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第一专题：水产养殖技术与设施

不同颜色肝胰腺对成年雌性中华绒螯蟹营养品质的影响

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摘要：中华绒螯蟹在养殖过程中出现了白肝症，病蟹的肝胰腺颜色会逐渐变浅。因此，本研究对比分析了不同颜色（黄色，黄白色和白色）肝胰腺成年雌蟹的组织指数，总可食率，以及肝胰腺、卵巢和肌肉的营养成分，旨在为不同颜色肝胰腺雌蟹的营养价值评定提供基础数据和理论依据。

关键词：食用部位；中华绒螯蟹；营养品质；白肝症；黄白色肝胰腺

Comparison on nutritional quality of adult female Chinese mitten crab (*Eriocheir sinensis*) with different colored Hepatopancreases

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Abstract: White hepatopancreas syndrome has recently emerged in Chinese mitten crab (*Eriocheir sinensis*) aquaculture. The hepatopancreas color of diseased crabs becomes gradually lighter. Therefore, this study compared and analyzed the tissue index, total edible yield and nutritional composition of hepatopancreas, ovaries and muscles of adult female crabs with different colors (yellow, yellow-white and white).The purpose of this study is to provide basic data and theoretical basis for the evaluation of nutritional value of female crabs with different colors of hepatopancreas.

Keywords: edible parts, *Eriocheir sinensis*, nutritional quality, white hepatopancreas syndrome, yellow-white hepatopancreas

不同河蟹放养密度对寒区稻蟹综合种养生产性能及水质的影响

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摘要：为明确我国高寒地区稻蟹综合种养系统的要素配比等关键技术参数，构建寒区稻蟹综合种养模式，本实验以水稻单作为对照，研究了不同河蟹放养密度对寒区稻蟹综合种养过程中河蟹和水稻的生长性能及稻田水质理化因子的影响。

关键词：稻蟹综合种养；寒区；河蟹密度；生产性能；水质

Effects of different crab stocking density on production performance and water quality under integrated cultivation of rice crab in cold areas

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Abstract: In order to clarify the Key technical parameters such as the element ratio of the rice crab co-culture system in the high-cold areas in our country and construct a integrated cultivation of rice crab in cold regions, in this experiment, rice single cropping was used as the control group, and the treatment groups were set according to the stocking density of Eriocheir sinensis to study the effect on growth performance of Eriocheir sinensis and rice, and water quality under integrated cultivation of rice crab in cold areas.

Key words: integrated cultivation of rice crab; cold areas; crab stocking density; production performance; water quality

陆基集装箱与传统池塘养殖大口黑鲈形态特征和营养品质的对比研究

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摘要：为揭示陆基集装箱与传统池塘养殖大口黑鲈（*Micropterus salmoides*）形体特征和营养品质的差异，本实验选取两种模式下体质量差异不显著（P>0.05）的大口黑鲈对其形体特征和营养品质进行比较分析。结果表明：在形体特征方面，集装箱养殖的大口黑鲈体长极显著高于池塘养殖组（P<0.01），肥满度和脏体比极显著低于池塘养殖组（P<0.01）。在营养品质方面，集装箱养殖的大口黑鲈肌肉硬度、咀嚼性、弹性、粗蛋白、DHA、DAA、K、2-丁酮和戊醛等含量均显著高于池塘养殖组（P<0.05），肌纤维直径、失水率、粗脂肪、Se、壬醛和 2,5-二甲基吡嗪等含量均显著低于池塘养殖组（P<0.05）。实验表明，养殖模式不会使大口黑鲈肌肉的营养物质种类产生差异，但是会对其体型和肌肉中营养物质的含量造成明显影响。

关键词：大口黑鲈；陆基集装箱；传统池塘；形体特征；营养品质

Comparative study on body characteristics and nutritional quality of *Micropterus salmoides* cultured in land-based container and traditional pond

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Abstract: In order to reveal the differences in body characteristics and nutritional quality between land-based container and traditional pond culture of largemouth bass (*Micropterus salmoide*s), in this experiment, the body characteristics and nutritional quality of largemouth bass with no significant difference in body weight between the two modes (P>0.05) were compared and analyzed. The results showed that in terms of body characteristics, the body length of largemouth bass cultured in containers was significantly higher than that in the pond culture group (P<0.01), the condition factor and viscerosomatic index were extremely significantly lower than those in the pond culture group (P <0.01). In terms of nutritional quality, the contents of muscle hardness, chewiness, springsness, crude protein, DHA, DAA, K, 2 - butanone, pentanal in the container-cultured largemouth bass were significantly higher than those in the pond-cultured group (P<0.05), and the muscle fiber diameter, water loss rate, crude fat, Se, nonanal and 2,5 - dimethylpyrazine were significantly lower than those in the pond-cultured group (P<0.05). The results showed that the culture mode did not make a difference in the types of nutrients in the muscle of largemouth bass, but it had a significant impact on the body characteristics and the content of nutrients in the muscle.

Keywords: *Micropterus salmoides*; Recirculating aquaculture system; Traditional pond system; Body characteristics; Nutritional quality

离心式滩涂贝类播苗装置设计与试验

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摘要：因目前滩涂贝类养殖无专用机械化播苗装备，人工播苗劳动强度大、效率低和均匀性差等问题十分突出，本文根据滩涂作业环境、贝苗特性及播苗作业规范，设计了离心式滩涂贝类播苗装置。以四角蛤蜊苗为研究对象，基于播苗过程受力及运动分析，建立其在离心叶轮盘上运动的动力学模型。应用 EDEM 进行播苗过程的离散元仿真，基于 Design-Expert 软件进行正交试验设计和响应曲面分析，并进行播苗装置参数的优化。经回归分析和优化得到最优组合参数为：叶片个数 4，叶轮转速 500rpm，行进速度 0.77m/s，在该条件下播苗作业分布变异系数为 9.33%，破碎率为 2.17%。基于离散元的播苗过程仿真分析可用于离心式滩涂贝类播苗装置参数优化，并获得较好的播苗均匀性。

关键词：滩涂养殖；贝类播苗装置；叶轮盘；离散元仿真；分布变异系数

Design and test of centrifugal shellfish seeding device for tidal aquaculture

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Abstract: Duo to lack of seeding equipment for tidal shellfish culture in China, shellfish seeding has been carried out manually, with high labour intensive, low efficiency, and poor uniformity, etc. A centrifugal clam seeding device for tidal aquaculture was designed according to the characteristics of juvenile clam, the seeding specifications, and the tidal culture environment. Based on the force and motion analysis of seeding process, the dynamic moving model of clams on impeller disc was established. With discrete element simulation of the seeding process by EDEM and orthogonal experiment design and response surface analysis by Design-Expert, Additionally, optimal parameters of the seeding device were determined. According to regression analysis and optimization, the optimal parameters combination is as follows: the number of blades is 4, the revolving speed of impeller disc is 500 rpm, and the moving speed of ship is 0.77m/s. Under these conditions, the variation coefficient of clam distribution is 9.33%, the broken rate is 2.17%. Therefore, the simulation analysis of seeding process based on discrete elements is effective in optimizing the parameters of the centrifugal shellfish seeding device, and higher seeding uniformity can be obtained.

Key words: tidal aquaculture; shellfish seeding device; impeller disc; discrete element simulation; coefficient of distribution variation

船型桁架结构网箱系泊系统失效风险评估

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摘要：为了了解船型桁架结构网箱在外海环境作用下系泊系统的稳定性和安全性，本研究通过比尺为 1:40 的物理模型试验，围绕网箱在波浪作用下的系泊力及升沉、纵摇和横摇等运动分量对两种系泊方案进行了比较分析。结果表明，正常工作时，网箱系泊力及运动响应均较小，具有较高的稳定性和安全性，而当系泊一侧失效后，网箱的运动受力出现了不同程度的增大，对网箱的安全运行产生了较大影响。在本试验工况下，网箱的系泊力较正常系泊时普遍增大，增幅为 6.1%~67.7%；运动分量也均有所增大，其中升沉运动最大增幅 39%；纵摇运动增幅较小，最大为 17%；横摇运动则出现大幅增大，增幅达 123%~585%。研究结果可为今后船型桁架结构网箱的系泊方案设计及海上安装提供理论依据和数据支撑。

关键词：船型网箱；系泊系统；波浪；动力学；模型试验

Failure risk assessment of mooring system of a deep-sea aquaculture cage with vessel-shaped truss structure

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Abstract: To ensure the safe operation and stable output of large-scale deep-sea aquaculture cage is the key to realize the sustainable development of cage industry. In order to understand the stability and safety of the mooring system of the cage with vessel-shaped truss structure in the offshore environment, the physical model test with a scale of 1 : 40 was carried out in this study to compare and analyze the two mooring schemes around the mooring force of the cage under wave action and the motion responses such as heave, pitch and roll. The results show that the mooring force and motion response of the cage are small in normal operation, and it has a high stability and safety. However, when the mooring side fails, the mooring force of the cage increases to varying degrees, which has a great influence on the safe operation of the cage. In this study, the mooring force of the cage is generally increased by 6.1%~67.7% compared with normal work. The motion components also increased, and the heave increased by 39%. The increase of pitch is small, the maximum is 17%. Rolling increased significantly, with an increase of 123%-585%. The results provide theoretical basis and data support for the mooring design and offshore installation of ship truss cages in the future.

Key words: vessel-shaped cage, mooring system, wave, kinetics, model test

基于计算机视觉的 3 种金枪鱼属鱼类形态指标自动测量研究

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摘要：形态指标作为研究金枪鱼类的生长、发育和生活史具有重要意义。因此，本文通过计算机视觉库 OpenCV 对 3 种金枪鱼类图像进行预处理，得到金枪鱼类形态轮廓图像。根据预先选定的特征点，利用计算机视觉技术遍历轮廓图像上所有的像素点，并自动定位出每张轮廓图像的预选特征点共 17 个。利用计算机视觉技术遍历得到的特征点位置，自动测量出 3 种金枪鱼的形态指标像素长度，并计算出形态指标实际长度。并对比分析自动测量与人工测量形态指标的绝对误差和相对误差。研究结果表明，通过计算机视觉技术对 3 种金枪鱼的形态指标的自动测量效果较好，大眼金枪鱼、黄鳍金枪鱼和长鳍金枪鱼的 12 个形态指标的绝对误差范围分别为 0.00~1.46cm、0.00~1.73cm、0.00~1.32cm，其相对误差范围分别为 0.01%~5.84%、0.00%~6.17%、0.00%~6.89%。以期为金枪鱼类智能识别提供前期工作基础。

关键词：计算机视觉；金枪鱼属；形态轮廓；特征点；形态指标；自动测量

Automatic measurement of Morphological Indices of 3 *Thunnus* species based on computer vision

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Abstract: Its morphological indices were of great significance for the study of the growth, development and life history of tunas. Therefore, in this paper, images of 3 *Thunnus* species were preprocessed by computer vision library (OpenCV) to obtain the contour images of tuna. According to the pre-selected feature points, the computer vision technology was used to traversal all the pixel points on the contour image, and 17 pre-selected feature points of each contour image were automatically located. By using the computer vision technology, the pixel length of the morphological index of the three species of tuna was automatically measured and the actual length of the morphological index was calculated. The absolute error and relative error between automatic measurement and manual measurement are compared and analyzed. The results showed that the computer vision technique was effective in the automatic measurement of the morphological indexes of the 3 Thunnus species. The absolute error ranges of 12 morphological indices of Thunnus obesus, Thunnus albacores and Thunnus alalunga were 0.00~1.46cm, 0.00~1.73cm and 0.00~1.32cm, respectively, and the relative error ranges were 0.01%~5.84%, 0.00%~6.17% and 0.00%~6.89%, respectively. It is expected to provide a basis for intelligent identification of tuna.

Key words: computer vision; *Thunnus*; morphological contour; feature points; morphological index; automatic measurement

光照对黄颡鱼生长性能的影响

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摘要：为了解光强对黄颡鱼（*Pelteobagrus fulvidraco*）生长性能的影响，本实验对 1~8W/㎡光强下黄颡鱼的增重率、特定增长率、饵料系数进行研究，并通过消化性能、抗氧化性能、免疫性能以及养殖水质的变化规律探索光强对黄颡鱼生长性能的影响机制，为实现黄颡鱼高效养殖提供理论依据。

关键词：黄颡鱼；光照强度；生长性能；消化酶性能；抗氧化性能；免疫性能

The effect of light intensity on the growth performance of *Pelteobagrus fulvidraco*

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Abstract: In order to understand the effect of light intensity on the growth performance of *Pelteobagrus fulvidraco*, the experiment studies the weight gain rate, specific growth rate and diet coefficient of *Pelteobagrus fulvidraco* in the range of 1~8 W/m^2. In addition, the experiment is going to explore the influence mechanism of light intensity on the growth performance through the changes of digestion, antioxidation, immunization performences and culture water quality, which provides a theoretical basis for establishing an efficient culture system of *Pelteobagrus fulvidraco*.

Key words: *Pelteobagrus fulvidraco*, light intensity, growth performance, digestive performance, antioxidant performance, immune performance

无人装备在海洋水产养殖业中的作用

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摘要：近年来，我国海洋经济进入空前的高速发展阶，海洋经济的持续发展，海洋战略的实施使得海洋经济日益受到重视。科技是海洋高新技术产业的孵化器,更是海洋产业转型升级与优化的助推器。本文概述了无人装备的发展和特点，并以有缆遥控水下机器人、无人船、无人机等无人装备为例，详尽的叙述了利用无人装备的技术特点和优势，如何与海洋水产养殖业等相关业务相结合，促进经济发展；分析了无人装备在海洋经济中的应用前景和需求。

关键词：无人装备；水产；养殖；

Role of unmanned equipment in marine aquaculture

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Abstract: In recent years, China's marine economy has entered an unprecedented stage of rapid development. With the sustainable development of marine economy and the implementation of marine strategy, marine economy has attracted more and more attention. Science and technology is not only the incubator of marine high-tech industry, but also the booster for the transformation, upgrading and optimization of marine industry. This paper summarizes the development and characteristics of unmanned equipment, and takes unmanned equipment such as cable remote-controlled underwater robot, unmanned ship and unmanned aerial vehicle as an example to describe in detail how to combine the technical characteristics and advantages of unmanned equipment with marine aquaculture and other related businesses to promote economic development; The application prospect and demand of unmanned equipment in marine economy are analyzed.

Key words: Unmanned equipment; Aquatic products; Breed

利用 Biolog Eco 板和 PICRUSt2 方法分析凡纳滨对虾养殖池塘末期细菌群落的功能多样性

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摘要：微生物在环境中的作用是通过群落功能来实现的，但是人们对凡纳滨对虾池塘水体和底泥中微生物群落的功能多样性仍知之甚少。本研究中作者将高通量测序技术和 Biolog Eco 方法相结合，研究凡纳滨对虾池塘养殖末期水体和底泥中细菌群落的结构和功能多样性，并评价了基于 Biolog Eco 板的微生物群落实际代谢特性与基于 PICRUSt2 的预测功能的相关性。

关键词：凡纳滨对虾池塘；细菌群落；功能多样性；高通量测序；Biolog Eco 板

Analysis of bacterial community functional diversity in late-stage shrimp (*Litopenaeus vannamei*) ponds using Biolog EcoPlates and PICRUSt2

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Abstract: The role of microorganisms in the environment is reflective of the function of the community; however, our understanding of the functional diversity of the bacterial microbiome found in water and sediment from shrimp ponds is currently fragmentary. This study utilized high-throughput sequencing techniques and community level physiological profiling (CLPP) methods to study the structural and functional diversity of the bacterial communities found in water samples and sediment from three intensive *Litopenaeus vannamei* culture ponds at late stage. The correlation between the presumptive functions using PICRUSt2 and the actual metabolic profiles via Biolog EcoPlates was evaluated.

Key words: *Litopenaeus vannamei* pond, bacterial community, functional diversity, high-throughput sequencing, Biolog EcoPlates

泉吉河青海湖裸鲤自然产卵场的无人机遥测识别与定量评估

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摘要：无人机测绘具有快速高效、机动灵活、成本低等特点，成为遥感测绘领域的新兴力量，对于分布于高原、野外作业难度大、不易达到的河流栖息地调查提供了一种便捷的方法。本研究利用无人机对青海湖入湖支流泉吉河约 60km 长的江段进行了航拍调查，同时，对产卵场生境特征参数进行了原位调查监测，最终，基于河道形态、沙洲分布、可视水深和曲折率等生境特征使用目视解译法和 AI 识别法实现了对泉吉河产卵场分布状况和规模评估。结果表明，在非洪水季节，泉吉河可筛选出 307 个适合于青海湖裸鲤繁殖的区域，总面积达 399,320 ㎡；其中，中游可供青海湖裸鲤产卵的区域数量最多、面积最大，分别为 190 个和 258,039 ㎡；其次是下游，分别为 97 个和 124,455 ㎡。泉吉河上游支流也可以提供产卵区域，但数量较少，面积仅仅只有 5471 ㎡。泉吉河众多的砂石浅滩（总面积约 33,154,341 ㎡）为青海湖裸鲤在涨水季节提供了潜在的产卵场，这些浅滩也是在中游数量最多、面积最大。本研究通过无人机测绘获得了泉吉河精细河道宏观生境特征，为今后开展青海湖裸鲤自然繁殖栖息地评估和保护提供了重要基础数据。

关键词：青海湖裸鲤；无人机；产卵场；生境；河道形态

Characteristics of Spawning Habitats *Gymnocypris przewalskii* in Quanji River by UAV (unmanned aerial vehicle) Surveys

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Abstract: UAV surveying has become a method of field investigation due to its flexibility and convenience.Through UAV survey and field investigation, this study concluded that quanji river has 307 spawning grounds suitable for *Gymnocypris przewalskii* breeding under normal conditions, with a total area of 339,320m^2. The middle reaches have the largest area (258,039m^2), followed by the lower reaches (124,455m^2), while the tributaries have the smallest area (5,471m^2). Quanji river has many shoals that can provide potential spawning sites in flood season (the total area is 33,154,341 ㎡), and it is also the largest area in the middle reaches. This study can provide important basic data for the assessment and protection of natural breeding habitat of *Gymnocypris przewalskii.*

Key words: *Gymnocypris przewalskii*, UVA, Spawning grounds, habitat

水产养殖尾水处理技术及运行参数优化研究

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摘要：为了获知水产养殖尾水处理装置的运行参数，以便在养殖中更好地处理养殖废水，本实验通过构建尾水循环模拟装置，研究各尾水处理单元的材料筛选、效果对比，以及各单元的运行参数包括单元配比和水利停留时间，得出最优的水产养殖尾水处理参数。

关键词：尾水处理；尾水循环；运行参数

Aquaculture tail water treatment technology and operation parameter optimization

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Abstract: In order to obtain the operation parameters of aquaculture tail water treatment device, so as to better treat aquaculture wastewater in aquaculture, this experiment constructs a tail water cycle simulation device to study the material screening and effect comparison of each tail water treatment unit, as well as the operation parameters of each unit, including unit ratio and hydraulic residence time, so as to obtain the optimal aquaculture tail water treatment parameters.

Key words: Tail water treatment; Tail water circulation; Operating parameters

剪裁斜率对中层拖网网囊水动力及形态的影响

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摘要：网囊水动力及形态变化受网目尺寸、剪裁斜率等因素影响。为了解剪裁斜率对中层拖网网囊水动力及形态的影响，本研究采用 6 顶剪裁斜率不同（无剪裁、6:1、5:1、4:1、7:2、3:1）的模型网囊，通过动水槽模型试验，比较分析 5 种流速条件下各网囊阻力及形态差异，并采用傅里叶级数拟合存在渔获物条件下网囊位置振荡和阻力振荡。结果显示：（1）各网囊空网条件下，剪裁斜率越小，网衣越容易展开；并且其网囊阻力随剪裁斜率的增加而增大；（2）各网囊在有渔获时，其位置和水阻力振荡振幅均随剪裁斜率的减小呈先减小后增大趋势，当剪裁斜率为 4:1 时，振幅最小；振荡周期不会随剪裁斜率的变化发生明显差异；（3）采用 2 级傅里叶级数拟合网囊位置振荡，拟合结果与实测结果具极强相关性为 93.3%；采用 3 级傅里叶级数拟合网囊阻力振荡，拟合结果与实测结果具极强相关性为 86.7%。综上建议，为确保网囊具较好稳定性和最小水阻力，建议采用 4:1 剪裁斜率网囊。

关键词：剪裁斜率；网囊；水动力性能；网具形态；傅里叶级数

Effects of cutting ratio on hydrodynamic performance and net shape of mid-water trawl codend

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Abstract: The codend is an important part of mid-water, and its hydrodynamic performance and net shape can be affected by mesh size and cutting ratio. In order to understand the effect of the cutting ratio on hydrodynamic performance and net shape of mid-water trawl codend, 6 model codends with different cutting ratios (no cutting, 6:1, 5:1, 4:1, 7:2, 3:1) were made and comparative tests were conducted at 5 current speeds in a professional test tank. We used the Fourier series to fit the measured value of codend with catch. The results show that: (1) Each empty codend, the smaller cutting ratio, the easier it is to unfold; and the drag force of each empty codend increased as the cutting ratio increased; (2) Each codend with catch, the amplitude of position and drag force oscillation will decrease first and then increase with the cutting ratio decrease, and the cutting ratio is 4:1, the amplitude is the smallest; the oscillation cycle will not change obviously with the cutting ratio changes; (3) The second-order Fourier series is used to fit the position oscillation of codend, and the fitted value has a strong correlation with the measured value of 93.3%; and the third-order Fourier series is used to fit the drag force of codend, and the fitted value has a strong correlation with the measured value of 86.7%. In summary, in order to ensure the best stability and minimum drag force of codend, it is recommended to use 4:1 cutting ratio codend.

