键词：网囊；阻力特性；振荡特性；渔获量；形态

The effect of the catch size on the hydrodynamic characteristics of the cod-end

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Abstract： Codend is an important part of the trawl system, which major role is to collect, store and select catches. The accumulates of catch will change the structure of the codend and lead to the change of the hydrodynamic characteristics, and then affect the selectivity and stability of the codend. In order to understand the relationship between hydrodynamic characteristics and catch of the codend of middle trawl. The drag force and shape of a codend model under different flow speeds and catch weights were measured by flume tank experiments, and the drag force, shape, oscillation and volume of the codend structure model were analyzed in this study. The results of this study can provide information to improve the hydrodynamic characteristics, spatial geometry and stability of mid-water trawl codend structure.

Key words: cod-end; drag characteristic; oscillation characteristic; catch weight; shape

水平扩张比和模拟渔获物参数对南极磷虾拖网整体形态影响

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摘要：网具形态能够直观反映渔具作业性能，对拖网形态开展研究具有重要意义，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）及渔获物对网具整体形态以及阻力与能耗系数的影响。研究表明，L/S 保持在 0.35，拖速为 3.0 kn 左右，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

The effects of horizontal opening ratio and simulation catch on the overall shape of Antarctic krill trawl net

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Abstract： The net configuration can directly reflect the performance of fishing gears. It is important to study the trawl configuration to understand the configuration changes of the gears under different working conditions. This study was conducted in the four - pieces krill trawl, which is used by the Antarctic krill fishing vessel "Longteng". A 1/35 scale trawl model net was manufactured based on modified Tauti's law and tested in a flume tank. The effects of current speed (v), horizontal opening ratio (L/S) and catch on the mouth opening overall shape, drag and energy consumption coefficient of model net were investigated.The research suggests to keep L/S of 0.35 and the towing speed of 3.0 kn, so that the trawl could operate with better fishing performance.

Key words: Antarctic krill; trawl; shape; catch; horizontal opening ratio

结合洄游模式的中西太平洋鲣鱼渔业资源评估

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摘要：鲣鱼（*Katsuwonus pelamis*）是世界上最重要的商业性金枪鱼鱼种之一，从上个世纪 80 年代开始，中西太平洋鲣鱼遭遇的捕捞强度逐年增长，但由于其渔业数量多、管理区域划分复杂等特点，渔业资源评估仍然存在较大不确定性。本研究将中西太平洋渔业划分为 8 个管理单元和 31 个船队，结合其分季节的种群洄游特点，使用 Stock Synthesis 3 (SS3)对其进行系统性的资源评估，并拟合不同年龄阶段的洄游状况。结果表明当前捕捞量不会引起资源型过度捕捞或捕捞型过度捕捞。此外，通过对比考虑和不考虑洄游模型的结果表明季节性洄游对金枪鱼的影响是显著的，而不同年龄的鱼群又有不同的洄游趋势和特点，低龄鱼群会在 5 和 8 区域聚集，但是从 8 区域出来的鱼群相对较少，高龄鱼群则会在 3 和 5 区域进行聚集，所有年龄鱼群在区域 4 和 7 活动最为频繁。建议应该将洄游考虑在资源评估之中，而针对不同特征鱼群采取有针对性的养护管理措施。

关键词：渔业资源评估；洄游模式；鲣鱼；中西太平洋

Incorporating the migration pattern in Stock Assessment of Western and Central Pacific Ocean Skipjack Tuna

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Abstract： Skipjack tuna (*Katsuwonus pelamis*) is one of the most important commercial tuna species in the world. Since the 1980s, the WCPO SKJ has been faced with escalating fishing pressure. In order to optimize the stock assessment model and reduce the uncertainty, this essay divides the fishery of WCPO SKJ into 8 management areas and 31 fleets with independent selectivity after integrating indeterminate elements, such as various fishing operating patterns, highly migratory behavior and complex management area delineation.The stock assessment result revealed the status of Skipjack tuna is safe.In addiation， simulation results also reveal that different age groups have different migration patterns: the lower aged groups congregate in area 5, while the higher aged groups congregate in areas 3 and 5. Overall, groups of all ages in different seasons are most active in area 4 and area 7. It is suggested that migration should be taken into account in the stock assessment.

Key words: Stock assessment; Migration pattern; Skipjack tuna; Western and Central Pacific Ocean

环境因子对印度洋长鳍金枪鱼补充量变动影响研究进展

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摘要：长鳍金枪鱼(*Thunnus alalunga*)是世界海洋渔业的主要捕捞对象之一，及时掌握其资源动态对我国金枪鱼渔业的发展具有重要意义。补充量是资源动态的一个重要方面，然而，各种海洋环境因子的变化会对补充量造成一定的影响。因此，研究印度洋长鳍金枪鱼补充量和环境因子之间的关系是十分必要的。本文对国内外补充量模型研究进展进行回顾，介绍了影响长鳍金枪鱼资源分布的主要环境因子，并对环境因子与补充量模型之间的研究方法进行了讨论。包括Ricker模型优化、贝叶斯模型平均法、广义线性模型（Generalized Linear Models，GLM）和广义加性模型（Generalized Addictive Models，GAM）等，为下一步根据海洋环境因子变动进行预测印度洋长鳍金枪鱼的补充量提供参考。

关键词：长鳍金枪鱼；环境因子；补充量模型；Ricker模型

Influence of environmental factors on albacore tuna recruitment in the Indian Ocean

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Abstract： Albacore tuna (*Thunnus alalunga*) is one of the main fishing objects of the world marine fishery, and timely grasp of its resource dynamics is of great significance to the development of tuna fishery in China. The recruitment is an important aspect of the resource dynamics, however, the changes of various marine environmental factors will have certain effects on the recruitment. Therefore, it is necessary to study the relationship between the recruitment of albacore tuna and environmental factors in the Indian Ocean. In this paper, we review the progress of recruitment model research at home and abroad, introduce the main environmental factors affecting the distribution of albacore tuna resources, and discuss the research methods between environmental factors and recruitment models.The methods provide a reference for the next step of predicting the supplementation of albacore tuna in the Indian Ocean based on the changes of environmental factors.

Key words: Albacore tuna (*Thunnus alalunga*); environmental factors; recruitment model; Ricker model

鲨鱼捕捞现状及其制品贸易初步分析

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摘要：鲨鱼养护和管理问题一直是国际社会和区域渔业管理组织的关注重点，尤其是部分鲨鱼品种的过度捕捞问题。本文分析了联合国粮食及农业组织（Food and Agriculture Organization of the United Nations, FAO）全球鲨鱼捕捞及贸易最新数据，分析全球鲨鱼捕捞和鲨鱼制品贸易现状，探讨执行鲨鱼资源养护和贸易管理中面临的现实挑战。通过分析联合国框架下，各国执行濒危野生动植物种国际贸易公约（Convention on International Trade in Endangered Species of Wild Fauna and Flora, CITES）及制定和执行鲨鱼养护和管理国家行动计划（National Plan of Action for the Conservation and Management of Sharks，NPOA-SHARKS）的情况，探究各国鲨鱼捕捞管控的成效和各区域渔业管理组织中，现行鲨鱼养护管理措施的执行效果。分析目前全球鲨鱼的有效管理，特别是根据香港鱼翅贸易管理现状，分析贸易管理对鲨鱼资源的积极影响。针对目前鲨鱼捕捞及贸易过程中出现的兼捕率增加、过度捕捞和缺乏科学数据收集等问题进行了讨论，针对以上问题提出建议，具体包括提高渔具选择性，使用船舶监控系统（fishing vessel monitoring system , VMS），实施许可证制度等。本文结合各项相关国际公约和区域渔业管理组织通过的养护管理措施分析鲨鱼资源养护和管理政策的缺陷和不足，以确保全球鲨鱼资源可持续利用，为鲨鱼资源的养护管理和负责任渔业提供建议。

关键词：鲨鱼捕捞；鲨鱼贸易；区域渔业养护和管理组织；

Preliminary Analysis of the Current Status of Shark Fishing and Trade in its Products

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Abstract： In recent years, the overexploitation of shark resources has aroused widespread international concern for the conservation and management of shark resources. Based on the latest global shark catch and trade data from the Food and Agriculture Organization of the United Nations (FAO), this paper examines the challenges faced in the management of shark fisheries and trade in shark products in the context of the current status of global shark fisheries and trade in shark products. The report specifically analyzes the current conservation and management measures for sharks in regional fisheries management organizations, the implementation of the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) by countries under the UN framework, the effectiveness of the National Plan of Action for the Conservation and Management of Sharks (NPOA-SHARKS) in controlling shark fisheries and the current status of shark fin trade management in Hong Kong. The above measures in international and regional fisheries management organizations have a positive impact on the conservation and management of sharks in the world, but there are still problems in shark fishing and trade, such as increased bycatch rates, illegal fishing, overfishing and inaccurate identification of shark species. This paper proposes recommendations and approaches to address these problems, including changes in fishing gear, the introduction of a vessel monitoring system of fishing vessel (VMS) and implementation of a licensing system. In addition, this paper combines international conventions and conservation management measures of regional fisheries management organizations to ensure the conservation and management of shark resources at the legal and regulatory levels in order to maintain the sustainable use of shark resources worldwide. This research will provide basic information for the conservation, management and sustainable development of shark resources.

Key words: shark fishing; shark Trading; regional fisheries conservation and management organizations

在不同时间尺度下环境变量对西北印度洋灯光罩网渔业的 CPUE 和渔场空间分布的影响

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摘要：为更好地发展和保护西北印度洋的中上层渔业,中国渔业企业长期以来一直在该海域生产中上层渔业。本研究基于 2016 - 2020 年西北印度洋灯光罩网渔船捕捞日志数据,分析了不同时间尺度对灯光罩网渔场渔获率和渔场重心的影响。我们还利用渔场重心、随机森林模型(RF)和广义相加模型(GAM)探究了不同时间尺度与单位捕捞努力量渔获量(CPUE)的关系。结果如下：(1) 2016 - 2020 年,共捕获 76,576 吨,作业网具 16,496 网；(2)西北印度洋渔场重心整体向东北方向移动,各月渔场重心先向南部移动后向北部移动；(3) RF 模型(R 2 = 0.709 , RMSE = 0.2034 ,预测精度为 55.8 %),优于 GAM 模型(R 2 = 0.632 , RMSE = 0.2242 ,预测精度为 37.3 %)。在 RF 模型中,时间变量对 CPUE 的重要性依次为周、年、作业时间、月相；在 GAM 模型中,它是周、年、月相和作业时间。从整体上看,长时间尺度(年、周)的重要性大于短时间尺度(月相和作业时间)。(4) RF 模型和 GAM 模型表明,最关键的环境变量是 SST、DO、SSS 和 Chla,最不重要的是 SSH、Δ 50 和 CV50。SST、Chla 和 DO 显著影响远洋渔业和 CPUE,是预测西北印度洋灯光罩网渔场的重要参考指标。(5) 95%置信区间表明,RF 模型中时间、空间和环境变量的适宜区间远小于 GAM 模型；

关键词：西北印度洋；单位捕捞努力量；时间尺度；环境因素；随机森林；广义加性模型

Environment variables affect CPUE and spatial distribution of fishing grounds on the light falling gear fishery in the northwest Indian Ocean at different time scales

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Abstract：To better develop and protect the pelagic fishery in the northwest Indian Ocean, China’s fishing enterprises have been producing pelagic fisheries in the said area for a long time. Based on the fishing log data of light falling gear in the northwest Indian Ocean from 2016 to 2020, this study analyzed the impact of different time scales on the catch rate and fishing ground center of gravity of light falling gear fishing grounds. We also explored the relationship between different time scales and catch per unit effort (CPUE) by using the fishing ground center of gravity, the Random Forest model (RF), and the generalized additive model (GAM). The results were shown as follows: (1) From 2016 to 2020, 76,576 t were captured, and 16,496 nets were operated; (2) The gravity center of fishing ground in the Northwest Indian Ocean moved to the northeast as a whole, and the monthly fishing ground gravity center changed first to the Southern and then to the northern; (3) RF model (R^2 = 0.709, RMSE = 0.2034, and prediction accuracy is 55.8%), which is better than the GAM model (R^2 = 0.632, RMSE = 0.2242, and prediction accuracy is 37.3%). In the RF model, the importance of time variables on CPUE was in the order of week, year, operation time, and lunar phase; in the GAM model, it was week, year, lunar phase, and operation time. On the whole, the importance of the long time scale (year, week) is greater than that of the short time scale (lunar phase and operation time). (4) The RF model and GAM model show that the most critical environmental variables were SST, DO, SSS, and Chla, and the least important were SSH, Δ 50, and CV50. SST, Chla, and DO significantly impact pelagic fishing and CPUE and are critical reference indexes for predicting the Northwest Indian Ocean light falling gear fishing ground. (5) The 95% confidence interval showed that the suitable interval of time, space, and environmental variables in the RF model was much smaller than in the GAM model.

Key words: northwest Indian Ocean; catch per unit effort; time scale; environment factors; random forest model; generalized additive model

属性参数和工况条件对网片水动力性能影响研究进展

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摘要：网片是网渔具的重要组成部分，在水流等因素的作用下易产生形变，是一种复杂的柔性结构物。开展网片的水动力特性的研究是优化网渔具的基础工作。本研究综述了影响网片水动力特性的主要因素与利用数值模拟探究网片与流场变化规律的研究。结果表明：（1）影响因素包括网片的网目参数、占空率、网线材料等属性参数和冲角、流速、波浪等工况条件；（2）数值模拟的研究内容主要是网片变形、阻力及周围流场分布规律，模拟网片与水流的流固作用今后主要研究方向。

关键词：网片；水动力；流场；数值模拟；模型试验

The effects of attribute parameter and operating condition on hydrodynamic characteristics of netting

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Abstract： Net is an important part of net fishing gear, which is easy to deform under the action of water flow and other factors. It is a complex flexible structure. The research on the hydrodynamic characteristics of net is the basic work of optimizing net fishing gear. This paper reviews the main factors affecting the hydrodynamic characteristics of the mesh and the research on the variation of mesh and flow field by numerical simulation. The results show that :(1) the influencing factors include mesh parameters, duty ratio, network material and other attributes of the mesh, and the operating conditions such as attack Angle, flow rate and wave; (2) The research content of numerical simulation is mainly the mesh deformation, resistance and the distribution law of the surrounding flow field. The fluid-solid interaction between the simulation mesh and water flow is the main research direction in the future.

Key words: Netting; Hydrodynamics; The flow field; Numerical Simulation; Simulation test

中西太平洋金枪鱼围网渔业中鲸类的兼捕研究

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摘要：大洋性金枪鱼渔业对鲸类（*Cetaceans*）的影响在近年来得到广泛的关注，但国际上对该渔业兼捕鲸类的情况还认识较少。根据中西太平洋渔业委员会(WCPFC) 科学机构提供的 2013－2020 年期间金枪鱼渔业和鲸类兼捕数据，对金枪鱼围网兼捕鲸类的情况进行量化分析。结果显示：累计兼捕到 30 种鲸类，共计 9,881 头，年兼捕率为 1.781～4.214 头·百网-1，兼捕主要发生在巴布亚新几内亚、所罗门群岛、密克罗尼西亚、马绍尔群岛、瑙鲁、基里巴斯和图瓦卢之间的海域（130°E－180°W、5°N－10°S）；与围网渔业频繁互动的主要物种包括伪虎鲸（*Pseudorca crassidens*）、糙齿海豚（*Steno bredanensis*）、短肢领航鲸（*Globicephala macrorhynchus*）、瓶鼻海豚（*Tursiops truncatus*）、飞旋原海豚（*Stenella longirostris*）、布氏鲸（Balaenoptera edeni）、塞鲸（Balaenoptera borealis）和东方瓶鼻海豚（*Tursiops aduncus*），其中，糙齿海豚和瓶鼻海豚易受到围网的影响而发生死亡；齿鲸（*Odontoceti*）和须鲸（*Mysticeti*）的兼捕率以及净兼捕率存在显著性差异（P＜0.05）；瓶鼻海豚、短肢领航鲸和塞鲸的兼捕率与金枪鱼的渔获率呈一定正相关关系，抹香鲸（*Physeter macrocephalus*）和里氏海豚（*Grampus griseus*）呈负相关关系。研究结果有助于提高中西太平洋海域金枪鱼围网渔业对鲸类兼捕的认识，以更合适的方式实施鲸类兼捕的减缓措施。

关键词：鲸类；兼捕；金枪鱼围网；中西太平洋

A research study on bycatch of cetaceans by tuna purse seine fishery in Western and Central Pacific Ocean

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Abstract: Increasing attention has been paid to fisheries, which may impact cetacean populations, but the magnitude of cetacean is still poorly known. A quantitative analysis of cetacean bycatch in tuna purse seine fishery was conducted based on fishery and bycatch data released by the Secretariat of the Western and Central Pacific Fisheries Commission from 2013 to 2020. The results showed that a total of 9,881 cetaceans classified as 30 species interacted with purse seine fishery. The annual bycatch rate ranged from 1.781 per hundred sets to 4.214 per hundred sets. The interactions were mainly distributed in the sea area between Papua New Guinea, Solomon Islands, Micronesia, Marshall Islands, Nauru, Kiribati, and Tuvalu (130° E-180° W, 5° N-10° S). The main cetaceans that interacted frequently with the purse seine were false killer whales (*Pseudorca crassiden*s), rough-toothed dolphins (*Steno bredanensis*), short-finned pilot whales (*Globicephala macrorhynchus*), bottlenose dolphins (*Tursiops truncatus*), spinner dolphins (*Stenella longirostri*s), bryde’s whales (*Balaenoptera edeni*), sei whales (*Balaenoptera borealis*) and indo-pacific bottlenose dolphins (*Tursiops aduncus*), of which the rough-toothed and bottlenose dolphins were vulnerable to purse seine. In addition, there were significant differences (P < 0.05) in bycatch and net bycatch rates for odontoceti and mysticeti. Furthermore, bottlenose dolphins, short-finned pilot whales and sei whales were positively associated with tunas. On the contrary, sperm whales (*Physeter macrocephalus*) and risso’s dolphins (*Grampus griseus*) were negatively associated with tunas. The results of this research may improve the understanding of cetacean bycatch and implement adequate monitoring and mitigation in the Western and Central Pacific Ocean.

Key words: cetaceans; bycatch; tuna purse seine fishery; Western and Central Pacific Ocean

阿拉斯加狭鳕太平洋群系资源评估和参考点估算

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摘要：阿拉斯加狭鳕是北太平洋重要的底栖类关键种，分析阿拉斯加狭鳕的资源状况对其可持续发展具有重要意义。依据日本中央水产研究所提供的 1981-2018 年阿拉斯加狭鳕太平洋群系的资源调查数据和生物学数据，利用基于 Beverton-Holt 模型的实际种群分析和单位补充量产量模型对其资源现状进行评估及其管理参考点的制定，分析阿拉斯加狭鳕太平洋群系的资源开发情况和制定管理策略。研究结果表明，历年阿拉斯加狭鳕太平洋群系资源量波动较大，总体呈现下降趋势，但仍保持较高水平，2018 年资源量为 7.6 万 t，0-8 龄鱼捕捞死亡系数波动较大呈现下降趋势，近 5 年平均捕捞死亡系数 F2014-2018 为 0.24，单位补充量产卵生物量是未开发时的 37%，该资源群体不存在生长型过度捕捞和补充型过度捕捞，处于健康状态。并且建议使用 F0.1 为 0.33 作为管理参考点进行渔业资源管理。

关键词：阿拉斯加狭鳕；实际种群分析；单位补充量产量模型；管理参考点；太平洋群系

Resource Assessment and Reference Point of Alaska pollock (*Gadus chalcogrammus*) biomass in the Pacific Ocean

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Abstract： Alaska pollock (*Gadus chalcogrammus*) is an important economic species in the North Pacific Ocean, analyzing its resource status and formulating reasonable management reference point are of great significance for its development, utilization and scientific management. According to the fishery data of the Pacific group which is supplied by Japan’ s central fisheries research institute from 1981 to 2018. The paper evaluates based on analysis of virtual population analysis(VPA) and yield per recruitment(YPR) models. The results showed that the resource amount of pollock in the Pacific Ocean fluctuated greatly over the years, and generally showed a decreasing trend, and maintained a stable level in the past decade. The resource amount in 2018 was 76,000 t. The fishing mortality coefficient of each age group showed a fluctuating downward trend. The average fishing mortality coefficient F2014-2018(0.24) was lower than F0.1(0.33), and the oviposition biomass per unit replenishment was 36% of that in the unexploited period, much higher than the standard warning line of 20%. These results indicated that the species was neither in growth overfishing nor in supplementary overfishing, and the resources were in good condition. It is suggested to use F0.1 as a reference point for fishery resource management to ensure the rational development and utilization of resources.D

Key words: *Gadus chalcogrammus*; VPA; YPR; management reference point; Pacific stoc

江苏近海南部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及年际变化，根据 2009—2020 年春、秋两季在江苏近海南部的底拖网调查数据，结合综合性指标与多元统计分析方法研究了该海域的渔业生物群落结构的年际变化。结果表明：江苏近海南部调查共捕获渔业生物 169 种，物种数呈下降趋势，全年相对资源量波动上升。江苏近海南部优势种主要为三疣梭子蟹、鮸和小黄鱼等，季节变化明显。聚类分析（Cluster）、多维标度排序（MDS）与单因子相似性分析（ANOSIM）表明，研究期间，春季可划分为 A、B 两个年份组，组间相异性系数为 79.68；秋季可划分为 C、D 两个年份组，组间相异性系数为 57.14。相似性百分比分析（SIMPER）显示，A 组与 B 组的组间分歧种主要为葛氏长臂虾等；C 组与 D 组的组间分歧种主要为短吻舌鳎等。本研究为江苏近海南部渔业资源保护及可持续利用研究提供了理论参考。

关键词：群落结构；多元统计分析；江苏近海南部；相对重要性指数

Interannual changes in fishery organisms community structure in the southern coastal waters of Jiangsu Province, China

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Abstract: Based on the data collected from the bottom trawl surveys in the southern coastal waters of Jiangsu Province from 2009 to 2020 in two seasons, multivariate statistical analysis and other integrated indiceswere used to analyze the variation in the community structure of fishery assemblage over time. The results showed that 169 species had been caught, the species number showed decrease over time. The fluctuation of annual relative biomass showed increase. The main dominant species were Portunus trituberculatuns, Miichthys miiuy and Larimichthys polyactis with significant seasonal alternations. The results of Cluster, MDS and ANOSIM showed that station groups in spring cound be divided into Group A and B, while Group C and D in autumn. SIMPER showed that the main discriminating species of Group A and B were Palaemon gravieri, while they were Cynoglossus abbreviatus of Group C and D. Our results might contribute to the sustainable utilization of fishery resources in the southern Jiangsu.

Key words: community structure; multivariate statistical analysis; southern coastal waters of Jiangsu Province; index of relative importance

西非塞拉利昂沿岸海域大眼裸颌鲈生长特征及资源现状

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摘要：大眼裸颌鲈（*Brachydeuterus auritus*）是非洲西海岸重要的经济性鱼种，具有重要的生态价值。本研究利用塞拉利昂沿岸海域的调查资料，对大眼裸颌鲈的资源开发状况进行了评价。结果显示，大眼裸颌鲈的 L∞为 20.47 cm，渐进体重（W∞）为 238.71 g，理论初始年龄（t0）为 0.38 a，拐点年龄（tip）为 1.03 a，生长效能指数Φ’=2.51。LBB 分析显示，参数 L95th/L∞=0.95，Lmean/Lopt=1.07，Lc/Lopt=1.10，M/K=1.53，F/K =1.37，E=0.45，B/B0=0.44，B/Bmsy=1.2。这些参数表大眼裸颌鲈的捕捞死亡率低于自然死亡率，存在一定数量的大个体群体，资源的开发率小于 0.50，资源结构健康，具有一定的开发潜力。

关键词：大眼裸颌鲈；体长频率数据；生长状况；LBB；资源评估；塞拉利昂

Resource assessment and growth characteristics of big-eye grunt (*Brachydeuterus auritus*) in the coastal waters of Sierra Leone, West Africa

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Abstract：Big-eye grunt (*Brachydeuterus auritus*) is an important economic fish species in the west coast of Africa and has important ecological value. Based on the survey data of the coastal waters of Sierra Leone, this study evaluated the resource development status of the large-eye grunt. The results showed that the L∞ of the large-eye grunt was 20.47 cm, the progressive weight (W∞) was 238.71 g, the theoretical initial age (t0) was 0.38 a, the inflection point age (tip) was 1.03 a, and the growth efficiency index Φ’= 2.51。LBB analysis showed that the parameters L95th/L∞=0.95，Lmean/Lopt=1.07，Lc/Lopt=1.10，M/K=1.53，F/K =1.37，E=0.45，B/B0=0.44，B/Bmsy=1.2。These parameters showed that the fishing mortality rate of big-eyegrunt was lower than the natural mortality rate, there were a certain number of large individual groups, the resource development rate was less than 0.50, the resource structure was healthy, and there was a certain development potential.

Key words: Big-eye grunt; length-frequency data; growth equation; LBB; stock assessment; Sierra Leone

岩藻多糖和海带多糖通过激活 intelectin 增强团头鲂巨噬细胞的吞噬作用

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摘要：岩藻多糖和海带多糖通过激活免疫细胞和诱导细胞因子的表达来调节免疫反应。在鱼类免疫反应中巨噬细胞占据重要位置。之前的研究表明，团头鲂内凝集（MaINTL）在免疫反应发挥重要作用，增强了巨噬细胞对嗜水气单胞菌的吞噬和杀伤能力。因此，本研究关注岩藻多糖和海带多糖通过激活 MaINTL 对巨噬细胞的吞噬作用的影响。结果表明岩藻多糖和海带多糖通过激活 MaINTL 的表达改变巨噬细胞骨架，进而增强巨噬细胞吞噬能力。

关键词：岩藻多糖；海带多糖； intelectin；巨噬细胞；吞噬

Fucoidan and laminarin enhance the phagocytosis of Megalobrama amblycephala macrophages via activation of intelectin

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Abstract： Fucoidan and laminarin modulate immune responses by activating immune cells and inducing the expression of cytokines. Macrophages play an important role in fish immune responses. Previous studies have shown thatMegalobrama amblycephala intelectin (MaINTL) plays an important role in the immune response, enhancing the phagocytosis and killing ability of macrophages against Aeromonas hydrophila. Therefore, this study focused on the effect of fucoidan and laminarin on the phagocytosis of macrophages by activating MaINTL. The results show that fucoidan and laminarin alter the macrophage cytoskeleton by activating the expression of MaINTL, thereby enhancing the phagocytic ability of macrophages.

Key words: fucoidan; laminarin; intelectin; macrophage; phagocytosis

渔业产地环境中双酚类污染物的毒性风险与机制

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摘要：双酚类化合物是使用量最大的环氧树脂原材料，可通过多种途径进入到渔业产地环境，对养殖生物和食用者的健康风险亟需重视。前期研究表明，中枢神经系统和代谢系统是双酚 A 替代物作用于生物的敏感靶标，是评价其健康风险的理想指示物。本文以斑马鱼为模式生物，以用量大且检出率高的三种双酚类污染物（双酚 A、双酚 F 和双酚 AF）为研究对象，识别出双酚类污染物长期暴露，会引起鱼类认知障碍和肝脏脂肪化等毒性影响。进一步的脑组织单细胞转录组测序结果发现，认知异常的斑马鱼脑中细胞组成发生了显著改变化，包括神经元比例下降和小胶质细胞等免疫细胞比例上升，这些改变可能与导致了认知障碍的发生有关。而通过对肠道组织的单细胞转录组分析发现，斑马鱼肠上皮细胞占比上升，且伴随脂质吸收基因激活，以上改变可能引起肠道对脂质的过量吸收，进而引起肝脏脂肪化，解释了双酚类污染物引发肝脏脂肪化的原因。

关键词：双酚类污染物；神经毒性；代谢效应；细胞异质性响应；斑马鱼

Toxic risk and mechanism of bisphenol analogues in fishery production environment

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Abstract： Bisphenol analogues can enter the environment of fishery production areas through various approaches, and it is urgent to pay attention to their risks toward cultured organisms and consumers. In this paper, zebrafish was used as the test model to investigate the toxic risk of three mainly used bisphenol analogues (BPA, BPF and BPAF). Based on our results, exposure of bisphenol analogues would result in cognitive impairment and liver steatosis in zebrafish. Single-cell transcriptome sequencing of brain tissue found that there were significant changes in cell composition in the cognitively abnormal zebrafish brain, including a decrease in the proportion of neurons and an increase in the proportion of immune cells such as microglia. In addition, the proportion of intestinal epithelial cells in zebrafish increased after bisphenol exposure, and with the activation of lipid absorption genes, which may further induce excessive absorption of lipids in the intestine and liver steatosis.

Key words: Bisphenol analogues; neurotoxicity; metabolic effect; cell heterogeneous response; zebrafish

饲料中添加肽聚糖对中华绒螯蟹生长性能、血清抗氧化机能的影响

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摘要：为研究饲料中添加肽聚糖对中华绒螯蟹幼蟹生长性能、血清抗氧化机能的影响，在基础饲料中分别添加 0（对照组）、62.5、125 和 250mg/kg 的肽聚糖，配制成 4 组实验饲料，分别投喂初始体质量为(32.7±1.4)g 的中华绒螯蟹 28d。结果显示，实验蟹的增重率随着饲料中肽聚糖添加量的提高先升后降，在添加量为 125mg/kg 饲料组达到最大值，显著高于对照组。相比于对照组，添加 125~250mg/kg 饲料的肽聚糖组实验蟹血清中总抗氧化能力（T-AOC）、超氧化物歧化酶(SOD)活性和过氧化氢酶（CAT）活性显著提高；肽聚糖添加量为 125mg/kg 饲料组实验蟹血清溶菌酶（LZM）活性达到最大值，且与对照组差异显著。研究表明，饲料中适量添加肽聚糖可显著提高中华绒螯蟹幼蟹的生长性能、增强血清抗氧化能力。

关键词：中华绒螯蟹；肽聚糖；生长性能；抗氧化能力

Effect on peptidoglycan level on growth performance and serum antioxidant activity of Chinese mitten crab (Eriocheir sinensis)

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Abstract: An experiment was conducted to investigate the effects of peptidoglycan content on growth performance and serum antioxidant activity of Eriocheir sinensis. Peptidoglycan levels of 0, 62.5, 125 and 250mg/kg were supplemented to basal diet to formulate four diets. Each diet was randomly assigned to triplicate cages of 60 crabs with an initial average weight of (32.7±1.4)g for 28 days. The results showed that the WGR first increased and then decreased with the increase of peptidoglycan, and reached the maximum when the dietary supplementation was 125 mg/kg, which were significantly higher than those of the control group. Compared with the control group, T-AOC, SOD and CAT were significantly increased. The maximum of LZM appeared in the 125mg/kg group, which were significantly different from those of the control group. All these results indicated that the suitable peptidoglycan supplementation could significantly improve growth performance, enhance the serum's antioxidant capacity.

Key words: Chinese mitten crab; peptidoglycan; growth performance; antioxidant capacity

基于 SecA 基因的鰤鱼诺卡氏菌 qPCR 检测方法的建立及进化分析

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摘要：为对诺卡氏菌病进行快速早期诊断，建立了鰤鱼诺卡氏菌 TaqMan qPCR 检测方法。以鰤鱼诺卡氏菌的管家基因 SecA 为靶标设计引物和探针，进反应条件优化，制作标准曲线，对灵敏性、重复性和特异性测试，并将建立的方法应用于临床样品的检测。结果表明，引物和探针终浓度分别为 0.3 μmol/L 和 0.1 μmol/L，退火延伸温度 60℃时，qPCR 在 9.85×1010~9.85×100 copies 范围内呈良好的线性关系，灵敏度最高达 9.85 copies；重复性较好，组间和组内变异系数均小于 1%；特异性较高，对弗氏柠檬酸杆菌、维氏气单胞菌等 12 种病菌均无扩增；大口黑鲈样品进行临床检测，qPCR 检出率比比普通 PCR 提高 14.24%，SecA 基因在传代中和种内高度保守。本研究建立的鰤鱼诺卡氏菌 qPCR 检测方法可用于对鰤鱼诺卡氏菌病的早期诊断和定量检测，为诺卡氏菌病的早诊断早治疗提供有效手段。

关键词：大口黑鲈；鰤鱼诺卡氏菌；qPCR；诺卡氏菌病

Establishment of qPCR detection assay and phylogenetic analysis based on Nocardia seriolae SecA gene

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Abstract： In order to perform diagnosis of N.seriolae infection quickly and early, a TaqMan qPCR detection method for N.seriolae was established. The Primers and probes were designed with the housekeeping gene SecA of N.seriolae as the target,The assay of qPCR showed high linearity in the range of 9.85×1010~9.85×100 copies with a sensitivity of up to 9.85 copies under the optimal final concentrations of primer and probe (0.3 μmol/L and 0.1 μmol/L)and the optimal annealing extension temperature 60℃. CV between groups and within groups is less than 1%.The specificity showed that there was no amplification for 12 pathogens such as C.freundii and A.veronii.The result of the clinical samples from diseased M.salmoides,qPCR was 14.24% higher than that of normal PCR. SecA gene is highly conserved in passage and within species.The qPCR method can be used in early diagnosis and quantitative detection of N.seriolae, and provides an effective tool for early diagnosis and treatment of nocardiosis.