Key words: cutting ratio, codend, hydrodynamic characteristics, net shape, the Fourier series

倾斜状态对 V 型网板水动力和周围流场特征的影响

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摘要：为了探究 V 型网板在各种工作姿态下水动力特性的变化规律，作者采用数值模拟方法对比了 4 个展弦比(0.4、0.5、0.6、0.7)和 4 个板面夹角(16°、19°、22°、25°)的网板的水动力性能，遴选出水动力性能最佳的 V 型网板，并分析其在不同姿态下的水动力系数、周围流场分布和表面压力变化规律，结果表明：1）展弦比 λ=0.7、板面夹角 Γ=16° 的 V 型网板的水动力性能最优，升力系数在冲角为 37.5°时最大，为 1.482，冲角为 10°时扩张效率最大。2）随着冲角的增大，13 号网板迎流面的压力逐渐增大，网板迎流面和背流面的速度差亦呈增大趋势。3）13 号网板发生不同程度的前后倾或内外倾时，升力系数降低，阻力系数则随着倾角的增大而减小。4）当网板发生内外倾斜时，随着倾角的增加，迎流面压力中心向网板前端移动，网板中心面后涡旋变化不明显；当网板前后倾斜时，网板迎流面压力分布变化明显，即随着倾角的增加，压力中心分别逐渐向前端上下两侧移动，并且网板中心面后涡旋逐渐变小。本研究结果可以为预测不同工作姿态网板水动力特性变化，调整网板稳定性提供科学参考。

关键词：V 型网板；稳定性；压力分布；流场分布；水动力系数

The effect of tilt state on the hydrodynamics and surrounding flow field characteristics of V-shaped otter board

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Abstract: V-type otter board is an important part of single ship bottom trawl system. In order to explore the variation of hydrodynamic of V-shaped otter board in various working postures, Author applied numerical simulation method to compare the hydrodynamic characteristics of the otter board with different aspect ratios (0.4, 0.5, 0.6, 0.7) and the different Dihedral angle (16°, 19°, 22°, 25°) and select one V-shaped otter board with better hydrodynamic characteristic, then the hydrodynamic coefficient, surrounding flow field distribution and surface pressure variation of the better otter board under different postures were analyzed. The results show that: 1) the V-shaped otter board with aspect ratio λ=0.7 and Dihedral angle Γ=16° has the best hydrodynamic performance. The lift coefficient reaches the maximum at 37.5°, which is 1.482. The expansion efficiency reaches the maximum when the Angle of attack is 10°.2) With the increase of the Angle of attack, the pressure on the headstream surface of the No.13 otter board gradually increases, and the velocity difference between the headstream surface and the back flow surface of the otter board also increases.3) When the No.13 otter board has different degrees of forward and backward inclination or inside and outside inclination, the lift coefficient decreases, and the drag coefficient decreases with the increase of inclination Angle.4) With the increase of the inclination Angle, the pressure center of the headstream surface moves to the front of the otter board, and the change of the back vortices on the center of the otter board surface is not obvious. When the otter board is tilted back and forth, the pressure distribution of the otter board’s flow face changes obviously, that is, with the increase of the inclination, the pressure center gradually moves up and down the front end, respectively, and the vortex of the otter board 's center surface gradually decreases. The results of this study can provide scientific reference for predicting the variation of hydrodynamic characteristics of otter board with different working positions and adjusting the stability of otter board.

Key words: V-shaped otter board; stability; Pressure distribution; flow field distribution; hydrodynamic coefficients

栅型兼捕减少装置的规格和倾角对网囊水动力及形态的影响研究

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摘要：为了减少副渔获物的兼捕，提高拖网渔具选择性，栅型兼捕减少装置已在底拖网渔业中广泛应用。兼捕减少装置的水动力变化影响着鱼类接触后的行为反应，从而决定着装置的分隔效率和选择性效果。为了了解栅型兼捕减少装置对网囊阻力及形态的影响，本研究通过动水槽模型试验方法，探究了 3 种不同规格的栅栏（Grid-0.3 栅、Grid -0.4 栅、Grid -0.5 栅）分别在倾角 30°、45°和 60°，3 种状态下对网囊网目张开程度、空间形态和阻力的影响效果。结果表明：(1)无栅栏网囊的网目平均张开角度为 22°±5°。设置 Grid-0.4 栅和 Grid-0.5 栅网囊的网目平均张开角度较无栅栏网囊分别增大了 3.3%和 18.8%；而设置 Grid-0.3 栅网囊的网目平均张开角度减少了 9.2%。(2) Grid-0.4 栅对网囊形态影响程度最小，贴合网囊流线型；Grid-0.3 栅和 Grid-0.5 栅使网囊发生扭曲形变。(3)设置 Grid-0.3 栅的网囊，在不同倾角下的阻力与无栅栏网囊的阻力相近。以不同倾角设置 Grid-0.4 栅和 Grid-0.5 栅的网囊，平均阻力分别比无栅栏网囊的阻力分别大 12.7%、24.4%。

关键词：栅型兼捕减少装置；阻力；形态；规格；倾斜角度

The effects of size and inclination angle of sorting grid on the hydrodynamic performance and shape of trawl codend

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Abstract: The sorting grid has been widely used in trawl fishery to reduce by-catch and improve the selectivity of trawl net. The change in hydrodynamic force of the by-catch reduction device affects the behavioral response of fish after contact, which determines the separation efficiency and selectivity result of the device. In order to understand the effects of sorting grid on the hydrodynamic performance and shape of trawl codend, this study investigated the effects of three grids with different sizes(Grid-0.3, Grid-0.4, Grid-0.5) on the mesh opening angle, spatial geometry and drag of codend under three different inclination angles of（A-30°、A-45°、A-60°）by flume tank test. The results showed that: (1) The average mesh opening angle of Grid-free codend is (22°±5°). Compared with Grid-free codend, the average mesh opening angle of Grid-0.4 codend and Grid-0.5 codend is increased by 3.3% and 18.8%, respectively. The average mesh opening angle of Grid-0.3 codend is reduced by 9.2%. (2) Grid-0.4 has the least influence on the shape of the codend, it is streamlined to fit the codend; Grid-0.3 and Grid-0.5 make the codend distorted. (3) The average drag of Grid-0.3 codend is similar to the drag of Grid-free codend. The average drag of Grid-0.4 codend and Grid-0.5 codend at different inclination angles is 12.7%, 24.4% higher than that of the average drag of Grid-free codend.

Keywords: Sorting grid；drag；shape；size；inclination angle

基于 ANSYS/LS－DYNA 的紫菜切割动力学仿真分析

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摘要：为解决我国紫菜采收劳动强度大，生产效率低等问题。设计了一种滚刀式紫菜切割装置，该装置由网帘支撑辊轴、分段直刀、防护栏和液压系统等结构组成。为避免切割时紫菜的漏割和重割，探究紫菜切割状态，分别对刀具的运动轨迹和刀具旋转切割角与紫菜受力关系进行了分析，结果表明：刀具旋转切割角与紫菜剪切应力成反比，与拉伸应力成正比，当刀具旋转切割角为 90°时，紫菜切割状态为完全拉断。基于 ANSYS /LS-DYNA 建立切割装置与紫菜叶状体互作刚柔耦合模型，通过响应面仿真试验研究了不同进给速度、刀具转速、刀具延伸长度和倾角对紫菜所受切割力的影响关系，结果显示最优参数组合为 0.77m/s、94.25rad/s、40mm 、110°，此时紫菜所受切割力最小，为 4.21N。该研究为紫菜机械化采收装备设计研究提供理论参考。

关键词：紫菜；切割装置；刚柔耦合模型；切割动力学；仿真研究

Dynamic simulation analysis of laver cutting based on ANSYS/LS-DYNA

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Abstract: In order to solve the problems of high labor intensity and low production efficiency in the harvesting of laver in China. A roll type laver cutting device was designed. It includes a net support roller, a segmented straight knife, a guard rail and hydraulic system, etc. To avoid missing and repeat cutting of laver during harvesting, explore the cutting state, the trajectory of the knife roller blade of the cutting device and the relationship between the cutting angle of the cutter and the stress condition of laver were analyzed respectively, the results showed that the shear stress and tensile stress of laver are directly proportional to the cutting angle of the cutter. when the cutting angle of the cutter was 90°, the broken state of laver was completely tenside rupture. The rigid-flexible coupling model of the laver fronds cutting was established based on ANSYS/LS-DYNA, to analyze the influence of different advance speeds, cutter rotating speed, cutter lengths and inclination angles on the cutting force of laver，the response surface simulation experiments were carried out. The result showed optimal parameter combination is 0.77m/s, 94.25rad/s, 40mm and 110° respectively, the minimum cutting force on laver is 4.21N. This study provides a theoretical reference for the design and research of laver mechanized harvesting equipment.

Keywords: laver, cutting device, rigid-flexible coupling model, cutting dynamics, simulation research

杂交鲷及黑鲷投喂频率的比较研究

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摘要：本文研究比较了杂交鲷(黑鲷(*Acanthopagrus schlegelii*)♀×真鲷(*Pagrus major*)♂杂交子二代)与黑鲷幼鱼在不同投喂频率下的差异表现，旨在为新品种选育提供基础依据。实验设 4 个投喂频率组：1 次/d、2 次/d、3 次/d、4 次/d(记作 1 T、2 T、3 T、4 T)，养殖实验共 40 d。结果显示：投喂频率从 1 T 升至 2 T，两种鱼的增重率(WGR)、特定生长率(SGR)、成活率(SR)、*igf1* 及 *lpl* 基因表达量均显著升高，消化酶活力显著降低。继续升高投喂频率，上述指标无显著变化，抗氧化酶活力先升高后显著降低。两种鱼相比，2 T 组杂交鲷的生长性能、消化酶活力、生长及脂代谢相关基因表达均显著高于黑鲷。研究结果表明，杂交鲷及黑鲷幼鱼的适宜投喂频率为 2 T，且 2 T 组中杂交鲷在生长代谢等方面均有优于黑鲷的表现。

关键词：投喂频率；杂交鲷；黑鲷；生长性能；生理生化指标；基因表达量

Comparative study on feeding frequency of the hybrid porgy and black porgy

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Abstract: This paper studied and compared the different performance between the hybrid porgy (HF_2) of *Acanthopagrus schlegelii*♀ (black porgy) ×*Pagrus major*♂ (red porgy) and black porgy under different feeding frequencies, the aims to provide the basis for the breeding of new varieties. set 4 feeding frequency groups: once·d^{-1}, twice·d^{-1}, 3 times·d^{-1} and 4 times·d^{-1} (marked as 1 T, 2 T, 3 T, 4 T), the breeding experiment lasted for 40 days. The results show that the weight gain rate (WGR), specific growth rate (SGR), survival rate (SR), *igf1* and *lpl* gene expression of the HF_2 and black porgy increased significantly, and the activity of digestive enzymes decreased significantly when the feeding frequency increased from 1 T to 2 T. With the continuous increase of feeding frequency, there was no significant change in the above indexes; and the antioxidant enzyme activities increased at first and then decreased significantly. Compared with the two fishes, the growth performance, digestive enzyme activity, growth and lipid metabolism related gene expression of HF_2 in 2 T group were significantly higher than those in black porgy. Therefore, the optimum feeding frequency of the HF_2 and black porgy juveniles was 2 T, and the growth and metabolism of HF_2 was better than that of black porgy in 2 T group.

Key words: feeding frequency, the hybrid porgy, black porgy, growth performance, physiological and biochemical indicators, gene expressiona

东海区三疣梭子蟹刺网的选择性

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摘要：为探讨单片刺网对三疣梭子蟹的选择性，我们使用 6 种网目尺寸(100、110、120、130、140 和 150 mm)进行选择性试验来确定三疣梭子蟹刺网的最佳网目尺寸。试验于 2018 年 7 月 25 日至 29 日在东海传统捕蟹海域进行。采用四种选择性曲线进行拟合，运用极大似然法估算模型参数。本试验中，6 种网目尺寸的刺网共捕获 436 只三疣梭子蟹。其头胸甲长范围为 46.2-83.7 mm，所有的三疣梭子蟹均被缠绕(即身体或肢体)捕获。当网目尺寸大于 100 mm 时，幼蟹(头胸甲长＜60 mm)的捕获量不到总捕获量的 20%。甲宽、甲高与甲长均呈现线性关系。以最小 AIC 值为基础的正态分布模型较好地描述了三疣梭子蟹刺网选择性。正态分布模型计算的最佳头胸甲长分别为 49.8、54.8、59.8、64.8、69.8 和 74.8mm。

关键词：东海区；三疣梭子蟹；刺网；选择性; 网目尺寸

Gillnet selectivity for swimming crab *Portunus trituberculatus* in the East China Sea

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Abstract: To explore the gillnet selectivity for swimming crab Portunus trituberculatus, six mesh sizes (100, 110, 120, 130, 140 and 150 mm) were tested to determine the optimal mesh size for swimming crab. The experiments were conducted in the traditional area for fishing crab in the East China Sea from 25–29 July 2018. Four kinds of selectivity curves were used for fitting, and the maximum likelihood method was used to estimate the model parameters. In this experiment, 436 swimming crabs were caught with six different mesh sizes. The carapace length range was 46.2–83.7 mm, and all crabs were caught by entanglement (i.e. body or limb). When the mesh size was larger than 100 mm, the proportion of juvenile crab (carapace length < 60 mm) was less than 20% of the total catch. A linear relationship between the carapace width and height and the carapace length of the crab was observed. Gillnet selectivity for swimming crab was well described by the normal model based on the smallest AIC value. The optimum length calculated by the normal model were 49.8, 54.8, 59.8, 64.8, 69.8 and 74.8mm for six mesh sizes, respectively.

Key words: The East China Sea, Swimming crab, Gillnet, Selectivity, Mesh size

对虾生物絮团养殖系统细菌群落组成、共现网络稳定性及其构建过程

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摘要：为了阐明对虾生物絮团养殖系统中细菌群落的互作关系，以便进行微生物调控促进对虾健康，本研究利用 16S rRNA 高通量测序技术系统研究了水体、絮团和肠道三个生境中细菌群落组成、共现网络稳定性及其构建过程差异，发现生物絮团养殖可以定向增加三个生境中细菌群落的趋同和稳定性。

关键词：对虾；生物絮团；细菌群落; 共现网络；构建过程

Bacterial community composition, co-occurrence network and assembly process in the biofloc-based shrimp culture system

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Abstract: A full understanding of the bacterial community relationships in the biofloc-based shrimp culture system is helpful for shrimp health through manipulating its microbiota. In this study, we systematically analyzed the differences of bacterial community composition, co-occurrence network stability and assembly process in three habitats (water, bioflocs and gut). The results indicated that bioflocs directionally enhanced the bacterial community convergence and network stability of the culture system.

Key words: Shrimp, Bioflocs, bacterial community, co-occurrence network, assembly process

小球藻及芽孢杆菌对罗非鱼养殖水体的影响

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摘要：随着鱼类养殖产量大幅度提高，养殖对象的排泄、残饵的腐化分解、药物的滥用及工业废水和生活污水未经处理直接排放，严重污染到养殖水体。本实验利用小球藻及菌发现对罗非鱼养殖水体有显著净化效果。

关键词：藻类；芽孢杆菌；沉积物；有机物降解

Effects of Chlorella and Bacillus on tilapia culture water

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Abstract: With the substantial increase of fish breeding output, the excretion of breeding objects, the decay and decomposition of residual bait, drug abuse and the direct discharge of industrial wastewater and domestic sewage without treatment seriously pollute the breeding water body. In this experiment, Chlorella and bacteria were used to purify tilapia culture water.

Key words: Algae; Bacillus; Sediment; Organic degradation

池塘工程化圈养系统内养殖密度对草鱼生长性能及甲状腺机能的影响

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摘要：本实验构建了一种新型池塘内循环养殖模式“池塘工程化圈养系统”，并以草鱼为研究对象，设置高、中、低三个密度养殖 120 天。结果表明，高密度（HSD）养殖会抑制草鱼生长性能。HSD 会引起鱼类拥挤胁迫，导致鱼体甲状腺激素（THs）水平显著变化，抑制鱼类生长。为了探究本系统中拥挤胁迫对草鱼甲状腺机能的影响，研究了 THs 及相关脱碘酶的代谢。结果显示，草鱼血清 T3，血小板生成素(TPO)随养殖密度增加而降低；III 型脱碘酶(Dio3)、葡糖醛酸转移酶(UDPGT)随养殖密度增加而升高。HSD 引起 Dio3 活力增加，加速 TH 内环脱碘导致 TH 失活。影响肝脏 UDPGT 活力，提高 TH 清除率，使 TPO 受抑制干扰 TH 合成。

关键词：池塘工程化化圈养系统；草鱼；养殖密度；生长性能；甲状腺激素

An in-pond tank culture system: Effect of stocking density on growth and thyroid function of grass carp

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Abstract: In this experiment, a new type of pond recirculating system "In-pond tank culture system" was constructed. In this system, grass carp was cultured with high stocking density, medium stocking density, and low stocking density for 120 days. The results showed that high stocking density (HSD) would inhibit the growth performance of grass carp. HSD can cause fish crowding stress, leading to significant changes in fish thyroid hormone (THs) levels and inhibiting fish growth. In order to explore the impact of crowding stress on grass carp thyroid function, the metabolism of THs and related deiodinases was studied. The results showed that grass carp serum T3 , thrombopoietin (TPO) decreased with the increased of stocking density; type III deiodinase (Dio3), glucose Aldyltransferase (UDPGT) tends to increase with the increased of stocking density. HSD increases the vitality of Dio3, accelerates the deiodination of the inner loop of TH, leads to inactivation of TH. Affects the vitality of liver UDPGT, improves TH clearance rate, inhibits TPO interferes with TH synthesis.

Key words: In-pond tank culture system；grass carp, stocking densities；growth performance； thyroid hormone

波流条件下桩网分离式围网网衣受力的研究

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摘要：围网养殖是一种新的生态养殖模式，主体由桩柱、网衣、纲绳等结构组成。网衣系统安全是决定围网养殖工程安全的关键所在。本文提出桩网分离式新型围网工程结构，采用集中质量点法建立围网网衣数值模型，利用 Stokes III 阶波波浪理论，研究波浪、水流和波流联合对桩网分离式围网网衣纲绳和网线最大受力、最大偏移、系缚点受力的影响。

关键词：波浪；数值模拟；水动力；受力；

Study on the mechanical characteristics of pile-net-separation mesh under wave-current conditions

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Abstract: Net Enclosure Aquaculture (NEA) is a new and innovative ecological aquaculture model, in which piles, nets, ropes, and other structures form the main body. The net system is the most important part which affects the security of the whole NEA system. This paper proposes a new type of pile-net-separate net enclose equipment, a numerical model of Net Enclose is established by using the method of concentrated mass point, Using Stokes 3th order wave theory, studies the influence of wave, current and combined action of wave and current on the pile net separation engineering mesh and the maximum force and maximum displacement of the pile net rope.

Key words: wave; numerical simulation; hydrodynamic force; force;

芽孢杆菌制剂对海水贝塘浮游生物群落结构的影响

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摘要：通过对养殖水体环境基因组 DNA 中 16S 和 18S rRNA 基因进行高通量测序和生物信息学分析，研究了在海水贝塘中泼洒芽孢杆菌制剂对养殖水体浮游生物群落的影响。在海水滩涂贝类养殖过程中，芽孢杆菌制剂的常规使用（5 天 1 次，终浓度 1×10^3 CFU/mL）不是浮游生物群落的主要影响因素。

关键词：芽孢杆菌制剂；浮游生物；海水贝塘；高通量测序；16S rDNA；18S rDNA

Impact of bacillus probiotics on plankton community in seawater shellfish pond

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Abstract: Through high-throughput sequencing and bioinformatics analysis of 16S and 18S rRNA genes in the environmental genomic DNA of aquaculture water, the effects of spraying Bacillus on the phytoplankton community in aquaculture water were studied. Therefore, the routine use of Bacillus preparations (once every 5 days, with a final concentration of 1×10^3 CFU/mL) is not the main influencing factor of plankton community in the process of shellfish cultivation in tidal flat.

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

水下机器人在海洋经济发展中的作用

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摘要：海洋是生命的摇篮，是资源的宝库，是人类可持续发展的重要战略空间，具有潜在的巨大经济利益和战略地位。我国海洋经济持续发展，海洋战略的实施使得海洋经济日益受到重视。科技是海洋高新技术产业的孵化器,更是海洋产业转型升级与优化的助推器。本文以有缆遥控水下机器人（Remotely Operated Vehicle，简称 ROV）为例，简述了利用 ROV 的技术特点和优势，详尽的叙述了如何与海洋经济建设等相关业务相结合，以及在水产工业化养殖中发挥的作用，分析了 ROV 在海洋经济中的应用前景和需求，最后对 ROV 在海洋相关领域中的应用前景进行了展望。

关键词：水下机器人；海洋；经济

Role of ROV in marine economic development

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Abstract: The ocean is the cradle of life, the treasure house of resources and an important strategic space for human sustainable development. It has potential huge economic benefits and strategic position. With the sustainable development of China's marine economy and the implementation of marine strategy, marine economy has attracted more and more attention. Science and technology is not only the incubator of marine high-tech industry, but also the booster for the transformation, upgrading and optimization of marine industry. Taking the cable remote control underwater vehicle as an example, this paper briefly describes the technical characteristics and advantages of ROV, describes in detail how to combine with marine economic construction and other related businesses, as well as its role in aquaculture industrialization, analyzes the application prospect and demand of ROV in marine economy, and finally prospects the application prospect of ROV in marine related fields.

Key words: ROV，Marine，Economy

小黄鱼仔稚鱼着底期间摄食习性的变化分析

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摘要：小黄鱼是黄海和东海的关键物种之一，对当地生态系统有重大影响，然而近几十年资源衰退显著。本研究针对长江口小黄鱼的后期仔鱼和早期稚鱼的摄食习惯，采用 DNA 条码来检查其胃肠含物，基于 TA 克隆和 Miseq 高通量测序方法分别进行两组实验以相互补充和比对。结果显示，随着体长的增加，桡足类在饮食中的主导地位下降。后期仔鱼（体长小于 17mm）主要以桡足类为食。在后期仔鱼到稚鱼的过渡期（体长 17～19mm）个体开始摄取较大的生物，如鱼类、糠虾和桡足类。较大的稚鱼（体长>20mm）捕食更广泛的食物，标志着其成功的定居。两种鉴定方法相比较，Miseq 组的物种数量明显大于 TA 克隆组的物种，使得 Miseq 组内的趋势更加明显。建议在未来通过结合 Miseq 和目检来研究仔稚鱼的食性。

关键词:仔鱼；小黄鱼；食性；发育变化；高通量测序

Analysis of small yellow croakers (*Larimichthys polyactis*) feeding habits shifting during settlement

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Abstract: The small yellow croaker, *Larimichithys polyactis,* is a keystone species in the Yellow Sea and the East China Sea that significantly affect the local ecosystems, has been through decades of resource decline. Settlement of post-larvae is another period with high mortality other than first feeding, thus affect the recruitment and survival. The current study was conducted to examine the feeding habits of 49 post-larvae and early juveniles of *L. polyactis* in the Yangtze River estuary. In order to obtain more detailed feeding habits, the method of DNA barcode was used to examine the gastrointestinal contents. Two groups are carried out by TA cloning and Miseq high-throughput sequencing, respectively. The results of both groups revealed that the dietary breadth enlarged with body length increase. The dominance of copepods in diet decreased with body length increasing. Post-larvae (< 17 mm in body length in the current study) mainly feed on copepods. At the beginning of settlement (17 mm-19 mm in body length), *L. polyactis* ingested larger organisms like fishes and mysids, along with copepods. Larger early juveniles (> 20 mm in body length) have a much wider dietary breadth, implying successful settlement. The species numbers in the Miseq group are significantly larger than ones in the TA clone group, making the trend more pronounced within the Miseq group. In conclusion, the current study recommended investigating the feeding habits of larvae by combining Miseq and visual examination in the future.