Key words: Micropterus salmoides; Nocardia seriolae; quantitative PCR; nocardiasis

脊尾白虾“僵尸病”的转录组研究

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摘要：探究患“僵尸病”后脊尾白虾（病原：二尖梅奇酵母）的分子响应机制，为深入了解脊尾白虾应对该病原的分子机制和疾病控制研究提供参考。利用高通量测序技术进行脊尾白虾感染前后转录组测序分析，对所得基因进行比对和注释，并对差异基因进行鉴定和分析。共组装注释获得了 67,811 个基因，平均长度 905bp，筛选得到 1991 个差异表达基因,其中 1224 个上调,767 个下调，与免疫相关的基因主要与模式识别受体、溶酶体、氧化应激、细胞凋亡密切相关；此外部分差异基因参与甘油磷脂代谢、蛋白质消化和吸收等代谢途径。脊尾白虾感染后会上调 CTL 增强对病原的识别并激活免疫系统，同时上调 CTSB, ARSB 促使溶酶体降解外源性病原；此外 GST，LPSAT, Plg 等基因的表达受到抑制，进而损伤虾体的抗氧化系统、甘油磷脂代谢及蛋白质消化吸收途径。

关键词：脊尾白虾；僵尸病；二尖梅奇酵母；转录组；免疫；代谢

Transcriptome analysis reveals mechanisms of organismal response in Exopalaemon carinicauda with "Zombie Disease"

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Abstract： Exopalaemon carinicauda is one of the important economic species in China. In recent years, an epidemic disease called "Zombie Disease" by local farmers has appeared in the E. carinicauda breeding area of Jiangsu Province, and the pathogen was found to be Metschnikowia bicuspidata after isolation and identification. The immune responses of M. bicuspidata to the E. carinicauda infection is not fully characterized. To investigate the immune response of E. carinicauda against M. bicuspidata, we performed transcriptome analysis of the E. carinicauda hepatopancreas with and without M. bicuspidata infection using transcriptome high-throughput sequencing. After assembly, 67,811 high quality unigenes were obtained from transcriptome high-throughput sequencing. Differential expression analysis revealed the existence of 1991 significantly differently expressed genes (DEGs) at 60 h post infection, with 1224 up-regulated and 767 down-regulated genes. The expression levels of 8 DEGs were randomly validated by qRT-PCR, and the results showed that are consistent with the RNA-seq data. The enrichment analysis of DEGs showed that the immune-related genes were closely related to pattern recognition receptors (CTL), lysosome (CTSB, ARSB), stress-related process (GST), apoptosis (Casp2). Moreover, a large number of DEGs related to metabolic function such as glycerophospholipid metabolism (LPSAT, LPEAT), protein digestion and absorption (Plg). These new experimental results reveal the immune and metabolic mechanisms of the hepatopancreas in response to M. bicuspidata infection in E. carinicauda, providing a reference for further understanding of host response mechanisms to pathogens in aquatic systems.

Key words: Exopalaemon carinicauda; Zombie Disease; Metschnikowia bicuspidata; Transcriptome; Immunity; Metabolism

基于稳定同位素比值的鲍鱼指纹特征及产地溯源研究

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摘要：随着人们对水产品的需求量日益增加，原产地信息不清、以假乱真、以次充好等问题逐渐显现出来。稳定同位素蕴含了丰富的产地环境信息，其指纹分析技术是产地溯源最具应用前景之一。为了保护消费者合法权益，实现对鲍鱼产地来源的追溯，本研究应用稳定同位素比质谱仪，分析了连江、长岛、荣成和大连四个地点鲍鱼的贝柱、裙边、消化腺性腺以及外套膜中的碳、氮稳定同位素比值，利用 Fisher 判别分析建立产地溯源模型，并结合留一交叉验证法验证模型，指出了不同产区鲍鱼稳定同位素比值的指纹特征，并评估了鲍鱼不同组织的δ13C、δ15N 值对产地溯源的识别能力。研究结果表明，全部组织的总体产地判别的原始正确判别率为 90.5%，交叉验证正确判别率为 89.0%，其中连江和荣成两个产区的鲍鱼溯源效果最好。此外，每个部位单独进行产地溯源结果普遍小于全部组织整体判别分析，建议全部组织结合溯源，以提高产地溯源准确率，但连江鲍鱼可单独使用外套膜作为溯源指标进行产地溯源。本研究提供了鲍鱼产地溯源方法，为完善水产品的产地溯源模型奠定基础。

关键词：鲍鱼；稳定同位素；判别分析；产地溯源；指纹特征

Study on the fingerprint characteristics and origin tracing of abalone based on stable isotope ratio

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Abstract： With the increase of people's demand for aquatic products, some problems have gradually emerged, such as unclear information about the origin, confusing the real with the false, shoddy and so on. Stable isotope contains abundant environmental information of origin, and its fingerprint analysis technology is one of the most promising applications in origin traceability. To protect the legitimate rights and interests of consumers and trace the origin of abalone. In this study, abalone samples were collected from Fujian, Changdao, Rongcheng and Dalian. The stable isotope ratios of carbon and nitrogen in the Gastropod muscle, Muscle edge, Digestive glands and gonads and Mantle of abalone were analyzed by stable isotope mass spectrometer. Establishing origin traceability model by Fisher discriminant analysis, and it was verified by leave-one-out method. The fingerprint characteristics of stable isotope ratios of abalone in different regions were pointed out, and the recognition ability of stable carbon and nitrogen isotopes in different tissues to the origin traceability was evaluated. The results show that the original correct discrimination rate of the overall origin discrimination of all tissues was 90.5%, and the correct discrimination rate of cross validation was 89.0%. Among them, Fujian and Rongcheng regions have the best effect on abalone traceability. Furthermore, the results of origin traceability for each part were generally less than that of the whole tissue discriminant analysis. It is suggested that all organizations should combine traceability to improve the accuracy of origin traceability. However, the abalone in Lianjiang can be traced to the origin by using the outer coating alone as the traceability index. This study provides the method of origin traceability of abalone and lays a foundation for perfecting the origin traceability model of aquatic products.

Key words: Abalone; Stable isotope; Discriminant analysis; Origin traceability; Fingerprint characteristics

黄颡鱼春季暴发病小 RNA 病毒基因组特征与宿主敏感性研究

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摘要：为研究黄颡鱼小 RNA 病毒的致病机制，对从发病黄颡鱼组织中分离的小 RNA 病毒（*Pelteobagrus Fulvidraco Picornavirus* 1，YCPrV-1）YCPrV21316 毒株进行基因组特征与宿主敏感性研究。根据以前获得的 YCPrV-1 基因组序列设计引物，扩增获得 YCPrV21316 毒株的基因组序列，近全长 7360 bp，含有两个编码框，与已报道的病毒基因组序列最高同源性为 28.04%；通过 YCPrV21316 对黄颡鱼、草鱼和鳙鱼的攻毒试验，发现可引起黄颡鱼和草鱼的死亡，死亡率分别为 62.5%和 40%，以上结果表明，黄颡鱼小 RNA 病毒是一种具有多宿主致病性的新病毒，肾脏是其主要靶器官，病毒的体外培养可为其生物学特性与疫苗的研究提供基础。

关键词：黄颡鱼；小 RNA 病毒；荧光定量 PCR；敏感宿主

Genomic characteristics and host sensitivity of the spring outbreak small RNA virus in Pelteobagrus Fulvidraco

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Abstract： To study the pathogenic mechanism of Pelteobagrus Fulvidraco small RNA virus (*Pelteobagrus Fulvidraco* 1, YCPrV-1) YCPrV21316 strain isolated from diseased Pelteobagrus Fulvidraco tissues, genomic characteristics and host sensitivity were studied. Based on the previously obtained YCPrV-1 genome sequence, the sequence of YCPrV21316 was amplified, which was nearly 7360 bp in length and contained two coding frames. The highest homology with the reported virus genome sequence was 28.04%. YCPrV21316 was tested on Pelteobagrus Fulvidraco, grass carp and bighead carp. It was found that YCPrV21316 could induce the death of Pelteobagrus Fulvidraco and grass carp. The mortality rates were 62.5% and 40% respectively. The results indicated that the small RNA virus of Pelteobagrus Fulvidraco is a new virus with multi-host pathogenicity, and the kidney is its main target organ.

Key words: Pelteobagrus Fulvidraco; Small RNA virus; Fluorescent quantitative PCR; Sensitive host

外源一氧化氮对脊尾白虾体内虾肝肠胞虫载量和免疫力的影响

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摘要：为探究外源一氧化氮(NO)对脊尾白虾体内虾肝肠胞虫（*Enterocytozoon hepatopenaei*, EHP）载量和免疫力的影响，本研究向脊尾白虾围心腔注射10 µL浓度为0 µg/L（对照组）、0.3 µg/L、0.6 µg/L、0.9 µg/L的硝普纳（作为外源NO供体），观察脊尾白虾在投放EHP的养殖水中5 d内肝胰腺的EHP载量、组织结构，及血液中诱导型一氧化氮合酶（iNOS）活性和NO含量的变化。研究结果表明，0.3、0.6和0.9组第5 d的EHP载量显著低于对照组（$P<0.05$）。组织切片发现，第3 d和5 d各组肝小管空泡化加重，而对照组的肝小管受损最严重且萎缩形。0.3组血淋巴中iNOS活力和NO含量先下降后上升，而NO含量变化区间小于对照组。研究发现注射外源NO能降低感染EHP脊尾白虾体内的EHP载量和减缓肝胰腺结结构的病变程度,作用机制可能与iNOS有关。

关键词：脊尾白虾；虾肝肠胞虫；一氧化氮；非特异性免疫

Effects of exogenous nitric oxide on Enterocytozoon Hepatopenaei copy number and immunity of Exopalaemon carinicauda

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Abstract：Nitric oxide (NO) can participate in immune defense reaction.In order to explore the effect of exogenous NO on the carrying capacity and immunity of *Enterozoon hepatoopenaei* (EHP) in Exopalaemon carinicauda, we injected 10 µL of Sodium Nitroferricyanide Dihydrate (SNP, as an exogenous NO donor) at concentrations of 0 µg/L(control group), 0.3 µg/L, 0.6 µg/L and 0.9 µg/L into the pericardial cavity of Exopalaemon carinicaud. We observed the changes of EHP copy number of hepatopancreatic, hepatopancreatic structure, superoxide dismutase (SOD) activity, alkaline phosphatase (AKP) activity, inducible nitric oxide synthase (iNOS) activity and NO content in the blood of NO injected Exopalaemon carinicauda, within 5 days after being put into EHP culture water.The results showed that the EHP load of groups 0.3, 0.6 and 0.9 on the 5th day was significantly lower than that of the control group ($P < 0.05$), and the EHP load of groups 0.3 and 0.6 was lower than that of group 0.9. The histological sections showed that spores were observed in the hepatic tubules of each group on the first day. On the third and fifth days, the vacuolation of the hepatic tubules in each group was aggravated and the number of spores increased. The hepatic tubules in control group were seriously damaged and appeared atrophy and deformation. INOS activity and NO content in hemolymph of group 0.3 decreased first and then increased. On the 5th day, there was no significant difference in iNOS activity between group 0.3 and control group ($P > 0.05$), but the change interval of NO content in group 0.3 was smaller than that in control group. It was found that injection of exogenous NO could reduce the EHP copy number and slow down the pathological degree of hepatopancreas structure in EHP infected Exopalaemon carinicauda, and the mechanism of action might be related to the increase of iNOS activity.

Key words: Exopalaemon carinicauda; Enterozoon hepatoopenaei; Nitric oxide; Nonspecific immunity

氟苯尼考与槲皮素联用治疗凡纳滨对虾急性肝胰腺坏死综合征的效果评价

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摘要：评价了槲皮素（CGA）和氟苯尼考（FFC）联合使用对凡纳滨对虾感染致急性肝胰腺坏死综合征副溶血弧菌（VPAHPND）的治疗效果。与FFC和CGA单独使用相比，FFC和CGA联用组的虾在感染后5天内的累积死亡率显著降低（$p < 0.05$）。此外，在药物联用组中，弧菌密度始终比仅感染组和药物单用组低，免疫参数始终高于药物单用组（$p < 0.05$）。联合用药组的对虾肝胰管结构和完整性优于药物单用组。因此，与FFC和CGA单独使用相比，二者联用提高了受VPAHPND攻击的虾的存活率、抗病性和免疫力。在获得更好的治疗效果的同时，可以减少抗生素的使用量，缓解水产养殖中细菌耐药性的发生。

关键词：凡纳滨对虾；VPAHPND；槲皮素；氟苯尼考

Effects of combined florfenicol and quercetin to treat acute hepatopancreatic necrosis disease in Litopenaeus vannamei caused by Vibrio parahaemolyticus

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Abstract： The survival, disease resistance, and immunity of Litopenaeus vannamei infected with Vibrio parahaemolyticus causing acute hepatopancreatic necrosis syndrome (VPAHPND), and treated with quercetin and florfenicol, alone or in combination were evaluated. Compared with either drug alone, the shrimps in the florfenicol and quercetin combination groups showed significantly lower cumulative mortality over 5 days after infection ($p<0.05$). Moreover, in the drug combination groups, the vibrio density were consistently lower and the immune parameters were consistently higher than those in single drug groups ($p<0.05$). In the drug combination groups, the hepatopancreatic tubule structure and integrity were better than those in the single drug groups. Thus, the use of florfenicol and quercetin combined improved the survival rate, disease resistance, and immunity of shrimp challenged with VPAHPND compared with either drug alone. The use of florfenicol could be reduced to gain an improved therapeutic effect.

Key words: Litopenaeus vannamei; VPAHPND; Florfenicol; Quercetin

茶多酚改善双酚 A 诱导斑马鱼卵巢中线粒体功能基因表达下调

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摘要：内分泌干扰物广泛存在于环境中，干扰生物体内分泌系统诸多环节，主要靶器官是生殖系统，导致受精下降，性腺发育和生殖行为异常。增塑剂双酚 A 是一种典型的内分泌干扰物，研究表明双酚 A 暴露会导致生殖毒性，受精异常和不育。然而，低浓度双酚 A 对生殖系统的作用机制和治疗措施尚未完全明确。本研究以斑马鱼为模型探索了雌性斑马鱼卵巢的转录组，转录组数据显示，双酚 A 暴露组线粒体 NADH 脱氢酶（mt-Nd）基因表达显著降低，而茶多酚共同处理组线粒体 NADH 脱氢酶基因表达显著升高。为进一步探索 mt-Nd 基因的表达模式，本研究通过 qRT- PCR 分析了 6 个 mt-Nd 基因在对照组，双酚 A 暴露组和双酚 A-茶多酚共同处理组斑马鱼卵巢不同时期的表达，结果显示 0.1mg/L 双酚 A 暴露会对斑马鱼卵巢的线粒体呼吸链产生不利影响，可能会导致生殖障碍。最后，本研究表明茶多酚对低浓度双酚 A 暴露的雌性斑马鱼卵巢线粒体功能障碍起保护作用。

关键词：斑马鱼；双酚 A；茶多酚；转录组；线粒体 NADH 脱氢酶

Tea polyphenols improve down-regulation of mitochondrial functional gene expression induced by bisphenol A in zebrafish ovaries

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Abstract：Endocrine disrupting chemicals are widely present in the environment and interfere with many aspects of the endocrine system of organisms. The main target organ is the reproductive system, resulting in decreased fertilization, abnormal gonadal development and reproductive behavior. The plasticizer bisphenol A is a typical endocrine disrupting chemical, studies demonstrated that exposure to bisphenol A can cause reproductive toxicity, abnormal fertilization, and infertility. However, the mechanisms of low-concentration bisphenol A on the reproductive system and treatment measures have not been fully determined. In this study, we used the zebrafish as a model to explore the transcriptomic profiles of female zebrafish ovaries. The transcriptomic data revealed that mitochondrial NADH dehydrogenase (mt-Nd) genes were significantly decreased in the bisphenol A-exposed group, while the co-administration of tea polyphenols remarkably elevated the expression of mt-Nd genes. To further explore the expression pattern of the mt-Nd, we analyzed the expression of six mt-Nd genes on different days by qRT-PCR in control, bisphenol A-exposed, and bisphenol A-tea polyphenols ovaries. Here, we found that 0.1 mg/L bisphenol A exposure adversely affects the mitochondrial respiratory chain in ovaries and may lead to reproductive disorders. Finally, our study demonstrated that tea polyphenols play a protective role in ovarian mitochondrial dysfunction in low-concentration bisphenol A-exposed female zebrafish.

Key words: zebrafish; bisphenol A; tea polyphenols; transcriptome; mitochondrial NADH dehydrogenase

突发公共卫生事件中食品安全网络舆情主题与情感演化研究

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摘要：探索突发公共卫生事件中食品安全网络舆情主题与情感演化规律，为食品安全网络舆情的引导与治理提供决策支持。基于舆情生命周期的不同阶段，选取新冠肺炎疫情期间进口冷链水产品事件微博舆情数据为研究对象，结合 LDA 主题挖掘、社会网络分析和机器学习的情感分析方法构建突发公共卫生事件中食品安全网络舆情的主题与情感演化分析模型，对舆情主题和情感演化规律进行分析。结果表明，突发公共卫生事件中的食品安全网络舆情可以分为潜伏期、突发期、蔓延期和终结期四个阶段，各阶段网民关注内容主题侧重不同，官方通告与媒体报道内容会对网民关注主题产生影响；网民评论总体情感表现为消极，呈现出波动-发泄-缓和-蔓延的变化趋势；网民关注主题与情感演变之间存在相互作用关系。因此，本文提出应基于不同发展阶段、网民关注主题与社会集体参与三方面提升食品安全网络舆情的治理水平。

关键词：突发公共卫生事件；食品安全网络舆情；主题挖掘；主题演化；情感演化

Research on the theme and emotional evolution of food safety network public opinion in public health emergencies

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Abstract: To explore the theme and emotional evolution of public opinion on food safety networks in public health emergencies, and to provide reference for public opinion guidance and governance; [Method/process] Based on the different stages of the public opinion life cycle, the Weibo public opinion data of the imported cold chain aquatic products incident during the new crown pneumonia epidemic was selected as the research object, and the theme and emotion analysis model of network public opinion in public health emergencies were constructed by combining LDA theme mining, social network analysis and machine learning emotion analysis methods, and the theme of public opinion and the law of emotional evolution were analyzed; [Result/conclusion] There are four stages of public opinion coverage, including the end of the incubation period and the postponement of public opinion, which can focus on the topics of public health emergencies, and the results can be divided into four stages; The overall emotion of comments is negative, showing a trend of fluctuation - venting - easing - spreading. Based on this, this paper proposes to improve the governance level of food safety network public opinion from three aspects: different development stages, Internet users' attention to the theme and social collective participation.

Key words: Keywords; Public health emergencies; Food safety network public opinion; Topic mining, Theme Evolution; Emotional evolution.

西伯利亚鲟链球菌肠炎转录组及 NLRs 的表达分析

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摘要：海豚链球菌是一种危害水产养殖业的兼性胞内菌，其感染引起的细菌性肠炎是鲟鱼养殖中的常见疾病，然而肠炎的发生发展机制尚不清楚。因此，本研究通过肛门灌注 2×107 CFU/mL 海豚链球菌构建西伯利亚鲟肠炎模型，基于疾病活动指数、髓过氧化物酶、组织病理损伤和炎症因子分析，揭示海豚链球菌感染后西伯利亚鲟经历了渗出（1-3d）、坏死（4-6d）到增生（7-10d）的肠炎过程。对发病关键期坏死性肠炎阶段的瓣肠转录组测序发现 DEGs 富集在 NLR 信号通路，转录组数据库挖掘获得 33 个 NLR 家族基因，包括 8 个 NLR-A，20 个 NLR-C 和 5 个其他 NLR。对肠炎各阶段 NOD1、NOD2、NLRC3L 和 NLRC4L 与 IL-1β的表达水平进行相关性分析，相关系数分别为 0.995、0.401、0.327 和 0.089，提示 NOD1 可能在海豚链球菌肠炎中发挥重要作用。本研究为阐释西伯利亚鲟链球菌肠炎发生发展机制奠定基础。

关键词：海豚链球菌；西伯利亚鲟；肠炎；NOD 样受体；炎症反应

Transcriptome and NLRs expression analysis of Streptococcal enteritis in Siberian sturgeon

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Abstract： Streptococcus iniae is a facultative intracellular bacterium that endangers aquaculture. Bacterial enteritis caused by S. iniae infection is a common disease endangered sturgeon aquaculture. However, the mechanism of enteritis is still unclear. Therefore, an enteritis model of Siberian sturgeon was constructed by anal infusion of 2×107 CFU/mL S. iniae based on the Disease activity index, Myeloperoxidase, histopathology damage and the expression of inflammatory factors. Predominant symptoms of exudative inflammation, metamorphic inflammation and proliferative inflammation on days 1-3, 4-6, and 7-10 post infection were shown, respectively. The transcriptome of the valve intestine at the critical stage showed that DEGs were enriched in the NOD-like receptor (NLR) signaling pathway. 33 NLR family genes containing NACHT domains were obtained from the transcriptome database, including 8 NLR-A, 20 NLR-C and 5 other NLRs. The mRNA expression levels of NOD1, NOD2, NLRC3L and NLRC4L were detected and correlated with IL-1β in different stages of enteritis, and the correlation coefficients were 0.995, 0.401, 0.327 and 0.089, respectively. These results suggested that NOD1 may play an important role in S. iniae enteritis. This study laid a foundation for explaining the mechanism of S. iniae enteritis in Siberian sturgeon.

Key words: Streptococcus iniae; Siberian sturgeon; enteritis; NOD-like receptor; inflammatory response

罗氏沼虾病原非 O1 霍乱弧菌致病性及全基因组分析

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摘要：2017 年至 2018 年，中国江苏省高邮县罗氏沼虾（*Macrobrachium rosenbergii*）养殖场发生大规模死亡事件。从罗氏沼虾中分离的细菌根据生化特征和分子技术鉴定为非 O1 型霍乱弧菌（non-O1 Vibrio cholerae）。在攻毒试验中，感染 GXFL1-4 的罗氏沼虾表现出与自然患病对虾相似的病理症状。GXFL1-4 的毒力因子检测表明该细菌产生酪蛋白酶、脂肪酶等，并携带 toxR、txA 等毒力基因。此外，我们对 GXFL1-4 的全基因组进行了测序，以揭示其致病性和抗生素耐药性。研究发现其携带 372 个潜在毒力基因，148 个耐药基因和 320 个与病原体-宿主相互作用相关的基因。本研究揭示了非 O1 霍乱弧菌对罗氏沼虾的致病性，该研究结果将为预防非 O1 霍乱弧菌引起的罗氏沼虾病提供理论支持。

关键词：罗氏沼虾；非 O1 霍乱弧菌；致病性；基因组特征；毒力因子

Pathogenicity and complete genome analysis of non-O1 Vibrio cholerae isolated from Macrobrachium rosenbergii

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Abstract: From 2017 to 2018, outbreaks of mass mortalities occurred in *Macrobrachium rosenbergii* farms in Gaoyou county, Jiangsu Province of China. The bacterial isolated from M. rosenbergii were identified as non-O1 Vibrio cholerae according to biochemical characteristics and molecular identification. In challenge test, M. rosenbergii infected with GXFL1-4 developed similar pathological signs to the naturally diseased prawns. Detection virulence factors of GXFL1-4 showed that the bacteria produced caseinase, lipase, and etc, and carried toxR, txA, and etc. In addition, we sequenced the whole genome of GXFL1-4 for revealing the pathogenicity and antibiotic resistance. It was found to carry 372 potential virulence genes, including 148 resistance genes in 320 pathogen-host interactions genes. This study revealed the pathogenicity of non-O1 V. cholerae to M. rosenbergii, and the findings will provide theoretical support for the prevention of M. rosenbergii disease caused by non-O1 V. cholerae.

Key words: Macrobrachium rosenbergii; Non-O1 Vibrio cholerae; Pathogenicity; Genomic characterization; Virulence factors

绿茶源化合物 EGCG 抗石斑鱼虹彩病毒作用机制及免疫性能的影响

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摘要：为解决石斑鱼虹彩病毒(*Singapore grouper iridovirus*, SGIV)在水产养殖业中造成的威胁，本研究对绿茶活性成分 EGCG 抗 SGIV 感染作用进行了机制研究。本研究根据前期验证 EGCG 具有良好的抗 SGIV 作用效果(抑制率可达到 99%以上) 为基础，通过光学显微镜观察、RT-qPCR 技术以及 Western Blot 等技术进行研究。结果发现，EGCG 对病毒粒子结构有一定的破坏作用，同时对病毒的吸附、侵入和复制阶段也有一定的影响，根据主要衣壳蛋白的表达量来分析其抑制率分别为 82.31%、85.07%、79.77%，该结果与流式结果相一致，结果说明 EGCG 可以直接作用于病毒，已减少其对细胞的侵害作用。本研究也针对 EGCG 对宿主细胞的免疫性能影响，结果发现 EGCG 可以提高宿主细胞 IRF3、TNF-a、IL-6 等免疫因子的表达，说明 EGCG 可以提高机体免疫性能来提高自身抗病毒作用。

关键词：石斑鱼虹彩病毒；EGCG；病毒粒子；侵染过程；免疫因子

The inhibitory effect and immune performance of EGCG from green tea components against grouper iridovirus infection

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Abstract: In the past decade, the infectious disease caused by grouper iridovirus (SGIV) has seriously threatened groupers aquaculture. To control the viral diseases caused by iridovirus, the generation of effective drugs against iridovirus is necessary. Green tea components have been proved their various benefits against viral diseases. In this study, the mechanism of EGCG against SGIV infection was investigated. Based on the previous results that natural ingredient EGCG isolated from green tea could effectively inhibit SGIV replication, and the inhibition rate can reach more than 99%. Optical microscopy, RT-qPCR and Western Blot were used to investigate. The results showed that EGCG could damage the virion structure, and it also affected the stages of virus adsorption, invasion and replication, the inhibition rates were 82.31%, 85.07% and 79.77% respectively, according to the expression of major capsid proteins. The antiviral effect of aptamerQ5c was consistent with the results of RT-qPCR. The results indicated that EGCG exerted the direct antiviral activity against SGIV infection. This study also targeted the effect of EGCG on host cells immune performance. The results showed that EGCG could increase the expression of IRF3, TNF-α, IL-6 and other immune factors in host cells. It suggested that EGCG can improve the immune performance of host cell. In conclusion, EGCG from green tea components not only has a direct inhibitory effect on SGIV, but also can improve the immune performance of the host cell. It means that some green tea components might be promising candidates for developing effective medicines for preventing and controlling SGIV infection in grouper aquaculture industry.

Key words: grouper iridovirus; EGCG; virion; infection process; immune factor

卵形鲳鲹 ISG15 的鉴定及其在病毒和细菌感染中的作用研究

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摘要：干扰素 (IFN) 刺激基因 15（Interferon-stimulated gene, ISG15）是一种控制微生物感染至关重要的泛素样蛋白。卵形鲳鲹（*Trachinotus ovatus*）是我国南方沿海珍贵的海洋经济鱼类之一，常感染虹彩病毒和神经坏死病毒。迄今为止，卵形鲳鲹干扰素相关基因在病原感染中的作用在很大程度上仍旧未知。因此，本研究克隆并鉴定了卵形鲳鲹 ISG15 同源基因 (ToISG15)，并探讨了 ToISG15 在病毒与细菌感染中的作用。研究发现，ToISG15 的 ORF 由 465 个碱基组成，编码 154 个氨基酸，与已知的其他鱼类 ISG15 同源物具有不同的相似性。ToISG15 包含两个泛素样 (UBL) 域和一个泛素结合域 (LRGG)。ToISG15 主要位于卵形鲳鲹细胞的细胞质中，并能被 SGIV、NNV 或 poly I:C 显着诱导表达。ToISG15 在细胞中的过表达能够显着抑制 SGIV 的复制，但对 NNV 的抑制作用较弱。此外，ToISG15 在金鲳细胞中的过表达还能显着抑制嗜水气单胞菌的生长，这是首次发现鱼类 ISG15 具有抗菌功能。综上所述，卵形鲳鲹的 ISG15 具有抗病毒及抗菌功能，表明鱼类的 ISG15 在病毒和细菌感染的免疫反应中发挥重要作用。

关键词：卵形鲳鲹；ISG15；病毒与细菌感染；免疫应答

Identification of ISG15 in golden pompano, Trachinotus ovatus，and its role in virus and bacterial infections

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Abstract： Interferon (IFN)-stimulated gene product 15 (ISG15) is a ubiquitin-like protein critical for the control of microbial infections. Golden pompano, *Trachinotus ovatus* is one of the precious marine economic fish in the southern coast of China, always suffer from virus infection, including iridovirus and nodavirus. To date, the roles of golden pompano genes, especially interferon related genes in virus infection remained largely unknown. Here, the ISG15 homolog (ToISG15) was cloned from golden pompano and its immune response to Singapore grouper iridovirus (SGIV) and nervous necrosis virus (NNV) was investigated. The whole ORF of ToISG15 was composed of 465 bp and encoded a polypeptide of 154 amino acids with 37～68% identity with the known ISG15 homologs from other fish species. ToISG15 contained two ubiquitin-like (UBL) domains and an Ub-conjugation domain (LRGG). Expressional analysis showed that ToISG15 was located mainly in the cytoplasm of golden pompano cells, and dramatically induced by SGIV and GNNV infection, or poly I:C treatment. Overexpression of ToISG15 in vitro inhibited the replication of SGIV significantly, but the inhibitory effect on NNV was weak. Furthermore, overexpression of ToISG15 could also significantly restrain the growth of Aeromonas hydrophila, this was the first time to find that fish ISG15 possessed antibacterial function. Taken together, the results indicated that fish ISG15 might exert important roles against virus and bacterial infection.

Key words: Trachinotus ovatus; ISG15; immunity; virus and bacterial infection

嗜水气单胞菌灭活疫苗和 OmpA 亚单位疫苗对团头鲂幼鱼的免疫保护效果比较研究

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摘要：为评估灭活疫苗和重组外膜蛋白 A（OmpA）亚单位疫苗对团头鲂幼鱼抗嗜水气单胞菌的免疫保护作用，本研究评估了接种和未接种幼鱼的累积死亡率和各种疫苗的免疫原性，以及团头鲂的非特异性和特异性免疫反应。结果表明，与未接种组相比，灭活疫苗和 OmpA 亚单位疫苗均提高了感染后幼鱼的存活率。在感染后 14 天（dpi），亚单位疫苗组中，嗜水气单胞菌 OmpA 蛋白特异性血清免疫球蛋白 M（IgM）水平显著上调，显示出更好的免疫保护效果。疫苗接种还通过调节肝脏和血清抗微生物酶的活性来提高宿主的杀菌能力。各组免疫相关基因的表达均增加，在接种组中更为显著。此外，免疫组化检测显示，免疫阳性细胞的位置和数量在感染后的接种组中增加，显示不同的表位。这些结果表明，接种灭活疫苗或 OmpA 亚单位疫苗可增强宿主对嗜水气单胞菌的免疫应答，其中 OmpA 亚单位疫苗提供了更有效的保护，是一种理想的抗嗜水气单胞菌候选疫苗。

关键词：嗜水气单胞菌；灭活疫苗；亚单位疫苗；免疫原性；免疫保护作用

Comparative evaluation of the immunogenicity and protective effects of inactivated and OmpA subunit vaccines against Aeromonas hydrophila infection in Megalobrama amblycephala

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Abstract： Aeromonas hydrophila is a kind of zoonotic pathogen, and the bacterial septicemia in fish caused by its infection has lead to great economic loss of global aquaculture. To evaluate the immune protective effects of inactivated and recombinant outer membrane protein A (OmpA) subunit vaccines against A. hydrophila in juvenile Megalobrama amblycephala, the present study investigated the cumulative motality rate and bacterial load in vaccinated and non-vaccinated M. amblycephala post A. hydrophila infection, as well as the immunogenicity of various vaccines, and the nonspecific and specific immune responses of M. amblycephala. The results showed that both inactivated and OmpA subunit vaccines improved the survival rates of M. amblycephala upon infection compared to that of the non-vaccinated group, which should be attributed to the reduced bacterial load in experimental fish and enhanced host immunity. ELISA assay showed that the levels of serum immunoglobulin M (IgM) specific to OmpA protein of A. hydrophila up-regulated significantly in the subunit vaccine groups at 14 d post infection (dpi), which exhibited better immune protective effects. Moreover, vaccination also increased host bactericidal abilities by regulating the activities of hepatic and serum antimicrobial enzymes. Furthermore, the expression of immune related genes (SAA, iNOS, IL-1 β, IL-6, IL-10, TNF α, C3, MHC I, MHC II, CD4, CD8, TCR β, IgM, IGD and IgZ) increased in all groups post infection, which were more significant in the vaccinated groups. In addition, the location and number of immunopositive cells exhibiting different epitopes (MHC II, CD8, IgM, IgD and IgZ) detected by immunohistochemical assay increased in the vaccinated groups post infection. These results indicated that juvenile M. amblycephala inoculated with inactivated vaccine or OmpA subunit vaccine enhanced host immune responses against A. hydrophila, among which OmpA subunit vaccine provided more effective protection as an ideal candidate vaccine against A. hydrophila.

Key words: Aeromonas hydrophila; Inactivated vaccine; Subunit vaccine; Immunogenicity; Immune protective effects

小棚养殖南美白对虾“滴星病”的研究

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摘要：为探究如东地区部分小棚养殖的凡纳滨对虾（*Litopenaeus Vannamei*）“滴星病”的发生原因。于2022年5月从濒死的患病对虾中分离得到一株优势菌MRY0520，通过人工回感实验确认了该菌株的致病性；对菌株MRY0520进行了形态学观察和生理生化鉴定，并利用16S rRNA基因对其进行了分子生物学鉴定。经表型生物学观察和分子生物学分析，鉴定该菌株MRY0520为美人鱼发光杆菌美人鱼亚种（*Photobacterium damselae subsp. damselae*）。该菌在血琼脂平板上呈现β溶血，回感结果显示该菌对凡纳滨对虾的半数致死量LD50为2.15×105 CFU/g，药敏结果显示MRY0520对新霉素、多西环素等多种药物敏感。结果表明，引起本次凡纳滨对虾出现死亡现象的病原菌为美人鱼发光杆菌美人鱼亚种，该菌对凡纳滨对虾具有致病性，可致对虾死亡。

关键词：凡纳滨对虾；美人鱼发光杆菌美人鱼亚种；分离鉴定；药敏实验

Study on “Dropstar disease” of Litopenaeus Vannamei Cultured in small shed

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Abstract： In order to explore the causes of abnormal death of *Litopenaeus Vannamei* in some greenhouse culture in Rudong area. A dominant strain MRY0520 was isolated from dying diseased shrimp in May 2022, and its pathogenicity was confirmed by artificial challenge. The strain MRY0520 was observed morphologically, identified physiologically and biochemically, and identified by molecular biology using 16S rRNA gene. Through phenotypic biological observation and molecular biological analysis, the strain MRY0520 was identified as *Photobacterium damselae subsp. damselae*. The bacteria appeared β hemolysis on the blood agar plate and the results of artificial challenge showed that the LD50 of the bacteria to Litopenaeus Vannamei was 2.15 × 105 CFU/g. The drug sensitivity test showed that strain MRY0520 was sensitive to neomycin, doxycycline and other drugs. The results showed that the pathogen causing the death of Litopenaeus Vannamei was Photobacterium damselae subsp. damselae, which was pathogenic to Litopenaeus vannamei and could cause the death of it.

Key words: Litopenaeus Vannamei; Photobacterium damselae subsp; damselae; Isolation and identification; Drug sensitivity test

尼罗罗非鱼 Igλ单抗的制备及 Igλ+ B 细胞亚群的研究

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摘要：免疫球蛋白（Ig）是介导体液免疫的重要效应分子。免疫球蛋白由两条重链和两条轻链组成，在硬骨鱼类中，已报道的重链包括 Igμ、Igδ和 Igτ，轻链包括 Igk、Igλ和 Igσ。相比于重链，对硬骨鱼类轻链的研究极少，原因是缺乏识别轻链的抗体。本研究制备了鼠抗尼罗罗非鱼 Igλ的单抗，能够特异性识别血清中 Igλ+ 的抗体及组织中 Igλ+的 B 细胞。本研究利用该抗体和鼠抗罗非鱼 IgM 重链单抗分析了罗非鱼 IgM+和 Igλ+ B 细胞亚群的组成，结果显示头肾和外周血中 IgM+Igλ+ 占总 IgM+B 细胞的约 30%，而脾脏中约 45%；头肾和外周血中 IgM-Igλ+ 占 Igλ+ B 细胞的约 45%，脾脏中约 25%，推测这一群细胞为 IgT+ B 细胞。在无乳链球菌感染后，利用此抗体我们发现识别无乳链球菌表面抗原 Sip 的特异性抗体增加，表明此抗体可用于检测罗非鱼免疫后的抗体水平，为罗非鱼疫苗的研发和免疫效果的评价奠定了基础。

关键词：尼罗罗非鱼；单克隆抗体；Igλ；B 细胞

Preparation of the monoclonal antibody of Nile tilapia Igλ and study on the Igλ+ B cell subsets in Nile tilapia

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Abstract： Immunoglobulins (Ig) are important effector molecules that mediate humoral immunity. Immunoglobulin consists of two heavy and two light chains. In teleosts, three heavy chain isotypes (Igμ, Igδ and Igτ) and three light chain isotypes (Igκ, Igλ and Igσ) have been identified. Compared to heavy chains, teleost light chains have been poorly studied due to the lack of antibodies. In this study, a mouse anti-Nile tilapia Igλ monoclonal antibody (mAb) was prepared, which can specifically recognize Igλ+ antibody in serum and Igλ+ B cells in tissues. Further, the composition of IgM+ and Igλ+ B cell subsets was analyzed using this antibody and a mouse anti-tilapia IgM heavy chain mAb. The ratio of IgM+ Igλ+ B cells to total IgM+ B cells in head kidney and peripheral blood was about 30%, while that in spleen was about 45%; the ratio of IgM-Igλ+ B cells to total Igλ+ B cells in head kidney and peripheral blood was about 45%, while that in spleen was about 25%. The IgM-Igλ+ B cells was speculated to be IgT+ B cells. Finally, we detected an increase in the level of specific antibodies against the surface antigen-Sip of Streptococcus agalactiae in serum after S. agalactiae infection, indicating that mouse anti-Igλ mAb can be used to detect the antibody level after immunization of Nile tilapia, which lays a foundation for the development of tilapia vaccine and the evaluation of immunization effect.

Key words: Nile Tilapia; monoclonal antibody; Igλ; B cell

红鳍东方鲀可变剪切的鉴定及其响应哈氏弧菌侵染的调控分析

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摘要：本实验利用三代测序构建了红鳍东方鲀脾脏的全长转录组。对其进行生物信息学分析，共鉴定出 54860 条全长非冗余转录本、3736 个新基因、8571 项可变多聚腺苷酸化事件、4221 条长链非编码 RNA 和 421 条融合转录本。结合二代转录组数据，预测了其中存在 153591 个可变剪切事件，共鉴定出 5 种不同的类型，包括外显子跳跃，内含子保留，可变 3’剪切位点，可变 5’剪切位点和外显子互斥。通过 rMATS 软件筛选出在感染哈氏弧菌后不同时间点红鳍东方鲀的差异可变剪切事件分别为 974、1196 和 1911。GO 功能富集分析结果主要参与先天性免疫应答、ATP 结合、酪氨酸磷酸化等；KEGG 主要富集在剪切体、细胞凋亡和 JAK-STAT 信号通路等多条信号通路。研究从基因转录后调控水平阐释了红鳍东方鲀感染哈氏弧菌后的调控机制，揭示了可变剪切在红鳍东方鲀免疫应答过程中的重要作用，为解析红鳍东方鲀的免疫调控机制研究提供了支撑。

关键词：红鳍东方鲀；哈氏弧菌；三代测序；可变剪切事件

Assessment of the Alternative Splicing and Regulation Analysis of Response to Vibrio harveyi Infection in Japanese Pufferfish

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Abstract： This study is the first one to analyze the full-length transcriptome of the spleen in T. rubripes. By the bioinformatic analysis of the full-length transcript, a total of 54860 full-length non redundant transcripts, 3736 novel genes, 8571 alternative cleavage and polyadenylation events, 4221 lncRNAs and 421 fusion transcripts were identified. Combining NGS transcriptome data of the spleen in T. rubripes under Vibrio harveyi infection, the presence of 153591 alternative splicing events were predicted, which led to the identification of five different types of events including exon skipping, intron retention, variable 3 'splicing sites, variable 5' splicing sites, and exon mutual exclusivity. Differential alternative splicing events in T. rubripes at different time points after Infection with V. harveyi were screened by rMATS software, which were 974, 1196 and 1911, and the DAS genes were functionally enriched. The results of GO functional enrichment analysis are mainly involved in congenital immune response, ATP binding, and tyrosine phosphorylation. KEGG enrichment analysis demonstrated the DAS genes in several signaling pathways like spliceosome, apoptosis, and JAK-STAT pathway. The study elucidated the regulatory mechanisms after T. rubripes infection with V. harveyi at the level of post-transcriptional regulation, revealed the significant role of alternative splicing during the immune response progress in T. rubripes, and provided support for dissecting the mechanism of immune regulation in T. rubripes.

Key words: Japanese pufferfish; Vibrio harveyi; Pacbio sequencing; alternative splicing event

江苏典型稻虾及稻蟹共作系统中除草剂残留非靶向动态筛查及污染特征

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摘要：为掌握江苏地区稻虾及稻蟹共作系统内除草剂残留情况，在两种系统内各选择 3 家典型养殖基地，采用超高效液相色谱-四极杆飞行时间高分辨质谱联用技术（UPLC-Q-TOF MS），对整个养殖周期内，虾、蟹和环境样品（稻田水体、底泥）除草剂残留进行动态非靶向筛查，同时，对检出频率高及检出浓度较高的除草剂进行定量分析，结合风险熵（RQ）及混合风险熵（MRQ）评估生态风险。结果显示除草剂残留主要集中于环境样品，尤其是底泥中，在虾、蟹中残留较少，且残留主要集中于养殖前期，至成品收获期检出频次及浓度均较低；虾、蟹总体上处于中风险，而稻田水体及底泥总体上均处于高风险，尤其稻田底泥检出的 11 种除草剂，单个除草剂有 10 种处于高风险（RQ＞1）。表明江苏典型稻虾及稻蟹共作系统中除草剂污染程度为稻田底泥＞稻田水体＞虾、蟹，稻田底泥中残留的除草剂对周边环境存在潜在的生态风险，虾、蟹在收获期除草剂残留风险较小。

关键词：除草剂；非靶向筛查；高分辨质谱；污染特征；稻虾共作；稻蟹共作

Dynamic Non-target Analysis and Occurrence of Herbicides Residues in Rice-Crayfish and Rice-Crab Co-culture Systems at Jiangsu Province

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Abstract： To evaluate the herbicides residues in Rice-Crayfish and Rice-Crab systems at Jiangsu Province, select 3 typical breeding bases in the two systems, the dynamic non-target analysis and occurrence of herbicides residues in biological samples (crayfish, crab) and the environmental samples (field water, field sediment) were conducted with ultra high performance liquid chromatography coupled with quadrupole-time of flight mass spectrometry (UPLC-Q-TOF MS) during the entire breeding cycle. Herbicide residues were mainly concentrated in environmental samples, especially in field sediment, less in crayfish and crab, and the residues are mainly concentrated in the early stage of aquaculture, the frequency and value detected were controllable overall at the harvest time. The ecological risk assessment results showed that the comprehensive ecological risk of herbicides in crayfish and crab were medium risk, while the risk of field water and field sediment were both high, in particular, 10 of the 11 herbicides detected in field sediment were high risk. In this study, it was evident that the low to high degree of herbicides pollution in Rice-Crayfish and Rice-Crab Co-culture Systems at Jiangsu Province were field sediment, field water and aquatic product（ crayfish and crab），all the results indicate that herbicide residues in field sediment have a potential risk to the surrounding water environment， and the risk of aquatic product （ crayfish and crab ） were controllable overall.

Key words: Herbicide; Non-target analysis; High-resolution mass spectrometry; Occurrence; Rice-Crayfish system; Rice-Crab System

超高效液相色谱-三重四级杆串联质谱法测定干制鱼制品中游离活泼羰基化合物

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摘要：近年来，游离活泼羰基化合物中的 4-羟基己烯醛（HHE）和 4-羟基-壬烯醛（HNE）已被作为氧化应激损伤的重要生物标志物。本研究基于超高效液相色谱-三重四级杆串联质谱联用技术（UPLC-QQQ-MS/MS），建立一种同时测定干制鱼制品中游离 HHE 和 HNE 的方法。样品经衍生后经硅胶固相萃取小柱净化，以 ACQUITY UPLC HSS T3 为色谱柱，乙腈-乙酸溶液（pH = 3.55）为流动相进行梯度洗脱。在多反应检测、负离子电离模式，同位素内标法定量。结果显示：HHE 和 HNE 在 10~300 μg/L 范围内线性关系良好，相关系数均大于 0.99。本研究方法在不同干制鱼制品中的检出限和定量限分别为 20μg/kg 和 100 μg/kg。回收率为 88%～100.15%，相对标准偏差≤15%。该法操作简便，灵敏度高，适用于干制鱼制品中游离 HHE 和 HNE 的测定。

关键词：超高效液相色谱-串联质谱；准确定量；活泼羰基化合物；干制鱼制品

Determination of free reactive carbonyl compounds in dried fish products by ultra-performance liquid chromatography-triple quadrupole tandem mass spectrometry

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Abstract：Free reactive carbonyl compounds HHE and HNE have been used as important biomarkers of oxidative stress damage in recent years. Based on UPLC-QQQ-MS/MS, a determination of free HHE and HNE in dried fish products was developed. The samples were purified on a silica solid phase extraction column. Using acetonitrile-acetic acid solution (pH = 3.55) as the mobile phase in gradient elution mode. Qualitative analysis was performed under the multiple reaction monitoring mode with negative electrospray ionization by using the isotope internal standard method. Results showed good linear relationships in the range of 10-300 μg/L with correlation coefficients greater than 0.99. The limits of detection and limits of quantification of the method were 20 μg/kg and 100 μg/kg, respectively. The spiked recoveries ranged from 88.44% to 100.15%. The relative standard deviation was less than 15%. The method is suitable for accurately determining free HHE and HNE in dried fish products.

Key words: ultra-performance liquid chromatography-tandem mass spectrometry; accurate quantification; reactive carbonyl compounds; dried fish products

一株大鲵虹彩病毒的分离及鉴定

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摘要：2020 年 5 月，广东广州某野生动物保护基地爆发疑似病毒引发的疾病。现场采样发现，病鲵体长约 2 m， 反应迟钝，体表有出血点或溃疡症状。本研究采用胖头鲤肌肉细胞系（fat head minnow epithelial cells，FHM）培养、超薄切片透射电镜观察、病毒主要衣壳蛋白（ major capsid protein，MCP） 克隆与测序分析等方法，从患病大鲵中分离得到一株病毒，鉴定其属于虹彩病毒科蛙病毒属，命名为大鲵虹彩病毒广州分离株（CGSIV － GZ）。FHM 经患病大鲵组织匀浆液接种后出现细胞圆缩、死亡、脱落等典型的细胞病变症状。将感染后的 FHM 细胞制 作超薄切片，通过电镜观察发现，FHM 细胞中存在大量直径约 100 ～ 120 nm 具囊膜的正六边形成熟病毒粒子， 形态与虹彩病毒相似。根据虹彩病毒 MCP 基因保守区域序列设计特异性引物对病鲵组织样本进行 PCR 扩增，获得了 431 bp 的目的基因片段，测序后经采用 BLAST 软件分析，发现其与 GenBank 中的蛙病毒衣壳蛋白基因同源性达 96% ～ 99% 。确认本次野生动物保护基地大鲵发生大规模死亡是蛙病毒感染所致。

关键词：大鲵(*Andrias davidianus*) ；虹彩病毒科；透射电镜；胖头鲤肌肉细胞系；分离鉴定

Characterization of one strain of iridovirus isolate from Andrias davidianus

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Abstract：: One suspected virus－induced disease broke out in May 2020 in a Wildlife conservation base in Guangzhou，Guangdong Province. The diseased Andrias davidianus showed a slow reaction. The body length of diseased A. davidianus samples was 2m with typical clinical signs such as hemorrhages on the skin and ulcer symptoms. Fat head minnow epithelial cells(FHM) were cultured，the ultrathin section of transmission electron microscope and major capsid protein(MCP) cloning and sequencing were used in the experiment. One strain of virus from diseased A. davidianus was isolated， identified， and named as Guangzhou isolate of A. davidianus iridovirus(named CGSIV － GZ) . The tissue homogenate of diseased fish could cause typical cytopathic effect such as cell shrinkage，death，and exfoliation in FHM cells. Electron microscopy observation showed a large number of virus particles about 100 ～ 120 nm in diameter in infected FHM cells，which was similar to the iridescent virus. The conserved region of the major capsid protein(MCP) gene of iridovirus was amplified by PCR， and a 431bp specific gene fragment was obtained. Sequence alignment analysis of the DNA fragment showed that CGSIV － GZ shared a high identity(96% ～ 99%) with the published MCP gene sequence of iridovirus. It was confirmed that the large － scale death of A. davidianus was caused by frog virus infection in the wildlife conservation base. This study will provide some reference basis for the prevention and control of disease induced by CGSIV in A. davidianus culture.

Key words: *Andrias davidianus*; Iridoviridae; transmission electron microscope; fat head minnow epithelial cells; FHM; isolation and identification

镰刀菌的比较基因组学及镰刀菌 1-Jan 致病基因分析

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摘要： *Fusarium solari*. 1-Jan 毒株可引起凡纳滨对虾亲虾的严重流行病。导致虾体全身出现对虾黑斑病，包括头部、胸甲、腹甲、游泳足和尾扇等。真菌流行病造成的经济损失巨大，但目前对 *Fusarium solari*. 1-Jan 菌株的发病机制知之甚少。因此，我们采用 PacBio DNA 测序来揭示 1-Jan 基因组序列草图并确定假定的致病基因，以探寻病原体的工作机制。我们通过在 PacBio 平台上进行全基因组测序，生成了 1-Jan 菌株的基因组序列草图。基因组序列组装为 51.8 Mbp，scaffold 为 54，N50 scaffold 长度为 1,974 Kb。 AUGUSTUS 基因组分预测程序预测了 9,769 个推定基因，利用 NR、GO、KEGG、KOG 和 Swiss-Prot 数据库进行了基因功能注释。此外，使用 PHI、FCPD、DFVF 和 CAZy 数据库搜索 1-Jan 候选致病基因，分别生成 1,101、126、479 和 497 个注释。此外，预测了 538 种分泌蛋白。比较基因组学分析表明 1-Jan 菌株与 F.solani.JS-169 和 *N.haematococca* 相似。在 1-Jan 基因组中，737 个潜在致病基因中发现了 SNP 突变位点，4255 个单拷贝基因中有 859 个为潜在致病基因。此外，1-Jan 菌株 967 个独特基因中有 95 个是潜在致病基因，其中 27 个与几丁质降解功能有关，表明在对虾 1-Jan 菌株的发病机制中起重要作用。需要在细胞和分子水平上进一步分析这些致病基因，以阐明这些因子对凡纳滨对虾的功能机制。总之，这里介绍的 *F.solari*.1-Jan 基因组序列和假定的致病因素将有助于确定致病机制，并更好地进行对虾的真菌性疾病防治研究。

关键词：镰刀菌；比较基因组学；对虾感染；碳水化合物活性酶基因；致病基因；毒力因子；次级代谢；小分泌蛋白；基因簇

Genome description of the *Fusarium solari* isolate 1-Jan with comparative genomic analysis on pathogenic genes of *Fusarium* fungi

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Abstract： We have generated the draft genome sequence of 1-Jan strain by conducting whole-genome sequencing on a PacBio platform. The assembled genome sequence was 51.8 Mbp. The scaffold number was 54, with an N50 Scaffold length of 1,974 Kb. The AUGUSTUS gene prediction program predicted 9,769 putative genes, which were annotated with the NR, GO, KEGG, KOG, and Swiss-Prot databases. Additionally, searches for candidate 1-Jan pathogenicity genes using PHI, FCPD, DFVF, and CAZy databases, generating 1,101, 126, 479, and 497 annotations, respectively. Also, 538 secreted proteins were predicted. Comparative genomic analysis showed that 1-Jan strain was close to F.solani.JS-169 and *N.haematococca*. In the 1-Jan genome, SNP mutation sites were found in 737 potential pathogenic genes, and 859 of 4,255 single-copy genes were potential pathogenic genes. Also, 95 of 967 the unique genes in the 1-Jan strain were potential pathogenic genes, 27 of which were related to chitin-degradation functions, suggesting an essential role in the pathogenesis of 1-Jan strain in prawns. The further analyses of these pathogenic genes on the cellular and molecular level are required to elucidate the functional mechanisms of these factors on Fannabin prawns. Take together, the *F.solari*.1-Jan genome sequence and putative pathogenic factors presented here will facilitate the identification of pathogenicity mechanisms and ultimately lead to a better management of fungal infection in prawns.

Key words: Fusarium solari; comparative genomics; prawn infection; carbohydrate-active enzyme genes; pathogenic genes; virulence factors; secondary metabolism; small secreted proteins; gene clusters

rpoN 基因对拟态弧菌应激反应、生物膜形成及毒力影响的功能研究

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摘要：拟态弧菌作为弧菌病的病原菌可以引起水产动物发病死亡，且死亡率较高。在细菌中，*rpoN* 是调节细菌压力反应、生物膜形成及毒力一种 sigma 因子。为了研究 *rpoN* 在拟态弧菌中的作用，本研究构建 *rpoN*-RNAi 菌株，并通过表型和转录组测序对其进行分析。结果表明，*rpoN* 正向调控拟态弧菌对氧胁迫、乙醇胁迫和酸胁迫的抗性，负向调控其对碱胁迫和热胁迫的抗性，而对渗透压胁迫的抗性没有明显的调控作用。此外，在 12-72 小时内 *rpoN*-RNAi 菌株的生物膜形成能力比野生型菌株降低了 0.29 至 0.84 倍。人工感染试验表明，与野生株相比，rpoN-RNAi 菌株的 LD50 从 6.16×105 下降到 3.92×106 CFU/mL。转录组分析表明，很多毒力相关基因在 rpoN-RNAi 菌株中下调，包括 VI 型分泌系统（*vipB*，*vipA*，*trbL*，*impI*，*vasA*）、IV 型菌毛组装蛋白（*flpB-G*）、外膜蛋白（*ompU*，*ompA*）、溶血素等。此外，热休克蛋白、氧化还原酶、醛脱氢酶、群体感应系统等的一些应激保护基因也受到 rpoN 的调控。在 *rpoN*-RNAi 菌株中，这些差异表达基因的转录组分析与观察到的表型一致。这些结果表明，rpoN 对细菌适应性和致病性起重要作用，为进一步揭示 *RpoN* 调控网络奠定了基础。

关键词：拟态弧菌；rpoN 基因；应激反应；生物膜形成；毒力

Involvement of *RpoN* in Regulating Stress response, Biofilm Formation and Virulence of *Vibrio mimicus*

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Abstract: *Vibrio mimicus*, the causative agent for vibriosis, causes high mortality in a wide range of aquatic animals. *RpoN* is an alternative sigma factor regulating the stress response, biofilm formation, and virulence of bacteria. Herein, the *rpoN*-RNAi strain was constructed to investigate the roles of *rpoN* in V. mimicus by phenotypic and RNA-seq analysis. The data indicated that *rpoN* positively regulated the resistance of V. mimicus to H2O2, ethanol and acid, negatively regulated the resistance to alkali and heat, and had no influnence on the resistance to NaCl. The biofilm formation ability of the *rpoN*-RNAi strain was decreased from 0.29 to 0.84 fold than the wild-type strain over a period of 12-72 h. Furthermore, the LD50 of *rpoN*-RNAi strain decreased from 6.16×105 to 3.92×106 CFU/mL compared with wild strain by artificial infection test. The transcriptome analysis demonstrated that the well-known virulence-related genes were down-regulated in *rpoN*-RNAi strain, including type VI secretion system (*vipB, vipA, trbL, impI, vasA*), type IV pilus assembly protein (*flpB-G*), outer membrane protein (*ompU, ompA*), hemolysin, etc. Some stress-protective genes encoded heat shock protein, oxidoreductase, aldehyde dehydrogenase, quorum sensing system, etc., were also regulated by rpoN-RNAi. Transcriptome analysis of these DEGs were inconsistent with the phenotypes observed in the *rpoN*-RNAi strain. These results revealed that rpoN is a critical determinant for bacterial fitness and pathogenicity, and lay the groundwork for further revealing the characterization of *RpoN* regulatory networks.

Key words: Vibrio mimicus; rpoN gene; stress response; biofilm formation; virulence

荚膜多糖在 B 族链球菌逃逸罗非鱼巨噬细胞吞噬中的功能

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摘要：B 族链球菌（GBS）是罗非鱼以及多种水生动物的重要致病菌，其唾液酸化荚膜多糖（cps）是 GBS 的主要毒力因子。目前，cps 影响硬骨鱼巨噬细胞（MΦ）吞噬 GBS 的作用机制尚不清晰。本研究采用 cps 缺失型突变体Δcps 和唾液酸（sia）缺失型突变体ΔneuA，对 cps 在 GBS 逃逸罗非鱼 MΦ吞噬过程中的功能开展探究。结果显示，GBS 可通过 cps 和 sia 干扰非调理性吞噬作用，抑制氧化应激活性和抵抗杀伤。此外，在血清中的补体或抗体介导下，MΦ对Δcps 和ΔneuA 的调理性吞噬作用显著增强。另外，我们发现一些非调理性和调理性吞噬受体在 MΦ吞噬 WT 过程中下调表达，这表明 GBS 可能通过 cps 或 sia 直接或间接抑制吞噬受体的表达从而来抵抗 MΦ的吞噬作用。

关键词：B 族链球菌；荚膜多糖；唾液酸；罗非鱼；吞噬作用

The function of capsular polysaccharides in Group B Streptococcus escape from phagocytosis of tilapia macrophages

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Abstract： Group B Streptococcus (GBS) is an important pathogen for many aquatic animals, especially farmed tilapia. Sialylated capsular polysaccharides (cps) is a major virulence factor of GBS. At present, the mechanism of cps affecting the phagocytosis of GBS by teleost macrophages (MΦ) remains unclear. Using Δcps and ΔneuA in this experiment, the role of cps in the GBS escape from tilapia MΦ phagocytosis was explored. The results demonstrated that GBS can interfere with nonopsonic phagocytosis, inhibit oxidative stress activity and resist killing via cps and sia. Further, the opsonic phagocytosis of Δcps and ΔneuA by MΦ was significantly enhanced under complement or antibody mediated in serum. Moreover, we found that some nonopsonic and opsonic phagocytic receptors were down-regulated during MΦ phagocytosis of WT, which indicated that GBS might resist phagocytosis of MΦ by directly or indirectly inhibiting the expression of phagocytic receptors through cps or sia.

Key words: Group B Streptococcus; capsular polysaccharides; sialic acid; tilap; a phagocytosis

转运子 ZupT 参与嗜温性杀鲑气单胞菌毒力调控的分子机制初步研究

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摘要：杀鲑气单胞菌可引起多种淡水和海水鱼类的疖病，给水产养殖业造成严重的经济损失。杀鲑气单胞菌 SRW-OG1 是首次从温水鱼斜带石斑鱼中分离得到的中温致病菌株。根据之前的 RNA-seq 结果，我们发现 zupT 基因在 28℃时显著上调。因此，本实验旨在探讨杀鲑气单胞菌 SRW-OG1 感染过程中 zupT 基因的作用。结果表明，与野生株相比，zupT-RNAi 菌株在正常条件下以及在 Zn2+和 Fe2+限制条件下均受到严重的生长限制；与野生株相比，沉默株的毒力在人工感染以及毒力表型试验中均有不同程度的减弱。这些发现表明 zupT 基因在杀鲑鱼气单胞菌 SRW-OG1 的锌转运和毒力调节中起重要作用。

关键词：杀鲑气单胞菌；斜带石斑鱼；zupT；毒力调控

Effect of the zinc transporter ZupT on virulence mechanism of mesophilic Aeromonas salmonicida

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Abstract：Aeromonas salmonicida can cause furunculosis in a variety of freshwater and marine fish, causing serious economic losses to the aquaculture industry. A. salmonicida SRW-OG1 was a mesophilic pathogenic strain isolated from the warm water fish Epinephelus coioides for the first time. According to the previous RNA-seq results, it was found that the zupT gene was significantly up-regulated at 28℃. Therefore, the experiment is aimed at exploring the role of zupT during A. salmonicida SRW-OG1 infection at high temperature.Compared with the wild-type, the virulence of the zupT-RNAi strain was attenuated to varying degrees in artificial infection and virulence phenotype tests. In conclusion, these findings indicated that zupT gene played a vital role in Zn-transport and virulence regulation of A. salmonicida SRW-OG1.

Key words: Aeromonas salmonicida; Epinephelus coioides; zupT; Virulence regulation

rpoS 基因在罗氏沼虾病原阴沟肠杆菌生存和毒力中的功能研究

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摘要：阴沟肠杆菌广泛存在于各种水环境中，已经成为多种水产动物的致病菌，尤其给罗氏沼虾产业造成巨大损失。细菌可以在不良环境下抵抗压力长期存活，从而导致水产动物疾病反复暴发，rpoS 已经被证实是许多病原菌生存和毒力调控的重要基因。本研究采用 RNAi 技术构建阴沟肠杆菌 rpoS 基因稳定沉默株， qRT-PCR 结果显示，沉默株中 rpoS 的表达量相对于野生株降低了 82.62%。对沉默株与野生株进行转录组测序分析，筛选得到 488 个差异表达基因，包括上调基因 30 个，下调基因 458 个，其中环境应答、生物被膜形成、细菌 II 型分泌系统、鞭毛蛋白、菌毛蛋白、细菌趋化性等与生存及毒力相关基因的表达在沉默株中显著下调表达。同时 rpoS 沉默后导致其生存能力、物被膜形成能力、运动能力、黏附能力、定植能力以及对罗氏沼虾的致病性显著降低。研究结果表明 rpoS 基因在阴沟肠杆菌逆境生存和毒力调控中发挥重要的调控作用。

关键词：阴沟肠杆菌；rpoS 基因；抗胁迫；毒力调控

The role of rpoS in stress resistance and virulence of pathogenic Enterobacter cloacae from diseased Macrobrachium rosenbergii

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Abstract： Enterobacter cloacae is widely distributed in aquatic the environment, and has been identified as a pathogen to many aquatic animals recently, particularly caused serious economic losses of M. rosenbergii industry. Bacteria have developed strategies to survive in harsh environments, rpoS has been proven to play important roles in stress response and virulence in several bacteria. In this study, the rpoS of E. cloacae was silenced by RNAi technology. The qRT-PCR results showed the expression of rpoS in the rpoS-RNAi strain was reduced by 82.62%. The transcriptome analysis showed stress response and virulence related genes were down-regulated significantly in the rpoS-RNAi strain. RNAi-treated bacteria showed significantly impaired abilities of survival in environmental stresses, biofilm production, movement, adhesion, pathogenicity to M. rosenbergii. These results indicated that the rpoS plays important roles in environmental stresses adaptation and virulence of E. cloacae.

Key words: Enterobacter cloacae; rpoS; stress resistance; virulence regulation

翘嘴鳜病原维氏气单胞菌致病性及全基因组特征分析

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摘要：为确定翘嘴鳜大量死亡的原因，本研究从濒死翘嘴鳜溃疡处分离到优势生长细菌，通过形态观察、理化特性测定及 16S rRNA、gyrB 基因同源性分析进行分离菌的种属鉴定，并通过人工感染试验确定其致病性。结果表明，引起翘嘴鳜大量死亡的病原为维氏气单胞菌，分离菌 SJ4 对翘嘴鳜的 LD50 为 3.6×105 CFU/mL。对分离菌全基因组序列进行测定，组装与功能分析结果显示该基因组大小为 4562694bp，GC 含量为 58.95%，共注释到 3721 个蛋白质编码基因与 165 个代谢通路。通过与毒力因子数据库比对，共预测到 910 个毒力相关因子。通过与耐药基因数据库比对，结果显示 SJ4 中含有四环素类、氟喹诺酮类、氨基糖苷类等的耐药相关基因。本研究对致病性维氏气单胞菌 SJ4 进行了病原学及全基因组比较分析,为防控鱼类维氏气单胞菌感染提供了一定的参考依据。

关键词：翘嘴鳜；维氏气单胞菌；分离鉴定；全基因组；毒力及耐药

Isolation, characterization and complete genome sequencing of fish pathogenic Aeromonas veronii from diseased Siniperca chuatsi

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Abstract： Aeromonas veronii is an important opportunistic pathogen in aquatic environment and could cause diseases in various kinds of aquatic animals. However, there were few cases of A. veronii infections reported in Siniperca chuatsi. In this study, a dominant bacterium SJ4 was isolated from S. chuatsi, and was identified as A. veronii according to the morphological, physiological and biochemical characteristics, as well as 16S rRNA and gyrB gene sequences analyses. Additionally, the complete de novo assembled genome of A. veronii SJ4 consisted of a 4562694 bp circular chromosome. Genes encoding for several virulence factors were detected. Besides, drug resistance genes related to antibiotic target alteration, target replacement, antibiotic inactivation were also present. The results of our study suggested that A. veronii was etiological agent causing the mass mortalities of S. chuatsi and reports the first complete genome sequence of fish pathogenic A. veronii from S. chuatsi.

Key words: Aeromonas veronii, Siniperca chuatsi; pathogenicity; Genome sequencing; Virulence factors; Antibiotic resistance

铜离子胁迫下中华绒螯蟹鳃转录组分析

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摘要：本研究对 CuSO4·5H2O（0.7 mg·L-1） 浸泡 0 h（对照组）、12 h 和 24 h 时的鳃组织样品进行转录组分析。结果显示，胁迫 12 h 和 24 h 后，分别有 3713 和 3741 个差异表达基因（$P＜0.05$ 且 log2FC＞2），其中共同上调 424 个基因，共同下调 495 个基因。结合 GO 与 KEGG 富集分析，胁迫 12 h，与蛋白质折叠相关的热休克蛋白（Hsp40、Hsp70、Hsp90、sHSF）基因显著上调；胁迫 24 h 时， 与能量代谢相关的 V 型 ATP 酶（ATPeV1C、ATPeV0E）基因被显著抑制。免疫方面，细胞凋亡通路上调，炎症抑制因子（IκBα）基因先下调后上调，多种抗菌肽蛋白（Crustin1、Crustin2、ALF1、ALF2、ALF3）表达呈上升趋势。本研究初步阐明了中华绒螯蟹应对 Cu2+胁迫时的响应机制，为中华绒螯蟹养殖过程中的污染防治、生态修复提供新参考。

关键词：Eriocheir sinensis; Copper; Transcriptome; Heat shock protein; V-type ATPase

Transcriptome analysis of gill of Eriocheir sinensis under copper stress

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Abstract: In order to explore the response mechanism of Cu2+influence on E. sinensis, transcriptome analysis was performed on gill soaked in CuSO4·5H2O (0.7 mg·L-1) for 0 h (control group), 12 h and 24 h. The results showed that there were 3,713 and 3,741 differentially expressed genes (DEGs) ($P<0.05$ and log2FC>2) after 12 and 24 h Cu2+ treatment, respectively. 926 DEGs were co-expressed, including 424 co-up-expressed genes and 495 co-down-expressed genes. Combined with GO and KEGG enrichment analysis, the genes of heat shock proteins (Hsp40, Hsp70, Hsp90 and sHSF) related to protein folding were significantly up-regulated after 12 h Cu2+ stress. At 24 h Cu2+stress, the genes of V-type ATPase (ATPeV1C and ATPeV0E) related to energy metabolism were significantly inhibited. In terms of immunity, “apoptosis” pathway was up-regulated, NF-κ-B inhibitor α (Iκbα) gene was down-regulated and then up-regulated and the expression of antimicrobial peptides (Crustin1, Crustin2, ALF1, ALF2, and ALF3) showed an increasing trend. This study preliminarily elucidated the response mechanism of Cu2+ stress in E. sinensis, and provided a new reference for pollution control and ecological restoration in the process of E. sinensis culture.