Keywords: larval fish, small yellow croaker, feeding habits, ontogenetic shift, Miseq sequencing

第二专题：水产生物技术与育种

极端盐碱环境下达里湖瓦氏雅罗鱼局域适应的基因组学研究

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摘要：为了从基因组尺度深入解析达里湖瓦氏雅罗鱼耐受极端盐碱环境的适应性机制，本研究采集了达里湖高碱耐受种群、邻近姊妹湖岗更湖淡水种群和松花江淡水种群个体进行深度基因组重测序和遗传变异信息的挖掘，通过消除空间背景差异聚焦异质水环境，群体遗传结构和适应性进化研究发现，一些与离子和渗透压调节、血管发育、炎症免疫反应等过程相关的关键基因受到正向选择压力，参与盐碱局域适应。其中达里湖种群的血管活性肠肽受体基因 vipr1 多个位点受到强选择，使其编码蛋白具有更高效的配体结构域，可能通过 VIPR1-PACAP/VIP-PRL-NCC 轴参与 Na+/Cl-离子转运。本研究结果将对全面深入解析达里湖瓦氏雅罗鱼盐碱适应的遗传机制奠定基础。

关键词：瓦氏雅罗鱼(*Leuciscus waleckii*)；全基因组重测序；盐碱适应性；选择压力；局域适应

Genetic signatures into local adaptation of Amur ide (*Leuciscus waleckii*) in the Lake Dali Nor under extreme alkali-saline environment

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Abstract: To uncover the genetic basis of Amur ide (Leuciscus waleckii) alkali-saline adaptation, three populations, including one alkali form from Lake Dali Nor, one freshwater form from its adjacent sister Lake Ganggeng Nor, and one freshwater form from its historical origin, namely, the Songhua River, were analyzed using resequencing technology for mining of genetic variation information. A set of key regulated genes associated with osmoregulatory regulation, inflammation and immune responses, and cardiorespiratory development were identified by eliminating spatial background differences, genetic diversity comparison, and selective sweep analysis. Among them, a few sites of the vasoactive intestinal peptide receptor (vipr1) in the Dali Nor population were strongly selected to give its encoded protein a more efficient ligand-binding domain, which may be involved in Na+/Cl- ion transport through the VIPR1-PACAP/VIP-PRL-NCC axis. Our findings provide a basis for further study and reveal key genes for alkali-saline adaptation in Amur ide.

Key words: Amur ide (*Leuciscus waleckii*), whole-genome resequencing, alkali-saline adaptation, selective pressure, local adaptation

碱胁迫下杂交鲟“鲟龙一号”（*Huso dauricus*♀×*Acipenser Schrenckii*♂）鳃组织结构变化及转录表达特征

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摘要：为了探究杂交鲟“鲟龙一号”（*Huso dauricus*♀×*Acipenser Schrenckii*♂）鳃对碱胁迫的响应机制，本实验采用组织学和转录组学的方法研究了高碱胁迫下“鲟龙一号”鳃的组织学变化规律与转录组学表达特征。

关键词：碱胁迫；杂交鲟；鳃；组织学；转录组

Changes of gill structure and transcriptional expression characteristics of hybrid sturgeon（*Huso dauricus*♀×*Acipenser schrenckii*♂）under alkali stress

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Abstract: In order to explore the hybrid sturgeon (*Huso dauricus* ♀ × *Acipenser schrenckii* ♂）, the histological changes and transcriptomic expression characteristics on gills of hybrid sturgeon under high alkali stress were studied by the methods of histological and transcriptomic.

Key words: alkali stress; hybrid sturgeon（*Huso dauricus* ♀ × *Acipenser schrenckii* ♂）; gills; histology; transcriptome

大菱鲆 PPARs 家族基因在高温胁迫下对脂质代谢的调控作用

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摘要：大菱鲆是我国重要的海水经济鱼类，属于冷水性鱼类，对养殖水温要求严格。高温对大菱鲆的影响研究已经成为新的关注方向，并取得显著进展。基于本实验室前期对高温下大菱鲆转录组分析发现，PPAR 信号通路在大菱鲆高温应激下发挥重要作用。PPAR 信号通路以 PPARs 为核心，在脂质代谢调节中起着关键作用。本研究克隆了大菱鲆 PPARs 家族基因，共鉴定到三个亚型 α、β 和 γ。然后分别检测了 PPARs 三个亚型和脂质代谢基因在高温胁迫下的表达模式。同时我们首次利用 RNAi 技术和抑制剂处理分别在大菱鲆体内和细胞中敲降 PPARs 后检测三个亚型下游脂代谢靶基因的表达以进行功能分析。本研究结果将有助于解释 PPARs 家族基因在高温胁迫下调控大菱鲆脂质代谢的作用机制，并为其他海洋鱼类耐热机制的研究提供新的参考。

关键词：PPARs；大菱鲆；高温胁迫；脂质代谢

Effects of PPARs family genes on lipid metabolism in Scophthalmus maximus under high temperature stress

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Abstract: Scophthalmus maximus is an important marine economic fish in China, which belongs to cold water fish, so the aquaculture water temperature is strictly required. The effect of high temperature on turbot has become a new focus and significant progress has been made. Based on our previous transcriptome analysis of Turbot under high temperature conditions, we found that PPAR signaling pathway plays an important role in turbot under high temperature stress. PPAR signaling pathway, with PPARs as its core, plays a key role in lipid metabolism regulation. In this study, PPARs family genes of Turbot were cloned and identified as α, β and γ subtypes. Then, the expression patterns of PPARs subtypes and lipid metabolism genes under heat stress were detected. At the same time, we used RNAi technology and inhibitor treatment for the first time to knock down PPARs in turbot and cells respectively, and then detected the expression of downstream lipid metabolism target genes of the three subtypes for functional analysis. The results of this study will help to explain the mechanism of PPARs family genes regulating lipid metabolism in turbot under high temperature stress, and provide a new reference for the study of heat tolerance mechanism in other Marine fishes.

Key words: PPARs, Scophthalmus maximus, lipid metabolism, high temperature,

海参体壁胶原蛋白小分子稳定剂的构效关系研究

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摘要：为了稳定海参体壁胶原蛋白，实现即食类海参产品的常温贮藏，本研究以双重美拉德反应交联胶原蛋白形成稳定的网状结构为基本思路，以还原糖为原型，制备出一系列有交联活性的小分子糖类衍生物,并从分子成环及异构化方式、还原端自由度、氢键供受体等多个角度探究其构效关系，据此优化结构，进一步提升其稳定化海参的活性。

关键词：交联；海参；非酶失稳；胶原蛋白；室温贮藏

Research of the structure-function relationship of small-molecule sea cucumber bodywall collagen stabilizer

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Abstract: The aim of this study is to develop crosslinking agents that can stabilize sea cucumber collagen, and realize the room-temperature storage of instant sea cucumber products. The basic strategy is to use double Maillard reaction to crosslink collagen and yield a stable network. A series of saccharide derivatives with crosslinking activity was prepared from reducing sugars, and the structure-function relationship was explained from the aspect of structural cyclization and isomerization, the degree of freedom of the reducing ends and hydrogen bond donor/acceptors, etc. The structure of the crosslinking agents was then optimized which yielded higher activity on sea cucumber stabilization.

Key words: Cross-link, sea cucumber, non-enzymatic deterioration, collagen, shelf-stable

贝类肌红蛋白研究进展

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摘要：目的：目前对贝类肌红蛋白（Mb）的研究较琐碎，为更全面认识贝类肌红蛋白， 方法：本文从肌红蛋白的基本概念、形态结构，贝类肌红蛋白的分类、进化与功能来梳理贝类肌红蛋白的研究进展。根据肌红蛋白及软体动物珠蛋白等相关文献梳理归纳提炼研究进展。结果结论：1.肌红蛋白具有较高多样性，与血红蛋白关系密切，与珠蛋白E 有较高同源性。贝类与脊椎动物的肌红蛋白是不同的。2.主要有单体、二聚体两种聚集形态，并且是以此分为两类，二者间在氧合力等方面具有差别，推测聚集形态与其功能有密切关系，二聚体形态较高级。3.聚集形态的分化可能是独立进化而来。4.肌红蛋白功能主要与氧气结合运输、能量代谢有关。展望：目前软体动物肌红蛋白的研究还不系统深入，值得深入研究其分类与进化，从软体动物肌红蛋白的一级和空间结构分析将是一个有效深入了解肌红蛋白分类和进化的方式，包括对它们内含子位置和序列的研究。意义：整合梳理了软体动物肌红蛋白的研究进展，意使读者对软体动物的肌红蛋白有一个更全面的认识；有观点推测肌红蛋白与血红蛋白存在进化关系，故研究肌红蛋白将可能有助于其它珠蛋白的研究，故本文可供对肌红蛋白及珠蛋白、软体动物相关研究人员参考。

关键词：贝类；肌红蛋白；分类；进化；功能

Research progress of shellfish myoglobin

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Abstract: Objective: at present, the research on shellfish myoglobin (Mb) is relatively trivial, in order to have a more comprehensive understanding of shellfish myoglobin, Methods: this paper reviews the research progress of shellfish myoglobin from the basic concept, morphological structure, classification, evolution and function of shellfish myoglobin. The research progress of myoglobin and mollusc globin was summarized according to the related literature. Results and conclusions: 1. Myoglobin has high diversity, is closely related to hemoglobin and has high homology with globin E. The myoglobin of shellfish is different from that of vertebrates. 2. There are mainly two kinds of aggregation forms: monomer and dimer, and they are divided into two types. There are differences in oxygenation force between them. It is speculated that the aggregation form is closely related to its function, and the dimer morphology is more advanced. 3. The differentiation of aggregation forms may have evolved independently. 4. The function of myoglobin is mainly related to oxygen binding transport and energy metabolism. Prospect: at present, the study of myoglobin in molluscs is not systematic and in-depth, and it is worth studying its classification and evolution. The analysis of the primary and spatial structure of myoglobin in molluscs will be an effective way to understand the classification and evolution of myoglobin, including the study of the position and sequence of their introns. Significance: this paper combs the research progress of myoglobin in molluscs, which means that readers can have a more comprehensive understanding of myoglobin in molluscs. it is speculated that there is an evolutionary relationship between myoglobin and hemoglobin. therefore, the study of myoglobin may be helpful to the study of other globins, so this paper can be used as a reference for the researchers of myoglobin, globin and molluscs.

Key words: Shellfish; myoglobin; classification; evolution; function

青鱼体型相关的基因复制研究

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摘要：青鱼（*Mylopharyngodon piceus*）属鲤科，是长江流域重要的渔业资源。我们报道了一个大小为 975 MB 的青鱼 survey 基因组，共注释了 27,541 个编码基因，它与草鱼和斑马鱼具有较高的同源性。青鱼与草鱼、斑马鱼分化时间在大约 13 百万年前和 57 百万年前。通过对 8 种鱼类扩增基因家族的鉴定，发现涉及发育相关途径的基因在青鱼和草鱼等大型鱼类中发生了复制。这些复制基因编码的蛋白质所构建的功能互作网络，在青鱼、草鱼中调控生长发育通路使其体型增大，但是在河鲀中表达生长抑素受体，调控抑制生长激素分泌的生长抑素的分泌，造成河鲀鱼与草鱼、青鱼体型的差异。

关键词：基因组；序列；基因复制；进化；鱼；基因家族

Survey genome sequence of black carp provides insights into body-size-related gene duplications

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Abstract: Black carp (*Mylopharyngodon piceus*) is a species of Cyprinidae with an important fishery resource in the Yangtze River. Here, we reported a black carp survey genome with 975 MB in size. A total of 27,541 protein-coding genes were annotated, which exhibited a high synteny with grass carp and zebrafish. Phylogenetic analysis estimated that black carp diverged from grass carp and zebrafish around 13 and 57 million years ago, respectively. Identification of expanded gene families among eight fish species revealed that the genes involved in development-related pathways underwent the duplications in the large body fishes, black carp and grass carp. The constructed functional interaction networks of proteins encoded by these replication genes regulate the growth and development pathways that increase the body size of black carp and grass carp. However, the expression of somatostatin receptor in takifugu regulates the secretion of somatostatin which inhibits GH secretion, resulting in the body size difference between puffer fish and grass carp and black carp.

Key words: genome, sequence, gene duplication, evolution, fish, gene family

克氏原螯虾养殖群体的 SLAF 测序及遗传多样性分析

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摘要：为了获知是否需要及时引种和群体间杂交以改善养殖群体种质，本实验采用一种简化基因组测序技术——特定区点扩增片段测序技术（SLAF-seq），对来自五省的克氏原螯虾主要产地的 14 个养殖群体的 120 个个体进行测序，对多态性位点数据进行群体遗传学分析。通过利用鉴定出的 741147 个单核苷酸多态性（SNP）位点进行群体系统进化分析表明，14 个群体的种源主要来自浙江金华和江苏宿迁，然后再向各地引种迁徙,同时发现各群体均接近遗传多样性中等水平的下限。

关键词：克氏原螯虾；SLAF-seq；SNP；遗传多样性; 群体遗传学

Analysis of genetic diversity among the farmed *Procambarus clarkii* populations using the SLAF-seq technology

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Abstract: In order to know whether timely introduction and interpopulation hybridization are needed to improve the breeding population germplasm, a Specific-Locus Amplified Fragment Sequencing (SLAF-seq) technology, one of the restriction site-associated DNA sequencing technologies, was applied to sequence 120 individuals of 14 farmed populations from the five provinces to identify the single nucleotide polymorphism (SNP) loci and compare the genetic variations. Using the identified 741147 SNPs, the phylogeny and admixture analyses were performed among the sequenced individuals, which suggested two probable origins, Jinhua and Suqian, of the 14 populations. Also it was found that each population was close to the lower limit of medium genetic diversity.

Key words: *Procambarus clarkii*; SLAF - seq; SNP; genetic diversity; population genetics

MSTN 基因对脊尾白虾蜕皮间期肌肉生长发育的作用及调控机制研究

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摘要：生长性状是水产动物育种研究中重要的衡量指标，甲壳动物的生长发育主要依赖于蜕皮过程中肌肉的重塑和生长速率。肌肉生长抑制素（MSTN）基因是哺乳动物肌肉生长发育及分化的重要负调控基因，但在甲壳动物中，MSTN 基因对肌肉生长的作用及调控机制仍不明确。本实验以脊尾白虾为对象，探究 MSTN 基因对其蜕皮间期肌肉生长发育的作用及其调控机制。结果表明：（1）脊尾白虾 MSTN 基因包括 3 个外显子和 2 个内含子，有两个 SNP 位点 g.Mstn220 和 g.Mstn567 与体重和体长性状显著相关；（2）MSTN 在脊尾白虾的多个组织中均有表达，在腹部肌肉的表达量显著高于其它组织， MSTN 基因的表达量从无节幼体期开始显著增加；（3）MSTN 基因在肌肉组织中的表达量与生长性状呈负相关，敲降 35 天后，脊尾白虾体重性状与对照组相比显著增加，过表达 MSTN 基因 24 h 后，生长相关基因的表达显著下降，说明 MSTN 基因对脊尾白虾生长发育起负调控作用；（4）敲降 MSTN 导致其下游的 TGF-β、MAPK 和 PI3K-Akt 信号通路的部分基因上调表达，提示 MSTN 可能通过调控 MAPK 和 PI3K-Akt 信号通路进而对生长起负调控作用。

关键词：生长；脊尾白虾；蜕皮间期；过表达

The role and regulation mechanism of MSTN in the muscle growth and development during intermolt period of *Exopalaemon carinicauda*

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Abstract: Muscle growth in crustacean is a complicated process where the muscle grows and develops through muscle restoration, and the growth rate depends on the net muscle gain during molting. Myostatin (MSTN) is a conserved inhibitor of muscle growth in vertebrates, but until now solid evidence supporting a similar function of MSTN in invertebrates has been lacking. There were three exons and two introns in MSTN, and two SNP loci g.Mstn220 and g.Mstn567 were markedly associated with both body weight and body length. MSTN was expressed in a wide range of tissues, but predominantly detected in the abdominal muscle. Low expression was detected in the cleavage, blastula and gastrula stages in the early development stages, increasing after the nauplius stage. MSTN expression was negatively correlated with the growth traits. The growth-related genes were down regulated after MSTN overexpression, and the body weight increased significantly after 35 days of long-term knockdown of MSTN. The knockdown of MSTN may lead to up-regulation of TGF-β, MAPK and PI3K Akt signaling pathways, suggesting that MSTN regulates growth by regulating MAPK and PI3K Akt signaling pathways.

Key words: growth, *Exopalaemon carinicauda*, intermolt, overexpress

对虾科物种线粒体基因组特征和系统发育分析

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摘要：本研究综合分析了对虾科（Penaeidae）21 个物种线粒体基因组的全序列，同时采用 ML（maximum likelihood）和 BI（bayesian inference）方法构建系统发育树。为快速鉴定对虾科生物提供了可靠的分子标记，为分析对虾科物种遗传多样性提供理论依据。

关键词：对虾科；线粒体基因组；结构特征；系统发育

Characteristics and phylogenetic analysis of mitochondrial genome in the Penaeidae

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Abstract: In this study, we comprehensively analyzed the complete sequence of the mitochondrial genomes of 21 species in the Penaeidae. At the same time, this study adopted more systematic and comprehensive ML (maximum likelihood) and BI (bayesian inference) methods to construct a phylogenetic tree. And this study provides reliable molecular markers for the rapid identification of Penaeidae species, and provides a theoretical basis for analyzing the genetic diversity of Penaeidae species.

Key words: Penaeidae; mitogenome; structure characteristic; phylogeny

低温胁迫下野生罗非鱼脑的转录组分析

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摘要：为了了解野生罗非鱼对低温的应激反应机制，对野生罗非鱼与养殖的尼罗罗非鱼的脑组织进行了转录组测序和比较转录组分析。结果发现，昼夜节律和凋亡信号通路中的基因在野生罗非鱼和养殖罗非鱼脑组织的低温胁迫下存在着差异表达。野生罗非鱼的相关基因在低温胁迫的早期(14℃,120h)，显著上调(如 camk2b1 、MPP5、 PER2 、hmgb1a、lmnb2、ptpn13、ptpn13、dffa 和 casp2)，而在长期低温胁迫（288h 时）后，这些基因表达明显下调。但养殖罗非鱼的这些基因，在这个过程中，表达始终不断的上升。此现象表明，野生罗非鱼可能对低温胁迫的应激机制有所差异。

关键词：罗非鱼；脑；低温；转录组

Analysis of brain transcriptome data in wild tilapia under low temperature stress

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Abstract: To investigate the stress response mechanism of wild tilapia in cold tolerance, a transcriptome sequencing and a comparative transcriptome analysis were performed on the brain tissues of wild tilapia and farmed Nile tilapia. It was found that the genes involved in circadian rhythm and apoptosis signaling pathways were differentially expressed between the wild and farmed tilapias during the prolonged low temperature stress. In wild tilapia, the related genes (camk2b1, MPP5, PER2, hmgb1a, lmnb2, ptpn13, ptpn13, dffa and casp2) were significantly up-regulated at the early stage of low temperature stress (14℃,120h) but down-regulated after a long time of low temperature (288h). Comparatively, those genes of the farmed tilapias were constantly increased during this process. It was suggested that the wild and farmed tilapias probably have different mechanisms in low temperature stress.

Keywords: tilapia; brain; low temperature; transcriptome

黄颡鱼白介素 22（IL-22）基因克隆及表达分析

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摘要：以黄颡鱼（*Pelteobagrus fulvidraco*）肝脏 RNA 为模板，分离克隆得到 IL-22 基因序列，蛋白质编码区（CDS）包含 546 个核苷酸，共编码 181 个氨基酸。同源比对发现，黄颡鱼 IL-22 和其它几种物种 IL-22 氨基酸序列有较高的相似度。多重比对发现，其与其它物种的 IL-22 氨基酸序列相似性为 43.03%~97.99%。qRT-PCR 发现，IL-22 在黄颡鱼肝脏、肠、脑、鳃、脾脏、肾脏、心脏、肌肉中均有表达，鳃组织表达量最高，肠组织次之。低氧胁迫 24h 和 48h 后，IL-22 表达量均显著上升。本研究为探究在低氧胁迫下 IL-22 基因发挥的功能提供了基础材料。

关键词：黄颡鱼；IL-22；基因克隆；组织表达；低氧胁迫

Cloning and expression analysis of interleukin-22 (IL-22) gene from *Pelteobagrus fulvidraco*

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Abstract: The kidney RNA of *Pelteobagrus fulvidraco* was used to be the template to isolate and clone the full-length cDNA sequence of interleukin 22 (IL-22). The coding sequence(CDS) contained 546 nucleotides, encoding 181 amino acids. Homologous comparison showed that the alignment of IL-22 amino acid sequence with several other species was more than 90% similar. The distribution analysis of IL-22 showed that IL-22 was expressed in tissues (liver, intestine, brain, gill, spleen, kidney, heart and muscle) of *Pelteobagrus fulvidraco*, with the highest expression level in gill, next was intestine. These studies laid a foundation for exploring the role of IL-22 in the immune regulation of teleost fish.

Keywords: *Pelteobagrus fulvidraco*; IL-22; Bioinformatics analysis; Expression analysis

全基因组测序揭示解淀粉芽孢杆菌 CQN-2 的潜在益生功能

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摘要：解淀粉芽孢杆菌 CQN-2 分离自健康仿刺参肠道，经安全性试验证明不会导致仿刺参损伤或者死亡，并且对仿刺参病原菌塔氏弧菌具有体内和体外抗菌活性。为了进一步探讨 CQN-2 菌株的潜在益生功能，本研究对 CQN-2 菌株进行了全基因组测序，获得两个环状复制子，一个 3929751 bp 的染色体,GC 含量 46.5%,编码 4260 个 CDS，一个 161917 bp 的质粒,GC 含量 33.5%，编码 76 个 CDS。数据库注释表明，33 个基因参与细胞内运输分泌和囊泡运输，110 个基因参与次生代谢产物的生物合成、运输和分解代谢，基因组中包含细菌趋化性、鞭毛组装等可影响定植的通路。次生代谢产物主要包含非核糖体肽合成酶和聚酮合酶。通过 BAGEL4 挖掘潜在的细菌素、RiPPs 基因簇，CQN-2 染色体中含有合成 Amylocyclicin、ComX3、LCI 和 Lanthipeptide_class_II 的基因簇。结果表明解淀粉芽孢杆菌 CQN-2 具有益生菌应用潜力。

关键词：解淀粉芽孢杆菌；仿刺参；益生菌；全基因组测序

The complete genome sequence of *Bacillus amyloliquefaciens* CQN-2 reveals potential probiotic functions

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Abstract: *Bacillus amyloliquefaciens* CQN-2 was isolated from the intestinal tract of healthy *Apostichopus japonicus*. It has been proved by safety tests that it will not cause injury or death of *A. japonicus*, and it has antibacterial activity against *Vibrio tubiashii* in vivo and in vitro. In order to further explore the potential probiotic function of the CQN-2 strain, the whole genomet sequencing of the CQN-2 strain was performed. It revealed a chromosome of 3929751 bp, with 46.5% GC content. , encoding 4260 CDS, a plasmid of 161917 bp , with 33.5% GC content , encoding 76 CDS. Database annotations indicate that 33 genes are involved in intracellular trafficking secretion and vesicular transport, 110 genes are involved insecondary metabolites biosynthesis, transport and catabolism. The genome contains pathways that can affect colonization, such as bacterial chemotaxis and flagella assembly. The secondary metabolites mainly include non-ribosomal peptide synthase and polyketide synthase. Potential bacteriocin and ripps gene clusters were excavated through BAGEL4. The chromosome of strain CQN-2 contained gene clusters that synthesized Amylocyclicin, ComX3, LCI and Lanthipeptide_class_II. The results showed that *B. amyloliquefaciens* CQN-2 had the potential application of probiotics.

Key words: *Bacillus amyloliquefaciens*, *Apostichopus japonicus*, probiotic, whole-genome sequence

高温胁迫对南移仿刺参热休克蛋白基因和免疫酶活力的影响

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摘要：为了探究南移养殖仿刺参在高温胁迫下的应答特征，测定了南移仿刺参在不同温度下热休克蛋白基因 *hsp10*、*hsp60*、*hsp70*和 *hsp90*的表达变化，以及不同温度下超氧化物歧化酶(SOD)、总抗氧化能力(T-AOC)、过氧化氢酶(CAT)、酸性磷酸酶(ACP)、碱性磷酸酶(AKP)和溶菌酶(LSZ)的活性变化。结果发现，实验组(20 ℃、24 ℃、28 ℃、32 ℃)相比于对照组(16 ℃)，仿刺参热休克蛋白基因的表达量有不同程度的变化，尤其在 28 ℃和 32 ℃高温组中，各基因的表达量显著提高。仿刺参体壁中 SOD 和 LSZ 活性随着温度升高呈先升高后降低的趋势，而 T-AOC、CAT、ACP 和 AKP 的活性随温度升高呈下降趋势。

关键词：仿刺参；高温胁迫；热休克蛋白；免疫酶活力

Effects of high temperature stress on heat shock protein gene and immune enzyme activity of *Apostichopus japonicus* moved southward

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Abstract: In order to explore the response characteristics of *Apostichopus japonicus* transplanted to the south under high temperature stress, and to determine the expression changes of heat shock protein genes *hsp10*, *hsp60*, *hsp70* and *hsp90* at different temperatures. And the activity changes of superoxide dismutase (SOD), total antioxidant capacity (T-AOC), catalase (CAT), acid phosphatase (ACP), alkaline phosphatase (AKP) and lysozyme (LSZ) at different temperatures. The results showed that the expression of heat shock protein genes in the experimental group (20 ℃, 24 ℃, 28 ℃, 32 ℃) was different from that in the control group (16 ℃), especially in the high temperature groups of 28 ℃ and 32 ℃. The expression of each gene increased significantly. The activities of SOD and LSZ in body wall of *Apostichopus japonicus* increased firstly and then decreased with the increase of temperature, while the activities of T-AOC, CAT, ACP and AKP decreased with the increase of temperature.

Key words: *Apostichopus japonicus*; high temperature stress; heat shock protein; Immune enzyme activity

基于微卫星多重 PCR 技术的红螯螯虾亲子鉴定

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摘要：红螯螯虾是较为名贵的淡水经济虾类之一，具有重要的商业价值。为防止红螯螯虾种群的种质资源退化，迫切需要对其种质资源进行保护。本研究基于红螯螯虾全基因组序列筛选微卫星标记，结合毛细管电泳方法，建立适用于红螯螯虾亲子关系鉴定的实验体系。通过不断优化组合的退火温度、引物浓度和循环次数，使用 20 个扩增效果良好、多态信息含量（PIC）丰富的四碱基微卫星标记，构建了 5 组微卫星多重 PCR 体系。利用 Cervus 3.0 软件对 12 个已知系谱信息的红螯螯虾家系进行亲子鉴定。结果表明，从 20 个位点共扩增出 112 个等位基因。选取 5 个组合时，累积实际鉴定率达到 100%。本研究构建的微卫星多重 PCR 体系可为红螯螯虾的分子系谱构建、群体选育和家系管理提供便捷有效的途径。

关键词：红螯螯虾；四碱基重复微卫星；多重 PCR；亲子鉴定

Parentage assignment of *Cherax quadricarinatus* using multiplex pcr of microsatellites

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Abstract: *Cherax quadricarinatus*, commonly known as valuable freshwater crayfish, possesses important commercial benefits. In order to prevent the germplasm degradation of *C. quadricarinatus* population, it is urgent to protect its germplasm resources. In this study, microsatellite markers were screened based on the whole genome sequence of *C. quadricarinatus.* Combining microsatellite markers with capillary electrophoresis, an experimental system suitable for parentage assignment of *C. quadricarinatus* was established. By continuously optimizing the annealing temperature, primer concentration, and cycle numbers of the combination, 20 tetranucleotide microsatellite loci with good amplification effect and the high polymorphism information content (PIC) were obtained, and five groups of microsatellite multiplex PCR systems were constructed. Parentage assignment of 12 families of *C. quadricarinatus* with known pedigree information using Cervus 3.0 software. The results showed that 112 alleles were amplified from the 20 loci. Furthermore, after selecting five combinations, the rate of correct identification reached 100%. The microsatellite multiplex PCR system constructed in this study can provide a convenient and efficient way for molecular pedigree construction, population breeding, and family management of *C. quadricarinatus*.

Keywords: *Cherax quadricarinatus,* tetrameric microsatellite markers, multiplex PCR, parentage assignment

碳酸氢盐胁迫对碱水型和淡水型瓦氏雅罗鱼血清离子和鳃转运蛋白的影响

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摘要：为了解生存在内蒙古达里湖中的碱水型瓦氏雅罗鱼对高碱环境适应的离子调节机制，本研究围绕生理指标与分子机制对高碱胁迫下碱水型和淡水型瓦氏雅罗鱼的应答差异进行分析，提出碱水型瓦氏雅罗鱼维持离子和酸碱平衡的模型，为其适应极端碱性条件的生理反应提供了新的见解。

关键词：瓦氏雅罗鱼(*Leuciscus Waleckii*)；碱性水体；离子调节；离子转运蛋白

Effects of Bicarbonate Stress on Serum Ions and Gill Transporters in Alkali and Freshwater Forms of Amur Ide

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Abstract: In order to understand the ion regulation mechanism of alkaline form Amur ide in Lake Dali of Inner Mongolia in adapting to the high-alkali environment, this study analyzed the response difference between alkaline form and freshwater form Amur ide under high alkali stress around physiological indicators and molecular mechanism, and proposed a model for alkaline form Amur ide to maintain ion and acid-base balance. It provided a new insight into the physiological response of alkaline form Amur ide to adapt to extreme alkaline conditions.

Keywords： Amur ide (*Leuciscus waleckii*); alkaline water; ionoregulation; ion transporters

黄河鲤 SCoT 分子标记 PCR 反应体系的建立及引物筛选

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摘要：为建立黄河鲤 SCoT-PCR 的最佳反应体系并筛选能在黄河鲤中扩增的多态性引物和最适温度，本实验采用 L_{25}（5^3）正交设计与单因素实验的方法优化反应体系中 2xTap PCR MasterMix、模板 DNA 及引物的用量。然后按照 8 个梯度筛选引物多态性和退火温度（49~62℃）。结果表明：黄河鲤 SCoT-PCR 的最佳反应体系（20μl）为 2×Tap PCR MasterMix 用量 10μl、模板 DNA 用量 1μl（25ng/μl）、引物用量 1μmol/L、ddH$_2$O 用量 8μl；通过此最佳反应体系，从 80 条引物中筛选出扩增稳定、条带清晰且多态性较高的引物 39 条。本研究结果为 SCoT 分子标记在黄河鲤中的应用提供了参考。

关键词：黄河鲤（*Cyprinus carpio haematopterus*）；SCoT；PCR 体系；引物；筛选

Establishment of SCoT Molecular marker PCR reaction system and primer screening in *Cyprinus carpio haematopterus*

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Abstract: To establish the optimal reaction system of start codon targeted polymorphism polymerase chain reaction of Yellow River Carp *(Cyprinus carpio haematopterus*) and screen the polymorphic primers and optimal temperature that can be amplified in Yellow River carp, in this experiment, $L_{25}(5^3)$ orthogonal design and single factor experiment were used to optimize the dosage of 2xTap PCR MasterMix, template DNA and primers in the reaction system. Then screen primer polymorphism and annealing temperature (49~62℃) according to 8 gradients. The result shows: The best reaction system (20μl) for Yellow River Carp SCoT-PCR is the dosage of 2xTap PCR MasterMix is 10μl、the dosage of is Template DNA 1μl (25ng/μl)、the dosage of the primer is 1 μmol/L、ddH$_2$O 8μl; Through this optimal reaction system, 39 primers with stable amplification, clear bands and high polymorphism were selected from 80 primers. The results of this study provide a reference for the application of molecular markers of SCoT in Yellow River carp.

Key words: Yellow River carp (*Cyprinus carpio haematopterus)*; SCoT; PCR System; Primer; Screen

人工养殖过程中大刺鳅间性个体的发现

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摘要：我们通过对大刺鳅（*Mastacembelus armatus*）连续 4 年的养殖试验，发现大刺鳅雌雄性别比例严重偏离 1:1，雌性比例较高且个体较小。进而从形态学、解剖学和性腺组织学水平首次证明了大刺鳅在人工养殖条件下出现间性个体。通过对大刺鳅不同性腺转录组分析，鉴定出的性别差异候选基因 Dmrtb1/Dmrt6，特异性表达于精子细胞、精子、精原细胞和精母细胞中。通过单细胞转录组分析，发现间性性腺中存在具有双向性别分化的潜力的细胞群。

关键词：性别二态性；DM 结构域；dmrtb1/dmrt6；间性；单细胞 RNA 测序

Bulk and single-cell RNA-seq reveal the sexually dimorphic expression pattern of dmrtb1 in zig-zag eel (*Mastacembelus armatus*)

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Abstract: Sequential hermaphroditism, whereby the sex of one individual changes during its development, has been described in many fish species. Here, we report the characterization of intersexual differences in an aquacultural fish, the zig-zag eel (*Mastacembelus armatus*), based on 4 years of artificial breeding. A DM-domain candidate gene, dmrtb1, was identified from gonadal transcriptome data screening. The expression of dmrtb1 was restricted to testis, similar to dmrt1, which is one of the conserved sex-determining genes in vertebrates. Interestingly, dmrtb1 was expressed at the onset of sex change (early stage), and gradually increased in expression in the intersex gonads until the late stage of differentiation. Dmrtb1 was also expressed in the seminiferous lobules containing cysts with germ cells. A mixed cell population from ovotestis was identified by single-cell RNA sequencing, and included mitotic fetal germ cells, meiotic prophase fetal germ cells, and gonad endothelial cells. Spermatocyte and oocyte marker genes were both enriched in the same gonadal cell population, indicating this cell population might have the potential of bisexual differentiation.

Keywords: Sexual dimorphism, DM-domain, dmrtb1/dmrt6, Intersex, Single-cell RNA sequencing

厚壳贻贝甲腺原氨酸脱碘酶基因调控幼虫变态的作用研究

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摘要：厚壳贻贝幼虫的附着变态过程是苗种培育的关键时期。甲腺原氨酸脱碘酶是甲状腺素信号通路的重要调控因子。本实验室前期从双壳类厚壳贻贝（*Mytilus coruscus,* Mc）中克隆得到两个脱碘酶基因（*McDx*和 *McDy*）全长。本研究利用原位杂交方法研究了 *McDx*和 *McDy*基因在厚壳贻贝幼虫各发育阶段的时空表达。结果显示：在担轮幼虫时期，*McDx*和 *McDy*都表达在端毛轮和环毛轮，*McDx*同时在壳区域也有表达。在 D 型幼虫时期，*McDx*和 *McDy*表达在外套膜区域，表明主要与壳的生成相关。在壳顶幼虫和眼点幼虫时期，*McDx*和 *McDy*在胃肠区域都有表达。值得注意的是，*McDx*在眼点幼虫脑神经节、足神经节和内脏神经节也有表达，表明其对神经节发育具有重要作用。为研究厚壳贻贝脱碘酶基因在幼虫变态发育过程中的作用，采用 siRNA 电转染技术分别敲降了 *McDx*和 *McDy*基因的表达，qPCR 结果显示 *McDx*和 *McDy*基因的表达量较对照组显著下降（$P<0.05$），且敲降后幼虫变态率与对照相比显著下降（$P<0.05$）。本研究揭示了厚壳贻贝脱碘酶基因参与了幼虫的生长和变态发育，为研究贝类幼虫变态的分子机制提供数据支撑。

关键词：厚壳贻贝；甲腺原氨酸脱碘酶；幼虫变态；RNA 干扰

Effects of two iodothyronine deiodinase genes on larval metamorphosis of the mussel *Mytilus coruscus*

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Abstract: Larval metamorphosis in *Mytilus coruscus* is the key stage of seedling cultivation. Iodothyronine deiodinase is an important regulator of the thyroid hormone signaling pathway. The full-length of two deiodinase genes *(McDx* and *McDy*) were cloned from *Mytilus coruscus* (Mc). In this study, we detected the mRNA expression of *McDx* and *McDy* in the different developmental stages of larval development by *in situ* hybridization. The results showed that both *McDx* and *McDy* were expressed at the prototroch and telotroch of trochophore larvae, and *McDx* was also expressed at the shell field of trochophore larvae. *McDx* and *McDy* were expressed in the mantle in the D-veliger larvae, indicating that *McDx* and *McDy* may involve in shell formation. In umbo and pediveliger stages, *McDx* and *McDy* were widely expressed in gastrointestinal. It is noted that *McDx* was also expressed in the cerebral (cg), pedal (pg) and visceral (vg) ganglia of pediveliger larvae, suggesting that *McDx* may play an important role in ganglion development. Knock-down of the *McDx* and *McDy* genes in pediveliger larvae of *M. coruscus* significantly reduced the mRNA expression of *McDx* and *McDy* ($P<0.05$), and the larval metamorphosis was decreased significantly compared to the control larvae ($P<0.05$). The results of this study indicate that *McDx* and *McDy* are involved in larval growth and metamorphosis development.

Keywords: *Mytilus coruscus*; iodothyronine deiodinase; larval metamorphosis; siRNA

鳜牙齿形态结构及与不同种属间比较观察

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摘要：牙齿是肉食性鱼类重要的摄食器官。为探究鳜牙齿形态结构，采用解剖镜观察了鳜牙齿分布、形态与数量，并比较其与大眼鳜、斑鳜及中国少鳞鳜牙齿差异。采用茜素红染色、组织切片、扫描电镜、X 射线能谱及红外光谱观察并检测了鳜牙齿结构、元素组成和化学成分。结果显示，鳜牙齿具上颌齿、下颌齿、犁齿、腭齿和咽齿。茜素红染色显示，犬齿和绒毛状齿外层均为透明的牙釉质，内层为包裹髓腔的牙本质。扫描电镜显示，犬齿和绒毛状齿表面均由釉柱组成。X 射线能谱显示，犬齿和绒毛状齿主要元素都为碳、氧、氮、钙和磷。红外光谱显示，犬齿和绒毛状齿主要无机成分为碳酸羟基磷灰石。结果表明，鳜牙齿发达，上、下颌齿有犬齿，犬齿和绒毛状齿结构与组成基本相似。

关键词：鳜；牙齿；牙釉质；牙本质

Tooth Morphology and Structure of *Siniperca chuatsi*: Comparison with Different Species and Genera

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Abstract: Tooth is an important feeding organ of carnivorous fish. The distribution, morphology and number of teeth in *Siniperca chuatsi* were observed, and compared with *S. kneri*, *S. scherzeri*, *Coreoperca whiteheadi*. The dental structure, element composition and chemical composition of *S. chuatsi* were further studied with alizarin red staining, tissue sections, scanning electron microscopy, as well as X-ray energy spectrum and infrared spectrum analyses. The results showed that *S. chuatsi* had maxillary teeth, mandibular teeth, vomerine teeth, palatal teeth and pharyngeal teeth. Alizarin red staining showed that the outer layer of canine and villous teeth was enamel, and the inner layer was dentin. Scanning electron microscopy showed that the surface of canine and villous teeth was composed of enamel prisms. X-ray energy spectrum showed that the main elements of canine and villous teeth were carbon, oxygen, nitrogen, calcium, phosphorus. Infrared spectrum showed that the main component of canine and villous teeth was carbonated hydroxyapatite. The results show that *S. chuatsi* has more advanced teeth with canines in maxillary and mandibular teeth, and the structure and composition of canines and villous teeth are similar.

Key words: *Siniperca chuatsi*, teeth, enamel, dentine

低盐胁迫对缢蛏生理特性的影响

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摘要：为探究缢蛏(*Sinonovacula constricta*)在低盐条件下的生理适应机制，本研究设置低盐组 1‰、3‰、5‰、10‰和对照组 20‰，开展了 7 天的低盐胁迫实验。结果表明：低盐胁迫导致缢蛏血淋巴渗透压降低，1‰时降低至 105.6 mOsmol·kg-1 H_2O； 与对照组相比，所有低盐度处理组缢蛏肌肉水含量显著增加（$P < 0.05$）； 低盐处理组缢蛏鳃的 Na+/K+-ATPase 活性均显著高于对照组（$P < 0.05$），其中 10‰最高，达到 2.39 μmol·g^{-1}·h^{-1}。采用全自动氨基酸分析仪对缢蛏血淋巴中游离氨基酸含量进行检测，结果显示：牛磺酸、丙氨酸、精氨酸、鸟氨酸是缢蛏血淋巴中主要的游离氨基酸，低盐胁迫导致牛磺酸、精氨酸和鸟氨酸在血淋巴总游离氨基酸的占比增加，而丙氨酸的占比减少，其中牛磺酸在 10‰组中增加了 40.5%， 丙氨酸在 3‰组中减少了 37.25%，表明血淋巴中游离氨基酸在缢蛏渗透压调节方面起重要作用。组织学分析发现鳃血管内组织增生明显，表明低盐胁迫导致鳃组织发生适应性变化。本实验初步揭示了缢蛏在低盐胁迫下通过调节体内 Na+/K+-ATPase 活性与游离氨基酸的含量以适应盐度变化，研究结果为开展缢蛏内陆低盐养殖提供数据参考。

关键词：缢蛏；低盐胁迫；渗透压；游离氨基酸

Effects of low salt stress on physiological characteristics of razor clams *Sinonovacula constricta*

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Abstract: In the present study, a 7-day low salinity (LS) stress experiment was conducted to investigate the physiological adaptation mechanism of razor clams (*Sinonovacula constricta*) under LS conditions by setting up LS groups of 1‰, 3‰, 5‰, 10‰ and a control group of 20‰. The results showed that LS stress reduced hemolymph osmolality to 105.6 mOsmol·kg-1 H_2O at 1‰. The muscle water content in all LS groups was significantly increased compared to the control group ($P < 0.05$). The Na+/K+-ATPase activities of gills in the LS groups were significantly higher than that of the control group ($P < 0.05$), with the highest at 2.39 μmol·g^{-1}·h^{-1} for 10‰. Taurine, alanine, arginine and ornithine were the main free amino acids in the hemolymph of razor clams, which were detected using an automatic amino acid analyzer. LS stress resulted in an increase in the proportion of taurine, arginine, and ornithine in the total free amino acids in the hemolymph and a decreased one of alanine, with taurine increasing by 40.5% in the 10‰ group and alanine decreasing by 37.25% in the 3‰ group, indicating that free amino acids in the hemolymph play an important role in the regulation of osmolality in razor clams. Histological analysis revealed significant tissue hyperplasia within the gill vasculature, suggesting LS stress resulted in an adaptive change in the gill. This study reveals that razor clams adapt to salinity changes by regulating the Na+/K+-ATPase activity and free amino acid content under LS stress, and the results provide data for inland LS culture of razor clams.