Key words: Eriocheir sinensis; Copper; Transcriptome; Heat shock protein; V-type ATPase

Vvrr2：一种新的弧菌 ncRNA，通过转录后调控参与多种生物膜基质胞外多糖的动态合成、生物膜结构和毒力

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摘要：多年来，溶藻弧菌是人类疾病中报道的第二大常见弧菌种，因此迫切需要更好地了解溶藻弧菌感染的致病机制。我们之前通过 RNA-seq 在溶藻弧菌中发现了一种新的 ncRNA，可能与其粘附调控有关，并将其命名为 Vvrr2。在本研究中，我们发现 Vvrr2 通过一种负调控模式参与了环境适应。同时，vvrr2 过表达菌株在粘附、生长、生物膜、运动性、耐药性和毒力等方面均受到不同程度的损害。此外，共聚焦激光显微镜和扫描电镜显示，Vvrr2 的过表达导致了生物膜结构的失败。我们还通过拉曼光谱证实了 Vvrr2 对生物膜中多糖、蛋白质和核酸的类型和含量的影响。

关键词：溶藻弧菌；ncRNA；Vvrr2；毒力；生物膜的形成

Vvrr2：A new Vibrio ncRNA involved in dynamic synthesis of multiple biofilm matrix exopolusaccharides, biofilm structuring and virulence via post-transcriptional regulation

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Abstract： For many years, Vibrio alginolyticus is the second most common Vibrio species reported in human illness, thus a better understanding of the pathogenic mechanism of V. alginolyticus infection is urgently needed. We previously discovered a novel ncRNA in V. alginolyticus by RNA-seq that might be related to its adhesion regulation and named it Vvrr2. In the present study, we found that Vvrr2 was involved in environmental adaptation through a negative regulatory mode. Meanwhile, the Vvrr2-overexpression strain was impaired to varying degrees in adhesion, growth, biofilm, motility, drug resistance, and virulence. Furthermore, confocal laser microscopy and scanning electron microscopy showed that overexpression of Vvrr2 resulted in failing of biofilm structuring. We also confirmed the effect of Vvrr2 on the type and content of polysaccharides, proteins and nucleic acids in biofilm by Raman spectroscopy.

Key words: Vibrio alginolyticus; ncRNA; Vvrr2; Virulence; Biofilm formation

鲤疱疹病毒 II 型 SH-01 株的全基因组和分子表征分析

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摘要：鲤疱疹病毒 II 型（CyHV-2）感染养殖鲫和金鱼会引发疱疹病毒造血器官坏死病（HVHN）。在本项研究中，我们对从上海当地一家养殖场的患病鲫体内分离得到的一个新毒株 CyHV-2 SH-01 进行了全基因组测序和分析，并与其他几个近缘毒株的基因组结构做了比较。SH-01 的基因组大小为 290,428 bp，存在一些变异，包括核苷酸突变、缺失和插入，以及基因重复、重排和水平转移等。值得注意的是，SH-01 与 ST-J1 的基因组具有 99.98%的序列相似性。基因组共线性分析表明，SH-01 与其他三个 CyHV-2 分离株的基因组具有高度共线性关系，与 CyHV-1、CyHV-3 和 CaHV 总体上亲缘关系较近，而与 AngHV-1 的基因组共线性程度最低。总之，通过基因组测序和进一步的序列挖掘，本研究的发现为更好地了解 CyHV-2 的基因组结构和潜在的分子致病机制提供了新线索。

关键词：鲤疱疹病毒 II 型；鲫；疱疹病毒造血器官坏死病；全基因组测序；分子表征；基因组共线性

Complete genome and molecular characterization of Cyprinid herpesvirus 2 (CyHV-2) SH-01 isolated from cultured crucian carp

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Abstract： Cyprinid herpesvirus 2 (CyHV-2) is the pathogen causing herpesviral hematopoietic necrosis (HVHN) in farmed crucian carp and goldfish. In this study, we analyzed the genomic characteristics of a new strain, CyHV-2 SH-01, isolated from diseased crucian carp at a local fish farm in Shanghai. Complete genome of SH-01 is 290,428 bp. Compared to the genomes of other closely viruses, several variations were found in SH-01, including nucleotide mutations, deletions, and insertions, as well as gene duplications, rearrangements, and horizontal transfers. Notably, the genome of SH-01 shares 99.98% identity with that of ST-J1. Genomic collinearity analysis showed that SH-01 has a high degree of collinearity with another three CyHV-2 isolates, and it is generally closely related to CyHV-1, CyHV-3, and CaHV, and the most distantly related is AngHV-1. Overall, the results provide new clues to better understand the CyHV-2 genome and potential molecular pathogenic mechanisms through sequence mining.

Key words: Cyprinid herpesvirus 2 (CyHV-2); herpesviral hematopoietic necrosis (HVHN); crucian carp; complete genome sequencing; molecular characterization; genome collinearity

补体分子 C3a、C4a 和 C5a 来源的抗菌肽及其抗菌机制研究

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摘要：补体分子 C3a、C4a 和 C5a 是脊椎动物重要的先天性免疫分子。现有研究表明，在人类中，只有 C3a 和 C4a 具有抗菌肽功能，而 C5a 不具有。然而，C3a、C4a 和 C5a 在脊椎动物中的抗菌特性仍待阐明。我们的研究表明，C3a、C4a 和 C5a 的抗菌特性在脊椎动物中出现了趋异进化。脊椎动物 C3a、C4a 和 C5a 所带净电荷差异极大，但结构却很保守，且其来源多肽的抗菌活性与其所带净电荷正相关；此外，来源于脊椎动物 C3a、C4a 和 C5a 的非活性多肽如果突变为带有足够的净正电荷的突变体时，则具有了抗菌活性，表明净电荷是决定脊椎动物 C3a、C4a 和 C5a 抗菌活性的核心因子。更重要的是，多个脊椎动物 C3a、C4a 和 C5a 来源的多肽，尤其是象鲨 C3a 和 C4a 来源的多肽，具有高抗菌活性，但没有溶血活性，显示了脊椎动物 C3a、C4a 和 C5a 来源的多肽在抗感染治疗中的应用潜力。

关键词：C3a；C4a；C5a；净电荷；抗菌机制；脊椎动物

Antibacterial peptides derived from complement molecules C3a, C4a, and C5a and their antibacterial mechanisms

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Abstract: C3a, C4a, and C5a are important immune molecules in vertebrates. Although they diverged from a common ancestor, only C3a and C4a, but not C5a, can act as antibacterial peptides in Homo sapiens. However, the antibacterial properties of C3a, C4a, and C5a across vertebrates still require elucidation. Here, we show that, unlike those in H. sapiens, the antibacterial properties of C3a, C4a, and C5a have evolved divergently in vertebrates. The extremely different net charge and the conserved structure of vertebrate C3a, C4a, and C5a suggesting that net charge is the key factor determining the antibacterial activities of those molecules. The inactive overlapping peptides derived from vertebrate C3a, C4a, and C5a can become antibacterial peptides if mutated to possess enough net positive charges strongly supported the speculation. More importantly, many vertebrate C3a, C4a, and C5a derived peptides, especially Callorhinchus milii C3a and C4a derived peptides, possess excellent antibacterial activities yet exhibit no hemolytic activities, suggesting the application potential of vertebrate C3a, C4a, and C5a derived peptides in anti-infective therapy.

Key words: C3a; C4a; C5a; Net charge; Antibacterial mechanism; Vertebrate

Intelectin 通过 CDC42-WASP-Arp2/3 信号轴增强团头鲂巨噬细胞吞噬功能的调控机制研究

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摘要：内凝集素是一种存在于许多脊椎动物体内的凝集素，在机体免疫中起着重要作用。我们以前的研究发现，重组团头鲂内凝集素蛋白（rMaINTL）能促进巨噬细胞的吞噬功能，但其机制尚不清楚。本研究表明，rMaINTL 可与巨噬细胞结合并诱导伪足延伸。rMaINTL 处理的巨噬细胞和团头鲂幼鱼的数字基因表达谱鉴定了大量差异表达的基因，包括 Rac1、CDC42、WASP、Arp2/3 等。WB、qRT-PCR 和抑制剂阻断验证表明，rMaINTL 激活了 CDC42，进而激活了下游信号分子 WASP 和 Arp2/3 复合体，从而促进了肌动蛋白聚合和细胞骨架重构。此外，CDC42 和 WASP 抑制剂可阻断 rMaINTL 蛋白诱导的团头鲂巨噬细胞吞噬功能的增强。这些结果提示 MaINTL 通过激活 CDC42-WASP-Arp2/3 复合体而增强了团头鲂巨噬细胞的吞噬功能。

关键词：团头鲂；内凝集素；巨噬细胞；吞噬作用；信号通路

Intelectin enhances the phagocytosis of macrophages via CDC42-WASP-Arp2/3 complex in Megalobrama amblycephala

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Abstract： Our previous studies found that recombinant Megalobrama amblycephala intelectin protein (rMaINTL) enhanced the phagocytosis of macrophages, but the underlying mechanisms remained unclear. The present study revealed that rMaINTL could bound with macrophages and induce pseudopodia elongation. Digital gene expression profiling of rMaINTL treated macrophages and juvenile M. amblycephala identified amounts of differentially expressed genes, including Rac1, CDC42, WASP, Arp2/3 and the like. WB, qRT-PCR and inhibitors blocking verification revealed that rMaINTL activated CDC42 and then the downstream signaling molecules WASP and Arp2/3 complex, which thereby facilitated actin polymerization and cytoskeleton remodeling. Moreover, the enhanced phagocytosis of M. amblycephala macrophages upon rMaINTL protein treatment was blocked by CDC42 and WASP inhibitors. These results suggested that MaINTL enhanced the phagocytosis of M. amblycephala macrophages by activating the CDC42-WASP-Arp2/3 complex.

Key words: Megalobrama amblycephala; Intelectin; Macrophages; Phagocytosis; Signaling pathway

基于机器学习的一种抗菌肽优化算法开发

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摘要：抗菌肽（AMPs）是一类广泛存在于自然界生物体内的小分子多肽物质，为机体天然免疫的重要组成部分，对细菌、真菌、病毒和寄生虫等均具有较好的抑杀作用。AMPs 具有无污染及不易产生耐药性等特点，是传统抗生素的优良替代品。抗脂多糖因子（ALFs）是对虾抗菌肽重要成员之一。但由于目前鉴定和分离的众多天然抗菌肽活性并不理想，因此对其进行设计和改造成为克服此类缺点的首选方法，有助于新型抗菌肽的开发。基于此，我们提供了一种基于机器学习的 ALF 优化方法，即适用于 ALF 家族脂多糖结合域（LBD）氨基酸序列的改造算法，并通过测定经算法预测的排名前七位的改造短肽的最小抑菌浓度（MIC），有 6 条短肽的 MIC 均较原肽有大幅度降低。我们选取 LBDA 对其核磁共振（NMR）液体结构进行了解析，并通过体内外实验验证其具有较强且广谱的杀菌功能。本项目的实施将为水产养殖业抗生素替代药物的开发提供技术创新和物质基础。

关键词：机器学习；抗菌肽；ALFs；改造；抑菌功能

A machine learning-based algorithm for the development of activity enhanced anti-lipopolysaccharide factor

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Abstract： Antimicrobial peptides (AMPs) are groups of small molecular polypeptides, which are important parts of host innate immune system, having perfect inhibiting effects or killing effects against bacteria, virus and parasites. Due to their non-pollution and no drug resistance, AMPs are expected to replace antibiotics in the prevention. Anti-lipopolysaccharide factor (ALFs) is one of the important members of antimicrobial peptides in shrimp. However, at present, the activity of many natural antimicrobial peptides identified and isolated is not ideal, so the design and modification of them has become the preferred method to overcome such shortcomings, which is helpful to the development of new antimicrobial peptides. Based on this, we provided a machine learning-based algorithm for the development of activity enhanced anti-lipopolysaccharide factor, which means a modified algorithm suitable for lipopolysaccharide binding domain (LBD) of ALF family for the amino acid sequence. By measuring the minimum inhibitory concentration (MIC) of the top seven modified peptides predicted by the algorithm, the MIC of 6 short peptides is significantly lower than that of the original peptide. We selected LBDA to analyze the liquid structure of nuclear magnetic resonance (NMR) and verified its strong and broad-spectrum bactericidal function in vivo and in vitro. The implementation of this project will provide technological innovation and material basis for the development of antibiotic alternatives in aquaculture.

Key words: machine learning; Antimicrobial peptides; ALFs; Modification; Bacteriostasis

长江石首江段鱼类群落结构特征及其年际变化

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摘要：基于 2018 年，2020~2022 年在长江石首江段监测的鱼类数据，采用多样性指数和多元统计方法分析该江段的鱼类群落结构特征，4 年共监测到鱼类 62 种，隶属于 4 目 10 科 37 属。其中鲤形目 41 种，优势十分明显。不同年份间的鱼类物种数差别较大，全流域禁捕的 2021 年监测到的鱼类种类数要多于其他年份。鱼类多样性指数显示，Margalef 丰富度指数和 Shannon-Wiener 指数波动较大，2021 年最大分别为 6.22 和 4.08；Pielou 均匀度指数和 Simpson 优势度指数波动较小，各年份之间相差不大。ABC 曲线及 W 统计表明 2018 年鱼类群落结构相对稳定，优势种以大个体的种类为主。2020~2021 年鱼类群落主要以生命周期短、个体小的种类为主。2022 年较 2020~2021 年鱼类规格有所提升，鱼类群落相对稳定。

关键词：石首江段；鱼类群落结构；物种多样性；年际变化

Interannual variation of the fish community structure in the Shishou section of the Yangtze River

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Abstract：Abstract: Based on monitoring data of fish community in Shishou section of the Yangtze River from 2018 and 2020 to 2022, the fish community structure and species diversity were described using Shannon-Wiener diversity index，Simpson dominance index，Margalef 's richness index，Pielou's evenness index and multivariate statistical analysis，respectively. A total of 62 fish species from 37 genera, 10 families and 4 orders were collected during monitoring periods. They were dominated by cypriniforme. And there was significant interannual difference in fish species number, more fish species were monitored in 2021, when the entire catchment was fishing ban, than in other years. Fish diversity index showed that Margalef richness index and Shannon-Wiener index fluctuated greatly, with the maximum values of 6.22 and 4.08 in 2021, respectively. The Pielou evenness index and Simpson dominance index had little fluctuation, and there was little difference between the years. ABC curve and W statistics showed that the structure of fish community was relatively stable in 2018, and the dominant species was large individual species. From 2020 to 2021, the fish community was moderately disturbed, and the dominant species were the species with short growth cycle and small individuals. Compared with 2020~2021, the fish specifications in 2022 were improved, and the fish community was relatively stable. The fish community structures in the four years were divided into two groups by using cluster analysis and nonmetric multidimensional scaling (NMDS) methods. No obvious difference between these two groups was found by the ANOSIM analysis. The similarity percentage (SIMPER) analysis showed that compared with 2020-2022, the abundance of fish adapted to lotic environment and benthic omnivorous species decreased in 2018, while the abundance of fish adapted to standing water, benthic carnivorous species and semi-migratory species increased. On the whole, the fish community in the Shishou section of the Yangtze River was stable, and the fish size tended to increase.

Key words: Shishou section; Fish community structure; Species diversity; Interannual variation

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：摘要：以池塘养殖大口黑鲈（LY1）为对照，分别于池塘传统养殖大口黑鲈放入工厂化循环水养殖系统中的第 10 天（LY2）、第 20 天（LY3）和第 40 天（LY4）进行了肌肉营养成分与挥发性风味物质的鉴定与分析，并建立了四组大口黑鲈肌肉挥发性风味的指纹图谱。结果显示，大口黑鲈肌肉中总氨基酸含量和 EPA+DHA 含量均以 LY4 组最高，但 PUFA 含量却以 LY4 最低；工厂化循环水养殖对大口黑鲈肌肉挥发性气味物质种类及含量影响显著。对不同组大口黑鲈肌肉挥发性风味物质进行主成分分析（PCA），筛选出 2 个变量的贡献率为 87%，并且 4 个组别大口黑鲈无重叠区域，可明显区分开。大口黑鲈肌肉中共检测出 56 种挥发性风味化合物，相较于池塘传统养殖组，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，具有改善肌肉营养和风味的潜能。

关键词：工厂化循环水；大口黑鲈；肌肉；营养品质；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 largemouth bass (LY1) as a control, the muscle nutrient components and volatile flavor compounds were identified and analyzed on the 10th (LY2), 20th (LY3) and 40th (LY4) days after the traditional pond cultured largemouth bass was put into the factory circulating aquaculture system, and the fingerprints of the volatile flavor compounds of the muscle of four groups largemouth bass were established. The results showed that: the total amino acid content and EPA + DHA content in muscle of largemouth bass were the highest in LY4 group, but the PUFA content was the lowest in LY4 group; 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 largemouth bass, which has the potential to improve the volatile flavor compounds of largemouth bass muscle.

Key words: actory recirculating aquaculture; Micropterus salmoides; muscle; nutritional quality; volatile flavor

灌喂牡丹籽油对草鱼急性肝损伤的保护作用

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摘要：为明确牡丹籽油（PSO）对草鱼急性肝损伤的保护作用，共设置 5 个实验组：对照组（0g/kg），CT 组（注射 CCL4），PSO2.5 组（2.5g/kg），PSO5.0 组（5.0g/kg）和 PSO7.5 组（7.5g/kg）。实验选取草鱼 75 尾，随机分入 15 个网箱；灌喂 7d，末次灌喂 3h 后注射 2.25ml/kgCCL4，24h 后取样；检测血清生化指标，血清及肝胰脏中抗氧化酶活性。结果显示，PSO7.5 组血清中 ALT、AST 水平显著降于 CT 组；PSO5.0 和 PSO7.5 组的血清和肝胰脏中的 TG、LDL-C 含量显著低于 CT 组，HDL-C 显著高于 CT 组；PSO7.5 组血清中 SOD 活性显著升高，且肝胰脏中 SOD 和 CAT 的酶活性显著升高。结果表明牡丹籽油均可缓解 CT 引起的草鱼肝脏脂质蓄积，7.5g/kg 牡丹籽油可以提高草鱼血清及肝脏中 SOD 和 CAT 活性。研究结果为开发水产动物功能性饲料添加剂提供了基础数据。

关键词：牡丹籽油；四氯化碳；抗氧化；脂代谢；草鱼

Protective effect of drenching peony seed oil on acute liver injury in grass carp (*Ctenopharyngodon idella*)

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Abstract： In order to clarify the protective effect of peony seed oil (PSO) on acute liver injury in grass carp, five experimental groups were set up in this experiment: control group (0 g/kg), CT group (CCL4 injection), PSO 2.5 group (2.5 g/kg), PSO 5.0 group (5.0 g/kg) and PSO 7.5 group (7.5 g/kg). 75 grass carps were randomly divided into 15 cages. The experimental period was 8 d, continuous drenching for 7 d, the last feeding 3 h after injection of 2.25 ml/kg CCL4, 24 h after sampling. The biochemical indexes in serum and the activities of antioxidant enzymes in serum and hepatopancreas were detected. The results showed that compared with the CT group, the serum ALT and AST levels in the PSO 7.5 group were significantly lower ($P<0.05$). The contents of TG and LDL-C in serum and hepatopancreas in PSO 5.0 group and PSO 7.5 group were significantly lower than those in CT group ($P<0.05$), while the content of HDL-C was significantly higher than that in CT group ($P<0.05$). The activity of SOD in serum of PSO 7.5 group was significantly increased (P<0.05), and the activity of SOD and CAT in hepatopancreas was significantly increased ($P<0.05$). The results showed that peony seed oil could alleviate CT-induced liver lipid accumulation in grass carp, and 7.5 g/kg peony seed oil could also increase SOD and CAT activities in serum and liver of grass carp. The results provide basic data for the development of aquatic animal functional feed additives.

Key words: peony seed oil; carbon tetrachloride; antioxidant; lipid metabolism; grass carp

饲料中不同比例混合植物油替代鱼油对黄颡鱼线粒体融合分裂以及脂肪酸β氧化的影响

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摘要：脂肪酸的组成差异和线粒体结构稳态极大地影响脂肪酸β氧化速率,但相关作用机制尚不明确。本实验以鱼油为对照料,用混合植物油（棕榈油：菜籽油=1:1）替代对照料中 16.67%，33.33%，50.00%，66.67%以及 83.33%鱼油。本实验中，利用 6 组等氮等脂饲料饲喂 8 周的黄颡鱼以及脂肪酸孵育分离的原代肝细胞，探究饲料中不同比例混合植物油对线粒体融合以及脂肪酸β氧化的影响以及分子机制。结果表明，混合植物油可能通过影响线粒体融合和脂肪酸β氧化进而降低肝脏脂肪沉积。

关键词：植物油；黄颡鱼；脂肪酸β氧化；线粒体融合分裂；脂肪沉积

Effects of replacing fish oil with different proportions of mixed vegetable oil on mitochondrial fusion and fission and fatty acid β-oxidation in yellow catfish Pelteobagrus fulvidraco

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Abstract：Different composition of fatty acids and structural homeostasis of mitochondria can greatly affect the efficiency of fatty acid β-oxidation, but the underlying mechanisms are unknown. In this study, fish oil was used as the control group, and mixed vegetable oil (palm oil : rapeseed oil = 1 : 1) was used to replace 16.67 %, 33.33 %, 50.00 %, 66.67 % and 83.33 % fish oil in diets. In this experiment, we used six iso-nitrogenous and iso-lipidic diets to feed yellow catfish for 8 weeks and primary hepatocytes incubated by fatty acids to explore the effects and molecular mechanisms of mitochondrial fusion and efficiency of fatty acid β-oxidation. The present study revealed mixed vegetable oils may reduce liver lipid deposition by affecting mitochondrial fusion and fatty acid β-oxidation.

Key words: Vegetable oil; Pelteobagrus fulvidraco; Fatty acid β-oxidation; Mitochondrial fusion and fission; Lipid deposition

中枢食欲因子甘丙肽影响西伯利亚鲟下丘脑食欲信号促进摄食

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摘要：甘丙肽在哺乳动物中是促食欲因子，但其在鱼类中的摄食调节机制研究少。本研究探讨了 Galanin 调节鲟鱼摄食的作用及机制。首先克隆了甘丙肽及其受体的 cDNA 序列，分别长 557 和 710 bp，且发现二者均在下丘脑中高表达。通过短期禁食、腹腔注射和脑室注射试验确定甘丙肽对西伯利亚鲟的摄食调节作用。结果表明：禁食 1 和 3 h，甘丙肽表达量显著升高。注射实验表明，甘丙肽腹腔注射对鲟鱼摄食无显著影响，但其脑室注射显著促进摄食。甘丙肽与 spexin 共脑室注射发现 spexin 显著逆转了 galanin 的促食欲作用，且甘丙肽并不影响 galr3 表达，而 spexin 显著降低 galr3 表达。进一步检测脑室注射后食欲因子表达情况，结果显示中枢甘丙肽通过下调下丘脑的厌食信号 cart、ucn3 和 pyy 提高鲟鱼食欲，而 spexin 通过上调 cart 和 ucn3 表达并下调 npy 表达降低食欲。本研究为分析硬骨鱼类食欲调节机制提供依据。

关键词：西伯利亚鲟；甘丙肽；Spexin；甘丙肽受体 3；摄食调节机制

Galanin, a central appetite factor, affects appetite signals in the hypothalamus and promotes feeding in Siberian sturgeon (Acipenser baerii Brandt)

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Abstract： Galanin is a strong appetite promoting factor in mammals, but information about the mechanism of galanin in feeding regulation is very limited in fish. This study investigated the effects of galanin on food intake and explored the feeding regulation mechanism in Siberian sturgeon. Galanin and galanin receptor-3 (galr3) cDNA sequences of 557 bp and 710 bp were obtained respectively, and they were both abundantly expressed in the hypothalamus. Three experiments were performed to determine whether galanin affects food intake in Siberian sturgeon, including short-term fasting, intraperitoneal (i.p.) injection, and intraventricular (i.c.v.) injection. The results showed that galanin mRNA expression increased significantly after fasting for 1 ($P<0.05$) and 3 h ($P<0.01$). The galanin (0.50, 1.00, and 1.50 μg/g BW) i.p. injection did not significantly change food intake within 1, 3, or 6 h, but the galanin i.c.v. injection concentrations of 0.01, 0.05, and 0.10 μg/g BW significantly increased food intake within 3 h ($P<0.01$, $P<0.05$, $P<0.001$, respectively). An i.c.v. co-injection experiment with galanin and spexin was carried out to further explore the mechanism of galanin on the feeding regulation and to clarify the relationship between galanin and spexin. The results showed that 0.20 μg/g BW spexin significantly reversed the appetite promoting effect of 0.10 μg/g BW galanin ($P<0.05$). Moreover, galanin did not affect the expression of galr3, while spexin significantly decreased the transcriptional level of galr3 ($P<0.05$). The expression of 9 appetite factors (cart, ucn3, apelin, nucb2, npy, cck, galanin, spexin, and pyy), significantly changed among the four groups (saline, galanin, spexin, and galanin+spexin). These results indicate that central galanin promotes food intake by down-regulating anorexic signals, including cart, ucn3, and pyy in the hypothalamus, whereas spexin reduces appetite by up-regulating the expression of cart and ucn3, and down-regulating the expression of npy. This investigation provides a theoretical basis for an in-depth analysis of the feeding regulation mechanism in teleost.

Key words: Siberian sturgeon; galanin; spexin; galanin receptor-3; feeding regulation mechanism

MS-222 对地图鱼麻醉效果研究

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摘要：本文采用不同剂量 MS-222 对地图鱼进行急性麻醉和模拟长途运输慢性麻醉，研究不同剂量 MS-222 对鹦鹉鱼麻醉效果。结果表明，MS-222 对于地图鱼有很好的麻醉效果，起到了有效降低应激的作用。MS-222 为 30-90 mg/L 的剂量下，地图鱼可以进入麻醉状态，并且能够持续很长一段时间；不同浓度条件下，麻醉一定时间后，地图鱼的平均呼吸频率有不同程度的下降；在运输试验中，使用 50、60 mg/L 的 MS-222 麻醉地图鱼幼鱼，运输 4、8、12 h 后，鱼体谷丙转氨酶（ALT），谷草转氨酶（AST）的含量变化不显著（$P>0.05$），对皮质醇，总蛋白（TP）以及运输水体中氨氮含量均有一定的影响。高浓度急性麻醉条件下，MS-222 最佳麻醉浓度为 45-60 mg/L；在长途运输时，MS-222 的适宜浓度在 50 mg/L 左右。

关键词：MS-222；麻醉；应激；地图鱼

Anesthetic Effect of MS-222 on Astronotus ocellatus

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Abstract： Different doses of MS-222 was used for acute anesthesia of Astronotus ocellatus and simulated long-distance transport chronic anesthesia. The effects of different doses of anesthetic on Astronotus ocellatus were studied. The results of anesthesia experiment showed that MS-222 has a good anesthetic effect on Astronotus ocellatus and plays an effective role in reducing stress. MS-222 can be anesthetized at 30-90 mg/L and can last for a long time. Under different concentrations, after anesthesia for a certain period of time, the mean respiratory rate of the Astronotus ocellatus decreased to varying degrees. In the transportation experiment, MS-222 with 50 and 60 mg/L anesthetized juvenile map fish had no significant effects on alanine aminotransferase (ALT) and aspartate aminotransferase (AST) after transportation for 4, 8 and 12 h ($P>0.05$), and had certain effects on cortisol, total protein (TP) and ammonia nitrogen content in transportation water. The results of acute anesthesia experiments showed that the optimal anesthetic concentration of MS-222 was 40 mg/L under high concentration of acute anesthesia. During long-distance transportation, the suitable concentration of MS-222 is 50 mg/L.

Key words: MS-222; anesthesia; stress; Astronotus ocellatus

两种芽孢杆菌对克氏原螯虾幼虾生长的影响

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摘要：本文采用不同浓度的解淀粉芽孢杆菌（*Bacillus amyloliquefaciens*）SS-42 和地衣芽孢杆菌（*Bacillus licheniformis*）10-2 发酵液饲喂经过驯化的克氏原螯虾（*Procambarus clarkii*），通过观察、计算和分析幼虾存活率、残肢率和幼虾体重生长率，研究两种芽孢杆菌对克氏原螯虾（*P. clarkii*）幼虾生长的影响。实验结果显示，加菌处理组和对照组间死亡率和残肢率无显著变化，SS-42 每天的饲喂量为 105 CFU/尾时各项生长指标表现最佳，体重增长率为（29.44±1.26）%；相同饲喂量时，饲喂 SS-42 菌株处理的平均体重增长率显著高于饲喂 10-2 菌株的处理（P＜0.05）。可见，无明显胁迫条件下，连续饲喂芽孢杆菌（*Bacillus*）对克氏原螯虾（P. clarkii）幼虾生长情况总体上有显著提高作用，解淀粉芽孢杆菌（*B. amyloliquefaciens*）的提高效果明显高于地衣芽孢杆菌（*B. licheniformis*）。本试验为应用芽孢杆菌（*Bacillus*）生产克氏原螯虾（*P. clarkii*）发酵饲料打下基础。

关键词：克氏原螯虾；解淀粉芽孢杆菌；地衣芽孢杆菌；生长影响

Effects of two kinds of Bacillus on the growth of Procambarus clarkii

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Abstract： In this paper, using the different concentrations solution of Bacillus amyloliquefaciens SS-42 and Bacillus licheniformis 10-2 to feeding *Procambarus clarkii* after domestication in the lab. By the methods of observation, calculation and analysis of young shrimp mortality, the rate of the residual limb, and young shrimp weight growth rate, the effects of two kinds of Bacillus on the growth of P. clarkii were researched. The results showed that there were no significant differences in mortality and stump rates between the treatment group and the control group, and the growth indicators data were the best when the daily feeding amount of SS-42 was 105 CFU/tail.The increase in body weight was（29.44±1.26）%. At the same dosage, the average weight growth rates of the treatment group fed with SS-42 strain were significantly higher than that of the treatment group fed with 10-2 strain ($P < 0.05$). The reports indicated that continuous feeding of Bacillus had significant effects on the growth of *P. clarkii* under normal circumstance, and the improvement effects of *B. amyloliquefaciens* were significantly higher than that of *B. licheniformis*. This experiment laid a foundation of feeding *P. clarkii* on the fermentations of *B. amyloliquefaciens* and *B. licheniformis*.

Key words: Procambarus clarkii; Bacillus amyloliquefaciens; Bacillus licheniformis; influence on growth

低蛋白饲料中添加β-羟基-β-甲基丁酸对日本囊对虾生长性能、消化能力、TOR 通路及肌肉品质的影响

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摘要：本研究开展 8 周的养殖试验以评估低蛋白饲料中添加β-羟基-β-甲基丁酸（HMB）对日本囊对虾（初重：2.00 ± 0.01 g）生长和肌肉品质的影响。分别配制蛋白水平为 49%和 44%的饲料作为阳性（HP）和阴性（LP）对照组，同时在 LP 基础上添加 0.025%、0.05%、0.10%、0.20%和 0.40% HMB 配制另外五种饲料（HMB1、HMB2、HMB3、HMB4 和 HMB5）。结果表明与 LP 组相比，HP、HMB3 和 HMB4 组增重率和特定生长率显著升高，而饲料系数显著降低。同时上述三组肠道胰蛋白酶活性显著高于 LP 组。较高的饲料蛋白水平和 HMB 提高了肌肉中 TOR 通路相关基因表达及大部分游离氨基酸含量。添加 0.2% HMB 提高了对虾肌肉硬度和持水力，肌肉中总羟脯氨酸和胶原蛋白含量均随饲料 HMB 含量的增加而增加。此外，添加 0.2% HMB 显著提高了对虾肌纤维密度和肌节长度，降低了肌纤维直径。

关键词：β-羟基-β-甲基丁酸；饲料蛋白水平；日本囊对虾；生长性能；TOR；肌肉品质

Dietary β-hydroxy-β-methylbutyrate supplementation affects growth performance, digestion, TOR pathway and muscle quality in kuruma shrimp Marsupenaeus japonicus fed a low protein diet

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Abstract： An 8-week feeding trial was performed to evaluate the effects of dietary β-hydroxy-β-methylbutyrate (HMB) on growth and muscle quality of kuruma shrimp Marsupenaeus japonicus (initial weight: 2.00 ± 0.01 g) fed a low protein diet. The positive control diet (HP) with 49% crude protein and negative control diet (LP) with 44% crude protein were formulated. Based on the LP, 0.025%, 0.05%, 0.10%, 0.20% and 0.40% of HMB were added to design the other five diets (HMB1, HMB2, HMB3, HMB4 and HMB5). Results showed that compared with LP group, HP, HMB3 and HMB4 groups had significantly higher weight gain rate and specific growth rate, while lower feed conversion ratio. Higher dietary protein level and HMB increased the expressions of TOR pathway-related genes and most of free amino acids contents in muscle. Dietary 0.2% HMB improved muscle hardness and water holding capacity, remarkably elevated myofiber density and sarcomere length, while reduced myofiber diameter.