Keywords: razor clam, low salt stress, osmotic pressure, free amino acids

内分泌干扰物对三角帆蚌 *Cyp17a* 的影响及其在性腺发育中的作用

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摘要：雌激素和雄激素对贝类内分泌干扰作用非常大。三角帆蚌作为中国重要的水产养殖贝类，具有显著的经济效益。通过将幼贝在含有 17β-雌二醇（E2）和 17α-甲基睾酮（MT）的养殖水体暴露 28 天来评估雌雄激素对三角帆蚌雄性和雌性性腺中类固醇合成酶 *Hc-Cyp17a* 的影响。同时测定性腺发育四个阶段的 E2 含量、*Hc-Cyp17a* 在性腺发育中的表达变化及其在成熟性腺中的定位，探讨基因与激素的关系。

关键词：三角帆蚌；*Cyp17a*；17β-雌二醇；17α-甲基睾酮

Cyp17a effected by endocrine disruptors and its function in gonadal development of *Hyriopsis cumingii*

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Abstract: Endocrine disrupting effects of estrogens and androgens in shellfish are significant. As an important aquaculture shellfish in China, *Hyriopsis cumingii* has remarkable economic benefits. In this study, the effects of estrogen and androgen on the steroid synthase *Hc-Cyp17a* in the male and female gonads of the *H. cumingii* were assessed by exposing juvenile mussels to cultured waters containing 17β-estradiol (E2) and 17α-methyltestosterone (MT) for 28 days. At the same time, the E2 content in the four stages of gonadal development, the expression changes of *Hc-Cyp17a* in gonadal development and its localization in the mature gonad were measured to explore the relationship between genes and hormones.

Key words: *Hyriopsis cumingii*, *Cyp17a*, 17β-Estradiol, 17α-Methyltestosterone

高温胁迫下缢蛏 *p38MAPK* 基因的表达模式及其对细胞凋亡的影响

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摘要：*p38MAPK* 是 MAPK（丝裂原活化蛋白激酶）通路的一个重要分支，在细胞凋亡，细胞增殖和生长等生理过程起重要作用。本实验在缢蛏中筛选鉴定了 *p38MAPK*，该基因编码 359 个氨基酸，且在成体各个组织中广泛表达。在 34℃高温胁迫 12h、24h 时，该基因分别在肝胰腺和鳃组织中显著上调（$p < 0.05$）。进一步利用 dsRNA 干扰技术沉降 *p38MAPK* 基因，发现在鳃和肝胰腺组织中，下游抑凋亡基因 *Bcl-2* 上升，促凋亡基因 *Bax* 极显著下降（$p < 0.01$）；采用 TUNEL 染色技术检测干扰前后细胞凋亡情况，发现干扰 *p38MAPK* 后鳃和肝胰腺组织的细胞凋亡程度降低，ROS 含量极显著降低（$p < 0.01$）。本研究结果揭示了 *p38MAPK* 对缢蛏的高温耐受性具有一定的调控作用。

关键词：缢蛏；高温；*p38MAPK*；细胞凋亡；ROS

Expression pattern of *p38MAPK* in razor clam *Sinonovacula constricta* under high temperature stress and its effect on apoptosis

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Abstract: *p38MAPK* is an important branch of the MAPK (mitogen-activated protein kinase) pathway that plays an important role in physiological processes such as apoptosis, cell proliferation and growth. In this experiment, we screened and identified *p38MAPK* in *Sinonovacula constricta,* which encodes 359 amino acids and is widely expressed in various adult tissues. The gene was significantly up-regulated in liver and gill at 12h and 24h of high temperature stress at 34°C, respectively ($p < 0.05$). Further sedimentation of the *p38MAPK* using dsRNA interference revealed a rise in the downstream apoptosis suppressor gene *Bcl-2* and a highly significant decrease in the pro-apoptosis gene *Bax* in gill and liver ($p < 0.01$). TUNEL staining technique was used to detect apoptosis before and after interference, and it was found that the degree of apoptosis in gill and liver was reduced after interference with *p38MAPK*, and the ROS content was highly significantly reduced ($p < 0.01$). The results of this study reveal that *p38MAPK* has a regulatory role in the heat tolerance of razor clams.

Key words: *Sinonovacula constricta*, high temperature, *p38MAPK,* apoptosis, ROS

三角帆蚌 Hc-BMP10 基因的分子鉴定和表达分析

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摘要：为了探究 *Hc-BMP10* 基因三角帆蚌胚胎发育、生物矿化中的作用，本实验通过 RACE 技术克隆了全长，其全长为 2477bp。组织定量显示 *Hc-BMP10* 在三角帆蚌各组织和胚胎发育各时期均有表达，鳃中表达最高，中央膜次之；胚胎发育各时期中卵裂期表达最高，稚蚌期次之；在破壳后 24h 和 48h 表达上升；原位杂交结果表明，在三角帆蚌边缘膜上表皮细胞检测到较强的信号。结果表明 *Hc-BMP10* 基因三角帆蚌胚胎发育、生物矿化中起重要的作用。

关键词：三角帆蚌；*Hc-BMP10*；胚胎发育；生物矿化

Molecular identification and expression analysis of *Hc-BMP10* gene in *Hyriopsis cumingii*

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Abstract: In order to explore the role of *Hc-BMP10* gene in embryonic development and biomineralization of *Hyriopsis cumingii*, the full-length cDNA of *Hc-BMP10* gene was cloned buy RACE (Rapid-amplificiantion of cDNA ends) method, which was 1383bp. Tissue expression analysis showed that *Hc-BMP10* was expressed in all tissues and stages of embryonic development, with the highest expression in gills, followed by the central membrane. The highest expression was observed in the cleavage stage, followed by the juvenile stage. The expression of *Hc-BMP10* gene increased from 24h and 48h after shell breaking. The results of in situ hybridization showed that Hc-BMP10 the signal of *Hc-BMP10* was strong in the epidermal cells of *H. cumingii*. These results indicate that *Hc-BMP10* gene plays an important role in embryo development and biomineralization of *H. cumingii*.

Keywords：*Hyriopsis cumingii*, *Hc-BMP10*, embryonic development, biomineralization

三角帆蚌 ***MAP2K1*** 基因的克隆和功能研究

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摘要：为了研究 *MAP2K1*（*MEK1*）基因在三角帆蚌性别决定中的作用，采用 RACE 方法克隆了三角帆蚌 *MAP2K1* 基因序列；利用实时荧光定量分析比较 *MAP2K1* 基因在三角帆蚌不同组织（性腺、闭壳肌、肝胰腺、鳃、外套膜、斧足）、早期发育阶段（1～8 月龄）性腺和 1、2、3 龄雌雄性腺中的表达水平；利用 RNA 干扰技术（RNAi）对 *c-Mos* 基因进行干扰，然后观察下游基因 *MAP2K1* 在性腺中的表达情况，推测 *MAP2K1* 基因可能参与三角帆蚌的卵巢发育过程，在三角帆蚌中属于雌性高表达基因。

关键词：三角帆蚌；*MAP2K1* 基因；性别决定；原位杂交；RNAi

Cloning and function study of *MAP2K1* gene in *Hyriopsis cumingii*

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Abstract: In order to study the role of the *MAP2K1* (*MEK1*) gene in the sex determination of *H.cumingii*, the RACE method was used to clone the *MAP2K1* gene sequence;using real-time fluorescence quantitative analysis to compare *MAP2K1* gene in different tissues (gonads, adductor muscle, hepatopancreas, gills, mantle, foot), early developmental stage (1-8 months old) gonads and 1, 2, 3 years'level of expression in male and female glands at age of *H.cumingii;* using RNA interference technology (RNAi) to interfere with the *c-Mos* gene, and then observe the expression of the downstream gene *MAP2K1* in the gonads,it is speculated that *MAP2K1* gene may be involved in the ovarian development process of H.cumingii, and it is a female highly expressed gene in H.cumingii.

Key words: *Hyriopsis cumingii*, *MAP2K1*, Gender determination, In situ hybridization, RNAi

密度和盐度对缢蛏血清离子浓度、Na^+/K^+-ATPase 酶活性及 Na^+/H^+ antiporter 基因表达的影响

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摘要：缢蛏（*Sinonovacula constricta*）是我国重要的经济养殖贝类，密度和盐度是影响其养殖过程中的重要因子。本研究以缢蛏为实验对象，设置高密度组和低密度组，且每个密度组下设 2 个盐度，对其进行 72h 急性高密度、高盐度双因子胁迫实验，并检测鳃组织中 Na^+/K^+-ATPase 酶活性、Na+/H+ antiporter 基因的表达，血清 Na^+浓度、K^+浓度。结果表明 Na^+/K^+-ATPase 酶活性随盐度升高而升高，血清 Na^+浓度、K^+浓度随时间呈现先升高后趋于平稳，Na+/H+ antiporter 基因在鳃组织中的表达随时间呈现先升高后下降的趋势。研究结果对深入解析缢蛏在不同密度和盐度下适应环境变化的生理机制提供了一定的理论基础。

关键词：密度；盐度；离子浓度；Na^+/K^+-ATPase 酶；Na+/H+ antiporter；缢蛏

Effects of density and salinity on serum Ion concentration, Na^+/K^+ -Atpase activity and Na^+/H^+ Antiporter gene expression in *Sinonovacula constricta*

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Abstract: The razor clam (*Sinonovacula constricta*) is an important economically cultured shellfish in China, and density and salinity are important factors affecting its culture process. In this study, high-density and low-density groups were set up for razor clams, and two salinities were set up under each density group, and they were subjected to 72h acute high-density and high-salinity two-factor stress experiments, and the Na+/K+-ATPase enzyme activity, Na+/H+ antiporter gene expression, serum Na+ concentration and K+ concentration in gill tissues were detected. The results showed that Na+/K+-ATPase enzyme activity increased with salinity; serum Na+ concentration and K+ concentration showed a first increase and then leveled off with time, and the expression of Na+/H+ antiporter gene in gill tissue showed a trend of first increase and then decrease with time. The results of the study provide a theoretical basis for an in-depth analysis of the physiological mechanisms of the constrictor razor clams in adapting to environmental changes at different densities and salinities.

Keywords: Density, salinity, ion concentration, Na+/K+ -Atpase, Na+/H+ Antiporter, *Sinonovacula constricta*

高温胁迫对厚壳贻贝足丝分泌的影响及其调控机制初探

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摘要：厚壳贻贝是我国重要的海洋经济贝类，通过其足组织分泌的足丝蛋白固化形成足丝附着于岩石等固体表面。本研究比较了不同温度(21℃，27℃，31℃)下厚壳贻贝足腺体结构、5-羟色胺（5-HT）受体表达模式、5-HT 分布及 5-HT 拮抗剂注射对足丝分泌的影响。结果表明：高温胁迫显著影响了足丝分泌能力，与对照组相比，31℃处理后的足丝分泌能力显著降低($p < 0.05$)。31℃处理后贻贝足组织总腺体面积较 21℃和 27℃处理组显著降低($p < 0.05$)。NBT 染色结果显示 31℃染色颜色较浅，表明高温胁迫降低了足组织中合成足丝原料多巴醌的含量。对不同温度下 5-HT 受体表达分析发现，31℃处理后足组织中 6 个 5-HT 受体表达量显上升($p < 0.05$)。5-HT 免疫组化结果显示 31℃处理后足组织足沟附近 5-HT 分布增多，表明 5-HT 可能对足丝分泌存在调控作用。为进一步研究 5-HT 与足丝分泌关系，本研究对厚壳贻贝足组织注射 5-HT 及其受体拮抗剂米安色林（mianserin），结果显示 5-HT 和米安色林抑制了足丝的分泌。本研究初步揭示了环境温度影响足丝生成的能力，其机制可能是通过 5-HT 信号通路调控足丝发生。

关键词：厚壳贻贝；足丝；足腺体；5-羟色胺

Effect of high-temperature stress on byssus secretion in the mussel *Mytilus coruscus* and its regulation mechanism

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Abstract：Mussels anchor themselves to various substrates underwater by producing byssal threads with adhesive protein secreted by mussel foot. In the present study, the structure of the foot gland, the gene expression pattern of 5-hydroxytryptamine (5-HT) receptors, distribution of 5-HT and the effects of 5-HT antagonist injection on the secretion of byssus were analyzed under different temperatures (21℃, 27℃ and 31℃). The secretion ability of byssus was significantly decreased at 31℃ compared to the control group ($p < 0.05$). The total glandular area of mussel foot tissue treated at 31℃ was significantly lower than that treated at 21℃ and 27℃ ($p < 0.05$). The results of NBT staining showed that the color was lighter at 31℃, indicating that high-temperature stress reduced the content of dopa quinone in foot tissue. We found that the transcriptional expressions of six 5-HT receptors were significantly upregulated in the 31℃ group compared to other groups ($p < 0.05$). The distribution of 5-HT increased near the groove of the foot after 31℃ treatment, indicating that 5-HT may regulate the secretion of byssus. In order to further study the relationship between 5-HT and the secretion of byssus, we injected 5-HT and its receptor antagonist mianserin into the foot of mussels. The results showed that 5-HT and mianserin inhibited the secretion of byssus. This study revealed the effect of ambient temperature on byssogenesis, which may be regulated by the 5-HT signaling pathway.

Key words: *Mytilus coruscus*; byssus; foot gland; 5-HT

中华绒螯蟹性别特异性标记及基因组 BAC 文库 ZW 染色体 DNA 克隆的鉴定

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摘要：为了建立中华绒螯蟹单性养殖的性别控制技术和阐明性别决定和分化的分子机制，我们成功从已发表的中华绒螯蟹遗传图谱 LG48 中鉴定出一个性别特异性标记，并构建一个高度冗余的细菌人工染色体(BAC)文库，利用性别特异性标记分离 ZW 衍生的 BAC 克隆，对性别染色体 DNA 序列初步分析。

关键词：中华绒螯蟹；细菌人工染色体（BAC）；性别染色体；性别特异性标记

Identification of sex-specific marker and ZW-chromosome DNA clones from genomic BAC library in the Chinese mitten crab *Eriocheir sinensis*

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Abstract: In order to establish sex control techniques in monosex cultivation and elucidate molecular mechanism of sex determination and differentiation of *Eriocheir sinensis*, we successfully identified a sex-specific marker from LG48 in our previously published genetic map, and constructed a highly redundant genomic bacterial artificial chromosome (BAC) library from *Eriocheir sinensis*. ZW-derived BAC clones were isolated using sex-specific markers for initial analysis of the sex chromosomal DNA sequence.

Keywords**:** *Eriocheir sinensis*, bacterial artificial chromosome (BAC), sex chromosomes, sex-specific marker

瓦氏黄颡鱼全基因组微卫星的分布特征及其定位的初步研究

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摘要：为探究瓦氏黄颡鱼全基因组微卫星的分布特征及其规律，旨在为相关功能性微卫星分子标记的筛选提供依据，利用 MISA 软件对其全基因组微卫星进行筛查和分析，并对外显子中含有微卫星的基因进行了 GO 注释和 KEGG 富集分析，联合分析预测瓦氏黄颡鱼定位到外显子上的微卫星和其体内的生物代谢过程密切相关。

关键词：瓦氏黄颡鱼；基因组；微卫星；分布规律

Preliminary study on the distribution characteristics and positioning of microsatellites in the whole genome of *Pelteobagrus vachelli*

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Abstract: we explored the distribution and characteristics of microsatellites in the whole genome of *Pelteobagrus vachelli*, aiming to provide a basis for the selection of functional microsatellite markers. MISA (MIcroSAtellite identification tool) was used for screening and analysis. In addition, the genes containing microsatellites in the exon regions were subjected to GO annotation and KEGG enrichment, integrated analysis indicates that the microsatellites located in the exons of genes in *P. vachelli* are closely related to the biological metabolism processes.

Key words: *Pelteobagrus vachelli*, genome, microsatellite, distribution characteristics

渤海湾三疣梭子蟹遗传多样性分析

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摘要：利用 6 个 SSR 位点对渤海湾三疣梭子蟹野生和养殖群体进行遗传多样性分析，共检测到 132 个等位基因，平均值为 22。多态性信息含量(*PIC*)值在 0.5027-0.9204 之间，表明 6 个 SSR 位点具有高度多态性，能够提供丰富的遗传信息。野生群体的平均期望杂合度(*He*)和观察杂合度(*Ho*)分别为 0.8192，0.8028；养殖群体的平均值为 $He = 0.7404$ 和 $Ho = 0.8111$。*PIC* 平均值分别为 0.7874(野生)，0.7694(养殖)，均大于 0.5；群体间遗传分化系数 $F_{ST} = 0.0133$。结果表明，渤海湾三疣梭子蟹遗传多样性较高，野生和养殖群体间无遗传分化($F_{ST} < 0.05$)。另外，根据体重，我们采集了 4 个群体的 140 个三疣梭子蟹样本，分别为：野生大个体组(WL)，野生小个体组(WS)，养殖大个体组(CL)，养殖小个体组(CS)。利用 20 个多态性 SSR 位点对这 4 个个体组进行遗传多样性分析，发现遗传多样性均较高。另外，大个体组遗传多样性高于小个体组，即 WL($He = 0.819$，$Ho = 0.756$) > WS($He = 0.808$，$Ho = 0.771$)，CL($He = 0.770$，$Ho = 0.705$) > CS($He = 0.765$，$Ho = 0.697$)；4 个个体组之间无遗传分化($0.001 < F_{ST} < 0.032$)。上述研究为渤海湾三疣梭子蟹野生资源的保护和开发利用提供了基础数据，有助于了解影响体重的遗传机制，并为三疣梭子蟹的分子标记辅助育种提供有价值的信息。

关键词：渤海湾；三疣梭子蟹；SSR；遗传多样性

The analysis of genetic diversity on *Portunus trituberculatus* in Bohai Bay

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Abstract: Six SSR loci were used to analyze genetic diversity of wild and cultivated populations of *Portunus trituberculatus* in Bohai Bay. A total of 132 alleles were detected, with an average of 22. The polymorphism information content (*PIC*) value was between 0.5027-0.9204, indicating that the six SSR loci were highly polymorphic and could provide rich genetic information. The average expected heterozygosity (*He*) and observed heterozygosity (*Ho*) of wild population were 0.8192 and 0.8028, respectively; The average values of cultivated population were $He = 0.7404$ and $Ho = 0.8111$. The average values of *PIC* were 0.7874 (wild) and 0.7694 (cultivated), both of which were greater than 0.5. The coefficient of genetic differentiation among populations $F_{ST} = 0.0133$. The results showed that the genetic diversity of *P. trituberculatus* in Bohai Bay was high, and there was no genetic differentiation between wild and cultivated populations ($F_{ST} < 0.05$). In addition, according to body weight, we collected 140 individuals collected from four groups: Wild high body weight (WL), wild low body weight (WS), cultivated high body weight (CL) and cultivated low body weight (CS). Using 20 polymorphic SSR loci to analyze the genetic diversity of the four individual groups, it was found that the genetic diversity was high. In addition, the genetic diversity of large individual group was higher than that of small individual group: WL ($He = 0.819$, $Ho = 0.756$) > WS ($He = 0.808$, $Ho = 0.771$), CL ($He = 0.770$, $Ho = 0.705$) > CS ($He = 0.765$, $Ho = 0.697$); There was no genetic differentiation among the four individual groups ($0.001 < F_{ST} < 0.032$). The above research provides basic data for the protection, development and utilization of wild resources of *P. trituberculatus* in Bohai Bay, and contribute to our knowledge regarding genetic mechanisms which affect body weight and provide valuable information for molecular marker-assisted breeding of *P. trituberculatus*.

Key words: Bohai Bay, *Portunus trituberculatus*, SSR, genetic diversity

斑重唇鱼胚胎及早期仔鱼发育的初步观察

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摘要：本研究基于 2020 年 4-6 月在伊犁河流域利用人工驯化成熟的野生斑重唇鱼亲本开展的人工繁殖试验，采用体视显微镜观察并记录了 21 粒斑重唇鱼受精卵胚胎发育及仔鱼发育过程。结果表明：斑重唇鱼受精卵为亮黄色，呈卵圆形，卵径（2.32±0.12）mm，约 40 min 后吸水膨胀卵径达（3.38±0.19）mm。在水温 12℃下，受精卵 4 h 形成胚盘，5 h 30 min 进入卵裂期，22 h 进入囊胚期，74 h 30 min 进入原肠期，81h 进入神经胚期，105h 进入器官分化期，288 h 30 min 开始破膜而出，初孵仔鱼平均全长 10.33 mm。胚胎发育积温为 3462 h·℃，破膜后 14 d 仔鱼开始平游。本研究表明斑重唇鱼胚胎发育特征与其他裂腹鱼类有较大差异，显著差异为囊胚期胚体下部卵黄组织液开始有规则移动，直至神经胚期。本研究将为斑重唇鱼的资源保护提供基础资料。

关键词：斑重唇鱼；伊犁河；胚胎发育；早期仔鱼

Morphological Observation of Embryonic and Early Larval Development of *Distychus maculates*

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Abstract: This study is based on the artificial reproduction experiment carried out by the artificially domesticated breeding parents of wild *Distychus maculates* in the Yili River Basin from April to June 2020. The embryonic development and larval development of *D. maculates* were observed and recorded using a stereo microscope. The results showed that the fertilized eggs of *D. maculates* were bright yellow, oval in shape, with an egg diameter of 2.32±0.12 mm, and swelled to 3.38±0.19 mm after absorbing water in about 40 minutes. At a water temperature of 12℃, the fertilized egg forms the blastoderm at 4 hours, enters the cleavage stage at 5 hours 30 minutes, enters the blastula stage at 22 hours, enters the gastrula stage at 74 hours 30 minutes, enters the neural embryo stage at 81 hours, and enters the organ differentiation stage at 105 hours , 288 h 30 min began to break the membrane, and the average length of the newly hatched larvae was 10.33 mm. The accumulated temperature of embryonic development was 3462 h·℃, and the larvae began to swim flat 14 days after membrane rupture. This study shows that the embryonic developmental characteristics of *D. maculates* are quite different from those of other Schizothoracinae. It is manifested in the regular movement of the yolk tissue fluid in the lower part of the embryo body at the blastocyst stage until the neuroblast stage. This study will provide basic data for the conservation of the resources of *D. maculates*.

Key words: *Distychus maculates*; Yili River; embryonic development; early larvae

文蛤 CDK7 基因克隆及其在不同品系生长发育中的表达分析

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摘要：本文进行了文蛤 CDK7 基因（MmCDK7）克隆，以及该基因在不同品系生长发育中的表达分析。得到 MmCDK7 基因 cDNA 全长为 1296bp，其中 5'UTR 为 83bp，3'UTR 为 196bp，ORF 为 1017bp，共编码 338 个氨基酸。该基因氨基酸序列含有 S_TKc、TyrKc 催化结构域、T-loop 以及 cyclin 的结合部位 NRTAIRE 等。序列比对和进化树显示该基因在进化过程中具有较好的保守性。实时荧光定量 PCR 检测结果显示 MmCDK7 在文蛤 7 个组织及 8 个发育时期中均有表达，其中在性腺以及多细胞时期的表达量最高。且在相同养殖条件下，红文蛤相对于黄文蛤的壳长相对增长率在 2.79%-32.37%之间，除了第 2 组，红文蛤的壳长均显著大于黄文蛤，且这种趋势随着养殖周期越来越明显。且在大多数情况下，相同时间点的红文蛤 CDK7 表达量都高于黄文蛤。上述结果表明，MmCDK7 可能在文蛤生长发育过程中起到一定的调控作用。

关键词：文蛤；CDK7；基因克隆；时空表达；生长发育

Cloning of CDK7 gene of *Meretrix meretrix* and its expression during growth and development of different strains

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Abstract: In the present study, the CDK7 gene (MmCDK7) of *Meretrix meretrix* was cloned and its expression during the growth and development of different strains was analyzed.The full length cDNA of MmCDK7 gene was 1296bp, including 83 bp of 5'UTR, 196 bp of 3'UTR and 1017 bp of ORF, encoding 338 amino acids. The amino acid sequence of the gene contained S_TKc, TyrKc catalytic domain,T-loop and NRTAIRE(the binding site of cyclin).Sequence alignment and phylogenetic tree showed that the gene was highly conserved during evolution. The results of real-time quantitative PCR showed that MmCDK7 was expressed in 7 tissues and 8 developmental stages of the clam, among which the highest expression level was in gonad and multicellular stage. Besides, the relative growth rate of shell length between red clam and yellow clam was 2.79%-32.37% under the same conditions, and except for the second group, the shell length of red clam was significantly higher than that of yellow clam, this trend is more and more obvious with breeding cycle. In most cases, the expression of CDK7 in red clam was higher than that in yellow clam at the same time point.These results suggest that CDK7 may play a certain role in the growth and development of clam.

Key words: *Meretrix meretrix*, CDK7, gene cloning, spatiotemporal expression, growth and development

中国对虾性别决定机制解析及性染色体探究

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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。性成熟后的中国对虾表现出显著的性别二态性：雌性个体体型明显大于雄性，且身体颜色不同。然而，中国对虾的性别决定机制尚不明确。本研究基于中国对虾重测序数据，计算固定指数（F_{ST}）和核酸多态性（π）来检测不同性别群体之间的遗传分化。根据结果在中国对虾基因组中定位到了候选性染色体，并基于重测序数据在该染色体的覆盖深度初步判断中国对虾属于雌性异配型性别决定机制（ZW 型）。利用雌性混池重测序数据组装了雌性特异性（W 染色体特异性）序列，并对部分序列进行了分子验证，可作为中国对虾遗传性别鉴定的分子标记。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。转录组测序筛选到许多雄性偏好性表达的基因在 Z 染色体特异区域聚集，这些雄性偏好基因将进一步加剧 Z 染色体和 W 染色体之间的分化。

关键词：甲壳动物；中国对虾；性别决定；性染色体；重测序；转录组

Research on sex determination mechanism and sex chromosome of *Fenneropenaeus chinensis*

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Abstract: *Fenneropenaeus chinensis* is a commercially cultured shrimp in China. *F. chinensis* adults show significant sexual dimorphism; the females are larger than the males. However, sex determination of *F. chinensis* has not yet been elucidated. In this study, we calculated the fixation index (F_{ST}) to detect the genetic differentiation of the 2 sexes of *F. chinensis* on the basis of resequencing data. 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. We also assembled female-specific (W chromosome-specific) sequences, which could be used as molecular markers to identify the sex of *F. chinensis*. 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.

Key words: Crustacea, *Fenneropenaeus chinensis*, sex determination, sex chromosome, resequencing, RNA-seq

低氧胁迫和恢复对杂交黄颡鱼“黄优 1 号”肠道组织的影响

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摘要：目前国内外学者针对鱼类肠道组织的环境胁迫研究逐渐受到重视，为探究低氧胁迫和恢复对杂交黄颡鱼“黄优 1 号”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(1.0 ± 0.1 mg/L)胁迫和恢复下该鱼肠道氧化应激指标、组织结构形态、细胞凋亡以及微生物组成变化。研究结果可为解析低氧/恢复下杂交黄颡鱼“黄优 1 号”肠道组织内环境稳态调控机制提供理论依据。

关键词：杂交黄颡鱼“黄优 1 号”；低氧胁迫；肠道；氧化应激；细胞凋亡；微生物组成

Effects of hypoxia stress and recovery on intestinal tissue of hybrid yellow catfish "Huangyou-1" (*Pseudobagrus vachelli*♂×*Pelteeobaagrus fulvidraco*♀)

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Abstract: At present, scholars at home and abroad are gradually paying attention to the environmental stress research of fish intestinal tissues, in order to explore the effect of hypoxia stress and recovery on the intestinal tissues of hybrid yellow catfish “Huangyou-1”. In this study, the hybrid yellow catfish "Huangyou-1" was subjected to (1.0 ± 0.1) mg/L hypoxia stress for 0, 24, 48, 72 h, and then the dissolved oxygen (7.0 ± 0.5) mg/L treatment was restored for 24 h. Through enzyme activity determination, H&E, qRT-PCR, TUNEL detection and 16S *rRNA* technology methods, the oxidative stress indicators, structural morphology, cell apoptosis and microbial composition changes in the intestine were analyzed. The research results can provide a theoretical basis for analyzing the physiological regulation mechanism of hybrid yellow catfish "Huangyou-1" in response to hypoxia stress and recovery.

Key words: hybrid yellow catfish “Huangyou-1”; hypoxia stress; intestine; oxidative; apoptosis; microorganisms

盐度能够缓解低温胁迫下暗纹东方鲀鳃的生理反应

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摘要: 洄游鱼类在洄游过程中需要适应水温和盐度的变化。在本研究中，我们研究了冷胁迫(25、21、17 和 13°C)和盐胁迫(20、10 和 0 ppt)对暗纹东方鲀(*Takifugu fasciatus*)鳃显微结构、抗氧化酶活性和冷胁迫基因、渗透压调节基因及凋亡基因表达的影响。该环境双因子胁迫实验表明，低温胁迫和盐胁迫导致暗纹东方鲀鳃丝增厚，多伴有明显的液泡和增生。低温可加剧氧化应激水平，有效触发冷应激、渗透、凋亡等反应，威胁暗纹东方鲀的生存。结果还表明中等盐度(10 ppt)可缓解低温引起的鳃胁迫反应。本研究揭示了暗纹东方鲀在寒冷和盐度胁迫下的初级分子响应，可为研究洄游鱼类对环境变化的响应提供有价值的参考。

关键词:低温胁迫、盐胁迫、暗纹东方鲀、氧化应激、渗透、凋亡。

Mitigation of low temperature stress by increased salinity is associated with multiple physiological responses in the gills of *Takifugu fasciatus*

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Abstract: During migration, anadromous fish need to adapt to changes in water temperature and salinity. In this study, we examined the effects of cold stress (25, 21, 17 and 13°C) and salinity stress (20, 10 and 0 ppt) on gill microstructure, antioxidant enzyme activity, cold stress,osmotic pressure regulation and apoptotic gene expression of gills sampled from river pufferfish (*Takifugu fasciatu*s). This environmental bifactor stress experiment suggested these results suggested that moderate salinity (10 ppt) may alleviate the gill stress responses caused by low temperatures. This research exhibited the primary molecular responses of the anadromous fish *T. fasciatus* under cold and salinity challenges and could be a valuable reference for studying the response of migratory fish to environmental change.

Keywords: cold stress, salinity stress, *Takifugu fasciatus*, oxidation, osmosis, apoptosis.

选育大规格银鲳(*Pampus argenteus*)亲本形态性状与体重的通径分析及生长曲线拟合研究

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摘　要：银鲳在我国及东南亚国家说一种重要的水产养殖经济鱼类。为研究银鲳形态性状与体重之间的相关性，本研究从银鲳选育池中随机捞取大规格银鲳 241 尾，小规格银鲳 331 尾进行形态学测量。结果显示，大小不同规格银鲳体重与 11 个形态性状(全长、叉长、体长、体高、头长、吻长、眼径、躯干长、尾柄长、尾柄高及尾长)的相关系数分别是 0.094-0.884 和 0.142-0.912；通径分析发现，小规格组保留了全长、体高、尾柄高和尾长 4 个形态性状；大规格组保留了体长、体高和尾柄长 3 个形态性状，两组保留的形态性状与体重之间均达到了极显著水平($P < 0.01$)。发现通径分析与决定系数分析结果的变化趋势相一致。同时，筛选出了大小规格组中不同形态性状与体重的回归方程和最佳曲线拟合模型。综上，在以体重为主要目标进行亲本选育时，应以银鲳的体长为选育的主要性状，将体高和尾柄长作为育种的参考性状，从而能够有效提高大规格银鲳的选育效率，也可以为银鲳选育提供测量指标与基础参考。

关键词：银鲳，形态性状，体重，通径分析，相关性，曲线模型拟合

Broodstock selection of large-sized silver pomfret *Pampus argenteus by the correlation between body weight and m*orphological traits

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Abstract: Silver pomfret *Pampus argenteus* is an important economic fish for aquaculture industry in China and Southeast Asian countries. In order to study the correlation between morphological traits and body weight of *P. argenteus*, two size groups of age-1 *P. argenteus* were randomly selected from culture pool, including 241 large-sized and 331 small-sized *P. argenteus*, and their morphological traits were accurately measured. The analysis results showed that the Pearson correlation coefficients between body weight and 11 morphological traits (e.g., total length, fork length, body length, body height, head length, snout length, eye diameter, trunk length, caudal length, caudal height, and tail length) of *P. argenteus* were 0.094-0.884 (in large size group) and 0.142-0.912 (in small size group). Path analysis showed that total length, body height, caudal height, and tail length traits were retained in small size group, and body length, body height, and caudal length traits were retained in large size group. The correlation between the retained morphological traits and body weight was extremely significant in the two groups ($P < 0.01$). The variation trend of path analysis was consistent with that of determination coefficient analysis, and the best multiple linear regression equation and the best curve fitting model of the two groups were screened. In short, when selecting parents with body weight trait as the main objective, the body length of *P. argenteus* should be taken as the main trait of genetic breeding, and the body height and caudal length traits should be taken as the reference traits, so as to effectively improve the breeding efficiency of large-size *P. argenteus*.

Key Words: *Pampus argenteus*; Morphological traits; Body weight; Path analysis; Curve model fitting

光唇鱼源无乳链球菌的分离鉴定及遗传特征

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摘要：为查明浙江养殖光唇鱼大量死亡的病原，了解该病原的分子遗传特征，本工作对患病光唇鱼进行病原分离，结合形态特征、生理生化特性和 16S rRNA 基因序列同源性，对分离菌株进行鉴定；采用人工回感试验确定其病原性，并对分离株的血清型、多位点序列分型、毒力基因型和表面蛋白抗原基因型等遗传特征进行分析；此外，还测试了菌株的药敏特性。

关键词：光唇鱼、无乳链球菌、分子血清型、MLST、毒力基因

Identification and genetic characterization of *Streptococcus agalactiae* isolated from *Acrossocheilus fasciatus* cultured in Zhejiang

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Abstract: This study aimed to investigate pathogenesis of diseased *Acrossocheilus fasciatus* cultured in Zhejiang province and analyze genetic characteristics of the pathogen. We isolated and purified pathogens from diseased *A. fasciatus* and identified the pathogenic bacteria by analyzing the physiology biochemistry characteristics and 16S rRNA gene sequence. We also carried out artificial infection experiments to verify the pathogenicity of isolated strain to *A. fasciatus*. Then the genetic characteristics of the pathogen were analyzed by molecular serotyping, multilocus sequence typing (MLST) and PCR screening of surface protein antigen genes and virulence-related genes. Meanwhile, we tested its antimicrobial susceptibility by disc diffusion method.

Key words: *Acrossocheilus fasciatus, Streptococcus agalactiae,* molecular serotyping, MLST, virulence-related genes

牙鲆生殖干细胞移植技术的建立及代孕子代的产生

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摘要：生殖干细胞移植是一项重要的动物辅助生殖技术。本研究在牙鲆上建立了以性成熟成鱼作为受体的生殖干细胞移植技术。以 2 龄雄鱼为实验对象，28℃高温以 18 mg/kg 体重剂量注射 2 次白消安，使受体内源性细胞枯竭。通过非连续 Percoll 梯度离心纯化获得供体卵原细胞，并经生殖孔移植至受体精巢中。移植后，组织学和荧光观察发现卵原细胞在受体鱼精巢中增殖和分化。移植 10 个月后，17 尾受体中有 16 尾产生了精子，经微卫星基因分型鉴定出 2 尾产生了供体来源的精子。利用该 2 尾受体与野生型雌鱼进行人工受精，所获得的子代经微卫星亲子鉴定表明供体来源的子代占比分别为 45.5%和 43.0%。本技术的建立为牙鲆种质资源保护利用和品种改良提供了强有力的技术支撑。

关键词：生殖干细胞；生殖细胞移植；精子发生；Vasa;牙鲆

Production of donor-derived offsprings by allogeneic transplantation of oogonia in the adult Japanese flounder (*Paralichthys olivaceus*)

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Abstract: Germ cell transplantation (GCT) is a promising reproductive technology in animals, including teleost fish. Here, we established a GCT procedure in Japanese flounder (*Paralichthys olivaceus*). Two-year-old male Japanese flounder were treated with temperature (28ºC) and busulfan (two doses, 18 mg/kg) to deplete endogenous germ cells and were then used as recipients. The discontinuous Percoll gradient purified oogonia were used as donor germ cells and transplanted into the recipients' testes through the genital pore. Histological and fluorescent observations showed the colonization, proliferation, and differentiation of transplanted oogonia in the testes of recipient fish. Ten months after GCT, 16 of 17 recipients produced sperm, and among them, two recipients produced donor-derived sperm, which was confirmed by microsatellite genotyping. The sperm of these two recipients were used to fertilize the eggs of wild-type females, and the donor-derived germline transmission rates were 45.5% and 43.0%, respectively, based on the microsatellite paternity analysis of the hatched larvae. Our established protocol can be applied to accelerate the reproduction cycle and be used for generating valuable surrogate breeding material and conserving the germplasm resources of Japanese flounder.

Keywords: germline stem cells; germ cell transplantation; spermatogenesis; Vasa; *Paralichthys olivaceus*

高硫酸盐胁迫对ENU草鱼*(Ctenopharyngodon idella)*血清离子浓度、鳃组织结构及鳃酶活性的影响

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摘要：背景: 草鱼（*Ctenopharyngodon idella*）作为淡水养殖经济上必不可少的鱼类，在中国广泛养殖。虽然ENU诱变已用于鱼类，但高硫酸盐胁迫对ENU诱变草鱼血清离子浓度、鳃组织结构和鳃酶活性的影响鲜见报道。**方法：**建立ENU诱变草鱼幼鱼（*Ctenopharyngodon idella*），测定血清离子浓度、鳃组织结构和鳃酶活性。然后，对BIM基因进行扩增和测序。此外，系统发育树的构建用于进一步分析。最后，进行qRT-PCR检测以验证高硫酸盐胁迫下BIM基因的相对表达量变化。**实验结果：**在高硫酸盐胁迫下，ENU诱导的草鱼鳃组织在0h、24h、48h和72h发生了一些变化，例如血清离子浓度、鳃组织结构和鳃酶活性。 特别是高硫酸盐胁迫24 h后，Na^+浓度显着高于高硫酸盐胁迫0h。在鳃组织结构方面，鳃片层间基质厚度在24h时比0h时显着降低了66.8%。同时检测到在硫酸盐胁迫下，24小时、48小时和72小时检测出ENU诱变草鱼的总蛋白（TP）、白蛋白（ALB）、丙氨酸转氨酶（ALT）、谷氨酸-草酸转氨酶（AST）、胆固醇（CHO）、球蛋白（GLOB）等发生了差异变化。**结论：** 高硫酸盐胁迫下ENU草鱼Na+/K+-ATP酶活性随时间推移呈一定程度的升高，而高硫酸盐胁迫下鳃丝SOD活性呈下降趋势。同时，BIM基因在高硫酸盐胁迫24小时鱼鳃中表达量显著降低，而在高硫酸盐胁迫72小时鱼鳃中BIM基因表达量显著增加。

关键字：ENU草鱼 (*Ctenopharyngodon idella*) 硫酸盐胁迫 BIM 鳃 血清

Title：Effects of high sulfate stress on serum ion concentration, gill tissue structure and gill enzyme activities of ENU grass carp *(Ctenopharyngodon idella)*

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Backgrounds: As an economically essential fish species for freshwater culture, grass carp (*Ctenopharyngodon idella*) is widely cultured in China. Though ENU mutagenesis has been used in fish, the effects of high sulfate stress on serum ion concentration, gill tissue structure and gill enzyme activities of ENU mutagenized grass carp have been reported only rarely. **Methods:** The ENU mutagenized grass carp juvenile (*Ctenopharyngodon idella*) was established and bred to measure the serum ion concentration, gill tissue structure and gill enzyme activities. Then, BIM was amplified and sequenced and a qRT-PCR assay was performed to investigate the relative abundance change of BIM under high sulfate stress conditions. Moreover, the construction of a phylogenetic tree was used for further analysis. **Results:** There were some changes of ENU-induced grass carp gill tissue at 0h, 24 h, 48h and 72h under high sulfate stress, such as serum ion concentration, gill tissue structure and gill enzyme activities. Particularly, after 24 h of high sulfate stress, Na+ concentration was significantly higher than that of 0 h of high sulfate stress. As for gill tissue structure, the thicknesses of the interlaminar matrix of the gill lamella had a significant decrease of 66.8% at 24h than that at 0h. Under the high sulfate stress, the total protein (TP), albumin (ALB), alanine transaminase (ALT), glutamic-oxalacetic transaminease (AST), Cholesterol (CHO), globulin (GLOB) of ENU grass carp were detected at 24h, 48h and 72h.**Conclusion:** To some extent, the activity of Na+ / K+-ATPase increased under high sulfate stress as time went on, while SOD activity in gill filament decreased under high sulfate stress for ENU grass carp. In the meanwhile, BIM gene decreased significantly in gills under 24 hours of high sulfate stress but increased significantly in gills under 72 hours of high sulfate stress.

Keywords: ENU grass carp, sulfate stress, BIM, gill, serum.

亚硝酸盐对越冬红螯螯虾亲虾生理生化及肠道菌群的影响

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摘要：为了取得红螯螯虾离体胚胎较佳的孵化水质条件及探究亚硝酸盐对孵化后的幼虾生长的影响，本实验利用 ZISS 孵化器筛选适宜红螯螯虾离体胚胎孵化的 pH、氨氮、亚硝酸盐条件，并通过调节养殖水体亚硝酸盐浓度探究亚硝酸盐对初孵幼虾的影响。

关键词：红螯螯虾；离体孵化；水质条件

The effect of water quality indexes on artificial incubation of red claw crayfish *Cherax quadricarinatus* eggs and growth of juveniles

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Abstract: In order to obtain better hatching water quality conditions of Red Crayfish embryos in vitro and explore the effect of nitrite on the growth of young shrimps after hatching, this experiment used ziss incubator to screen the pH, ammonia nitrogen and nitrite conditions suitable for Red Crayfish embryos hatching in vitro, and explored the effect of nitrite on newly hatched young shrimps by adjusting the nitrite concentration in culture water.

Key words: *Cherax quadricarinatus;* red claw crayfish; artificial incubation; water quality indexes

缢蛏高盐敏感性及耐高盐性状与生长性能相关性分析

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摘要：缢蛏是我国重要水产经济物种，进行耐高盐新品种选育对平衡不同地区缢蛏良种养殖差异意义重大。本研究对经过两个月养殖的不同家系缢蛏幼贝（平均壳长 2.67 cm，平均体重 1.48 g）进行高盐胁迫，运用统计学方法和相关性分析探究了缢蛏高盐敏感性及耐高盐性状与生长性能相关性。结果显示，缢蛏家系间壳长、壳高、壳宽和体质量表型值差异较大，体质量变异系数达 15.53%。不同家系对高盐敏感性差异较大，家系间死亡率范围在 0~100%。胁迫实验共持续 9 天，各家系缢蛏首粒死亡历时在 1~9 天不等，而且死亡率较高的家系内缢蛏死亡时间离散程度较大，说明不同个体间高盐敏感性差异也较大。大量死亡时间在第 8 天。第 9 天部分家系死亡率高于 80%，说明缢蛏对高盐耐受存在一个阈值，超过该阈值会开始或大量死亡。皮尔逊和斯皮尔曼相关性分析显示，缢蛏存活时间和生长性状为正相关，其中存活时间与缢蛏壳长、体质量相关性均达到显著水平（$P<0.05$）。各家系缢蛏存活率与缢蛏体质量、生长速度均显著正相关（$P<0.05$）。整体而言，壳长长、体质量重的个体耐高盐性能较强，在高盐环境中具有生长优势。本研究为缢蛏及其它海水双壳贝类耐高盐选育工作提供了参考资料。

关键词：缢蛏; 耐盐性; 生长性能; 相关性分析

Study of high-salt sensitivity and correlation analysis between high salt tolerance trait and growth performance of razor clam *Sinonovacula constricta*

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Abstract: The razor clam, Sinonovacula constricta, is an important aquatic economic species in China. The selection and breeding of new high-salt tolerant varieties are of great significance to balance the quality of razor clams in different regions. In this study, the young shellfish cultured for two months from different families were used for the high salinity stress experiment. Statistical methods and correlation analysis were used to study high-salt sensitivity and correlation analysis between high salt tolerance trait and growth performance in razor clam. The results showed that there was wide variation in the phenotypic values of shell length, shell height, shell width and body weight among different families. The coefficient of variation of body mass was 15.53%. The mortality among different families ranged from 0 to 100%. Therefore, different families had great differences in high salt sensitivity. The family with high mortality had a large discrete degree of death time, which was indicated that there were great differences in high-salt sensitivity among different individuals. The duress experiment lasted for 9 days in total, and the razor clams died in large numbers on the 8th day. It showed that there was a threshold for high salt tolerance in razor clams, beyond which death will begin or be massive. Pearson and Spearman correlation analysis showed that the survival time of razor clam was significantly and positively correlated with shell length and body weight ($P<0.05$). The survival rate of razor clams in each family was significantly and positively correlated with body weight and the specific growth rate ($P<0.05$). Overall, razor clams with long shell length and heavy body weight had strong high salt tolerance and had growth advantages in the high salinity environment. This study provides a reference for the selection and breeding of razor clams and other marine bivalves for high salt tolerance

Key words: *Sinonovacula constricta*; high salt tolerance; growth performance; correlation analysis

黄鳍棘鲷精子冷冻保存方法探究

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摘要：黄鳍棘鲷(*Acanthopagrus latus*)是中国具重要商业价值的海水鱼类之一，对其精子开展冷冻保存可为黄鳍棘鲷育种提供一定的技术支持，有效预防其种质资源衰退，保持其养殖业的可持续发展。该研究以黄鳍棘鲷精子为实验材料，对其精子冷冻保存的稀释液、葡萄糖浓度、抗冻剂种类及浓度、精子与保护液稀释比例和降温程序等进行了筛选优化。结果表明，以含 10g·L^{-1} 葡萄糖、5%乙二醇的 MPRS 溶液按 1：2 的比例稀释，4℃平衡 30min，液氮面上 5cm 熏蒸 5min，最后投入液氮保存 2h 后，将黄鳍棘鲷冷冻精子于 37℃水浴解冻后活性最好，精子活力、运动时间和寿命可分别达到(85.17±3.66)%、(9.16±7.70)s 和(94.29±9.55)s。

关键词：黄鳍棘鲷；精子活力；冷冻保存技术；精子库

Cryopreservation of sperm of *Acanthopagrus latus*

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Abstract: *Acanthopagrus latus*, one of the important breeding species in China, whose sperm cryopreservation can provide technical supports for its breeding, prevent the decline of its germplasm resources and maintain its sustainable development of the breeding industry effectively. In this experiment, taking the spermatozoa of A. latus as experimental material, we screened the diluent, glucose concentration, antifreeze type and concentration as well as dilution ratio and cooling procedure. The results show that when dilutes the sperm by MPRS solution with 10g·L-1 glucose and 5% glycol at a ratio of 1:2, freeze at 4 ℃ for 30 min, fumigate at 5 cm above the surface of liquid nitrogen for 5 min, and finally preserve in liquid nitrogen for 2 h. The frozen sperm had the best motility after thawing in 37℃ water bath, the sperm motility, motility time and life span could reach (85.170±3.66)%, (9.16±70)s and (94.297±9.55)s, respectively.