Key words: β-Hydroxy-β-methylbutyrate; Dietary protein level; Marsupenaeus japonicas; Growth performance; TOR; Muscle quality

饲料胆碱调控 PERK 甲基化位点改善黄颡鱼高脂饮食引起乳糜微粒受损的作用机制

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摘要：乳糜微粒（CMs）是脂质吸收转运的唯一载体，其合成分泌是平衡肠道脂质代谢的基础。众所周知，胆碱能够改善高脂饮食（HFD）造成的应激失衡从而缓解脂质代谢紊乱。目前 HFD 影响 CMs 合成分泌的机制仍难以确定，并且忽视了胆碱作为甲基供体在其中发挥的作用。因此，本研究旨在探究 HFD 诱导的内质网应激（UPRer）影响 CMs 合成转运的机制，并揭示胆碱在其中的作用机制。我们结合活体养殖实验与离体细胞实验，通过甲基化检测，蛋白互作分析，乳糜微粒分离分析等实验，发现 HFD 通过激活 UPRer，抑制 perk 甲基化，进而导致 CMs 受损；而胆碱在其中起到缓解作用。有关分子机制，HFD 激活 UPRer 特殊传感器 Perk，并通过与 CMs 关键蛋白 Apo48 的互作调控 CMs 的合成分泌；而胆碱通过激活 Perk 启动子的-211 CpG 位点，抑制 perk 的启动子活性，进而改善 HFD 诱导的 CMs 损伤。

关键词：乳糜微粒，高脂饮食，胆碱，甲基化，Perk，Apo48

Dietary choline mitigates High-Fat Diet-Induced Impaired Chylomicron via CpG methylation sites of PERK

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Abstract：Chylomicrons (CMs) are the exclusive transporter of dietary lipids, and their assembly and secretion are the basis for ensuring the balance of intestinal lipid metabolism. Choline is known to improve the stress imbalance caused by high fat diets (HFD) and thus alleviate disorders of lipid metabolism. However, the molecular mechanisms by which HFD affects the assembly and secretion of CMs remain elusive, and the contribution of choline acting as methyl-donor in this process also have been overlooked. Consequently, the objective of this study is testing the molecular mechanism of HFD-induced UPRer impairing CMs biogenesis, and also to uncover the role of choline acting as methyl-donor. We combined in vivo culture experiments with in vitro cell experiments, through methylation assays, protein interaction analysis, and CMs isolation analysis, found that HFD inhibits perk methylation through activation of UPRer, which in turn leads to impaired CMs; and that choline plays a mitigating role in this. In terms of molecular mechanisms, we reveal an important regulatory role of Perk, one critical sensors and transducers for UPRer signaling pathway, in HFD impairing CMs assembly and secretion by protein-protein interaction with Apo48. Choline alleviated HFD-increased the expression of Perk via activating -211 CpG methylation sites of perk promoter. Taken together, our study will provide a better understanding of the molecular mechanism of CMs assembly and secretion and their potential role in HFD-induced lipid metabolic dysfunction.

Key words: Chylomicrons; High-fat diet; Choline; Methylation; Perk; Apo48

日粮添加甘露寡糖对团头鲂幼鱼非特异性免疫力、肠道健康及抗感染能力的影响

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摘要：甘露寡糖（MOS）作为饲料添加剂被广泛研究和应用，但其对团头鲂的免疫保护作用却鲜有报道，本研究探究其对幼鱼非特异性免疫力、肠道健康及抗感染能力的影响。研究发现，日粮添加 MOS 可增强幼鱼的免疫力，从而提高嗜水气单胞菌感染后试验鱼的存活率。MOS 可增强肝胰脏抗菌酶及抗氧化酶活性，并提高肠道杯状细胞的数量，通过较少肠道褶皱坏死及肠绒毛损伤来维持肠上皮屏障结构的稳定。qRT-PCR 分析表明日粮添加 MOS 后肠道免疫及紧密连接相关基因的表达上升，但其在细菌感染后表达上调幅度小于对照组，推测 MOS 抑制了肠道过度炎症反应所造成的损伤。日粮添加 MOS 还影响了肠道菌群的丰度和组成，通过增加肠道有益菌群的相对丰度改善了团头鲂幼鱼的肠道健康。综上，MOS 作为一种功能性饲料添加剂和免疫增强剂，通过增强机体抗感染免疫力与防止过度炎症反应之间的平衡来维持肠道内稳态并改善肠道健康，从而对团头鲂幼鱼具有显著的免疫保护作用。

关键词：甘露寡糖；团头鲂；非特异性免疫力；肠道健康；免疫保护作用

Dietary mannan oligosaccharides enhance the nonspecific immunity, intestinal health, and resistance capacity of juvenile Megalobrama amblycephala against Aeromonas hydrophila

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Abstract： The immunoprotective effects of Mannan oligosaccharides (MOS) on Megalobrama amblycephala were not well studied, the present study found that dietary MOS improved the survival rate of juvenile M. amblycephala upon infection, which may be attributed to the enhanced host immunity. For instance, dietary MOS increased the activities of hepatic antimicrobial and antioxidant enzymes, and maintained the stability of the intestinal epithelial barrier. Moreover, the expression of intestinal immune related genes in dietary MOS groups was not induced as notable as that in the control group post-infection, thereby suppressed the damage caused by excessive intestinal inflammation. Furthermore, dietary MOS increased the relative abundance of beneficial gut microbiota. In a word, dietary MOS exhibited significant immune protective effects to juvenile M. amblycephala, which is a functional feed additive and immunostimulant.

Key words: Mannan oligosaccharides; Megalobrama amblycephala; Non-specific immunity; Intestinal health; Immunoprotective effects

缢蛏高不饱和脂肪酸合成及其调控机制研究

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摘要：缢蛏是我国四大养殖经济贝类之一，营养价值丰富，尤其富含高不饱和脂肪酸（HUFA）。为解析缢蛏 HUFA 合成及其调控机制，作者围绕 HUFA 合成关键酶 Fad 和 Elovl、以及 HUFA 合成调控关键因子 SREBP 和 PPAR 开展了相关研究。通过酵母异源表达鉴定到两条Δ5 Fad、一条Δ6 Fad、一条 Elovl2/5、两条 Elovl4 和一条新型具有 Elovl4 活性的 Elovlc，表明缢蛏具备完整的 HUFA 合成通路，从而能够合成 ARA、EPA 和 DHA。通过基因组筛选鉴定到一条 SREBP 和两条 PPAR 同源基因，采用双荧光素酶报告系统表明 SREBP 和 PPAR 调控Δ6 Fad 转录。进一步利用凝胶电泳迁移实验证实Δ6 Fad 启动子区 5‘-GTGGGGTAACT-3’位点为 SREBP 转录调控结合位点。以上研究为阐明缢蛏 HUFA 代谢途径、理解缢蛏 HUFA 需求、以及揭示 HUFA 在缢蛏生长发育中的作用机制奠定了基础。

关键词：缢蛏；高不饱和脂肪酸；合成；调控

Synthesis of highly unsaturated fatty acids in Sinonovacula constricta and its regulation

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Abstract：As one of the four major aquaculture economic shellfish in China, Sinonovacula constricta is rich in nutrients, especially highly unsaturated fatty acids (HUFA). To clarify the synthesis of HUFA in this bivalve and its regulation, we carried out related research on the key enzymes of HUFA synthesis (Fad and Elovl), as well as the key factors in the regulation of HUFA synthesis (SREBP and PPAR). Two Δ5 Fad, one Δ6 Fad, one Elovl2/5, two Elovl4, and a new Elovlc with Elovl4 activity were identified by heterologous expression in yeast, indicating that S. constricta has a complete HUFA synthesis pathway. One SREBP and two PPAR homologous genes were identified by genomic screening, and Δ6 Fad transcription was regulated by both SREBP and PPAR. The 5'-GTGGGGTAACT-3' site in the Δ6 Fad promoter region was confirmed as the SREBP binding site. The above studies have laid a foundation for understanding the nutrition and metabolism of HUFA in S. constricta.

Key words: Sinonovacula constricta; highly unsaturated fatty acids; synthesis; regulation

水温对花鲈生长性能、免疫及抗氧化能力的影响

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摘要：为探究高温对花鲈造成的生理影响及其机制，试验设计 27℃、31℃及 35℃三个温度处理，每处理 3 个重复，每重复 40 尾鱼（9.50±0.20g），在温控系统中进行为期 60d 的养殖试验。结果表明：随着温度的升高，存活率（SGR）、增重率（WG）、饲料效率（FE）、肠道消化酶活性、肾脏碱性磷酸酶（AKP）、酸性磷酸酶（ACP）、一氧化氮合酶（NOS）活性及一氧化氮（NO）含量均呈下降趋势，并在 35℃组达到最低（$P<0.05$），但血清超氧化物歧化酶（SOD）活性、总抗氧化（T-AOC）能力及丙二醛（MDA）含量呈现上升的趋势，在 35℃组达到最高（$P<0.05$）。结论：高温诱导花鲈的热应激，降低了生长性能、饲料利用及免疫能力，同时造成了氧化应激，导致氧化损伤。

关键词：花鲈；水温；生长；免疫；抗氧化

Effects of water temperature on growth performance, immunity and antioxidant capacity of spotted seabass (Lateolabrax maculatus)

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Abstract: This study was designed to explore the physiological impact and mechanisms of high water temperature on the spotted seabass. Three temperature treatments, 27°C, 31°C and 35°C, were designed in the experiment, with 3 repetitions in each treatment and 40 fish (9.50 ± 0.20g) per repetition, a 60 days culture experiment was carried out in a temperature control system. The results showed that high water temperature significantly affected the growth performance, feed utilization capacity, immune capacity and antioxidant capacity of spotted seabass. With the increase of temperature, the survival rate (SGR), weight gain rate (WG), feed efficiency (FE), intestinal digestive enzyme activities, renal alkaline phosphatase (AKP), acid phosphatase (ACP), nitric oxide synthase (NOS) activities and nitric oxide (NO) content showed a downward trend, the lowest value was observed in the 35℃ group ($P<0.05$), while the activity of superoxide dismutase (SOD), total antioxidant capacity (T-AOC) and malondialdehyde (MDA) showed an upward trend, the maximum value was observed in the 35℃ group ($P<0.05$). Conclusion: high water temperature induced the heat stress, which reduced the growth performance, feed utilization effect and immune ability, and caused oxidative damage of spotted seabass.

Key words: Lateolabrax maculatus; water temperature; Growth; Immunity; Antioxidant

饲料蛋白质水平对牛蛙蝌蚪的生长性能、抗氧化能力和变态率的影响

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摘要：为了探究饲料蛋白质水平对牛蛙蝌蚪的生长性能、抗氧化能力和变态率的影响，本试验配制了 7 种等脂等能饲料，蛋白质水平分别为 24.61%、28.49%、33.74%、37.50%、44.06%、48.39%和 53.92%。每处理设 3 个重复，每个重复 26 只蝌蚪（0.009g），试验为期 77d。结果表明：增重率（WG），特定生长率（SGR），肝脏总抗氧化能力（T-AOC）和过氧化氢酶（CAT）活性及变态率均随饲料蛋白质水平的升高而升高，在 44.06%蛋白质水平时达到最高，之后则呈下降趋势。以末均重（FBW）和变态率为基础进行二次回归，得到蛋白质水平分别为 42.60%和 46.33%时，末均重和变态率有最大值。综上所述，牛蛙蝌蚪饲料的最适蛋白质水平为 42.60%-46.33%。

关键词：牛蛙蝌蚪；生长；蛋白质；甲状腺素；变态

Effects of dietary protein levels on growth, antioxidant capacity and metamorphosis rate of bullfrog (Lithobates catesbeianus) tadpoles

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Abstract： This study aimed to evaluate effects of dietary crude protein requirement on growth performance, antioxidant capacity, and metamorphosis rate of bullfrog (Lithobates catesbeianus) tadpoles. Seven iso-lipidic and iso-energetic diets were formulated with 24.61%, 28.49%, 33.74%, 37.50%, 44.06%, 48.39% and 53.92% crude protein. Triplicate replicates of tadpoles (0.009g) were fed for 77 days. Weight gain (WG), specific growth rate (SGR), the total antioxidant capacity (T-AOC) and catalase (CAT) activity in liver, and metamorphosis rate of bullfrog tadpoles all increased with increasing dietary protein level from 24.61% to 44.06%, and then decreased. Based on the second-order polynomial regression analysis of the final body weight (FBW) and metamorphosis rate vs. dietary protein level, the optimal dietary protein level for bullfrog tadpoles was 42.60% and 46.33%, respectively. In conclusion, the optimum dietary protein level of bullfrog tadpoles was estimated to be 42.60% and 46.33% of diet.

Key words: Bullfrog tadpoles; growth; protein; thyroxine; metamorphosis

大口黑鲈幼鱼对饲料中亮氨酸的需求量

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摘要：设计亮氨酸添加量为 0、4.0、8.0、12.0、16.0 和 20.0 g/ kg 的半纯化饲料，饲养投喂初始体质量为（18.0 ± 0.1）g 的大口黑鲈幼鱼 8 周。结果表明，亮氨酸显著影响鱼体的增重率（WG）、饲料系数（FCR）和蛋白质效率比（*P < 0.05*）。WG 和 FCR 对饲料亮氨酸水平呈现二次效应（*P<0.05*），且 Leu-8 组具有最高的 WG 和最低的 FCR。饲料亮氨酸对全鱼粗蛋白、氨基酸组成以及氨基酸、蛋白质和脂肪保留率的影响呈二次方（*P<0.05*）。此外，最佳亮氨酸水平显著上调大口黑鲈肌肉 IGF-1、TOR、S6K1 和 4EBP-1 基因的 mRNA 表达水平（P<0.001），且总体呈显着的正二次趋势（*P<0.001*）。综上所述，亮氨酸的最佳补充水平为 8.0 g/kg（Leu-8），即大口黑鲈幼鱼饲料中亮氨酸的需求量分别为 25.2 g/ kg 干物质。

关键词：亮氨酸；生长；大口黑鲈；基因表达；IGF-1

Dietary leucine requirement of juvenile largemouth bass (Micropterus salmoides) based on growth, nutrient utilization and growth-related gene analyses

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Abstract：450 fish (18.0 ± 0.1 g) were randomly divided into six groups, and offered semi-purified diets supplemented with crystalline L-leucine at 0, 4.0, 8.0, 12.0, 16.0 and 20.0 g/kg for eight weeks. The results showed that leucine significantly (*P<0.05*) influenced weight gain (WG), feed conversion ratio (FCR) and protein efficiency ratio (PER) of juvenile largemouth bass. WG and FCR presented a quadratic effect (*P<0.05*) against the dietary leucine levels. Moreover, whole-body crude protein, amino acid compositions, and amino acid, protein and lipid retention efficiencies were influenced quadratically (*P<0.05*) by the dietary leucine. Importantly, the optimal leucine level significantly (*P<0.001*) up-regulated mRNA expression levels of IGF-1, S6K1 and 4EBP-1 in fish muscle. All of the target genes in general showed a significant positive quadratic trend (*P<0.001*). Overall, the optimal supplementation level of leucine was 8.0 g/kg (Leu-8), corresponding to 25.2 g/kg dietary leucine.

Key words: Leucine; Growth; Largemouth bass; Gene expression; IGF-1

青蛤对不同浓度微藻的生理生化反应

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摘要：滩涂埋栖型贝类作为天然的水环境滤食者，对水域生态系统发挥着重要作用。海洋富营养化和池塘养殖水质过肥等环境条件对贝类的生理生化影响具有重要的科学和实践意义。本实验以中国沿海常见的滩涂养殖贝类青蛤为研究对象，以小球藻为饵料设置了 5 组饵料浓度，分别为 5×10^5 cell/L（T1）、1.25×10^6 cell/L（T2）、1.3×10^7 cell/L（T3）、1.25×10^8 cell/L（T4）、1.5×10^9 cell/L（T5），经 90d 饲养实验，结束时对各组青蛤生长指标进行测量，并通过测量酸性磷酸酶（ACP）、溶菌酶（LSZ）、超氧化物歧化酶（SOD）、胰蛋白酶（TPS）、淀粉酶（AMS）、脂肪酶（LPS）、乳酸脱氢酶（LDH）和琥珀酸脱氢酶（SDH）研究不同饵料浓度对青蛤的生长性能、消化、免疫、呼吸代谢的影响。利用 Illumina Hiseq 测序分析了在不同饵料浓度下的青蛤肝胰腺转录组表达水平，挖掘出差异表达基因和通路，为滤食性贝类在不同富营养化水体的生长、生理生化表现提供科学论据。总之，本文研究发现过高浓度的微藻饵料对滩涂贝类的生长与生存、消化与免疫代谢均有显著影响，在实践中应避免水体环境中的微藻浓度超过 5×10^5cell/L 以上。

关键词：青蛤；生长性能；消化酶；非特异性免疫酶；转录组测序；

Physiological and Biochemical Responses of Cyclina sinensis on Different Concentrations of Dietary Microalgae

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Abstract： As a natural filter feeder in the water environment, tidal flat burial shellfish play an important role in the aquatic ecosystem. Environmental conditions such as marine eutrophication and excessive fertilization of pond aquaculture water have important scientific and practical significance on the physiological and biochemical effects of shellfish. In this experiment, the common tidal flat cultured shellfish Cyclina sinensis in coastal China was used as the research object, and 5 groups of bait concentrations were set with Chlorella as the bait, which were 5×10^5 cell/L (T1) and 1.25×10^6 cell/L (T2).), 1.3×10^7 cells/L (T3), 1.25×10^8 cells/L (T4), and 1.5×10^9 cells/L (T5), after 90 days of feeding experiments, the growth indexes of each group were measured at the end of the experiment. And by measuring acid phosphatase (ACP), lysozyme (LSZ), superoxide dismutase (SOD), trypsin (TPS), amylase (AMS), lipase (LPS), lactate dehydrogenase (LDH) and succinate dehydrogenase (SDH) to study the effects of different feed concentrations on the growth performance, digestion, immunity and respiratory metabolism of clams. Illumina Hiseq sequencing was used to analyze the transcriptome expression levels of the hepatopancreas of the green clam under different feed concentrations, and the differentially expressed genes and pathways were mined, providing scientific evidence for the growth, physiological and biochemical performance of filter-feeding shellfish in different eutrophic water bodies. In this study, it was found that excessively high concentrations of microalgae bait would have a significant impact on the growth and survival, digestion and immune metabolism of tidal flat shellfish.

Key words: *Cyclina sinensis*; food concentration; growth performance; digestive enzyme; nonspecific immunity enzyme; comparative transcriptomic

江苏沿海四种不同海水养殖模式水体微生物群落比较研究

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摘要：微生物群落在不同养殖模式水环境中发挥着重要的作用，与环境质量及养殖动物的生长和疾病暴发密切相关。为考察江苏沿海不同养殖模式中的微生物群落状况，本研究基于16SrRNA测序技术，比较分析了四种江苏沿海重要的海水养殖模式（凡纳滨对虾小棚（LV）养殖；中国对虾、蛤蛏混养（FS）；日本对虾、梭子蟹混养（PP）；脊尾白对虾、梭子蟹混养（EP））水体微生物群落的差异。结果表明，四种养殖模式水体中主要微生物在门水平上均以变形菌门和拟杆菌门为主；功能分析显示，四种养殖水体中都富含大量化能异养菌，其存在提升了环境中微生物降解有机物、增强免疫与抗病等能力；环境因子关联分析发现，pH对四种养殖模式水体微生物群落结构影响贡献最大。高密度的凡纳滨对虾小棚模式和三种混养模式在各自养殖条件下，仍能保持养殖动物健康和高产量，水体微生物群落在其中发挥了举足轻重的作用，为进一步探究不同养殖模式的优缺点提供了科学依据。

关键词：海水养殖模式；微生物群落；16SrRNA

Comparative study on microbial communities in water bodies of different mariculture modes in Jiangsu Province

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Abstract： Microbial communities play an important role in the water environment of different mariculture modes and are closely related to environmental quality and the growth and disease outbreaks of farmed animals. In order to investigate the microbial community status in different mariculture modes along the Jiangsu coast, this study was conducted to compare and analyze the differences in microbial communities in the water column of four important mariculture modes along the Jiangsu coast (Litopenaeus Vannamei(LV) ;Fenneropenaeus Chinensis, Sinonovacula Constricta(FS); Penaeus Japonicus, Portunus Trituberculatus(PP);Exopalaemon Carinicauda , Portunus Trituberculatus(EP)) based on 16SrRNA sequencing technology The results showed that the microbial communities of the four mariculture modes were different. The results showed that the main microorganisms in the water bodies of the four mariculture modes were dominated by Amoebacteria and Bacteroides at the phylum level; the functional analysis showed that all four mariculture modes were rich in a large number of chemoenergetic heterotrophic bacteria, whose presence enhanced the ability of microorganisms in the environment to degrade organic matter and enhance immunity and disease resistance; the environmental factor correlation analysis revealed that pH had the greatest contribution to the microbial community structure in the water bodies of the four mariculture modes. The microbial community of the water column played a significant role in maintaining the health of farmed animals and high yields under the respective mariculture conditions in the high density of the small shed mode and the three mixed mariculture modes, which provided a scientific basis for further investigation of the advantages and disadvantages of the different mariculture modes.

Key words: mariculture mode; microbial communities; 16SrRNA

墨瑞鳕循环水养殖系统中不同生物膜反应器水处理效率及微生物群落对比分析

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摘要：将固定床生物膜反应器（FBBR）和移动床生物膜反应器（MBBR）并联接入实际生产的墨瑞鳕循环水养殖系统中，实现两者的同步连续运行（35 d），考察了它们的出水水质变化和微生物群落结构。结果显示，FBBR 和 MBBR 可以有效控制养殖水体中的 NH4+-N 和 NO2--N 浓度，但会导致 NO3--N 积累和 pH 下降；FBBR 与 MBBR 出水水质无显著差异，且硝化效率相似。FBBR 和 MBBR 在微生物群落上的相同点在于：优势菌群基本相同，硝化菌由亚硝化单胞菌属（*Nitrosomonas*）和硝化螺菌属（*Nitrospira*）构成, 且 Nitrospira 的相对丰度远高于 Nitrosomonas，两反应器中可能存在完全氨氧化菌。两反应器在微生物群落上的不同点在于：FBBR 微生物群落的丰富度和多样性以及硝化菌的相对丰度均高于 MBBR。

关键词：循环水养殖系统；固定床生物膜反应器；移动床生物膜反应器；硝化反应；微生物群落

Comparative investigation on water quality and microbial communities in different biofilm reactors of recirculating aquaculture system for Macculochella peeli

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Abstract： Parallel fixed-bed biofilm reactor (FBBR) and moving-bed biofilm reactor (MBBR) were joined to the full-scale recirculating aquaculture system for Macculochella peeli. FBBR and MBBR were simultaneously and continuously operated for 35 d to investigate their water quality variations and microbial community structures. Results indicate that both FBBR and MBBR could transform ammonia and nitrite to nitrate, which resulted in the nitrate accumulation and the pH decrease in aquaculture water. FBBR possessed higher richness and diversity of microbial community than MBBR, while they had similar predominant microbes, Nitrosomonas and Nitrospira constituted the nitrifiers in both FBBR and MBBR, but the relative abundance of nitrifiers was higher in FBBR. Furthermore, the relative abundance of Nitrospira was far higher than that of Nitrosomonas, indicating that complete ammonia oxidation bacteria might exist in FBBR and MBBR.

Key words: recirculating aquaculture system; fixed-bed biofilm reactor; moving-bed biofilm reactor; nitrification reaction; microbial community

$NaHCO_3$胁迫下杂交鲟（*Huso dauricus*♀×*Acipenser schrenckii*♂）皮肤的转录表达特征

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摘要：为了探明碱胁迫对杂交鲟“鲟龙 1 号”（*Huso dauricus*♀×*Acipenser Schrenckii* ♂）皮肤生理功能的影响，本研究采用转录组测序的方法和皮肤组织学切片研究观察了碱胁迫与正常养殖水质条件下杂交鲟皮肤组织的分子特征和组织结构。结果发现，对照组与胁迫组差异表达基因总数量（DEGs）为 1849 个，其中 1302 个基因在胁迫组的皮肤组织中上调基因，547 个基因下调。对差异表达基因进行 GO 聚类，主要富集在胞浆钙离子浓度的调节、肌肉收缩、肌钙蛋白复合物、肌钙蛋白 T 结合、肌钙蛋白 C 结合等 7 个 GO term 上。KEGG 富集分析发现，甘氨酸、丝氨酸和苏氨酸代谢、蛋白质消化吸收、淀粉和蔗糖代谢和氨基糖和核苷酸糖代谢等为显著富集通路。代谢通路互作网络分析发现，碱胁迫下鲟龙 1 号皮肤核心代谢途径为黏着斑、蛋白质消化吸收和血小板活化、补体和凝血级联及缺氧诱导因子-1 信号通路等途径为主效途径。组织切片结果显示杂交鲟在碱胁迫下皮肤组织和肾脏组织受到严重损伤，肾小球和肾小管发生明显皱缩，远曲小管萎缩尤为明显，肾小球上皮细胞体积减小，管壁变薄甚至脱落；皮肤组织的黏液细胞数量随碱度的升高而增多，棒状细胞细胞核发生固缩现象，在碱胁迫下排列更加紧密。本研究揭示了鲟龙 1 号皮肤组织碱胁迫响应相关基因的总体表达特征，同时可为鲟鱼盐碱驯养提供参考。

关键词：杂交鲟“鲟龙 1 号”；碱胁迫；转录组；皮肤；组织学切片；代谢通路网络

Transcriptome characterization of hybrid sturgeon (*Huso dauricus*♀×*Acipenser schrenckii*♂) skin under alkaline stress

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Abstract: To investigate the effect of alkaline stress on the skin physiology of hybrid sturgeon (*Huso dauricus*♀×*Acipenser Schrenckii*♂), we investigated the molecular characteristics of the skin tissue of hybrid sturgeon under alkaline stress and normal breeding water conditions by transcriptome sequencing.The total number of differentially expressed genes (DEGs) between control and stress groups was the result showed that was 391, of which 289 genes were up-regulated genes and 102 genes were down-regulated in the skin tissue of the stress group.GO clustering of differentially expressed genes showed that they were mainly enriched in seven GO terms, including regulation of cytoplasmic calcium ion concentration, muscle contraction, troponin complex, troponin T binding, and troponin C binding. KEGG enrichment analysis revealed that glycine, serine and threonine metabolism, protein digestion and absorption, starch and sucrose metabolism, and amino and nucleotide sugar metabolism were significantly enriched pathways.Interaction network analysis of metabolic pathways revealed that the core metabolic pathways of hybrid sturgeon skin under alkaline stress were the adherent patch, protein digestion and absorption and platelet activation, complement and coagulation cascade and hypoxia-inducible factor-1 signaling pathways as the main efficient pathways.Interaction network analysis of metabolic pathways indicates that the core metabolic pathways of hybrid sturgeon skin under alkaline stress were the adherent patch, protein digestion and absorption and platelet activation, complement and coagulation cascade and hypoxia-inducible factor-1 signaling pathways as the main efficient pathways.The results of histological sections showed that the skin and kidney tissues of hybrid sturgeon were severely damaged by alkaline stress, and the glomeruli and tubules were significantly wrinkled, especially the atrophy of the distal tubules, and the epithelial cells of the glomeruli were reduced in size, and the walls of the tubules were thinned or even detached; the number of mucous cells in the skin tissues increased with the increase of alkalinity, and the nuclei of rod-shaped cells were solidified and arranged more closely under alkaline stress.

Key words: hybrid sturgeon; Alkaline stress; transcriptome; skin; Histological sections,metabolic pathway networks

基于微生态网络分析不同碳源对生物絮团细菌共现模式和氮转化的影响

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摘要：细菌在 biofloc 系统中无机氮转化过程中起着至关重要的作用。然而，关于不同碳水化合物作用下微生态机制的报道很少。在本研究中，基于细菌共现网络分析三种不同水产养殖系统中絮团细菌相互作用关系：对照系统（CON 组）和使用葡萄糖或淀粉作为碳源的 BFT 系统（分别为 GLU 和 STA 组）。结果表明(ⅰ) 三个系统中的细菌组合是非随机的，每种碳水化合物都导致了细菌群落的独特生态位，同时，与 STA 组（55.59±16.26%和 15.30±11.08）相比，GLU 组表现出更高的脱氮效率和更高的 DOC/总无机氮比（68.80±9.18%和 19.19±6.78）；(ⅱ) 厚壁菌是 BFT 系统中的核心门，芽孢杆菌、肉杆菌和葡萄球菌是同时工作以维持 BFT 系统稳定脱氮的核心属；此外，细菌特性的非随机分布与其他宏观生态系统相似；(ⅲ) 在 GLU 组中，厚壁菌的丰度增加，这对应于鱼肠道中较高的厚壁菌/拟杆菌（F/B），从而促进宿主的原位生长性能。这项研究为细菌共生和 biofloc 中的氮调节机制提供了全新的、综合见解，也为后续研究 Biofloc 系统及其氮转移衍生系统提供了理论基础。

关键词：生物絮团；碳源；网络分析；微生物多样性；养殖废水处理

Different carbohydrates impact on the co-occurrence patterns of bacteria and nitrogen transformation by network analysis in biofloc systems

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Abstract： The complex aggregation of the bacteria floc (biofloc) plays a vital role in the inorganic nitrogen transformation process in biofloc systems. However, few report has been on the microecology mechanism of the floc under different carbohydrate. Herein the study, a correlation-based network was applied to analyze the bacterial interaction relationship of floc in three different aquaculture systems: a clear water system (CON group) and two BFT systems using glucose or starch as a carbon source (GLU and STA groups, respectively). The results showed that (i) the bacterial assembly in the three systems were non-random, each carbohydrate caused a unique niche of the bacteria communities, meanwhile, the GLU group exhibited higher nitrogen removal efficiency and higher DOC/total inorganic nitrogen ratio (68.80 ± 9.18% and 19.19 ± 6.78) than the STA group (55.59 ± 16.26% and 15.30 ± 11.08); (ii) Firmicutes was a core phylum in the BFT systems, and *Bacillus*, *Carnobacterium*, and *Staphylococcus* were the core genera that worked concurrently to maintain the BFT systems stable on the nitrogen removal; in addition, the non-random distribution of bacteria characteristics was similar to those of other macroecology systems; (iii) In GLU group the Firmicutes abundance was increased, which corresponding to higher Firmicutes/Bacteroidetes (F/B) in fish gut, thus to promote the growth performance of host in situ. This study offers novel and integrated insights into the bacterial co-occurrence and the nitrogen regulation mechanism in biofloc, also provides a theoretical basis for the subsequent research about biofloc systems and their derivative technology on nitrogen transfer.

Keywords: floc; carbohydrate; network analysis; microbial diversity; aquaculture wastewater treatment

凡纳滨对虾小型温棚模式养殖水体微生物群落的研究

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摘要：为从微生物学角度探究小棚模式养殖凡纳滨对虾（*Litopenaeus vannamei*）高产的原因，本研究采用高通量测序技术，揭示了小棚模式养殖水体的微生物群落组成和功能。结果表明，养殖中后期群落多样性显著高于前期；门水平主要优势菌为变形菌门、拟杆菌门、放线菌门，属水平主要为 Candidatus_Aquiluna、海命菌属（*Marivita*）、Cyanobium PCC-6307、黄杆菌属（*Flavobacterium*）和冷杆菌属（*Psychrobacter*）；功能分析显示，养殖后期小棚养殖水体中富集大量化能异养菌和少量益生菌，表达了降解有机物、增强虾免疫与抗病能力等功能；环境因子关联分析发现，总氮（TN）对小棚模式水体微生物群落结构影响最多。研究表明，小棚模式在高密度、高氨氮的养殖条件下，其水体微生物群落在保持水环境稳定和增强虾免疫与抗病能力方面发挥了重要作用。

关键词：小型温棚模式；凡纳滨对虾；养殖水体；微生物群落；高通量测序

Study on bacterial community structure in the small greenhouse of rearing water of shrimp, Litopenaeus vannamei

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Abstract： To explore the reasons for the high yield of *Litopenaeus vannamei* cultured in the small greenhouse from the perspective of microbiology, in this study, Illumina high throughput sequencing technology was used to analyze the microbial composition and function of L. vannamei pond. The results showed that the community diversity of L. vannamei pond was significantly higher in the middle and late periods than in the early period. At the phylum level, the dominant categories were Proteobacteria (51.5%), Bacteroidetes (23.6%) and Actinobacteria (11.3%). At the genus level, Candidatus_Aquiluna, Cyanobium PC-6307, Marivita, Flavobacterium, and Psychrobacter were the dominant categories. The functional prediction of aquatic microflora showed that large amount of Chemoheterotrophy and a small number of probiotics were enriched in the rearing water at the later stage of period, which expressed the function of degrading organic matter and enhancing immunity and disease resistance of shrimp. The correlation analysis of environmental factors showed that total nitrogen (TN) had the most influence on the structure of the water microbial community in the small greenhouse. These results indicated that under the high density and high ammonia nitrogen culture conditions, the water microbial community in the small greenhouse played an important role in maintaining the stability of water environment and enhancing the immunity and disease resistance of shrimp. This study provides key and practical references for further research on the role of microbial community in the small greenhouse.

Key words: the small greenhouse; Litopenaeus vannamei; rearing water of shrimp; bacterial community structure; Illumina high throughput sequencing

凡纳滨对虾与缢蛏串联养殖模式下虾蛏生长特性及水生态效应研究

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摘要：虾蛏串养模式作为海水围塘可持续发展的一种模式，但适宜于这种模式下虾蛏数量比尚不清楚。本研究设立了 LP 组（虾蛏数量配比 1:3）、MP 组（1:5）、HP 组（1:7），对虾蛏生长特性、养殖环境水质因子、消化与免疫指标、环境与蛏内脏团微生物群落进行探究。结果表明，LP 组和 MP 组虾蛏增重率和特定生长率显著高于 GP 组。水质营养盐浓度总体升高但有下降趋势。虾蛏对环境反应不同，缢蛏中淀粉酶和过氧化氢酶活性变化显著，对虾则是胰蛋白酶和超氧化物歧化酶活性变化显著。RDA 分析表明，总氮、活性磷酸盐是影响微生物群落关键因素。16s rRNA 分析表明，不同虾蛏不同数量配比对养殖环境以及缢蛏内脏团有较大影响，与 LP 组相比，MP 组和 HP 组微生物种类更多，且参与氮磷循环的微生物丰度增加。LP 组、MP 组虾蛏能良好生长且所处养殖环境能起到改善作用。研究结果有助于优化虾蛏串养模式，这对今后虾蛏串养模式健康发展非常重要。

关键词：凡纳滨对虾；缢蛏；串养模式；水质因子；微生物群落

Study on the growth characteristics and aquatic ecological effects of Litopenaeus vannamei and Sinonovacula constricta under the tandem culture model of shrimp and razor clams

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Abstract： The shrimp and razor clam tandem culture model is a sustainable model for the development of seawater ponds, but the appropriate shrimp and razor clam population ratio for this model is not clear. In this study, LP (shrimp and razor clam population ratio 1:3), MP (1:5) and HP (1:7) groups were established to investigate the growth characteristics of shrimp and razor clams, water quality factors in the culture environment, digestive and immune indicators, and microbial communities in the environment and razor clam viscera. The results showed that the weight gain rate and specific growth rate of shrimp and razor clams in LP and MP groups were significantly higher than those in GP group. Water nutrient concentrations were generally higher but tended to decrease. RDA analysis showed that total nitrogen and active phosphate were the key factors affecting the microbial community. 16s rRNA analysis showed that the different quantity ratios of different shrimp and razor clams had a greater impact on the culture environment and the visceral mass of razor clams, and the MP and HP groups had more microbial species compared to the LP group. The LP and MP groups were able to grow well and the culture environment was improved. The results of the study can help optimize the razor clam culture model, which is very important for the healthy development of razor clam culture model in the future.