Key words: *Acanthopagrus latus*; Sperm motility; Cryopreservation technology; Sperm cryobank

急性低氧胁迫对鲂鲌（团头鲂♀×翘嘴鲌♂）杂交种 F₃ 鳃组织及血液的影响

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摘要：为了解鲂鲌（团头鲂♀×翘嘴鲌♂）杂交种 F_3（MC_3）鳃组织与血细胞对低氧的适应性，以期为其育种和推广应用提供参考资料，本实验利用 TUNEL 染色、HE 染色、抗氧化酶活性测定等技术探究了低氧对 MC_3 鳃组织的影响，并测定红细胞数量和血红蛋白浓度等指标。结果显示：（1）低氧处理会增加 MC_3 血液中的红细胞数量和血红蛋白浓度，复氧后红细胞数量和血红蛋白浓度会有所降低；（2）随着低氧处理时间的增加，MC_3 的鳃组织中鳃小片变长、层间细胞团面积减小、凋亡指数增加，复氧后层间细胞团面积和凋亡指数有所恢复，且低氧胁迫会影响 MC_3 鳃组织的抗氧化酶活性。

关键词：鲂鲌杂交种 F_3；低氧；鳃；细胞凋亡；抗氧化酶；血液

Hypoxia tolerance in Hybrid F₃ of *Megalobrama amblycephala* and *Culter alburnus* under hypoxic stress

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Abstract: In order to understand the adaptability of gill tissue and blood of the Hybrid F_3 of *Megalobrama amblycephala* (♀) and *Culter albus* (♂) (MC_3) and provide reference for its breeding and popularization, the effects of hypoxia on gill tissue of MC_3 were studied by TUNEL staining, HE staining and antioxidant enzyme activity determination, Determination of red blood cell count and hemoglobin concentration .The results showed that : (1) Hypoxia treatment increased the number of red blood cells and hemoglobin concentration in MC_3 blood, and the number of red blood cells and hemoglobin concentration decreased after reoxygenation. (2) With the increase of hypoxia treatment time, the gill lamellae of MC_3 became longer, the area of interlamellar cell mass decreased, and the apoptosis index increased. After reoxygenation, the area of interlamellar cell mass and apoptosis index recovered, and hypoxia stress affected the antioxidant enzyme activity of MC_3 gill tissue.

Key words: Hybrid F_3 of *Megalobrama amblycephala* (♀) and *Culter albus* (♂), Hypoxia, gill, apoptosis, antioxidant enzymes, blood

低氧胁迫对团头鲂“浦江 2 号”鳃重塑及细胞凋亡的影响

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摘要：为了研究低氧胁迫及恢复后对团头鲂新品种“浦江 2 号”鳃重塑及细胞凋亡的影响，本实验利用光镜，扫描电镜，TUNEL 染色以及 qRT-PCR 等技术研究了鳃组织形态结构的变化和细胞凋亡的情况。在团头鲂中鉴定出 Bcl-2 蛋白家族中的抗凋亡蛋白 *Bcl-2* 和促凋亡蛋白 *Bad*，并分析了这两个基因的分子特征以及低氧胁迫下在鳃组织中表达量的变化。本研究在细胞层面和分子层面为低氧导致的团头鲂鳃重塑的机制提供了一个新的见解。

关键词：团头鲂；低氧胁迫；鳃重塑；细胞凋亡；*Bcl-2*；*Bad*

Effects of hypoxia stress on gill remodeling and apoptosis of blunt snout bream *Megalobrama amblycephala* “Pujiang No.2”

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Abstract: Blunt snout bream (*Megalobrama amblycephala*) is an important species of freshwater aquaculture, but it is also a hypoxia-sensitive fish. Since 2007, the selective breeding under hypoxia was conducted on a wild blunt snout bream population from Poyang Lake, China, and the new breed “Pujiang No.2” was obtained in 2020, which showed markedly improved hypoxia-tolerance. In this study, the changes of morphology and apoptosis in blunt snout bream “Pujiang No.2” gills were studied after exposed to 4, 7 days of hypoxia. Additionally, the *Bcl-2* and *Bad* were firstly identified in blunt snout bream, and their molecular characteristics were analyzed. Our results indicate that the increase of apoptosis and the changes of *Bcl-2* and *Bad* mRNA expression levels might be contributed to gill remodeling of blunt snout bream under hypoxia stress.

Keywords: *Megalobrama amblycephala*; Hypoxia; Gill remodeling; Apoptosis; *Bcl-2*; *Bad*

中华鲟后备亲本的血液生化特征

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摘要：对海水驯养条件下的中华鲟后备亲本血液生化指标进行了测定，探讨生化指标数值的稳定性及其相关应用前景。研究结果显示，葡萄糖等 15 项指标的变异系数小于 0.5，高密度脂蛋白等 12 项指标在 0.5-1.0 之间，载脂蛋白-A1 大于 1.0。

关键词：中华鲟；后备亲本；海水驯养；血液生化指标

Blood biochemical characteristics of reserve parents of *Acipenser sinensis*

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Abstract: The blood biochemical indexes of reserve parents of *Acipenser sinensis* under seawater domestication were monitored, and the stability of biochemical indexes and its related application prospects were discussed. The results showed that the coefficient of variation of 15 indexes such as the glucose (Glu) was less than 0.5, 12 indexes such as the high density lipoprotein cholesterin (HDL-C) was between 0.5-1.0, and the Apolipoprotein A1 (Apo-A1) was greater than 1.0.

Key words: Chinese sturgeon, reserve parents, seawater domestication, blood biochemical index

曼氏无针乌贼 PRQFVamide-like 基因的克隆、表达及定位

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摘要：为初步探究 *SjPRQFVamide-like* 基因在曼氏无针乌贼生理活动中潜在的调控功能，本实验克隆了曼氏无针乌贼中 *SjPRQFVamide-like* 基因的全长，采用 qRT-PCR 研究了该基因的时空表达分布情况，利用原位杂交技术在脑组织中对 *SjPRQFVamide-like* 的 mRNA 进行定位，并构建真核表达载体在 HEK293 细胞中进行亚细胞定位。本研究为进一步探索 *PRQFVamide-like* 在头足类中的作用机制奠定基础,为头足类的种质资源恢复提供理论支撑。

关键词：神经肽；PRQFVamide-like；曼氏无针乌贼；头足类

Identification, Characterization, and Expression of a PRQFVamide-like Neuropeptide in Common Chinese Cuttlefish, *Sepiella japonica*

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Abstract: Neuropeptides, function as neurotransmitters and neuromodulators, having a variety of physiological functions in the mollusk. We first cloned the full-length cDNA sequence of a *PRQFVamide-like* gene isolated from cuttlefish *Sepiella japonica* (designated as *SjPRQFVa-like*). The spatial-temporal gene expression pattern showed that *SjPRQFVa-like* mRNA was widely distributed among tissues and primarily expressed in the brain and optic lobe at five developmental stages. Subcellular localization analysis revealed that the *Sj*PRQFVa-like protein was localized in cytoplasm of HEK293 cells. *In situ* hybridization data indicated that *SjPRQFVa-like* was detected in several functional lobes of brain, suggesting that the gene might have a potential role in various physiological function in *S. japonica*.

Key words: Neuropeptide; PRQFVamide-like; *Sepiella japonica*; Cuttlefish；Cephalopod

淡水常见鱼类线粒体通用引物的设计与验证

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摘要：为了找寻适用性良好的能够运用于淡水常见鱼类研究的通用引物，在鱼类线粒体 16s 区域内筛选出了两对通用引物，通过对 29 种鱼类基因组 DNA 扩增后的分析得，引物 16s 200 和引物 16s 400 可以对大多数鱼类进行扩增，且引物 16s 200 的扩增效果好于引物 16s 400，研究为淡水鱼类通用引物的研究提供了参考。

关键词：淡水鱼类；通用引物；线粒体；扩增

Design and Verification of Universal Primers for Mitochondria of Freshwater Fishes

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Abstract： In order to find the universal primer which can be used in common freshwater fishes, two pairs of universal primers are screened out in the fish mitochondrial 16s region. Through amplifying the Genomic DNA of 29 species of fish, the result shows that Primers 16S 200 and 16S 400 can amplify most fishes. The amplification effect of 16s200 is better than that of 16s400. The research could contribute to the study on universal primers for freshwater fish.

Key words: freshwater fish; universal primers; Mitochondrial; amplification

日本沼虾核糖体蛋白 L24 (RPL24)基因的鉴定及其在卵巢发育中的作用

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摘要:为了阐明核糖体蛋白 L24 (RPL24) 在日本沼虾卵巢中的功能，本研究利用 RACE-PCR 方法克隆得到了日本沼虾 RPL24（MnRPL24）基因全长 cDNA 序列，并通过实时荧光定量 PCR (qPCR)、免疫组织化学 (IHC) 和 RNA 干扰 (RNAi) 技术研究了其对日本沼虾卵巢发育的作用。

关键词:日本沼虾；卵巢发育；*MnRPL24* 基因；基因功能；RNA 干扰

Identification of ribosomal protein L24 (RPL24) from the oriental river prawn, *Macrobrachium nipponense*, and its roles in ovarian development

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Abstract: In order to clarify the function of ribosomal protein L24 (RPL24) in the ovary of *Macrobrachium nipponense*, the full-length complementary DNA (cDNA) of M. nipponense ribosomal protein L24 (MnRPL24) gene was cloned in this study, and its role in ovarian development was investigated using quantitative real-time PCR (qPCR), immunohistochemistry (IHC) and RNA interference (RNAi) technologies.

Keywords: *Macrobrachium nipponense*; ovarian development; MnRPL24 gene; gene function; RNA interference

红鳍东方鲀 C 型溶菌酶基因的序列特征及表达分析

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摘要：本研究对红鳍东方鲀（*Takifugu rubripes*）C 型溶菌酶(*TrLyzC*) 基因进行了生物信息学分析以及表达模式的测定。*TrLyzC* 基因 cDNA 全长为 432bp，共编码 143 个氨基酸。实时荧光定量 PCR 检测显示 *TrLyzC* 基因在 9 个健康红鳍东方鲀组织中均有表达，且在哈氏弧菌感染后肝脏和肠组织中 *TrLyzC* 基因均显著上调。该结果有助于进一步解析红鳍东方鲀抵抗病原微生物的免疫机制。

关键词：红鳍东方鲀；溶菌酶；哈氏弧菌；基因表达

Molecular characterization and expression analysis of c-type lysozyme gene in Japanese pufferfish (*Takifugu rubripes*)

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Abstract: In this study, bioinformatic and expression analyses of *TrLyzC* gene in *Takifugu rubripes* were conducted. A 432bp cDNA of C-type lysozyme was identified from Japanese pufferfish, encoding 143 amino acids. Real-time quantitative PCR showed that *TrLyzC* gene was expressed in nine healthy tissues, while the *TrLyzC* gene was significantly upregulated in liver and intestine after *Vibrio harveyi* infection. These results set the foundation for elucidating the immune mechanism of Japanese pufferfish against pathogenic microorganisms.

Key words: *Takifugu rubrip*es; lysozyme; *Vibrio harveyi*; gene expression

亚东鲑基因表达分析中内参基因的筛选

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摘要：内参基因作为检测基因表达水平变化时常用的参照物，可校正上样量和上样过程中存在的试验误差，合适的内参基因可以保证试验结果的准确性。为了寻找亚东鲑合适的内参基因，本研究检测了 8 种内参基因（*GAPDH*、*RPL13a*、*EF1a*、*β-actin*、*hprt1*、*β2M*、*28S rRNA* 和 *RPS29*）在成年雌性亚东鲑 8 种不同组织中的表达，应用 3 种内参基因的筛选方法（Genorm、NormFinder、BestKeeper），综合分析了这 8 种内参基因表达的稳定性。结果表明，内参基因在不同组织内的稳定性排名为：*hprt1*＞*RPS29*＞*RPL13a*＞*EF1a*＞*β-actin*＞*β2M*＞*GAPDH*＞*28S rRNA*。研究结果证实了基因表达转录分析中内参基因选择的必要性，也为亚东鲑功能基因表达的定量分析提供了重要的参考。

关键词：亚东鲑；内参基因；RT-qPCR；筛选方法

Screening of reference genes in the gene expression analysis of *Salmo trutta*

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Abstract: The reference gene is used as a commonly used reference when detecting changes in gene expression levels, which can correct sample loading and test errors in the process of loading. A suitable reference gene can ensure the accuracy of the test results. In order to find suitable reference genes for *Salmo trutta*, this study detected the expression of 8 reference genes (*GAPDH*, *RPL13a*, *EF1a*, *β-actin*, *hprt1*, *β2M*, *28S rRNA* and *RPS29*) in 8 different tissues of adult female *Salmo trutta*, using three screening methods of reference gene (Genorm, NormFinder, BestKeeper), comprehensive analysis of the stability of the expression of eight reference genes. The results showed that the stability ranking of reference genes in different tissues was: *hprt1>RPS29>RPL13a>EF1a>β-actin>β2M>GAPDH>28S rRNA*. The research results confirmed the necessity of the selection of reference gene in gene expression transcription analysis, and provided an important reference for the quantitative analysis of the functional genes expression of *Salmo trutta*.

Key words: *Salmo trutta*, reference gene, RT-qPCR, screening method

团头鲂“浦江 2 号”连续两代雌核发育群体的微卫星遗传结构分析

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摘要：为了培育出团头鲂“浦江 2 号”纯合家系，以“浦江 2 号”作为亲本，采用冷休克抑制第二极体排出的方法获得异源雌核发育一代群体（Meio-G1）和二代群体（Meio-G2）。利用筛选出的 20 对微卫星引物，分析正常群体、Meio-G1 和 Meio-G2 的遗传特征。在正常群体、Meio-G1 和 Meio-G2 中，分别扩增出 129、99、84 个等位基因，结果表明 Meio-G2 和 Meio-G1 相较于正常群体其遗传多样性下降，其中 Meio-G2 的遗传多样性最小，Meio-G1 和 Meio-G2 出现了杂合子缺失的现象，而正常群体则表现为杂合子过剩。聚类分析结果显示，正常群体与 Meio-G1 共同汇聚成为一支，Meio-G2 单独成为一支，表明 Meio-G2 的纯合度高、遗传多样性低，是良好的育种材料，为团头鲂纯系的育种提供了重要的参考价值。

关键词：团头鲂;雌核发育;微卫星标记;遗传结构

Microsatellite genetic structure analysis of two successive generations of gynogenetic populations of *Megalobrama amblycephala* "Pujiang No.2"

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Abstract: To breed a *Megalobrama amblycephala* "Pujiang No.2" pure family, *M. amblycephala* varieties "Pujiang No.2" as breeding parents, using the cold shock inhibit the second polar body eduction method for heterogeneous gynogenesis generation group (Meio - G1) and gynogenesis second-generation group (Meio - G2). The genetic characteristics of “Pujiang No.2” normal population, Meio-G1 and Meio-G2 populations of *M. amblycephala* were analyzed using twenty microsatellite markers in this study. The mean value of number of alleles of normal population, Meio-G1 and Meio-G2 was 129, 99 and 84, respectively. The results showed that the genetic diversity of Meio-G2 and Meio-G1 decreased compared with the normal population, and the genetic diversity of Meio-G2 was the least. Using unweighted pair-group method with arithmetic means method based on their genetic distances, normal population and Meio-G1 population were grouped in one cluster, while Meio-G2 population was classified into another cluster, indicating a genetic differentiation between the two clusters. The results showed that MeiO-G2 was a good breeding material with high purity and low genetic diversity, and provided important reference value for breeding pure lines of *M. amblycephala*.

Key words: *Megalobrama amblycephala*; gynogenesis; microsatellite; genetic structure

坛紫菜 *Hsp22* 增强莱茵衣藻高温耐受性的分子机制解析

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摘要：全球变暖是影响我国南方大型经济海藻坛紫菜生长的主要因素之一。然而，坛紫菜耐高温的机制尚不清楚。前期研究表明，坛紫菜小热休克蛋白 22 基因(*PhHsp22*)在高温胁迫下表达上调，但其调控机制尚未完全阐明。本研究通过异源表达对 *PhHsp22* 进行了功能分析。结果表明，*PhHsp22* 的 c 端高度保守，并包含一个 a-晶体结构域。系统进化分析表明，*PhHsp22* 与其他物种的小热休克蛋白基因亲缘关系较远。在 33°C 处理 3 h 和 6 h 后，*PhHsp22* 表达量显著增加，并提高了转基因衣藻在高温下的存活率。转录组分析显示，*PhHsp22* 可能通过调控能量代谢、代谢物代谢和蛋白稳态等相关途径提升衣藻的耐高温能力。因此，*PhHsp22* 可能在坛紫菜响应高温胁迫中起至关重要的作用。

关键词： *PhHsp22*；坛紫菜；衣藻；高温胁迫；内稳态

Molecular mechanism underlying *PhHsp22*-mediated increase in the high-temperature tolerance of *Chlamydomonas reinhardtii*

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Abstract: Global warming is one of the key limiting factors affecting the cultivation of *Pyropia haitanensis*, which is an economically important macroalgae species grown in southern China. However, the mechanism underlying the high-temperature tolerance of *P. haitanensis* remains largely unknown. In a previous study, we proved that the expression of the small heat shock protein 22 gene (*Hsp22*) is upregulated in *P. haitanensis* in response to high temperature stress, but the associated regulatory mechanism was not fully elucidated. In this study, a transgenic *Chlamydomonas reinhardtii* expression system was used to functionally characterize *P. haitanensis Hsp22*. A phylogenetic analysis revealed *PhHsp22* is not closely related to small heat shock protein genes in other species. Additionally, *PhHsp22* expression significantly increased at 3 and 6 h after initiating 33°C treatment, which improved the survival rate of transgenic *C. reinhardtii* during the early stage of high temperature treatment. The further transcriptome analysis revealed that *PhHsp22* expression can promote pathways related to energy metabolism, metabolites metabolism, and protein homeostasis in transgenic *C. reinhardtii* cells exposed to high temperatures. Therefore, *PhHsp22* may be crucial for the response of Pyropia species to high temperature stress.

Key words: *PhHsp22; Pyropia haitanensis; Chlamydomonas;* High-temperature stress; Homeostasis

藻酸盐促进海假交替单胞菌生物被膜形成及厚壳贻贝幼虫的变态

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摘要：为探究藻酸盐对海假交替单胞菌生物被膜形成及厚壳贻贝幼虫附着变态的影响,本研究以海假交替单胞菌生物被膜为对照组，设置终浓度为 0.1、0.5、1.0、1.5、2.0 mg/L 的藻酸盐标准品溶液添加到海洋细菌菌液中共同形成生物被膜，并检测生物被膜对厚壳贻贝幼虫附着变态的影响。选择添加藻酸盐的最适浓度，比较分析藻酸盐对生物被膜的膜厚及胞外产物的影响。结果表明：生物被膜的细菌密度随添加藻酸盐浓度的增加而增加；当添加藻酸盐的浓度大于 0.5 mg/L 时，共同形成的生物被膜的膜厚，胞外多糖显著增加（$P<0.05$），诱导厚壳贻贝幼虫附着变态的能力增强。本研究对理解海洋贝类附着变态的诱导机制具有积极意义，为利用生物被膜提高贻贝育苗成功率提供理论依据。

关键词：藻酸盐；生物被膜；厚壳贻贝幼虫；幼虫变态

Alginate promotes the *Pseudoalteromonas marina* biofilm formation and larval metamorphosis of *Mytilus coruscus*

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Abstract: This study was in order to research the effects of alginate on the biofilm formation of *Pseudoalteromonas marina* and the roles of co-formed biofilm on larval metamorphosis of the *Mytilus coruscus*. The biofilm of *P. marina* was used as a control, and the alginate was added into the bacterial solution with the final concentration of 0.1, 0.5, 1.0, 1.5 and 2.0 mg/L to form biofilm, respectively. The effects of the biofilm on larval metamorphosis of the mussel larvae were detected. In addition**,** the optimal concentration of alginate was selected to compare and analyze the changes of density, thickness and extracellular products of biofilm. The results showed that, the bacterial density of biofilms increased with the increase of alginate concentration. When alginate concentration was higher than 0.5 mg/L, the thickness and extracellular polysaccharide of biofilm were significantly increased ($P < 0.05$), and finally increased biofilm-inducing activities. This study has positive significance for understanding the induction mechanism of marine shellfish larval metamorphosis, it also provides a theoretical basis for the use of biofilms to improve the success rate of mussel seedlings.