Key words: Litopenaeus Vannamei; razor clam; string culture model; water quality factors; microbial community

养殖牛蛙皮肤细菌群落组成和功能受到红腿综合症的影响

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摘要：皮肤微生物与宿主健康密切相关。因此，严重干扰皮肤微生态系统的稳定性可能引起疾病。牛蛙是一种重要的水产经济动物，养殖中发生的红腿综合征(RLS)等细菌性疾病，造成巨大经济损失。本文采用 16S rRNA 基因扩增子高通量测序技术对健康牛蛙和 RLS 牛蛙的皮肤细菌群落组成和功能进行研究。研究表明 RLS 牛蛙皮肤细菌群落的香农多样性较低，chao1 较高。健康牛蛙和 RLS 牛蛙皮肤细菌群落差异显著。RLS 牛蛙皮肤细菌群落中 Elizabethkingia、Flavobacterium 和 Streptococcus 等条件致病菌的丰度较高，而 shwanella 等益生菌的相对丰度较低。Tax4Fun 功能预测显示 RLS 牛蛙代谢相关基因的相对丰度显著高于 RLS 牛蛙。我们发现 RLS 显著改变养殖牛蛙皮肤细菌群落的组成和预测功能。本研究为预防和管理牛蛙养殖中的红腿综合征提供了理论基础。

关键词：牛蛙；红腿综合症(RLS)；细菌群落；细菌功能

The composition and function of skin microbiota was altered of red leg syndrome in farmed bullfrog (*Rana catesbeiana*)

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Abstract： Skin microbiota plays an important role in skin barrier function and is closely related to host health. Therefore, seriously disturbing the stability of the skin microecosystem may cause host disease. Bullfrog (Rana catesbeiana) is an important aquaculture economic animals. However, bacterial diseases, such as red leg syndrome (RLS), frequently occur in bullfrog farming and cause huge economic losses around the word. The emergence of RLS is unclear. Here, we compare the skin bacterial communities of healthy and RLS bullfrogs. 16S rRNA gene sequencing was used to study the microbial composition and function of healthy and RLS bullfrogs. [Results] Skin bacterial communities of RLS were lower Shannon diversity, but were more high the Chao1 estimator than those of healthy bullfrogs. The skin bacterial communities were significantly different between healthy and RLS bullfrogs. Compared with healthy bullfrogs, RLS bullfrogs had higher abundances of unclassified_f__Comamonadaceae,Acinetobacter, Chryseobacterium, Elizabethkingia, Flavobacterium and Streptococcus in skin bacterial communities, whereas the relative abundances of Peptostreptococcales-Tissierellales, Cetobacterium, Bacteroides and Shewanella were overrepresented in RLS bullfrogs. Tax4Fun functional prediction showed that the relative abundance of genes related to Nucleotide metabolism (Purine metabolism), Translation (Aminoacyl-tRNA biosynthesis), Nucleotide metabolism (Pyrimidine metabolism), Translation (Ribosome), Glycan biosynthesis and metabolism (Peptidoglycan biosynthesis) exhibited were significantly higher in RLS bullfrogs.Overall, we found that RLS significantly altered the composition and predictive function of the skin bacterial communities in farmed bullfrogs. Our findings enhance understanding of microbial ecology in aquatic ecosystems and contribute to the prevention and management of RLS in bullfrog farming.

Key words: bullfrog (Rana catesbeiana); red leg syndrome (RLS); bacterial community; bacterial function

养殖银鲳繁殖前后尾部神经分泌系统形态学和组织学观察

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摘要：硬骨鱼类尾部神经分泌系统（caudal neurosecretory system，CNSS）与繁殖密切相关，为研究养殖银鲳 CNSS 与繁殖期的关系，实验采用光镜和电镜技术对 CNSS 形态结构和繁殖前后结构变化进行观察，并检测其尾加压素 I（U-I）和 II（U-II）繁殖前后含量变化。结果显示：银鲳 CNSS 主要由 Dahlgren 细胞、轴突和尾垂体组成。尾垂体体积较大且有单个长条形和单个圆球形两种形态。轴突主要是无髓神经纤维；Dahlgren 细胞主要分布在尾部最后 3 节脊髓中；银鲳繁殖前，Dahlgren 细胞数量较多，细胞突起及末梢内充满两种类型分泌颗粒；繁殖后，Dahlgren 细胞数量和其内分泌颗粒显著减少。在 CNSS 中，U-II 含量繁殖后显著增加。在血清和性腺中，U-I 和 U-II 含量繁殖前后呈降低趋势。综上所述，养殖银鲳的 CNSS 形态及数量繁殖前后变化显著，与性腺发育密切相关参与调控银鲳繁殖。

关键词：银鲳；尾部神经分泌系统；尾垂体；Dahlgren 细胞；尾加压素

Morphological and histological observation of the caudal neurosecretory system before and after reproduction in artificially cultured silver pomfret, Pampus argenteus

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Abstract：The caudal neurosecretory system (CNSS) of the tail of teleost fish is closely related to reproduction. Our results showed that the CNSS is comprised of large magnocellular neuroendocrine cells (Dahlgren cells) located in the terminal vertebral segments of the spinal cord and clustered around the region of the central canal of the spinal cord, primary axons projected by Dahlgren cells and the neurohaemal release organ (urophysis) lying at the ventral side of the caudal extremity of the spinal cord. Dahlgren cell numbers and cellular endocrine granules were significantly reduced, and mitochondria were vacuolated after propagation. In CNSS, U-II content was significantly increased after reproduction than before reproduction. In serum and gonadal tissue, the content of U-I and U-II after reproduction showed a decreasing trend compared with before reproduction. In conclusion, the morphology and quantity of CNSS changed significantly before and after the breeding of artificially cultured silver pomfret, which was closely related to the development of gonads. It is speculated that it may participate in and regulate the reproduction of silver pomfret.

Key words: silver pomfret; CNSS; urophysis; Dahlgren cell; urotensins

虾肝肠胞虫极管蛋白 3 的鉴定

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摘要：对克隆的虾肝肠胞虫(*Enterocytozoon hepatopenaei*, EHP)极管蛋白 3 (Polar tube protein 3)基因进行生物信息学分析，构建其核心区域部分序列编码的蛋白原核表达载体，诱导表达、纯化，制备多克隆抗体。EHP PTP3 基因中最长的开放阅读框片段长 3390 bp，编码 1130 个氨基酸，预测蛋白分子质量为 125 kD。该蛋白有 13 个 N-糖基化位点和多个 O-糖基化位点，未发现信号肽结构域；有 117 个磷酸化位点，其中苏氨酸磷酸化位点约占 61%；二级结构中α螺旋占 41.77%，延伸链占 12.48%，随机卷曲占 39.29%，β转角占 6.46%。通过 Western blotting 验证了多抗的特异性，免疫荧光下观察了 PTP3 在极管弹射时的状态，确认了 EHP PTP3 在极管上的存在。以上结果均证实了 EHP PTP3 是虾肝肠胞虫中最新鉴定出的一种极管蛋白。

关键词：虾肝肠胞虫；极管蛋白 3；生物信息学分析；多克隆抗体

Preliminary identification of Enterocytozoon hepatopenaei Polar Tube Protein 3

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Abstract：Bioinformatics analysis of the cloned gene polar tube protein 3 (PTP3) of *Enterocytozoon hepatopenaei* (EHP) was carried out, and the prokaryotic expression vector of the protein encoded by part of its core region was constructed. After induction, expression and purification, polyclonal antibodies were prepared. The longest open reading frame fragment of EHP PTP3 had 3390 bp, encoding 1130 amino acids, and the predicted protein molecular weight was 125 KD. The protein had 13 N-glycosylation sites and multiple O-glycosylation sites, and no signal peptide domain was found. There were 117 phosphorylation sites, of which threonine phosphorylation sites accounted for about 61%. In the secondary structure α Helix accounted for 41.77%, extended chain accounted for 12.48%, random curl accounted for 39.29%, β And the corner accounts for 6.46%. The specificity of the polyclonal antibody was verified by Western blotting, and the state of PTP3 at the time of polar tube ejection was observed by immunofluorescence, confirming the existence of EHP PTP3 at the polar tube. The above results confirmed that EHP PTP3 was a newly identified polar tube protein in EHP.

Key words: *Enterocytozoon hepatopenaei;* polar tube protein 3; bioinformatics analysis; polyclonal anti-body

循环水养殖系统中基于纤维素的生物反应器脱氮性能和微生物多样性

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摘要：为解决对虾循环水养殖系统硝酸盐积累问题，将基于瓦楞纸板的固相反硝化反应器引入循环水养殖系统。研究结果显示，养殖过程中硝酸盐浓度被控制在 2.31±1.00 mg/L，养殖水体中 82.88%的氮被去除，进一步通过稳定同位素稀释法检测到反应器反硝化速率达到 0.74 mg/(L·day)。高通量测序分析显示，反应器中的瓦楞纸板被 *Lachnospiraceae*、*Saprospiraceae*、*Exiguobacterium*、*Mesoflavibacter* 等细菌降解，为 *Rhizobiaceae*、*Rhodobacteraceae*、*Bacillus*、*Nitratireductor*、*Sphingobium*、*Marinicella*、*Desulfovibrio*、*Marinobacter*、*Labrenzia* 等反硝化细菌提供碳源。大量的 amoA、nirK、nosZ 等氮循环功能基因表明，反应器可将氮元素高效转化为氮气。

关键词：固相反硝化；稳定同位素；微生物群落；功能基因；循环水养殖系统

Nitrogen removal performance and microbial diversity of bioreactor packed with cellulosic carriers in recirculating aquaculture system

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Abstract： In this research, a solid-phase denitrification reactor (SPDR) packed with corrugated paperboard was introduced into the recirculating aquaculture system (RAS) of Litopenaeus vannamei for nitrate removal. Results showed that 82.88% of the nitrogen was removed from the culture water with the denitrification rate of 0.74 mg/(L·day) and the concentration of nitrate was controlled at 2.31 ± 1.00 mg/L. High throughput sequencing analysis showed that the corrugated paperboard was degraded by *Lachnospiraceae*, *Saprospiraceae*, *Exiguobacterium*, *Mesoflavibacte*r, etc. to provide carbon source for denitrifying bacteria, including Rhizobiaceae, *Rhodobacteraceae*, *Bacillus*, *Nitratireductor*, *Sphingobium*, *Marinicella*, *Desulfovibrio*, *Marinobacte*r, and *Labrenzia*. The abundance of the functional genes amoA, nirK, and nosZ indicated that nitrogen can be efficiently converted into N2 in the SPDR.

Key words: Solid-phase denitrification; Stable isotope; Microbial community; Functional gene; RAS

珠三角地区水稻浮床对生鱼养殖池塘尾水中氮、磷处理效果的初步试探

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摘要：选择两口面积约为 7 亩的池塘，放养 7~8 万尾 7cm~10cm 规格的生鱼苗，日常养殖操作相同。当生鱼达到 150g~350g 时，其中一口池塘 10%面积覆盖泡沫浮床，以池塘底泥作杯盘基底种植优质水稻作试验设计；另一口池塘不做处理作对照。分别在水稻生长的分蘖前期、抽穗扬花期、灌浆期对二者进行总磷（TP）、磷酸盐、总氮（TN）、硝态氮、铵态氮、叶绿色 a 等水质指标检测。结果显示：叶绿素 a、TN 含量过高，生鱼养殖尾水属富营养化水体。试验期间，水稻对尾水中磷的吸收作用明显，试验池 TP 小于对照池；水稻对氮的吸收以铵态氮为主，试验池中铵态氮含量显著大于硝态氮，而对照池中硝态氮显著大于铵态氮。此外，在水稻分蘖前期，水稻吸收氮作用开始显现，但试验池和对照池无显著差异；在抽穗扬花期，试验池 TN（13.978mg/L）显著小于对照池 TN（18.884mg/L）；在灌浆期，试验池 TN 反而大于对照池。

关键词：水稻；浮床；生鱼；富营养化；氮；磷

The preliminary test of the floating plate that planted rice on the treatment effect of the nitrogen and the phosphorus in the pond that cultured Snakehead in the Pearl River Delta

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Abstract：Two ponds with an area of about 4,667 square meters were selected to culture 70,000 to 80,000 Snakeheads of size ranging from 7cm to 10cm , and fed with the same content of the same compound feed and bred on the same operation everyday. When the size of Snakehead reached 150g~350g, 10% of the area of one pond was covered with ffloating plates, which was planted high-quality rice with the bottom mud of the pond as the base being as the experimental design，and the other pond was left untreated as a control. Water quality indexes such as total phosphorus (TP), phosphate, total nitrogen (TN), nitrate nitrogen, ammonium nitrogen and Chlorophyll a were detected at early tiller stage, heading and flowering stage, and grain filling stage of rice. The results showed that the content of Chlorophyll a and TN was too high, and the tail water of culturing Snakehead belonged to eutrophic water. During the test, the phosphorus absorption effect of rice on the tail water was obvious,and the TP of test pool was less than that of control pool. The nitrogen absorption of rice was mainly ammonium, and the content of ammonium in the test pool was significantly higher than that of nitrate, while that of nitrate in the control pool was significantly higher than that of ammonium. In addition, nitrogen absorption began to show in the early tiller stage, but there was no significant difference between the test pool with and the control pool . At heading and flowering stage, the test pool with the TN of 13.978mg/L was significantly lower than that of 18.884mg/L in the control pool. In the grouting stage, the TN of the test pool was greater than that of the control pool.

Key words: Rice; The floating plate; Snakehead; Eutrophic water; Nitrogen; Phosphorus

微塑料对生物絮团形成、微生物群落结构和氮转化功能的影响

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摘要：生物絮凝技术常用于集约化水产养殖，可以促进微生物聚集体的形成。微塑料污染目前已经广泛存在于水产养殖水体中，且会改变周围微生物群落结构。本文探究了 MPs 对生物絮团形成、微生物群落结构和功能，特别是对氮转化的影响。研究结果表明，生物絮团与 MPs 形成了明显的聚集体，有微塑料的系统存在更多的生物絮团量。微生物 Alpha 多样性结果表明，细菌群落多样性没有显著差异，但真核生物群落多样性存在显著差异。PLS-DA 分析表明微生物群落组间存在显著差异。在氮转化过程中，没有 MPs 存在的系统亚硝酸盐氮的峰值浓度显著高于有 MPs 存在的系统，可能是由于有 MPs 的系统中存在更少的 hao 基因和更丰富的 nxrA 基因，这主要与 Alphaproteobacteria_bacterium 的丰度有关。综上结果表明 MPs 可与生物絮团形成聚集体，抑制生物絮团形成，通过改变微生物群落结构从而抑制氨氧化和促进亚硝酸盐氧化。

关键词：微塑料；生物絮团；硝化作用；微生物群落微

Microplastics inhibit biofloc formation and alter microbial community composition and function related to nitrogen transformation in aquaculture

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Abstract： Biofloc technology, extensively used in intensive aquaculture system, can prompt the formation of microbial aggregates. Microplastics (MPs) are detected abundantly in aquaculture waters. This study explored the effects of MPs on biofloc formation, microbial community composition and function, especially on nitrogen transformation. The formation process and settling performance of bioflocs in the presence of MPs were examined. High-throughput sequencing of 16S and 18S rRNA genes was used to investigate the bacterial and eukaryotic community compositions of bioflocs. Dynamic changes of nitrogen were monitored during the bioflocs incubation. Metagenomic sequencing were further used to explore the changes in functional microorganism and genes associated with nitrogen metabolism. In biofloc formation, the aggregates consisting of bioflocs and MPs formed clearly and the systems with MPs had more floc volume. In microbial community composition and function, no significant differences in bacterial diversity but significant differences in eukaryotic diversity were found. Significant separations between systems without and with MPs were observed. The peak concentration of nitrite nitrogen in systems without MPs was higher than that with MPs, which might be due to lower hao and enricher nxrA genes related to nitrogen metabolism in systems with MPs and be related to the abundance of Alphaproteobacteria_bacterium. The results could better reveal ecological risks of nitrogen transformation in MPs and have important significance for the health assessment of aquaculture water environment especially in the biofloc systems.

Key words: Microplastic; Biofloc technology; Nitrification; Microbial community

缢蛏海水池塘综合养殖模式及承载力研究

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摘要：本研究通过现场试验，在江苏南部海水池塘开展了缢蛏与脊尾白虾、黑鲷鱼综合养殖的研发试验，比较分析了缢蛏在 3 个不同放养面积条件下，与不同搭配种类综合养殖的效果。结果表明，“大面积缢蛏-黑鲷”在前期（6 月）表现出显著的生长优势，在养殖周期结束时，三个面积组的生长无显著性差异；“大面积缢蛏-脊尾白虾”在前期（6 月）表现出显著的生长优势，8 月份，“小面积缢蛏-黑脊尾白虾”试验组生长显著，在养殖周期结束时，三个面积组的生长无显著性差异；相同生物量条件下，适当提高放养密度对缢蛏生长影响较小，缢蛏成品养殖适宜放养密度 600-1200 粒/m2，两种模式下，缢蛏成活率及生长均较好，“缢蛏-黑鲷”模式较“缢蛏-脊尾白虾”的缢蛏壳长相对增长率高 11.96%。本研究为探索底栖贝类海水池塘养殖承载力，构建海水池塘贝类高效养殖模式提供理论依据。

关键词：缢蛏；海水池塘；承载力；养殖模式

Study on comprehensive culture model and bearing capacity of Sinonovacula constricta in seawater pond

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Abstract：In this study, through field experiments, the R & D experiments of Sinonovacula constricta, Exopalaemon carinicauda and Sparus macrocephlus were carried out in the seawater ponds in southern Jiangsu Province, and the effects of Sinonovacula constricta and different matching species in three different stocking areas were compared and analyzed. The results showed that " Large area Sinonovacula constricta - Sparus macrocephlus " showed significant growth advantages in the early period (June), At the end of the breeding cycle, there was no significant difference in the growth of the three area groups; "Large area Sinonovacula constricta - Exopalaemon carinicaudas with ridge tail" showed significant growth advantage in the early period (June). In August, the "small area Sinonovacula constricta - Exopalaemon carinicaudas with black ridge tail" test group grew significantly. At the end of the breeding cycle, there was no significant difference in the growth of the three area groups; Under the same biomass condition, properly increasing the stocking density has little effect on the growth of Sinonovacula constricta. The suitable stocking density for finished Sinonovacula constricta culture is 600-1200 grains / m2. Under the two mixed culture modes, the survival rate and growth rate of Sparus macrocephlus are better. “Sparus macrocephlus " mode is 11.96% higher than " Exopalaemon carinicauda" mode. This study provides a theoretical basis for exploring the bearing capacity of benthic shellfish culture in seawater ponds and building a high-efficiency culture model of shellfish in seawater ponds.

Key words: Sinonovacula constricta; sea water pond; Bearing capacity; culture mode

不同流速对豹纹鳃棘鲈摆尾频率和血液生理的影响

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摘要：为探究豹纹鳃棘鲈 (*Plectropomus leopardus*) 对不同流速的耐受能力，以豹纹鳃棘鲈 [体长 (11.38±1.48) cm，体质量 (34.71 ± 11.57) g] 为研究对象，设计静水对照组 (0 cm·s−1 或 0 bl·s−1、体长·秒−1) 和 3 组实验组 (11.4、22.8 和 34.2 cm·s−1 对应 1、2 和 3 bl·s−1)，探究 40 min 水流刺激对豹纹鳃棘鲈摆尾频率变化、血糖、血液中乳酸和皮质醇含量的影响。结果显示，摆尾频率与水流速度之间呈线性正相关关系；血糖和血液中皮质醇含量随摆尾次数增多呈线性增长趋势，而乳酸随摆尾次数增多呈非线性增长趋势。超过 2 bl·s−1 流速会导致豹纹鳃棘鲈血液中皮质醇含量显著升高 ($P<0.05$)。当流速达 3 bl·s−1 时，血液中乳酸和血糖含量显著升高 ($P<0.05$)。综上，豹纹鳃棘鲈对流速的耐受上限为 2 bl·s−1。

关键词：豹纹鳃棘鲈；水流；摆尾频率；血液生理

Effects of different flow velocity on tail beat frequency and blood physiology of Plectropomus leopardus

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Abstract： To investigate the tolerance of *Plectropomus leopardus* to different water currents, a control static water group (0 cm·s−1 or 0 bl·s−1, body length·s−1) and three test groups (11.4, 22.8 and 34.2 cm·s−1 corresponding to 1, 2 and 3 bl·s−1) were designed by using a homemade fish swimming test apparatus. A control group and three experimental groups were designed to investigate the effects of 40 min of water stimulation on the changes of tail swing frequency, blood glucose, lactic acid and cortisol contents of P. leopardus. The results showed that there was a linear correlation between the frequency of tail wagging and water velocity; the blood glucose and cortisol levels increased linearly with the number of tail wagging, and lactate increased nonlinearly with the number of tail wagging. Above 2 bl·s−1 flow rate resulted in a significant increase in cortisol in the blood of P. leopardus ($P<0.05$). When the flow rate reached 3 bl·s−1, the blood lactate and blood glucose levels increased significantly ($P<0.05$). In conclusion, the upper limit of tolerance to flow velocity of P. leopardus was 2 bl·s−1. When the flow velocity of cultured water was higher than 2 bl·s−1, the stress level and metabolic load increased significantly and stress effect appeared ($P<0.05$).

Key words: Plectropomus leopardus; Flow; Tail swing frequency; Blood physiology

过硫酸钠同时消解养殖尾水中总氮总磷的探索

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摘要：大部分池塘养殖尾水中总氮、总磷质量浓度偏高，测定过程中需要对样品进行稀释，耗时较长且影响准确度。实验室分析时，通常采用过硫酸钾对尾水样品进行消解，其配置过程对温度要求较高，易析出晶体，且耗时较长。而过硫酸钠易溶于水，受温度影响较小，易配制。因此，分别采用上述 2 种过硫酸盐消解液对样品进行消解并同时测定总氮、总磷的质量浓度，比较 2 种消解方式对校准曲线、加标回收率、养殖尾水实际样品测定的影响。结果表明，

关键词：过硫酸钠；过硫酸钾；消解；总氮；总磷；养殖尾水

Exploration of sodium persulfate for simultaneous digestion of total nitrogen and total phosphorus in cultured tailwater

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Abstract： The total nitrogen and total phosphorus content of tailwater from aquaculture ponds is usually higher than the highest measurable concentration. Thus, samples need to be diluted before measurement, which leads to an increase in measurement time and a decrease in measurement accuracy. In the laboratory, potassium persulfate is commonly used for digestion of tailwater samples. The disadvantages of potassium persulfate are that it is easy to precipitate in crystal form at low temperature and the preparation time is too long. On the contrary, sodium persulfate is easily soluble in water, less affected by temperature changes and easy to prepare. In this study, the samples were digested by two kinds of persulfate digestion solutions, respectively, and the contents of total nitrogen and total phosphorus of the digested samples were determined. Compare the effects of the two methods on calibration curves, standard recovery, and determination of aquaculture tailwater samples It was found that when the mass or material amount is equal to potassium persulfate, the sodium persulfate digestion solution can meet the requirements of total nitrogen and total phosphorus digestion. Moreover, the amount of sodium hydroxide added, and pH need not be adjusted when using sodium persulfate digestion solution, and the digestion effect is equal to that of potassium persulfate under equal amount of substance. In conclusion, equal amounts of sodium persulfate can replace potassium persulfate for digest

Key words: Sodium persulfate; Potassium persulfate; Digestion; Total nitrogen; Total phosphorus; Cultured tailwater

基于计算流体力学和机器学习的养鱼池水动力与能量利用的建模、开发与优化

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摘要：养殖池的水动力学在循环水养殖系统(RAS)中起着重要的作用，同时保持最大的有效能量利用率和均匀的涡流分布对鱼类生长是一个很大的挑战。为了解决这一问题，提出了一种利用计算流体力学(CFD)和机器学习(ML)优化八角形储罐物理参数的新方法。对八角罐的进出口直径、圆角半径、进口高度、进口角和流量等六个关键参数进行了数值计算。采用人工神经网络(ANN)和非支配排序遗传算法II (NSGA-II)相结合的建模开发和优化方法，获得了最大有效能量利用率和最小化涡流 STD 的帕累托前沿。研究结果表明:1)基于 CFD 数据训练的模型具有较高的预测能力，平均速度和涡 STD 的 RMSE 分别为 0.002 和 0.377。2)在平均速度和涡度 STD 的基础上，开发了 NSGA-II结合人工神经网络，并将其应用于优化过程中，得到 78 组最优 Pareto 前沿。3)在最接近的 Pareto 前沿之一，利用 LINMAP 获得一系列最优参数，优化结果。

关键词：流体动力学；多目标优化；物理参数；ML 和 CFD；八角形的文化罐

Modelling development and optimization on the hydrodynamics and energy utilization of fish culture tank based on computational fluid dynamics and machine learning

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Abstract： Hydrodynamics of culture tank plays an important role in the recirculating aquaculture system (RAS), meanwhile, maintaining the maximum effective energy utilization rate and uniform vortex distributions for fish growth is a great challenge. To solve this problem, a novel approach to optimize physical parameters of octagonal tank using computational fluid dynamics (CFD) and machine learning (ML) is proposed. Six vital parameters of octagonal tank including inlet and outlet diameters, fillet radius, inlet height, inlet angle and flow rate have been numerically investigated. Modelling development and optimization based method combining with Artificial Neural Network (ANN) and Nondominated Sorting Genetic Algorithm II (NSGA-II) was developed to obtain the Pareto front for maximizing effective energy utilization rate and minimizing the vortex STD. Some key findings are found that: 1) The model trained by CFD dates provides high predictive capability: RMSE of average velocity and vortex STD .

Key words: Hydrodynamics; Multi-objective optimization; Physical parameters; ML and CFD; Octagonal culture tank

不同虾-蟹混养池塘养殖周期中微生物群落结构变化和抗性基因的研究

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摘要：为探究不同品种三疣梭子蟹在虾-蟹混养池塘不同养殖时期中对环境微生物的种类、丰度及群落结构的影响，对两个不同品种三疣梭子蟹混养池的水体环境和底泥环境进行采样。利用 Illumina MiSeq 测序技术构建 Meta 基因组文库，经过 Metagenome 组装，进行基因预测、丰度分析、物种注释以及功能差异分析，并结合抗性基因数据库（CARD）对环境中的抗性基因进行注释分析。

关键词：宏基因组学；微生物群落结构；抗生素抗性基因；三疣梭子蟹

Different shrimp-crab-mixed pond breeding cycle in the breeding cycle of microbial community structures and resistance genes

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Abstract： In order to explore the influence of the types, abundance and community structures of different varieties of three warted crabs in shrimp-crab-mixed ponds during different breeding periods, the water body environment and bottom mud environment of the two different varieties of three warts. Sample. Using Illumina MISEQ sequencing technology to build the Meta genomic library, through Metagenome assembly to perform genetic predictions, abundance analysis, species annotations, and functional differences, and combine the anti -sex gene database (CARD) comments and analysis of the environment in the environment.

Key words: Acetic group; microbial community structure; antibiotic resistance gene; triple wart bull crab

野生和养殖褐菖鲉（*Sebastiscus marmoratus*）表观形态、机体生化组分及游泳代谢能力比较分析

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摘要：基于人工繁育苗种的增殖放流是当前修复海洋渔业资源的重要途径。然而，已有诸多研究表明，人工养殖环境可能会造成养殖群体与其野生同类之间存在明显的生物学特征差异。为了评估人工苗种在自然环境中的生存适应性，提高其野外存活率，有必要对野生和养殖群体之间存在的生物学特征差异开展比较研究。本研究对比分析了野生和养殖褐菖鲉（*Sebastiscus marmoratus*）在表观形态、机体生化组分及游泳代谢能力方面存在的差异。结果表明，野生与养殖褐菖鲉在表观形态上存在显著差异。养殖群体体型较宽（特别是头部和躯干部分）且尾柄较窄。在游泳代谢方面，养殖群体游泳速度较慢，代谢能力较差。在机体生化组成方面，野生群体机体蛋白质含量较高，脂肪含量较低。综上所述，养殖环境会对鱼类的形态特征及行为特征产生显著影响，在人工苗种繁育过程中应对育苗环境或策略做相应改进，以减小野生和养殖群体之间存在的生物学特征差异，确保增殖放流实践的长远健康发展。

关键词：几何形态测量学；爆发游泳速度；临界游泳速度；机体生化组分

Differences in external morphology, body composition and swimming performance between hatchery- and wild-origin marbled rockfish (*Sebastiscus marmoratus*)

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Abstract： Stock enhancement based on hatchery-reared fish has become one of the most common forms of management practices in marine fisheries resource restoration. However, unnatural rearing environments may cause hatchery-reared fish to diverge phenotypically from wild conspecifics, with negative consequences for post-release performance in the natural environments. To better evaluate the suitability of releasing hatchery-reared fish, it is necessary to understand the phenotypic effects of captive rearing, through comparisons with wild conspecifics. In this study, we compared body morphology, swimming performance, and biochemical body composition between hatchery-reared and wild marbled rockfish (*Sebastiscus marmoratus*) from the same general gene pool. The results show that the overall body profile differed significantly between the groups, with hatchery-reared individuals having a deeper body (in particular in the head and trunk regions), narrower caudal peduncles, and higher condition factor, as compared to wild conspecifics. Hatchery-reared marbled rockfish also had relatively shorter fins, for a given size. In terms of swimming performance, the hatchery-reared marbled rockfish performed worse than the wild, with slower burst swimming speeds and poorer endurance. Wild rockfish had higher body protein content but lower lipid levels compared to the hatchery-reared individuals. These results suggest that hatchery rearing conditions have a great impact on the phenotypic development, with possibly high effects on their post-release performance of the hatchery-reared marbled rockfish. Modifications for the hatchery environment and operation should be investigated with an aim to minimize the divergence in phenotypic development for production of more wild-like fish for stocking.

Keywords: morphological variation; geometric morphometrics; burst swimming speed; critical swimming speed; body composition

An assessment of the Atlantic bonito (*Sarda sarda, Bloch 1793*) stock in the Eastern Atlantic Ocean: a case study of the Senegalese Exclusive Economic Zone (SEEZ), using Bayesian State-Space Surplus Production models.

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Abstract： Atlantic bonito, *Sarda sarda* (Bloch, 1793), is a valuable small tuna species for coastal countries and local communities. This species is widely targeted by artisanal fisheries in the Senegalese exclusive economic zone (SEEZ). The common fishing gears used in artisanal fishing to harvest Atlantic bonito are gillnets, purse seines, longlines and sleeping nets. Though the catches of this species have been growing in recent years, little is still known regarding the Atlantic bonito catch per unit effort (CPUE) and the size selectivity in the region. Since this information is important as an input for many stock assessments, the present study used available catches, effort, and size data of Atlantic bonito harvested by different fishing gears for 15 years (2004-2018) to evaluate the nominal and standardized CPUE, size-frequency distribution, and length at retentions (50% and 95% selectivity) of the species. Generalized linear and additive models were used to standardize Atlantic bonito's CPUE using temporal, spatial, and environmental factors. The retention length at 50% and 95% for each year and fishing gear were calculated from the cumulative length frequency distribution as a proxy for selectivity. The optimal model standardization CPUE results presented a significant trend for gillnets values, ranging from 4.6 kg in 2005 to 92.65 kg in 2018. In contrast, sleeping nets showed lower CPUE values, varying from 2.12 kg in 2004 to 0.83 kg in 2018. Using the JABBA and JABBA-Select modeling frameworks, an assessment study was performed to estimate the Atlantic bonito stock status in the Senegalese Exclusive Economic Zone (SEEZ) based on standardized CPUE, size-frequency distribution, and length at retentions (50% and 95% selectivity), important inputs parameters aforementioned. The maximum sustainable yield (MSY) results estimated by JABBA ranged between 4,885 and 6,520 tons. For JABBA-Select, the MSY values ranged between 3,796 to 4,671 tons and 4,179 to 4,434 tons, respectively. The B/BMSY and F/FMSY results for JABBA ranged between 2.01 to 2.14 and 0.47 to 0.33, respectively. The range for B2004/K and B2018/K median values was 0.55 - 0.62 and 0.80 - 0.86, respectively. The estimated B/BMSY and F/FMSY for JABBA-Select ranged from 1.91 to 1.92 and 0.52 to 0.54, respectively, and from 0.76 to 0.69 for B2004/K, and 0.77 to 0.76 for B2018/K. The Kobe phase plots results of the base case scenarios ranged from 75% to 89% probability in the green area, indicating sustainable fishing pressure and a healthy stock size capable of producing high yields close to the MSY. Further, this study stated projections results with a proxy of the TACs for the stock of this species in 12 years. JABBA-Select provides less good performances than JABBA regarding the stock's fishing reference points results.

Keywords: Atlantic bonito; size-frequency; CPUE; GLM; GAM; Selectivity.

Assessment, JABBA, JABBA-Select, MSY, TAC, SEEZ

低磷通过 AMPK/ACC/CPTI 通路介导斑马鱼肝脏脂肪堆积

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摘要：开发低磷饲料可助力水产绿色养殖的发展，但是，低磷易导致鱼体肝脏脂肪异常堆积且具体机制尚不清楚。因此，本试验探究低磷是如何影响鱼类肝脂异常堆积。本试验配制两种不同磷水平的培养基，适宜磷培养基组（OP，磷水平 35mg/L）和低磷培养基组（LP，磷水平 0.7 mg/L）孵育斑马鱼肝细胞。结果表示，与 OP 组相比，LP 组的斑马鱼肝细胞脂沉积显著增加（$P<0.05$）。通过转录组分析发现，相较于 OP 组，LP 组显著提高脂合成（*ACC*，*SCD1*）相关基因的表达，抑制脂肪酸β-氧化（*CPTI*）基因的表达，并且该过程可能是通过 AMPK 信号通路介导的。5-氨基咪唑-4-羧酰胺核糖核苷酸（AIACR，AMPK 激活剂）可以有效的降低 LP 组的脂肪沉积，并且提高 p-AMPK/AMPK 和 p-ACC/ACC 比例以及 CPTI 的蛋白表达量（$P<0.05$）。综上所述，本试验发现低磷可以抑制 AMPK/ACC/CPTI 信号通路进而导致肝脏脂肪堆积。

关键词：磷；AIACR；脂肪堆积；AMPK 信号通路；斑马鱼肝细胞系

Low phosphorus-induced liver lipid deposition via the AMPK/ACC/CPTI in zebrafish

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Abstract: Lower dietary phosphorus supplied in fish matches both economic benefits and environmental sustainability. However, low phosphorus induced hepatic lipid deposition and the molecular mechanisms remain unknown. Therefore, the study was conducted to investigate the effects of low phosphorus on lipid metabolism. In this study, the zebrafish liver cell line (ZFL) was incubated by the optimal phosphorus medium (OP group, phosphorus concentration: 35 mg/L) and the low phosphorus medium (LP group, phosphorus concentration: 0.7 mg/L). Compared with the OP group, lipid accumulation was observed in ZFL from the LP group ($P<0.05$). Combined with the transcriptomics analysis, the lipid synthesis (*ACC*, *SCD1*) was enhanced, and fatty acid β-oxidation (CPTI) was reduced in the LP group. And the process might be mediated via the AMPK signaling pathway. 5-aminoimidazole-4-carboxamide ribonucleoside (AIACR, an AMPK activator) alleviated the lipid accumulation in the LP group compared with the OP group ($P<0.05$). The ratio of p-AMPK/AMPK, p-ACC/ACC, and the protein expression of CPTI were increased in the LP group incubation with AIACR ($P<0.05$). Overall, the findings implied that low phosphorus could increase lipid synthesis and reduce fatty acid β-oxidation to induce lipid deposition in the liver via AMPK/ACC/CPTI pathway.

Keywords: Phosphorus; AIACR; Lipid deposition; AMPK signaling pathway; Zebrafish liver cell line

水产源芽孢杆菌对不同病原菌的拮抗性、抗菌药物的敏感性以及消毒产品的抗性研究

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摘　要：本研究以水产源芽孢杆菌为材料，对其抗菌性、药物敏感性以及消毒产品耐性进行探究，分析探究其应用潜力。牛津杯法分析24株芽孢杆菌对常见6株病原菌(溶藻弧菌*Vibrio alginolyticus* VA1株和VA2株，副溶血弧菌*Vibrio parahaemolyticus* VP、哈维氏弧菌*Vibrio harveyi* VH、嗜水气单胞菌*Aeromonas hydrophila* AH和铜绿假单胞菌*Pseudomonas aeruginosa* PA)的拮抗性；K-B纸片法探究24株芽孢杆菌对6种常用水产药品(多西环素、氟苯尼考、新霉素、环丙沙星、恩诺沙星和复方新诺明)的敏感性等；稀释涂布法分析24株芽孢杆菌对8种常用水产消毒产品(聚维酮碘溶液、戊二醛苯扎溴铵溶液、复合碘溶液、苯扎溴铵溶液、浓戊二醛溶液、过硫酸氢钾、漂白粉和高锰酸钾)的抗性。24株菌株中，贝莱斯芽孢杆菌*Bacillus velezensis* BV1、BV2、BV3对6种致病菌均具有显著的拮抗作用，且拮抗能力的大小依次为BV1＞BV2＞BV3，而其他菌株对常见的水产致病菌则表现出部分或者不明显的拮抗效果。10株芽孢杆菌显示出耐药性，包括BV3，而其余14株菌均显示出新霉素中度敏感性。过硫酸氢钾、漂白粉以及高锰酸钾的常规消毒剂量对大多数的菌株无抑菌影响，但是聚维酮碘、戊二醛苯扎溴铵、复合碘、苯扎溴铵以及浓戊二醛的常规消毒剂量对菌株都有一定的抑菌效果。综合以上3个实验结果，选取BV1作为5种具有抑制效果的消毒产品的定量实验菌株，结果显示，高浓度的消毒产品会严重影响芽孢杆菌的活性，对于贝莱斯芽孢杆菌BV1来说，聚维酮碘、戊二醛和苯扎溴铵和浓戊二醛的消毒浓度不超过2 mg/L；复合碘和苯扎溴铵的消毒浓度不超过1 mg/L。水产源的贝莱斯芽孢杆菌BV1有较强的抗病原菌能力，对抗菌药物敏感，对常见的消毒产品抗性较好，可以作为潜在益生菌株用于后续水产动物饲料益生菌制剂的开发利用。此外，常用消毒产品用于水体泼洒的剂量最好不要超过建议使用剂量，会影响益生菌的活性。

关键词：芽孢杆菌；病原菌；抗菌药物；消毒产品；抗性

Study on the resistance of aqua-product borne *Bacillus* spp. to different pathogenic bacteria, antibacterial drugs and disinfection products

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Abstract： In this study, *Bacillus* spp. from aqua-product borne were used to explore antibacterial properties, drug susceptibility and resistance to disinfection products, and to analyze and explore their application potential. We analyzed the antagonism of 24 *Bacillus* strains from aqua-product borne against 6 common pathogenic bacteria (*Vibrio alginolyticus* VA1 and VA2 strain, *Vibrio parahaemolyticus* VP, *Vibrio harveyi* VH, *Aeromonas hydrophila* AH and *Pseudomonas aeruginosa*) by the Oxford cup method; The sensitivity of these strains to aquatic drugs (Doxycycline, Florfenicol, Neomycin, Ciprofloxacin, Enrofloxacin and Cotrimoxazole) was detected by the K-B paper method; Simultaneously, we used the dilution coating method to investigate the resistance of *Bacillus* strains to disinfection products (Povidone iodine, Glutaraldehyde benzalkonium bromide, Iodine compounds, Benzalkonium bromide, Concentrated glutaraldehyde, Potassium hydrogen persulfate, Bleaching powder, Potassium permanganate). The results showed that *Bacillus velezensis* BV1, BV2, and BV3 had significant antagonistic effects on 6 common aquatic pathogenic bacteria, and the order of antagonistic ability was BV1>BV2>BV3, while other strains showed partial or no obvious antagonistic effect. 10 strains showed neomycin-resistant, including BV3, while the remaining 14 strains showed moderate sensitivity to neomycin. The routine disinfectant doses of potassium hydrogen persulfate, bleaching powder and potassium permanganate had no bacteriostatic effect on the most strains, however, the routine disinfectant doses of povidone iodine, glutaraldehyde benzalkonium bromide, compound iodine, benzalkonium bromide and concentrated glutaraldehyde had a certain bacteriostatic effect on the *Bacillus* strains. Based on the results of the three experiments, BV1 was selected for the quantitative experiments. The results showed that high concentrations of disinfection products would seriously affect the activity of *Bacillus*. The disinfection concentration of povidone iodine, glutaraldehyde and benzalkonium bromide and concentrated glutaraldehyde did not exceed 2 mg/L; the disinfection concentration of iodine compounds and benzalkonium bromide did not exceed 1 mg/L. We found that *Bacillus velezensis* BV1 had strong resistance to pathogenic bacteria, was sensitive to antibacterial drugs, and had good resistance to common disinfection products, and therefore could be used as a potential probiotic strain for aquatic probiotic preparations development and utilization. In addition, the dose of commonly used disinfection products for water splashing should not exceed the recommended dose, which would affect the activity of probiotics.

Keywords: Bacillus; pathogenic bacteria; antibacterial drugs; disinfection products; resistant ability

环境DNA技术研究进展及其在长江流域中的应用前景分析

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摘要：长江流域鱼类资源丰富、生物多样性高，但近年来，受各种因素影响，鱼类资源急剧衰退；环境DNA技术能够更好地恢复其鱼类资源，拯救濒危动物栖息地并推进长江流域绿色健康发展。环境DNA作为一种高效灵敏且成熟的调查工具，技术日益成熟并快速发展；eDNA检测方法的敏感性使其非常适合于检测濒危、低密度入侵、瞬时和隐秘物种的存在，特别是当检测低密度物种的采样工作难以控制时，其敏感性、简单性和减少危害的优势愈加显现出来，该技术已被广泛应用于食品微生物、生物监测、群落生态学、古环境研究、保护生物学和生物入侵学等领域。本文综述了环境DNA定义、发展史、研究方法与优劣势；探究分析环境DNA技术的研究进展及其在长江流域的应用，以此总结分析环境DNA技术应用于长江流域生态监测，鱼类资源调查等，对环境DNA技术应用潜力进行了展望，以此推进长江流域绿色健康发展，恢复鱼类资源，拯救濒危动物栖息地。

关键词：环境DNA；长江流域；应用前景

Research progress of environmental DNA technology and its application in the Yangtze River Basin

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Abstract: The huge advantages of fishery resources and rich biodiversity in the Yangtze River Basin maintain the stable development of the ecosystem. However, due to various factors, the resources decline sharply. In order to better promote the green and healthy development of the Yangtze River Basin, restore the fish resources and save the habitat of endangered animals. With the increasing maturity of environmental DNA technology and the rapid development of biotechnology, as an efficient, sensitive and mature survey tool, Edna detection method is very suitable for detecting the existence of endangered, low-density invasive, transient and secret species, especially when the sampling of low-density species is difficult to control It has been widely used in food microbiology, biological monitoring, community ecology, paleoenvironment research, conservation biology and biological invasion. The definition, development history, research methods, advantages and disadvantages of environmental DNA were summarized; This paper explores the research progress of environmental DNA technology and its application in the Yangtze River Basin, summarizes the application of environmental DNA technology in ecological monitoring and fish resources investigation in the Yangtze River Basin, and prospects the application potential of environmental DNA technology, so as to promote the green and healthy development of the Yangtze River Basin, restore fish resources and save endangered animal habitats, Better promote the ecological protection of the Yangtze River Basin.

Keywords: Environmental DNA; Yangtze River Basin; application analysis

低蛋白饲料中添加β-羟基-β-甲基丁酸对日本囊对虾生长性能、消化能力、TOR 通路及肌肉品质的影响

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摘要：本研究通过开展为期 8 周的养殖试验评估低蛋白饲料中添加β-羟基-β-甲基丁酸（HMB）对日本囊对虾（初始体重：2.00±0.01 g）生长性能和肌肉品质的影响。分别配制蛋白水平为 49%和 44%的饲料作为阳性（HP）和阴性（LP）对照组，同时在 LP 基础上添加 0.025%、0.05%、0.10%、0.20%和 0.40% HMB 配制另外五种饲料（HMB1、HMB2、HMB3、HMB4 和 HMB5）。结果表明与 LP 组相比，HP、HMB3 和 HMB4 组的增重率和特定生长率显著升高，而饲料系数显著降低。同时上述三组对虾肠道胰蛋白酶活性显著高于 LP 组。较高的饲料蛋白水平和 HMB 上调了肌肉中雷帕霉素靶蛋白（*tor*）、核糖体蛋白 S6 激酶（*s6k*）、磷脂酰肌醇 3-激酶（*pi3k*）和丝氨酸/苏氨酸蛋白激酶（*akt*）表达，同时提高了肌肉中大部分游离氨基酸含量。在低蛋白饲料中添加 0.2% HMB 提高了对虾肌肉硬度和持水力，肌肉中总羟脯氨酸和胶原蛋白含量均随饲料 HMB 含量的增加而增加。此外，在低蛋白饲料中添加 0.2% HMB 显著提高了对虾肌纤维密度和肌节长度，降低了肌纤维直径。总之，在低蛋白饲料中添加 0.10%-0.20% HMB 改善了日本囊对虾的生长性能和肌肉品质，这可能与 HMB 提高胰蛋白酶活性，激活 TOR 通路，增加肌肉胶原蛋白含量，降低肌纤维直径，提高肌纤维密度和肌节长度有关。

关键词：β-羟基-β-甲基丁酸；饲料蛋白水平；日本囊对虾；生长性能；TOR；肌肉品质

Dietary β-hydroxy-β-methylbutyrate supplementation affects growth performance, digestion, TOR pathway and muscle quality in kuruma shrimp *Marsupenaeus japonicus* fed a low protein diet

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Abstract： An 8-week feeding trial was carried out to evaluate the effects of dietary β-hydroxy-β-methylbutyrate (HMB) supplementation on growth performance and muscle quality of kuruma shrimp *Marsupenaeus japonicus* (initial weight: 2.00 ± 0.01 g) fed a low protein diet. The positive control diet (HP) with 49% crude protein and negative control diet (LP) with 44% crude protein were formulated. Based on the LP, 0.025%, 0.05%, 0.10%, 0.20% and 0.40% of HMB were supplemented to design the other five diets named as HMB1, HMB2, HMB3, HMB4 and HMB5 respectively. Results showed that compared with the shrimp fed LP, the HP, HMB3 and HMB4 groups had significantly higher weight gain rate and specific growth rate, while significantly lower feed conversion ratio. Meanwhile, the intestinal trypsin activity was significantly elevated in the above three groups than that of the LP group. Higher dietary protein level and HMB inclusion up-regulated the expressions of target of rapamycin (*tor*), ribosomal protein S6 kinase (*s6k*), phosphatidylinositol 3-kinase (*pi3k*) and serine/threonine-protein kinase (*akt*) in shrimp muscle, accompanied by the increases in contents of most muscle free amino acids. Supplementation of 0.2% HMB in a low protein diet improved muscle hardness and water holding capacity of shrimp. The contents of total hydroxyproline and collagen in shrimp muscle both increased with increasing dietary HMB inclusion. Additionally, inclusion of 0.2% HMB in a low protein diet remarkably elevated myofiber density and sarcomere length, while reduced myofiber diameter of shrimp. In conclusion, supplementation of 0.10%-0.20% HMB in a low protein diet improved the growth performance and muscle quality of kuruma shrimp, which may be ascribed to the increased trypsin activity and activated TOR pathway, as well as higher muscle collagen content, reduced myofiber diameter, elevated myofiber density and sarcomere length caused by dietary HMB.

Keywords: β-Hydroxy-β-methylbutyrate; Dietary protein level; *Marsupenaeus japonicas*; Growth performance; TOR; Muscle quality

矛尾复鰕虎鱼浸泡免疫后的黏膜免疫反应研究

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摘要：浸泡免疫依赖于鱼类黏膜相关组织的应答反应，本实验以矛尾复鰕虎鱼为模型研究其浸泡免疫创伤弧菌灭活疫苗后的免疫应答反应。结果显示，血清中特异性抗体滴度逐渐升高并于免疫后的 21 天达到峰值，然而鳃黏液、皮肤黏液和肠黏液中的抗体滴度分别于第 3、5 和 7 天达到峰值。与内脏器官相比，黏膜相关组织（鳃、皮肤和肠）中的抗原摄入显著增加（$P < 0.05$），且皮肤和鳃中的抗原摄入于免疫后的第 12 小时达到峰值，显著高于其他组织（$P < 0.05$）。组织学结果显示，黏膜相关组织中的黏液细胞数量增加，并于第 3 天达到峰值。此外，黏液组分发生变化，从中性黏多糖向酸性黏多糖转变。黏液抗体滴度、黏膜相关组织抗原摄入量、黏液细胞数量变化以及黏液特性变化的综合分析为鱼类的黏膜免疫反应提供参考。该实验结果表明浸泡免疫的优势是激发高水平的局部免疫应答，使得浸泡免疫是激发鱼体免疫系统应对病原感染最理想的接种方式。

关键词：矛尾复鰕虎鱼；浸泡免疫；抗体滴度；抗原摄入；黏液细胞

Study on the mucosal response of javelin goby *Synechogobius hasta* after immersion vaccination

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Abstract: Immersion vaccination is dependent on the response of fish mucosa-associated tissues, and javelin goby *Synechogobius hasta* were immersed with *Vibrio vulnificus* bacterin to investigate mucosal immune responses and humoral responses. The results showed that the specific serum antibody titers gradually increased after vaccination and peaked at day 21, while the mucosal antibody titers in gill, skin and intestine showed a faster response, with the peak time at days 3, 5, and 7, respectively. For antigen uptake, a rapid and significant enhancement was detected in the mucosa-associated tissues (gill, skin and intestine) compared with the blood, spleen, kidney and liver ($P < 0.05$). Antigen uptake levels in the gill and skin both peaked at 12 h post-immersion and were significantly higher than the antigen uptake in other tissues ($P < 0.05$). The histological results showed that the mucous cell numbers in mucosa-associated tissues increased over time, peaked at day 3 post-immunization, and then decreased to the level of the control groups. Additionally, the mucin components in mucosa-associated tissues shifted from neutral mucopolysaccharide to acidic mucopolysaccharide. Integrations of antibody titers, antigen uptake in mucosa-associated tissues, mucous cell number changes and mucin characteristic changes provided valuable information for research on mucosal immunity in fish. All present findings suggest that a major advantage of immersion vaccines is the ability to elicit a high level of local immune response, making immersion vaccines an ideal mode of inoculation that induces protective immunity against a variety of pathogens.

Keywords: *Synechogobius hasta;* Immersion vaccination; Antibody titers; Antigen uptake; Mucous cells

低氧胁迫和复氧对长吻鮠鳃组织低氧应答基因和生理生化指标的影响

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摘 要：为了研究低氧胁迫(0.8±0.1 mg/L)和复氧(7.3±0.5 mg/L)对长吻鮠(*Leiocassis longirostris*)鳃组织氧传感蛋白、呼吸代谢、氧化应激、组织结构、细胞凋亡的影响。本文对长吻鮠进行了低氧胁迫(0h、2h、4h、6h)和复氧(2h、4h、6h)试验，采用 qRT-PCR、酶活性测定、H&E 染色和 TUNEL 切片检测等方法，分析该鱼鳃组织低氧应答基因、生理生化指标的变化。[结果]结果表明：在低氧胁迫下，长吻鮠鳃组织中氧传感蛋白相关基因(*HIF-1α*、*HIF-2α*、*PHDs* 和 *Vhl*)表达量显著升高，复氧后较对照组仍有显著差异(P＜0.05)；糖酵解相关酶(PFK、HK 和 PK)、无氧呼吸酶(LDH)、抗氧化酶(GSH-Px、CAT 和 SOD)和氧化应激指标(MDA 和 LPO)活性和含量显著升高，TCA 循环相关酶(SDH 和 MDH)活性显著降低，复氧后多数指标均逐渐恢复至对照水平；H&E 染色显示低氧胁迫下长吻鮠鳃组织上皮出现了抬升，部分血细胞大量聚集使鳃小片呈棒状尖端，发生线粒体丰富细胞肿胀和增生等组织变化现象，在溶氧恢复后低氧引起的变化并未得到改善；TUNEL 切片结果显示长吻鮠鳃组织凋亡细胞数量随低氧时间延长不断增加，凋亡相关基因(*Bax*、*Caspase 3*、*p53* 和 *Apaf-1*)表达量显著升高，*Bcl-2* 表达量显著降低，恢复溶氧后凋亡现象仍然存在。低氧胁迫和复氧能够显著影响长吻鮠鳃组织氧传感蛋白、呼吸代谢、氧化应激、组织结构、细胞凋亡等，该结果为探究鱼类低氧胁迫下分子调控机制奠定基础，为利用分子技术开展长吻鮠抗低氧新品种选育提供基础数据。

关键词：长吻鮠；低氧；鳃；低氧应答；生理生化

Effects of hypoxic stress and reoxygenation on hypoxic response genes and physiological and biochemical indexes in the gill tissue of *L. longirostris*

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Abstract: In order to study the effects of hypoxic stress (0.8 ± 0.1 mg/L) and reoxygenation (7.3 ± 0.5 mg/L) on gill tissue oxygen-sensing proteins, respiratory metabolism, oxidative stress, tissue structure, cellularity of L. longirostris effects of apoptosis. [Method] In this study, hypoxic stress (0h, 2h, 4h, 6h) and reoxygenation (2h, 4h, 6h) experiments were carried out on the L. longirostris. qRT-PCR, enzyme activity assay, H&E staining and TUNEL slice detection and other methods were used to analyze the changes of hypoxia response genes and physiological and biochemical indicators in the gill tissue of the fish. [Result]The results showed that: Under hypoxic stress, the expression levels of oxygen-sensing protein-related genes (HIF1α, HIF2α, PHD1, PHD2, PHD3 and Vhl) in the gill tissue of L. longirostris were significantly increased. After reoxygenation, there was still significant difference compared with the control group ($P<0.05$). The activities and contents of glycolysis-related enzymes (PFK, HK and PK), anaerobic respiration enzymes (LDH), antioxidant enzymes (GSH-Px, CAT and SOD) and oxidative stress indicators (MDA and LPO) were significantly increased, the activities of

TCA cycle-related enzymes (SDH and MDH) decreased significantly, and most indexes gradually recovered to control levels after reoxygenation. H&E staining showed that under hypoxia stress, the epithelium of the gill tissue was uplifted, and some blood cells gathered in large numbers to make the gill small pieces have rod-like tips, and tissue changes such as swelling and proliferation of mitochondria-rich cells occurred. After the recovery of dissolved oxygen, hypoxia-induced Gill tissue changes are not improved. The results of TUNEL sections showed that the number of apoptotic cells in the gill tissue of L. longirostris scorpion increased with the prolongation of hypoxia time, the expression of apoptosis-related genes (Bax, Caspase 3, p53 and Apaf-1) was significantly increased, and the expression of Bcl-2 was significantly decreased, the apoptosis phenomenon still exists after the recovery of dissolved oxygen. [Conclusion]Hypoxic stress and reoxygenation can significantly affect the tissue oxygen sensor proteins, respiratory metabolism, oxidative stress, tissue structure, and apoptosis of the gills. To provide a scientific basis for the selection and breeding of new hypoxia-resistant varieties of *L. longirostris* beetle using molecular technology.

Key words: *L. longirostris*; hypoxia stress; gill tissue; hypoxic response gene; physiological and biochemical indicators

三角帆蚌谷胱甘肽硫转移酶 P1 基因克隆表达及对类胡萝卜素代谢的影响分析

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摘要：类胡萝卜素是重要的天然色素，已有研究发现类胡萝卜素代谢与贝壳颜色显著相关，谷胱甘肽硫转移酶 P1 是一种类胡萝卜素结合蛋白，在类胡萝卜素转运中发挥重要功能。为明确三角帆蚌 *HcGSTP1* 基因在类胡萝卜素代谢中的功能，并探究该基因与三角帆蚌贝壳呈色的相关性，本实验克隆并鉴定了三角帆蚌 *HcGSTP1* 基因 cDNA 全长 1318bp，其中 ORF 区 618bp，编码 205 个氨基酸，包含一个 GST-N-pi 结构域和 GST-C-Pi 结构域。通过对白色、紫色三角帆蚌组织表达发现，除闭壳肌外，*HcGSTP1* 基因在紫色蚌各组织中的表达量均显著高于白色蚌（$P<0.05$）。原位杂交结果显示在外套膜的外褶、背膜区、腹膜区，外褶与中褶连接处以及部分中褶均出现该基因明显阳性信号。注射 dsRNA 干扰链后，*HcGSTP1* 基因在外套膜中的表达显著降低，干扰率达 83.74%，同时发现外套膜中 TCC 降低 30.12%（$P<0.05$）。研究结果表明 *HcGSTP1* 基因对三角帆蚌类胡萝卜素的代谢有着重要的作用，为深入研究三角帆蚌类胡萝卜素代谢与贝壳和珍珠颜色形成机制提供了理论基础。

关键词：三角帆蚌；*GSTP1* 基因；类胡萝卜素代谢

Cloning and expression of glutathione sulfur transferase P1 gene in *Hyriopsis cumingii* and its effect on carotenoid metabolism

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Abstract: Carotenoids are important natural pigments. Previous studies have found that carotenoid metabolism is significantly correlated with shell color. Glutathione sulfur transferase P1, a carotenoid binding protein, plays an important role in carotenoid transport. In order to clarify the function of *HcGSTP1* gene in carotenoid metabolism and explore the correlation between this gene and shell color, the total length of hyriopsis cumingii *HcGSTP1* cDNA was cloned and identified, including 618bp ORF region, encoding 205 amino acids. It contains a GST-N-pi domain and a GST-C-Pi domain. The expression of *HcGSTP1* gene in tissues of white and purple mussels was significantly higher than that in tissues of white mussels($P<0.05$). In situ hybridization showed obvious positive signals of the gene in the outer fold, dorsal membrane region, peritoneal region, the junction between outer fold and middle fold, and part of middle fold of the mantle. After dsRNA interference chain injection, the expression of *HcGSTP1* gene in the mantle significantly decreased, the interference rate reached 83.74%, and the TCC in the mantle decreased by 30.12% ($P<0.05$). Our results indicate that *HcGSTP1* gene plays an important role in carotenoid metabolism in *H. cumingii*, which provides a theoretical basis for further study of carotenoid metabolism and the mechanism of shell and pearl color formation in *H. cumingii*.

Key words: Hyriopsis cumingii; GSTP1 gene; Carotenoid metabolism

非法捕捞生态损害补偿的量化及其影响因素

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摘要：本研究选取了中国江苏省近十年来规模最大的非法捕捞案件作为研究对象，来验证不同假设下的量化结果的差异。在本研究中，我们假设非法捕捞渔获全部由鳀鱼组成，计算结果表明不同因素的引入使量化结果发生了显著变化，损害的量化范围为 2.74×10^7~8.73×10^9 元。除经济因素和生态因素外，社会因素也是在量化非法捕捞所造成的海洋生态破坏的过程中必须要纳入考量的因素。本研究建议拟定修正系数，对非法捕捞所造成的生态损害的定量结果进行调整，以平衡生态修复的效果与责任方的实际支付能力。这一修正系数是非法捕捞的社会影响的综合反映，包括非法捕捞的持续时长和频次、渔获量的多少、以及涉案海域的功能分区等，用以差异化不同程度的非法捕捞所造成损害的定量结果。

关键词：海洋生态损害补偿；非法捕捞；海州湾；多物种放流；社会因素

Quantification of ecological damage from illegal fishing: more than economic and ecological factors

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Abstract：In recent years, the research on compensation for marine ecological damage has made great progress in China, but the research on illegal fishing as a source of damage lags behind the whole, and cannot match the huge number of illegal fishing cases. In this study, we selected a typical case from Jiangsu Province, China, which was the largest illegal fishing case in a decade. We hypothesized that illegal catches are composed entirely of anchovy Engraulis japonicus to verify the quantification results under different scenarios. The results show that the introduction of different factors significantly changes the quantification results, and the value of damage quantified ranged from 2.74×10^7 to 8.73×10^9 yuan. A quantitative method based on market value is the most convenient, but it overemphasizes the utilization value of Marine organisms to human beings and ignores the ecological value of species, and resulted in the lowest value of 2.74×10^7 yuan. An approach based on ecological restoration costs seems more reasonable, but the introduction of different ecological factors radiatively changes the final results, ranged from 7.99×10^7 to 8.73×10^9 yuan, which means that special attention should be paid to the selection of different ecological factors in the actual quantification process. Multi-species release was a resource reconstruction measure in line with Marine biodiversity, and the price and proportion of different species affect the final cost. But whether potential losses from illegal fishing need to be included in the calculations is debatable. Social factors are also necessary for the quantification of Marine ecological damage, although they are illusory compared to the first two factors. It is suggested to formulate a correction coefficient to adjust the quantitative results to balance the effect of ecological restoration with the ability of the responsible party to pay. The correction factor reflects the social impact of illegal fishing, including the duration and frequency of violations, the amount of the catch, and the functional zoning of the sea, and differentiates the quantitative results of illegal fishing with different levels of severity.

Key words: Compensation of marine ecological damage; illegal fishing; Haizhou Bay; multi-species release; social factors

应用循环水装置批量化离体孵化红螯螯虾胚胎

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摘要：为解决红螯螯虾胚胎批量化离体孵化的瓶颈，我们运用循环水装置进行研究，结果表明：1. 选择胚胎发育至复眼色素形成期或 7 对附肢期时进行离体孵化的效果较好，孵化率与出苗率较高；2.每个孵化盒内放入 300 粒胚胎的孵化率显著高于 700 粒胚胎；每个孵化盒内放入 300 或 500 粒胚胎的出苗率显著高于 700 粒胚胎；3. 在孵化盒内插入细海绵条，可以显著提高出苗率；4. 孵化盒上端宽为 2.5cm 或 3cm 的组的出苗率显著高于 4cm 的组；5.选取 7 对附肢期或复眼色素形成期胚胎，以 300-500 粒/盒的密度放入孵化盒内，并将孵化盒（上端宽为 2.5cm）放入孵化装置进行孵化，孵化后将各组的孵化盒插入细海绵条，共培育 SPF 幼虾 240031 尾，孵化率为（85.34±4.56）%，出苗率为（61.31±9.58）%。

关键词：红螯螯虾；离体孵化；胚胎；技术优化

Mass artificial incubation of redclaw crayfish eggs in a recirculating mechanical pulling device

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Abstract：To solve the problems involved in the mass artificial incubation of redclaw crayfish eggs. The results were obtained: 1) the hatching rates or survival rates of the groups with 7 pairs of appendages and well-formed eye pigments were significantly higher; 2) the hatching rates of eggs incubated at densities of 300 eggs/incubator box were significantly higher. The survival rates of eggs incubated at densities of 300 or 500 eggs/incubator box were significantly higher; 3) the survival rates of the group whose incubator received a sponge attachment were significantly higher than those of the group without a sponge; 4) the survival rates of the group with 2.5 or 3 cm width of the upper end of boxes were significantly higher than those of the group with 4 cm; and 5) the eggs with 7 pairs of appendages or well-formed eye pigments were selected, with a density of 300-500 eggs/incubator box, and the box was 2.5-cm wide, and a total of 240,031 specific pathogen-free seedlings were cultivated.

牡蛎壳粉对养殖海水水体净化作用的研究

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摘 要：我国的渔业生产迅速的发展，引发水域生态环境除工业污染外，渔业的自身污染也有明显的增加趋势，养殖鱼类和水生动物病害频繁发生，解决养殖海水水体环境尤为重要。本研究将天然牡蛎壳加工成牡蛎壳粉，分别设定不同的牡蛎壳粉粒径大小、添加量、吸附时间，探究牡蛎壳粉对养殖海水中氨氮，总磷，硝酸盐，亚硝酸盐四项指标的吸附效率，并通过连续流动分析仪检测分析。实验结果表明牡蛎壳粉对水样中的四项指标有一定的吸附作用，粒径较小的牡蛎壳粉对污染水体有较好的吸附效率和吸附容量。为海水养殖水环境净化提供相应的参考。

关键词：牡蛎壳粉；粒径大小；吸附效率；水体净化

Study on the purification effect of oyster shell powder on aquaculture seawater

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Abstract: The rapid development of fishery production in my country has led to an obvious increase in the water environment in addition to industrial pollution, as well as the self-pollution of fisheries. The diseases of farmed fish and aquatic animals frequently occur, and it is particularly important to solve the water environment of aquaculture seawater. In this study, natural oyster shells were processed into oyster shell powder, and the particle size, addition amount, and adsorption time of oyster shell powder were respectively set to explore the effects of oyster shell powderon ammonia nitrogen, total phosphorus, nitrate, and nitrite in cultured seawater. The adsorption efficiency of the item index was detected and analyzed by a continuous flow analyzer. The experimental results show that the oyster shell powder has a certain adsorption effect on the four indicators in the water sample, and the oyster shell powder with smaller particle size has better adsorption efficiency and adsorption capacity for polluted water. Provide corresponding reference for the purification of marine aquaculture water environment.

Key words: oyster shell powder; particle size; adsorption efficiency; water purification

关于红螯螯虾雌雄性腺发育的转录组分析

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摘　要：红螯螯虾（*Cherax quadricarinatus*）俗称四脊滑螯虾、澳大利亚淡水龙虾、淡水小龙虾等，隶属于十足目、拟螯虾科、滑螯虾属，具有体型大、产量高、生长速度快、肉质细腻、抗压能力强等优点，具有广阔的养殖前景与良好的经济价值。同时，红螯螯虾雄虾的生长性能与外观均优于雌虾。为了对红螯螯虾性腺发育进行进一步了解。本实验采用illumina高通量测序技术，共得到50368条基因，其中25377条基因至少被一个数据库注释成功。根据转录组分析结果显示共有15206个差异基因其中包含9256个上调基因与5950个下调基因。其中包含三种热休克蛋白HSPA4、HSPA8、HSP90AA1，同样还有CREB3，这几个基因参与了精子的发生，进而可能促进了性腺的发育。

关键词：红螯螯虾；性腺；精子；转录组

Transcriptome analysis of male and female gonadal development in Cherax quadricarinatus

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Abstract: *Cherax quadricarinatus*, commonly known as four-spined crayfish, Australian freshwater lobster and freshwater crayfish, belongs to Decapoda, family Cheliceridae and genus Cheliceridae. It has the advantages of large body size, high yield, fast growth rate, fine meat quality and strong stress resistance, and has broad breeding prospects and good economic value. The growth performance and appearance of male crayfish were better than those of female crayfish. In order to further understand the gonadal development of red crayfish. In this study, a total of 50368 genes were obtained by Illumina high-throughput sequencing technology, of which 25377 genes were annotated successfully by at least one database. According to transcriptome analysis, there were 15206 differentially expressed genes, including 9256 up-regulated genes and 5950 down-regulated genes. These genes include three HSPA4, HSPA8, HSP90AA1, and CREB3, which are involved in spermatogenesis and may promote gonadal development

Keywords: Cherax quadricarinatus; gonad; sperm;transcriptome

青海湖裸鲤自主摄食节律与生长特性研究

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摘要：为了探究盐碱环境下鱼类自主摄食和生长特性，为耐盐碱鱼类增殖保护和盐碱水养殖提供基础数据，本文以青海湖裸鲤(*Gymnocypris przewalski*)为代表，研究其在盐碱水环境下的自主摄食节律，设置光暗交替和全暗环境处理组。结果表明湖水(盐度 15，碳酸盐碱度 28 mmol/L)和淡水环境中，青海湖裸鲤在自然光周期下均存在明显的日摄食节律，白昼摄食量最高，黎明和夜间的摄食量较低，判定其为白昼摄食类型鱼类。而在全暗环境下，青海湖裸鲤摄食的节律性减弱，各时段摄食量较为接近。经 63d 的自主摄食养殖，湖水组裸鲤在高盐碱环境下，其体长增长率、体质量增长率和特定生长率均分别显著低于淡水组裸鲤，表明生长受到抑制。湖水组和淡水组裸鲤的体长-体质量关系参数 b 均小于 3，表明青海湖裸鲤为负异速生长鱼类，其中湖水组 b 值小于淡水组，即湖水组体质量增长速率低于淡水组，一定程度上说明高盐碱环境导致青海湖裸鲤的生长特性发生变化。本试验通过探寻青海湖裸鲤在青海湖水环境以及淡水人工养殖中的摄食节律及生长规律，为青海湖裸鲤人工增殖投喂策略的制定提供理论依据，同时为盐碱生境鱼类的摄食习性研究提供基础数据。

关键词：盐碱环境；青海湖裸鲤；自主摄食节律；生长特性

Self feeding rhythm and growth characteristics of Gymnocypris przewalskii

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Abstract: In order to explore the characteristics of growth and self feeding of fish in saline-alkaline environment and provide basic data for the saline-alkaline aquaculture, naked carp (Gymnocypris przewalski) was taken as a representative in this paper to study its self feeding rhythm in saline-alkaline environment. Light-dark cycle group and continuous darkness group were set up. The results showed that naked carp had obvious daily feeding rhythm during natural photoperiod in fresh water and lake water. The food intake during the daytime was the highest, and the food intake at dawn and night were low. So naked carp was judged to be the type of daytime feeding. Whereas, in the continuous dark environment, the feeding rhythm of naked carp was weakened, and the food intake of each period was relatively close. After 63 days of self-feeding culture, the growth rate of body length, body mass and specific growth rate of naked carp in the lake water group were significantly lower than those in the fresh water group, indicating that the growth of naked carp was inhibited under high salinity and carbonate alkalinity environment. The body length-weight relationship parameter b of the naked carp in both the lake water group and the fresh water group was less than 3, which showed that the naked carp was a negative allometric growth fish. The b value of the lake water group was lower than that of the fresh water group, that is, the growth rate of body mass in the lake water group was lower than that in the fresh water group at the same growth rate of body length. To some extent, the change of the growth characteristics of naked carp is caused by the high salinity and alkalinity environment. This study explored the self-feeding rhythm and growth characteristics of naked carp in saline-alkaline Qinghai Lake and fresh water environment, which provided a theoretical basis for the formulation of artificial feeding strategy of naked carp, and provided basic data for the study of feeding habits of fish in saline-alkaline habitats.

Key words: Saline-alkaline environment; Gymnocypris przewalskii; Self-feeding rhythm; Growth performance

保存温度对生物絮团硝化性能和形态结构的影响

姜泽建

摘要：为探究生物絮团适宜的保存温度，将絮团在常温(25℃)、冷藏(4°C)和冷冻(-20°C)条件下分别密封保存了7、14、21和28天。结果发现，随着保存时间的延长，絮团的硝化性能在3种保存条件下较初始硝化性能均有不同程度的下降。在第28天，4 ℃保存条件下的絮团氨氧化速率为(0.16±0.10) mg /(L ·h)，显著高于25℃条件下的(0.08±0.09) mg /(L ·h)和-20 ℃条件下的(0.01±0.09) mg /(L ·h)，其中，-20℃保存条件下的絮团在第7天几乎丧失氨氧化活性，较初始氨氧化速率下降了99.52%。在第28 d，4 ℃保存条件的絮团亚硝氮氧化速率为(0.19±0.03) mg /(L ·h)，显著高于25℃保存条件下的(0.10±0.05) mg /(L ·h)和-20℃保存条件下的(0.14±0.02) mg /(L ·h)。显微观察的结果表明，25 ℃保存条件下絮团结构松散，絮团的体积平均粒径由初始的(245.92±21.51) µm减小到第28 d的(148.50±9.90) µm；在-20 ℃保存条件下，絮团的体积平均粒径由(245.92±21.51) µm增大到(310.82±29.67) µm；4℃保存条件下，絮团的形态结构和粒径均未受到显著变化。综上，4 ℃的保存条件可作为生物絮团的保存温度。

关键词：生物絮团；硝化性能；保存；温度

Effect of preservation temperature on the nitrification performance and morphological structure of bioflocs

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Abstract: To investigate the appropriate storage temperature for bioflocs, bioflocs were stored at room temperature (25°C), refrigerated (4°C) and frozen (-20°C) for7, 14, 21 and 28 d. The results showed that the nitrification performance of bioflocs decreased to different degrees compared with the initial nitrification performance under the three storage conditions with increasing storage time. At 28 d, the ammonia oxidation rate of the bioflocs at 4°C was (0.16±0.10) mg /(L ·h), which was significantly higher than that of (0.08±0.09) mg /(L ·h)at 25°C and (0.01±0.09) mg /(L ·h) at -20°C, with the bioflocs at -20 ℃ almost losing their ammonia oxidation activity at 7 d. The bioflocs stored at -20°C almost lost their ammonia oxidation activity at day 7, with a 99.52% decrease from the initial ammonia oxidation rate. At 28 d, the rate of nitrite oxidation for flocs stored at 4°C was (0.19±0.03) mg /(L ·h), which was significantly higher than that of (0.10±0.05) mg /(L ·h) for bioflocs stored at 25°C and (0.14±0.02) mg /(L ·h) for bioflocs stored at -20°C. The results of microscopic observation showed that the bioflocs were loosened under the storage condition at 25°C, and the volume average size of the bioflocs decreased from (245.92±21.51) µm at the beginning to (148.50±9.90) µm at the 28th day; under the storage condition at -20°C, the volume average size of the bioflocs increased from (245.92±21.51) µm to (310.82±29.67) µm;The morphological structure and particle size of the bioflocs did not change significantly under the storage condition at 4°C. In conclusion, the storage temperature of 4 ℃ can be used as the storage temperature for bioflocs.

Keywords: bioflocs; nitrification performance; preservation; temperature

脊尾白虾单日周期内肠道细菌群落、消化酶和免疫酶活性的比较分析

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摘要：生命活动以 24 小时左右为周期的变动称节律。昼夜节律对生物代谢、消化及免疫等生理活动有着非常重要的影响，但是对甲壳动物的节律研究很少。为了进一步研究甲壳类动物昼夜节律的生理机制。本研究对脊尾白虾的消化酶活性、免疫酶活性及肠道细菌群落的昼夜节律进行研究。结果表明脊尾白虾消化酶、免疫酶活性在一天的四个时间点有显著变化，在 24：00 出现最高值，在 12：00 出现最低值；肠道微生物群的结构、物种多样性及功能各不相同 24:00 的肠道微生物多样性最高，12:00 最低。24:00 肠道微生物丰度最高的是 Candidatus_Hepatoplasma，12:00 丰度最高的菌是 Marinomonas。本研究提高了对脊尾白虾消化酶活性、免疫酶活性以及肠道细菌群落结构昼夜节律的认识。对优化饲养时间，提高脊尾白虾的消化率和养分利用有重大作用。研究结果为进一步研究甲壳类动物肠道菌群日变化的生理机制提供了基础。

关键词：昼夜节律；消化酶活性；免疫酶活性；肠道细菌群落

Comparative analysis of gut bacterial community， digestive, and immune enzyme activity during a single day cycle in Exopalaemon carinicauda

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Abstract： Circadian rhythm has a very important influence on physiological activities such as biological metabolism, digestion, and immunity. In order to further study the physiological mechanism of the circadian rhythm of crustaceans. In this study, the activities of digestive enzymes and immune enzymes and the circadian rhythm of the intestinal bacterial community were studied. The results showed that the digestive enzyme activity, immune enzyme activity, intestinal microbial community structure, species diversity, and function of Exopalaemon carinicauda changed significantly at four-time points of the day, with the highest value at 24: 00 and the lowest value at 12: 00. This study improved the understanding of digestive enzyme activity, immune enzyme activity and circadian rhythm of intestinal bacterial community structure in Exopalaemon carinicauda. It plays an important role in optimizing feeding time and improving the digestibility and nutrient utilization of white shrimp.

Key words: Circadian Rhythm; Digestive Enzyme Activity; Immune Enzyme Activity; Intestinal Bacterial Community

日本沼虾(*Macrobrachium nipponense*)两种I型 Crustin 的鉴定及其免疫功能分析

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摘要： Crustins 作为一类阳离子抗菌肽，可以分为 I-Ⅴ五种类型，它们都在甲壳动物的先天免疫中发挥着重要作用。本研究从日本沼虾（*Macrobrachium nipponense*）中克隆出了两种 *Crustin* 基因（*MnCrustin1* 和 *MnCrustin2* 基因）的互补 DNA（cDNA）全长序列，并利用原核表达技术，体外和体内抗菌试验和 RNA 干扰（RNAi）技术研究了 MnCrustin1 和 MnCrustin2 的免疫功能。序列分析表明 *MnCrustin1* 基因的全长 cDNA 序列有 715 个碱基对（bp），包含一个 351 bp 的开放阅读框（ORF），编码 117 个氨基酸（aa）。*MnCrustin2* 基因的全长 cDNA 序列为 881 bp，ORF 区为 330 bp，编码 110 个 aa。在 MnCrustin1 和 MnCrustin2 的信号肽和乳清酸性蛋白（Whey acidic protein，WAP）结构域之间都有一个富含半胱氨酸（Cys）的区域。系统发育和多序列比对分析表明 MnCrustin1 和 MnCrustin2 属于 I 型 Crustin 家族。基因表达分析表明 *MnCrustin1* 和 *MnCrustin2* 基因的转录本广泛存在于日本沼虾的各组织中，其中在血细胞和鳃中最丰富。重组 *MnCrustin1* 和 *MnCrustin2* 蛋白的体外抗菌活性试验表明，这两种重组蛋白均对三种革兰氏阳性菌（枯草芽孢杆菌 *Bacillus subtilis*、溶壁微球菌 *Micrococcus lysodeikticus* 和金黄色葡萄球菌 *Staphylococcus aureus*）和三种革兰氏阴性菌（副溶血弧菌 *Vibrio parahaemolyticus*、嗜水气单胞菌 *Aeromonas hydrophila* 和大肠杆菌 *Escherichia col*i）的生长具有一定的抑制作用。体内抗菌和抗病毒活性试验表明，在日本沼虾感染嗜水气单胞菌和白斑综合征病毒（White spot syndrome virus，WSSV）后，*MnCrustin1* 和 *MnCrustin2* 基因在其肝胰腺、血细胞和鳃中的表达水平显著升高。RNAi 实验表明，*MnCrustin1* 和 *MnCrustin2* 基因被沉默的日本沼虾感染嗜水气单胞菌或 WSSV 后，其死亡率显著升高。以上研究结果证明 *MnCrustin1* 和 *MnCrustin2* 在日本沼虾抗细菌和病毒感染的免疫反应中起重要作用。

关键词：日本沼虾；Crustin；基因表达；RNA 干扰；免疫反应

Characterization and immune functional analysis of two type I crustin in the oriental river prawn *Macrobrachium nipponense*

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Abstract： Crustins, as cationic antimicrobial peptides, categorized into five types and play important roles in innate immunity of crustaceans. In this study, full-length cDNA sequences of two kinds of crustin genes were cloned from *Macrobrachium nipponense*, which were referred to as MnCrustin1 and MnCrustin2, respectively. The full-length cDNA of MnCrustin1 is 715 bp and contains a 351 bp open reading frame (ORF) encoding 117 amino acids. The full-length cDNA of MnCrustin2 is 881 bp, with a 330 bp ORF encoding 110 amino acids. There is a Cys-rich region between the signal peptide and WAP domain in both MnCrustin1 and MnCrustin2. The phylogenetic analysis and multiple sequence alignment indicated that MnCrustin1 and MnCrustin2 belong to the type I family. The transcripts of MnCrustin1 and MnCrustin2 were widely present in various tissues of M. nipponense, and the highest expression levels were found in hemocytes and gill. In vitro antimicrobial activity test of recombinant MnCrustin1 and MnCrustin2 showed that these two recombinant proteins all have certain resistance to the growth of three Gram-positive bacteria (*Bacillus subtili*s, *Micrococcus* *lysodeikticus* and Staphylococcus aureus) and three Gram-negative bacteria (Vibrio parahaemolyticus, *Aeromonas hydrophila* and *E. coli*). After A. hydrophila and white spot syndrome virus (WSSV) infection in vivo, *MnCrustin1* and *MnCrustin2* expression levels were significantly induced in hepatopancreas, hemocytes and gill of M. nipponense. RNA interference was employed to further study the roles of MnCrustin1 and MnCrustin2 in pathogen infection. The results showed that the silenced MnCrustin1 and MnCrustin2 accelerated the mortality rate of *M*. nipponense after challenged by *A. hydrophila* or WSSV. These results suggested that MnCrustin1 and MnCrustin2 play an important role in bacterial and viral infection in the immune response of *M. nipponense*.

Key words: *Macrobrachium nipponense*; Crustin; Gene expression; RNA interference; Immune respons

三丁基氯化锡对鲮鱼（*Liza haematocheila*）急性暴露的毒性：生物积累、抗氧化防御、组织学和转录组学分析

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摘要：鲮鱼面临着各种人为来源化学污染物的威胁，包括三丁基锡氯化锡(TBTC)。然而，TBTC 对鲮鱼的毒性机制尚不清楚。本研究设计了鲮鱼暴露于不同剂量(0、10%、20%和 50% LC50-96h) TBTC 中 96 小时的毒理学实验。结果显示，TBTC 在肝脏中生物累积性较高，发育状况有所改变。超氧化物歧化酶、过氧化氢酶和谷胱甘肽过氧化物酶的活性下降，同时丙二醛水平增加。TBTC 暴露导致活性氧大量产生，血清中血细胞总数减少，肝脏发生凋亡，表明在 TBTC 暴露引起了氧化应激。组织学结果显示，肝脏发生血管破裂、炎性细胞浸润以及肝细胞的空泡变性，鳃发生了肿胀、鳃丝融合甚至解体等现象。转录组结果表明，高剂量 TBTC 引起了 Jak-STAT 和脂肪细胞因子信号通路中细胞因子和脂肪细胞因子介导的能量紊乱、凋亡和脂肪生成受限。

关键词：脂质合成；凋亡；能量紊乱；TBTC

Toxicity of tributyltin chloride on haarder (*Liza haematocheila*) after its acute exposure: bioaccumulation, antioxidant defense, histological, and transcriptional analyses

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Abstract： Liza haematocheila is exposed to various chemical contaminants, including tributyltin chloride (TBTC). Yet the toxicity mechanism of TBTC on haarder remains unclear. In this study, haarder was exposed to different doses of TBTC. The results revealed its high bioaccumulation in the livers and significant alteration for development. The activities of SOD, CAT, and GPx decreased, accompanied by an increased MDA level. TBTC exposure caused the intense production of ROS, a reduction in total blood cell count, and apoptosis-related alterations, indicating that enhanced oxidative stress occurred after TBTC exposure. Histological results revealed angiorrhexis and infiltration of inflammatory cells, vacuolar degeneration of hepatocytes in livers, and swelling, fusion, and disintegration of gill organs. Transcriptional profiles indicated that high doses of TBTC caused energy disorder, apoptosis, and adipogenesis restriction mediated by cytokines in Jak-STAT and adipocytokine signaling pathways.

Key words: adipogenesis; apoptosis; energy disorder; TB

CXCL12-CXCR4 轴通过 PI3K/AKT 信号通路促进硬骨鱼 B 细胞的趋化和吞噬

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摘要：趋化因子在调节免疫细胞迁移和发育中发挥重要作用。CXCL12-CXCR4 轴在哺乳动物中已开展广泛研究，然而其在硬骨鱼中的调节机制仍不清楚。在本研究中，我们以尼罗罗非鱼(*Oreochromis niloticus*)作为硬骨鱼模型来开展 CXCL12-CXCR4 轴通过 PI3K/AKT 信号通路调控白细胞和 IgM+ B 细胞趋化和吞噬的研究。结果表明，CXCL12-CXCR4 轴参与调控白细胞的趋化活性（尤其是对 IgM^+ B 细胞具有较强的趋化活性），并促进 IgM^+ B 细胞的吞噬作用。同时，我们发现进化上保守的 PI3K/AKT 信号通路参与了罗非鱼感染无乳链球菌的免疫反应。用特异性抑制剂阻断 CXCR4 和 PI3K/AKT 信号通路可阻断病原体感染后白细胞和 IgM^+ B 细胞趋化进入外周血。此外，这些抑制剂显著抑制了相关蛋白的表达和磷酸化水平，以及体外 IgM^+ B 细胞的趋化活性和吞噬作用。总之，本研究在罗非鱼中阐述了 CXCL12-CXCR4 轴通过 PI3K/AKT 信号通路对 IgM^+ B 细胞的调节机制，并揭示了 B 细胞 CXCL12-CXCR4 轴的功能在哺乳动物和硬骨鱼中可能是保守的。

关键词：尼罗罗非鱼；CXCL12-CXCR4 轴；PI3K/AKT 信号通路；IgM^+ B 细胞

CXCL12-CXCR4 axis promotes the chemotaxis and phagocytosis of B cells via PI3K/AKT signaling pathway in a teleost fish

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Abstract： Abstract: Chemokines play important roles in regulating immune cell migration and development. CXCL12-CXCR4 axis has been extensively studied in mammals; however, its regulatory mechanism remains unclear in teleost fish. In the current study, we took Nile tilapia (Oreochromis niloticus) as a teleost model to investigate the mediation of the CXCL12-CXCR4 axis, which was performed in leukocytes and IgM^+ B cells and focused on the PI3K/AKT signaling pathway. The results demonstrated that the CXCL12-CXCR4 axis exhibited chemotactic activity on leukocytes (especially strong chemotactic activity on IgM+ B cells) and promoted phagocytosis of IgM^+ B cells. We discovered that the evolutionarily conserved PI3K/AKT signaling pathway was involved in the immune response during Streptococcus agalactiae infection in tilapia. Blockade of CXCR4 and the PI3K/AKT signaling pathway with specific inhibitors prevented the chemotaxis of lymphocytes and IgM+ B cells into the peripheral blood after pathogen infection. Moreover, the inhibitors severely impaired the expression and phosphorylation levels of the related proteins, as well as the chemotaxis and phagocytosis of IgM^+ B cells in vitro. Together, our study revealed the regulatory mechanismof the CXCL12-CXCR4 axis on IgM^+ B cells via the PI3K/AKT signaling pathway in tilapia, implying that the functions of the CXCL12-CXCR4 axis in B cells may be conserved between mammals and teleost fish.

Key words: Nile tilapia; CXCL12-CXCR4 axis; PI3K/AKT signaling pathway; IgM^+ B ce

高碳水化合物日粮导致大口黑鲈幼鱼代谢物转化、损害肝脏健康状况

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摘要：本研究旨在探讨饲料中三种不同碳水化合物水平对大口黑鲈幼鱼代谢的影响，用含 3 种碳水化合物水平 9.66%（L）、14.32% (M)和 19.11%（H）的等氮、等能饲料饲喂大口黑鲈幼鱼(初始体重 4.0 ± 0.2g)8 周。结果表明，在 H 组中大口黑鲈体重增长最小（15.75 ± 0.76g）。饲喂高碳水化合物饲料（HCD）会进一步导致血浆中丙酮酸（PA）、乳酸（LD）、甘油三酯（TG）和游离脂肪酸（NEFA）水平升高。此外，HCD 促进了大口黑鲈肝脏空泡化、糖原颗粒和脂质的积累。肝脏糖酵解相关酶(如己糖激酶、丙酮酸激酶和乳酸脱氢酶)的活性在不同处理之间没有显著差异（$P > 0.05$）。HCD 导致肝脏磷酸烯醇式丙酮酸羧激酶(PEPCK)和脂肪酶（LPS）活性增强，肝脏糖原和甘油三酯（TG）水平升高。此外，葡萄糖和脂质代谢相关基因如糖原磷酸化酶（PYG）和肉碱棕榈酰转移酶（CPT1，CPT2）的表达随着碳水化合物水平的增加而上调。HCD 组大口黑鲈肝脏过氧化氢酶（CAT）和谷胱甘肽过氧化物酶（GSH-PX）活性降低，总抗氧化能力（T-AOC）降低。UPLC-MS 代谢组学也进一步揭示了糖代谢、脂代谢和抗氧化防御系统受日粮中碳水化合物水平的影响。差异代谢物也在诸如半乳糖代谢、果糖和甘露糖代谢、不饱和脂肪酸生物合成、初级胆汁酸生物合成、胆固醇-丁酸盐代谢、谷胱甘肽代谢、丝氨酸和苏氨酸代谢途径中显著富集。

关键词：大口黑鲈；碳水化合物水平；代谢产物；新陈代谢；机体健康

High-carbohydrate diet altered conversion of metabolites, and deteriorated health in juvenile largemouth bass

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Abstract: To explore the effects of dietary carbohydrate level on nutrients metabolism, largemouth bass juveniles (initial weight, 4.0 ± 0.2 g) were fed three isonitrogenous and isoenergetic diets containing 9.66% (L), 14.32% (M) or 19.11% (H) carbohydrate for 8 weeks. The lowest weight gain (15.75 ± 0.76 g) was observed in group H. Feeding high carbohydrate diet (HCD) led to increased pyruvate (PA), lactic acid (LD), triglyceride (TG) and free fatty acids (NEFA) levels in plasma. Also, HCD enhanced vacuolation, glycogen granule and lipid accumulation in fish liver. Activities of hepatic glycolysis enzymes such as hexokinase, pyruvate kinase and lactate dehydrogenase did not significantly differ among treatments ($P>0.05$). HCD resulted in enhancement of hepatic phosphoenolpyruvate carboxykinase (PEPCK) and lipase (LPS) activities, and increased glycogen and triglyceride (TG) concentrations. Similarly, expression of glucose and lipid metabolism related genes such as glycogen phosphorylase (PYG) and carnitine palmitoyl transferases (CPT1, CPT2) were up-regulated with increasing carbohydrate level. Hepatic catalase (CAT) and glutathione peroxidase (GSH-PX) activities, and total antioxidant capacity (T-AOC) were decreased in HCD group. UPLC-MS metabolomics revealed that glucose metabolism, lipid metabolism, and antioxidant defense system were influenced by dietary carbohydrate level. Additionally, these differential metabolites were enriched in the metabolic pathways such as galactose metabolism, fructose and mannose metabolism, unsaturated fatty acid biosynthesis, primary bile acid biosynthesis, cholesterol-butyrate metabolism, glutathione metabolism, serine and threonine metabolism. Overall, our results revealed the details of metabolites conversion in juvenile largemouth bass fed HCD.

Key words: Largemouth bass; Carbohydrate level; Metabolites; Metabolism; Organism health

基于转录组学分析三疣梭子蟹蜕壳过程中的免疫变化

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摘要：蜕壳是甲壳动物最重要的生物学过程之一，众多分子机制促进了这一复杂的生理过程。目前，尚不清楚甲壳动物蜕壳过程中的免疫机制。鉴于此，本研究对处于蜕壳后期（AB）、蜕壳间期（C）、蜕壳前期（D）和蜕壳期（E）的三疣梭子蟹的血淋巴和肝胰腺进行了转录组测序。结果显示，三疣梭子蟹血淋巴和肝胰腺组织中共分离到78572个基因片段。进一步分析表明，98个差异表达基因（DEG）参与了血淋巴和肝胰腺的免疫反应，其中大部分DEG参与了信号转导、模式识别蛋白/受体和抗氧化酶系统的过程。综上，以上结果填补了蟹类蜕壳周期中差异基因连续转录变化的空白，为阐明蟹类蜕壳周期免疫调节的分子机制提供了有价值的信息。

关键词：三疣梭子蟹，蜕壳周期，免疫，抗氧化酶系统， 比较转录组

Comparative transcriptomics reveals the immune dynamics during the molting cycle of swimming crab Portunus trituberculatus

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Abstract： Molting is one of the most important biological processes of crustacean species, and a number of molecular mechanisms facilitate this complex procedure. However, the understanding of the immune mechanisms underlying crustacean molting cycle remains very limited. This study performed transcriptome sequencing in hemolymph and hepatopancreas of the swimming crab (Portunus trituberculatus) during the four molting stages: post-molt (AB), inter-molt (C), pre-molt (D), and ecdysis (E). The results showed that there were 78,572 unigenes that were obtained in the hemolymph and hepatopancreas of P. trituberculatus. Further analysis showed that 98 DEGs were involved in immunity response of hemolymph and hepatopancreas, and most of the DEGs participated in the process of signal transduction, pattern recognition proteins/receptors, and antioxidative enzymes system. Specifically, the key genes and pathway involved in signal transduction including the GPCR126, beta-integrin, integrin, three genes in mitogen-activated protein kinase (MAPK) signaling cascade (MAPKKK10, MAPKK4, and p38 MAPK), and four genes in Toll pathway (Toll-like receptor, cactus, pelle-like kinase, and NFIL3). For the pattern recognition proteins/receptors, the lowest expression level of 11 genes was found in the E stage, including C-type lectin receptor, C-type lectin domain family 6 member A and SRB3/C in the hemolymph, and hepatopancreatic lectin 4, C-type lectin, SRB, Down syndrome cell adhesion molecule homolog, Down syndrome cell adhesion molecule isoform, and A2M. Moreover, the expression level of copper/zinc superoxide dismutase isoform 4, glutathione peroxidase, glutathione S-transferase, peroxiredoxin, peroxiredoxin 6, and dual oxidase 2 in stage C or stage D significantly higher than that of stage E or stage AB. These results fill in the gap of the continuous transcriptional changes that are evident during the molting cycle of crab and further provided valuable information for elucidating the molecular mechanisms of immune regulation during the molting cycle of crab.

Key words： Portunus trituberculatus, molting cycle, immunity, antioxidative enzyme system, comparative transcriptome

通过转录组学和代谢组学研究
许氏平鲉响应饥饿胁迫的调控网络和潜在生物标志物

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摘要：无论是在水产养殖过程中还是在自然界，饥饿胁迫限制了鱼类的生长。本研究的目的是通过转录组和代谢组来阐明许氏平鲉应对饥饿胁迫的分子机制。转录组结果显示，与对照组（CG;每天投喂）相比，实验组（EG;饥饿 72 天）肝脏中与细胞周期和脂肪酸合成相关的基因下调，而与脂肪酸分解相关的基因则在上调。从肝脏代谢组的差异代谢物筛选出了五种脂肪酸作为饥饿胁迫潜在生物标志物。随后对这些差异基因与差异代谢物的进行相关性分析，发现这 5 种脂肪酸均与细胞周期和脂肪酸代谢差异基因显著相关。这些实验结果为了解饥饿胁迫下鱼类脂肪酸代谢和细胞周期的作用提供新的线索，为促进饥饿胁迫生物标志物鉴定和耐胁迫育种研究提供参考。

关键词：饥饿胁迫；转录组；代谢组；脂肪酸；细胞周期

Analyses of regulatory network and discovery of potential biomarkers for Korean rockfish (Sebastes schlegelii) in responses to starvation stress through transcriptome and metabolome

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Abstract：Whether in aquaculture or in nature, starvation stress limits the growth of fish. The purpose of the study is to clarify the detailed molecular mechanisms underlying starvation stress in Korean rockfish (Sebastes schlegelii) through transcriptome and metabolome. Transcriptome results showed that liver genes associated with cell cycle and fatty acid synthesis were down-regulated, whereas those related to fatty acid decomposition were up-regulated in the experimental group (EG; starved for 72 days) compared to control group (CG; feeding). Five fatty acids (Docosahexaenoic acid; Docosapentaenoic acid; Eicosapentaenoic acid; Eicosatetraenoic acid; γ-Linolenic acid) were selected as possible biomarkers of starvation stress from the differential metabolites of metabolome. Subsequently, correlation between these differential genes and differential metabolites were analyzed, and observed that all the five fatty acids were significantly correlated with the differential genes. These results provide new clues for understanding the role of fatty acid metabolism and cell cycle in fish under starvation stress. It also provides a reference for promoting the biomarker identification of starvation stress and stress tolerance breeding research.

Key words：starvation stress; transcriptome; metabolome; fatty acid; cell cycle

槲皮素对枝角类蚤状溞形态特征、代谢和抗氧化能力的影响

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摘要：以蚤状溞为研究对象，使用槲皮素（0、1、2.5、5、10 mg/L）处理，直到个体全部死亡，用电子显微镜观察形态，记录体长，并绘制生长曲线，计算平均寿命、净繁殖率、内禀增长率、世代周期以及蜕壳数，检测不同处理组蚤状溞体内代谢酶和抗氧化酶的活性。结果 槲皮素处理后的溞背部会出现“塌陷”现象，适量浓度的槲皮素处理后的蚤状溞寿命延长，前期对溞的体长没有显著性作用，随着处理时间的延长，体长增加也越显著；高浓度槲皮素会显著降低净生殖率、内禀增长率和世代周期。槲皮素可以调节蚤状溞消化酶的活性，长期处理会增强抗氧化酶活性。结论 适量的槲皮素对蚤状溞的形态有一定的影响，并对生长相关参数、抗氧化酶活性具有积极作用。

关键词：槲皮素；蚤状溞；代谢；抗氧化

Effects of quercetin on morphological characteristics, metabolism and antioxidation of the cladoceran Daphnia pulex

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Abstract： The effects of quercetin on Daphnia pulex were tested. Five concentrations were set (0, 1, 2.5, 5, 10 mg/L) . The body length, growth curve, average life span, net reproductive rate, intrinsic growth rate, generation cycle and molting number were detected. The activities of metabolic enzymes and antioxidant enzymes in different treatment groups of Daphnia pulex were tested. The results showed that the carapace of Daphnia pulex treated with quercetin would appear "collapse". The life span of Daphnia pulex treated with quercetin of appropriate concentration was prolonged, and there was no significant effect on the body length of Daphnia pulex in the early stage. However, with the extension of treatment time, the body length increased significantly; High concentration of quercetin can significantly reduce the net reproductive rate, intrinsic growth rate and generation cycle.

Key words： quercetin；Daphnia pulex；metabolize；antioxidant

藻菌共生型生物絮团系统中养殖密度对南美白对虾（N5-PL5）育苗的影响

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摘要：在藻菌共生型生物絮团系统中，探究了投放密度对南美白对虾从无节幼体 5 号（N5）到仔虾 5 号（PL5）的育苗的的影响。养殖密度分别为 200 尾/升（D200）、300 尾/升（D300）和 400 尾/升（D400）。在 14 天的实验中，没有进行水交换或添加额外碳源。与其他放养密度组相比，D400 放养密度组的总氨氮和亚硝酸盐氮浓度显著升高（分别为 0.55 和 0.66 mg/L）。硝态氮和总氮在整个试验过程中不断积累，三组之间没有显著差异。在实验的后期，三组的叶绿素-a 浓度、碱度和 pH 值均呈下降趋势。在养殖过程中，最低放养密度的对虾幼体存活率较高。D200 组的弧菌总数低于其他两组，但差异不显著。综上所述，我们发现，在藻菌共生型生物絮团养殖系统中，200 尾/L（N50）的放养密度有较好的成活率和水质条件。

关键词：凡纳滨对虾；无节幼体；藻菌共生型生物絮团；弧菌

Stocking Density Effects on Pacific White Shrimp Litopenaeus vannamei (N5–PL5) Hatchery Performance in Algal-Bacterial Biofloc Systems

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Abstract： The effects of stocking density of Pacific white shrimp Litopenaeus vannamei from hatchery stages nauplii 5 (N5) through postlarval 5 (PL5) were evaluated in algal–bacterial biofloc systems. Triplicate stocking densities of 200 (D200), 300 (D300), and 400 (D400) shrimp larvae/L were used. No water exchange or additional carbon source was conducted during the 14-d experiment. Compared with other groups, the D400 stocking density had significantly higher concentrations of total ammonia nitrogen and nitrite-nitrogen (0.55 and 0.66 mg/L, respectively). Nitratenitrogen and total nitrogen continuously accumulated throughout the experiment, with no significant difference among the three groups. The chlorophyll-a concentration, alkalinity, and pH of all three groups showed a downward trend in the later stage of the experiment. Shrimp larvae at the lowest stocking density had a higher survival during the rearing. Total Vibrio spp. count in the D200 group was lower than that of the other two but was not significantly different. In conclusion, we found that a stocking density of 200 shrimp larvae/L resulted in better survival and water quality conditions in the rearing systems tested.

Key words：Litopenaeus vannamei; Nauplius; Algal-bacterial biofloc systems; Vibrio