Key words: alginate; biofilm; *Mytilus coruscus*; larval metamorphosis

厚壳贻贝 caspase-3 基因的鉴定及其在幼虫变态中的功能分析

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摘要：为探究细胞凋亡及其效应基因 caspase-3 在海洋贝类变态中的作用，本研究通过 RACE 技术克隆并鉴定了厚壳贻贝（*Mytilus coruscus*）caspase-3 家族 3 个基因的 cDNA 全长，并分别将其命名为 *McCaspase 3-2*、*3-3* 和 *3-4*。利用实时荧光定量 PCR 技术对其在幼虫变态不同时期的潜在功能进行了分析，并通过抑制剂及 RNA 干扰实验分别验证了 3 个 caspase 基因在变态过程中的作用。结果显示，*McCaspase 3-2* 和 *McCaspase 3-4* 均参与了幼虫的早期变态过程，但 *McCaspase 3-2* 在其中的作用更强，*McCaspase 3-3* 则几乎不在变态过程中发挥作用。上述研究结果将有助于理解细胞凋亡在厚壳贻贝幼虫变态中的作用以及贝类变态的分子机制。

关键词：厚壳贻贝；细胞凋亡；Caspase-3；幼虫变态；RNAi

The identification of Caspase-3 and gene function analysis during *Mytilus coruscus* larval metamorphosis

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Abstract: To investigate the role of apoptosis and the effector gene caspase-3 in the metamorphosis of marine bivalves, the full cDNA sequences of three genes which belong to the caspase-3 family in *Mytilus coruscus* was cloned by RACE and were named as *McCaspase 3-2*, *McCaspase 3-3* and *McCaspase 3-4* respectively. Then, the potential functions of the three caspase genes in different larval metamorphosis stages were analyzed by real-time qPCR, and their roles were determined by inhibitors and RNA interference execution. The results show that *McCaspase 3-2* and *McCaspase 3-4* have the regulatory function in the early stage of metamorphosis, and *McCaspase 3-2* plays a more decisive role. *McCaspase 3-3* is almost not involved in the larval metamorphosis. These results can help to understand the role of apoptosis in the metamorphosis of *Mytilus coruscus*.

Keyword: *Mytilus coruscus*; Apoptosis; caspase-3; larval metamorphosis; RNAi

坛紫菜突变体库的初步构建

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摘要：为获得坛紫菜人工突变体，本研究利用不同强度的 γ 射线辐照处理坛紫菜幼苗。恢复培养后,藻体细胞的死亡量随着诱变剂量的增加而升高，镜检结果表明，突变的细胞数量随着辐射剂量增加呈先增后降的趋势。其中，经 1300 Gy 处理的藻体的色素突变细胞数量最多，因此，选取 1300 Gy 做为辐射剂量进行后续研究。利用酶解法获得单细胞后进行再生培养，从突变体中初步筛选出 21 份材料，并利用 11 个表型性状进行相关分析和聚类分析。结果表明，F_1 代表型性状的变异系数与对照组相差较大。而突变体的大部分性状间存在显著相关性,采用系统聚类的方法（遗传距离为 20）将 21 份材料分成了 4 个主要类群。此外，本研究还从上述群体中筛选出了具有选育价值的突变株 NYB26，其藻胆蛋白含量和氨基酸含量显著高于母本。综上所述，γ 射线对坛紫菜叶状体具有良好的诱变效果，本研究为丰富坛紫菜遗传育种研究以及选育优良新品种提供了丰富的基础材料。

关键词：坛紫菜；γ 射线；突变体；表型性状；氨基酸

Preliminary construction of mutant library of *Pyropia haitanensis*

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Abstract: In order to obtain artificial mutants of *P.haitanensis*, treatment of the gametophyte of *P.haitanensis* with different intensities of γ- ray irradiation. After recovery culture, the results showed that the amount of gametophyte cell death increased with increasing of mutagen. Microscopic examination revealed that the number of mutant cells increased and then decreased with increasing radiation dose. The gametophyte treated with 1300 Gy had the largest number of pigment mutation cells, which was the best mutagenic effect. The isolated cells were obtained by seedling raising enzymatical method and was regenerated into blades. Twenty-one materials were screened out preliminarily, and 11 phenotypic traits was analyzed by correlation analysis and system analysis. The results showed that the coefficients of variation of F_1 phenotypic traits was significantly differed from the control, Correlation analysis showed that most of the characters had significant correlation. The cluster analysis result showed that at Euclidean distance of 20, the 21 individuals were clustered into 4 groups Moreover, the mutant NYB26, with significantly higher phycobiliprotein content and amino acid content than NSD35, was initially selected for breeding. In conclusion, γ-ray has a good mutagenesis effect on the gametophyte of *P.haitanensis*. This study provides rich basic materials for the enrichment of *P.haitanensis* breeding research and its selection of excellent cultivars

Key words:*Pyropia haitanensis,* Gamma Ray, mutant, phenotypic character, cluster analysis

坛紫菜优良品系 WO144-3 经济性状评价

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摘要：性状评价是育种的核心工作，本研究对杂交选育坛紫菜品系 WO144-3 的生长、耐高温性能及藻胆蛋白含量进行测定，并与野生型 WT 做对比分析。结果表明：(1) 经过 20 天培养，WO144-3 品系叶状体平均日增长率为 17.59%，比 WT 显著高 1.92%，平均日增重率比 WT 显著高 1.05%。培养期间，WO144-3 品系的长宽比总是高于 WT，且差距越来越大。培养结束时，WO144-3 的长宽比达 129：1，表明 WO144-3 是一个窄叶品系。(2) 为模拟高温胁迫，将藻体在 30℃高温培养 10 天，发现 WO144-3 品系叶状体的生长速度比 WT 品系高 1.70 倍。此外，WO144-3 光系统 II 的最大光化学效率 *Fv/Fm* 没有显著下降，但 WT 显著降低了 59%。(3) WO144-3 品系的藻胆蛋白含量是 WT 品系的 2.05 倍。叶绿素 *a* 含量无显著差异。综上，虽然 WO144-3 是一个窄叶品系，但生长速度快，而且具有耐受高温胁迫和藻胆蛋白含量高的优点。

关键词：坛紫菜 生长性状 耐高温性能 藻胆蛋白

Characterization of the main economic traits of new *Pyropia haitanensis* strain WO144-3

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Abstract: Character evaluation is the core work of *P. haitanensis* breeding. The growth rate, high temperature resistance, and the contents of phycobiliprotein were measured on the hybrid selected strain WO144-3 and compared with a wild strain WT. The results showed that: (1) After 20 days of culture, the average daily growth rate of WO144-3 strain was 17.59%, significantly higher than WT by 1.92%, and the average daily wet weight rate was significantly higher than WT by 1.05%. The length/width ratio of WO144-3 strain was always higher than WT strain, and the difference became larger and larger. At the end of the culture, the length/width ratio of WO144-3 reached 129:1, which indicated that WO144-3 was a narrow-leaf strain. The blades were incubated at 30℃ for 10 days to test high temperature resistance, the growth rate of WO144-3 strain was 1.70 times higher than that of WT strain. In addition, the maximum photochemical efficiency of photosystem II Fv/Fm of WO144-3 didn't decrease significantly, but WT strain decreased by 59%. (4) The contents of phycobiliprotein of WO144-3 strain was 2.05 times higher than WT strain. There was no significant difference in chlorophyll *a* content both of them. The above results show that WO144-3 is a narrow-leaf strain, which has the advantages of rapid growth, tolerance to high temperature stress and high content of phycobiliprotein.

Keyword: *Pyropia haitanensis*, growth characters, high temperature resistance, phycobiliprotein

坛紫菜 *PhbZIP2* 基因克隆与功能验证

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摘要：高温影响坛紫菜的产量和品质，是制约坛紫菜产业发展的主要因素。研究发现，转录因子作为重要的调节因子在植物抵御逆境中发挥重要作用。前期研究发现，高温胁迫下坛紫菜的 bZIP2 基因显著上调表达，但其响应高温胁迫的分子机制尚不清楚。本研究通过分子生物学、生物信息学等技术手段对坛紫菜 *PhbZIP2* 的基因功能进行了分析。通过 PCR 技术克隆获取了该基因的基因序列，其开放阅读框长度为 1314 bp，共编码 437 个氨基酸。进化树分析结果表明，*PhbZIP2* 在红藻门中较为保守，与脐形紫菜亲缘关系较近。通过 qRT-PCR 结果发现，*PhbZIP2* 基因受到高温胁迫显著诱导。为进一步阐明 *PhbZIP2* 的分子功能，将其转入莱茵衣藻中进行功能验证。研究结果表明，转基因株系比野生型更耐受高温胁迫。本研究有助于阐明 bZIP 转录因子调控坛紫菜响应高温胁迫的分子机制，为指导耐高温新品种选育提供理论依据。

关键词：坛紫菜；高温；bZIP 转录因子；莱茵衣藻；转基因

The cDNA Cloning and Functional Verification of the *PhbZIP2* Gene from *Pyropia haitanensis*

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Abstract: Heat stress affects *Pyropia haitanensis* yield and quality, and is the main factor restricting the development of the *P. haitanensis* industry. Studies have shown that transcription factors play an important role in plant resistance to adversity as important regulatory factors. Previous studies found that the bZIP2 gene in *P. haitanensis* was significantly up-regulated under heat stress, but the molecular mechanism of its response to heat stress is unknown. In this study, the function of *PhbZIP2* gene was analyzed by molecular biology and bioinformatics. The gene sequence was cloned by PCR technology and found that its open reading frame length was 1314 bp, encoding 437 amino acids. Phylogenetic tree analysis showed that *PhbZIP2* was relatively conserved in the *Rhodophyta* and was closely related to *Porphyra Umbilicalis.* qRT-PCR results showed that *PhbZIP2* gene was significantly induced by heat stress. To further clarify its molecular function, the transgenic expression system of *Chlamydomonas reinhardtii* was constructed for functional verification. The results showed that Transgenic *C. reinhardtii* plants exhibited obvious tolerance to heat stress. This study helps to clarify the molecular mechanism of bZIP transcription factor regulating the response of *P. haitanensis* to high temperature stress, and provides theoretical basis for guiding the breeding of new varieties with high temperature tolerance.

Key words: *Pyropia haitanensis,* High temperature, bZIP transcription factor, *Chlamydomonas reinhardtii*, Transgenic

海带配子体β-碳酸酐酶的基因克隆与亚细胞定位

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摘要：碳酸酐酶（Carbonic anhydrase，CA），作为一种含锌金属酶，能够催化 CO_2 与 HCO_3^-之间的可逆水合反应，在藻类 CO_2 浓缩机制中发挥重要的作用。本研究采用 cDNA 末端快速扩增（RACE）等技术获得海带（*Saccharina japonica*）配子体细胞一个β-CA 基因的 cDNA 及 DNA 序列，将该基因命名为 *Sjβ-CA*。根据其 cDNA 序列设计引物，克隆不含信号肽的开放式阅读框序列，构建原核表达载体 pET28a-SjβCA，并将其转化至大肠杆菌（*Escherichia coli*）BL21pLysS 中以诱导表达，获得了分子量大小约为 36 kDa 的重组蛋白。利用 Bio-Scale Mini 预装滤柱纯化重组蛋白 *Sjβ-CA*，通过电极法测得该水合酶的比活力大小为 1.54 U/mg；利用重组的 *Sj-βCA* 免疫新西兰大白兔制备 *Sj-βCA* 多克隆抗体；利用该抗体对海带雌、雄配子体粗蛋白进行免疫印迹，结果证实了该抗体的特异性。并通过免疫共沉淀法证实该 CA 确实存在于海带配子体中。利用免疫胶体金电镜技术对其进行亚细胞定位，结果观察到绝大多数胶体金颗粒分布在海带配子体细胞的周质空间中，推测它可能是将海带细胞周围水环境中的 HCO_3^- 转化成 CO_2 以进入细胞甚至叶绿体促进光合作用。

关键词：碳酸酐酶；酶活；蛋白纯化

Molecular cloning and functional characterization of β- carbonic anhydrase (CAs) in the gametophytes of Saccharina japonica

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Abstract: Carbonic anhydrase (CA), as a zinc-containing metal enzyme, can catalyze the reversible hydration reaction between CO_2 and HCO_3。In this study, rapid amplification of cDNA ends (RACE) was used to obtain the cDNA and DNA sequence of a β-CA gene in gametophytic cells of kelp (Saccharina japonica), and the gene was named Sj-βCA. Then construct the prokaryotic expression vector pET28a-SjCA, and transform it into Escherichia coli BL21pLysS to induce expression, and obtain a molecular weight of approximately 36 kDa recombinant protein. The recombinant protein Sj-CA was purified using the Bio-Scale Mini pre-packed filter column, and the specific activity of the hydratase was measured by the electrode method to be 1.54 U/mg. The antibody was used to perform immunoblotting on the crude protein of kelp female and male gametophytes, and the results confirmed the specificity of the antibody. It was confirmed by immunoprecipitation that the CA did exist in the gametophytes of kelp. Using immunogold electron microscopy technology to perform subcellular localization, it was observed that most of the colloidal gold particles were distributed in the periplasmic space of the kelp gametophytic cells. It is speculated that it may be the conversion of HCO_3^- in the water environment around the kelp cells into CO_2. Enter cells and even chloroplasts to promote photosynthesis.

Key words: carbonic anhydrase; enzyme activity; protein purification

缺刻缘绿藻磷脂酶 A2（PLA2）的基因特征与功能鉴定

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摘要：磷脂酶 A2（PLA2）是一种水解酶（EC 3.1.1.4），它特异性地水解并释放甘油磷脂 sn-2 位的酰基，以释放溶血磷脂和游离脂肪酸，PLA2 参与膜脂的酰基修饰，并借助 Kennedy 等途径将某些特殊的脂肪酸合成为三酰甘油（TAG）。在缺刻缘绿藻（*Myrmecia incisa*）转录组高通量的测序数据中，我们筛选到一条与柑橘（*Citrus sinensis*）PLA2（ADF55750.1）编码序列具有 40.5%相似性且长 453 bp 的 Contig8456-14，基于该片段序列设计引物并利用 cDNA 末端快速扩增技术（rapid amplification of cDNA ends，RACE）克隆到该基因的全长序列。为了测其活性，本研究构建了原核表达载体 pET32a-PLA2，并将其转化至大肠杆菌（*Escherichia coli*）BL21（DE3）中通过 IPTG 诱导表达，然后利用 Bio-Scale Mini 预装滤柱纯化表达的重组蛋白。体外酶活的薄层色谱（TLC）结果显示，纯化的重组蛋白能将磷脂酰胆碱（PC）水解成溶血磷脂酰胆碱（LPC），从而鉴定了 MiPLA2 的基因功能。本研究有助于进一步探讨缺刻缘绿藻如何将花生四烯酸优先地合成为 TAG。

关键词：缺刻缘绿藻；磷脂酶 A2；三酰甘油；原核表达；酶活性

Gene cloning, prokaryotic expression and functional identification of phospholipase A2 (PLA2) from the *Myrmecia incisa*

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Abstract: Phospholipid phospholipase A2 (PLA2) is a hydrolytic enzyme (EC 3.1.1.4) that specifically hydrolyzes and releases glycerolipid sn-2 acylates to release lysophospholipids and free fatty acids. PLA2 participates in the acyl modification of membrane lipids and synthesizes some special fatty acids into triacylglycerols (TAG) by means of Kennedy. In the high-throughput sequencing data of the transcriptome of *Myrmecia incisa*, we screened a coding sequence of Citrus sinensis PLA2 (ADF55750.1) with a 40.5% homology to the 453 bp long Contig8456-14, and designed primers based on the sequence of the fragment. The cDNA full-length sequence of this gene was cloned by rapid amplification of cDNA ends (RACE). To measure its activity, the prokaryotic expression vector pET32a-PLA2 was constructed and transformed into *Escherichia coli* BL21 (DE3) to induce expression by IPTG, and then purified recombinant protein by using Bio-Scale Mini expression pre-filtration column. The results of in vitro thin layer chromatography (TLC) showed that the purified recombinant protein could hydrolyze phosphatidylcholine (PC) to lysophosphatidylcholine (LPC), thereby identifying the gene function of MiPLA2. This study is helpful to further explore how *Myrmecia incisa* preferentially synthesize.
arachidonic acid into TAG.

Keyword: *Myrmecia incisa*；phospholipase A2；TAG；prokaryotic expression；enzyme activity

海带 U 染色体及其性别决定区域的辨别

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摘要：褐藻中的重要经济物种海带(*Saccharina japonica*)具有典型的异型世代交替生活史和 UV 性别决定系统，但对于海带性染色体及性别决定区域（SDRs）的相关研究较少。本研究根据水云属(*Ectocarpus* sp.)的性别决定区域，开发了三个雌性连锁的(SJ-f_000170、 MSj68-58-2 和 FSMSJ-1294)性别特异性分子标记。根据单色荧光原位杂交(mono-color FISH)图谱，鉴定出海带假定的 U 染色体。后续利用连锁标记从已构建的海带雌配子体的细菌人工染色体(BAC)文库中筛选出阳性克隆并进行测序，最终结合海带雌、雄配子体比较转录组学分析结果，对海带 U 染色体的性别决定区域进行了初步辨别。

关键词：海带；性染色体；性别决定区域；性别连锁标记；荧光原位杂交; 细菌人工染色体；转录组

Discerning the putative U chromosome and the sex determining regions of *Saccharina japonica* (Phaeophyceae)

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Abstract: *Saccharina japonica*, an important economic species in brown algae, has a typical alternate life history of heteromorphic generations and UV sex determination system, but little is known about the sex chromosomes and sex determining regions (SDRs) in the *S. japonica*. In the present study, three female-linked (SJ-f_000170, MSj68-58-2 and FSMSJ-1294) sex-specific molecular markers, which were developed on the basis of the *Ectocarpus* sp. sex-determining regions. Discerning the putative U chromosome based upon the mono-color FISH profiles by these confirmed sex-linked markers. Bacterial artificial chromosome (BAC) clones were screened and sequenced from the constructed BAC libraries of *S. japonica* female gametophytes by female-linked markers. Combined with the result of different gene expression between male and female gametophytes of *S. japonica* using comparative transcriptome analysis, provide a preliminary identification of sex determining regions in *S. japonica* U chromosome

Key words: *Saccharina japonica*, sex chromosomes, sex determining regions (SDRs), sex-linked markers, fluorescence *in situ* hybridization (FISH), bacterial artificial chromosome (BAC), transcriptome

叶酸对斑马鱼胚胎心脏早期发育的剂量依赖性作用功能研究

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摘要：叶酸是 13 种必需维生素之一，在心血管发育中起着重要作用。叶酸合成基因 5,10-亚甲基四氢叶酸还原酶（MTHFR）突变与先天性心脏病的发生显著相关。然而 *mthfr* 基因调控心脏发育的机制尚不清楚。我们将斑马鱼胚胎暴露于过量的叶酸或叶酸代谢抑制剂中。利用 CRISPR/Cas9 在斑马鱼中建立了 *mthfr* 基因的敲除突变体。叶酸不足或过量的斑马鱼胚胎，以及 *mthfr*$^{-/-}$突变体均在受精后 3 天引起早期心包水肿和心脏缺损。此外，叶酸处理的胚胎在 5dpf 时出现异常运动。心脏标记基因 *hand2*、*gata4* 和 *nppa* 的表达水平在叶酸代谢异常的胚胎和 *mthfr*$^{-/-}$突变中发生变化，有证据表明它们与叶酸代谢变化引起的甲基化水平变化有关。总之，我们的研究为深入研究 *MTHFR* 基因和叶酸代谢提供了一个新的模型。我们的结果显示，叶酸对早期心脏发育具有剂量依赖性的双相效应。

关键词：*mthfr*；叶酸；斑马鱼；心脏发育；CRISPR/Cas9

Dose-dependent effects of folic acid on early cardiac development of zebrafish embryos

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Abstract: Folic acid, one of the 13 essential vitamins, plays an important role in cardiovascular development. Mutations in folic acid synthesis gene 5,10-methylenetetrahydrofolate reductase (MTHFR) is significantly associated with the occurrence of congenital heart disease. However, the mechanisms underlying the regulation of cardiac development by mthfr gene are poorly understood. Here, we exposed zebrafish embryos to excessive folate or folate metabolism inhibitors. And we established a knock-out mutant of mthfr gene in zebrafish by using CRISPR/Cas9. The zebrafish embryos of insufficient or excessive folic acid, and *mthfr*$^{-/-}$ mutant all gave rise to early pericardial edema and cardiac defect at 3 days post fertilization(dpf). The expression levels of cardiac marker genes *hand2, gata4* and *nppa* changed in the abnormality of folate metabolism embryos and *mthfr*$^{-/-}$ mutant, and there is evidence that they are related to the change of methylation level caused by the change of folate metabolism. In conclusion, our study provides a novel model for the indepth study of *MTHFR* gene and folate metabolism. And our results reveal that folic acid has a dose-dependent biphasic effect on early cardiac development.

Key words: *mthfr*; folic acid; heart development; zebrafish; CRISPR/Cas9

团头鲂转录组对急性低氧或急性低氧联合硼替佐米的响应

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摘要：团头鲂对低氧很敏感。为了克服这一缺点，研发了一个新的品系“浦江 2 号”。硼替佐米是蛋白酶体抑制剂，可以影响细胞对缺氧环境的适应。本文中，我们研究了与常氧组(NN)相比，急性低氧组(HN)与急性低氧联合硼替佐米组(HB)对肝脏结构和转录组表达的影响。HB 组的谷丙转氨酶和天冬氨酸转氨酶活性显著高于 HN 组。此外，HB 组出现严重的空泡、核萎缩、核裂解。对以上 3 组的肝脏进行转录组测序，KEGG 通路分析发现 FOXO、AMPK、PI3K-Akt 和 MAPK 信号通路中富集了许多表达差异基因。我们利用硼替佐米探索‘浦江 2 号’对缺氧胁迫的适应机制，并结合转录组分析，准确捕捉到与耐缺氧优势相关的基因。

关键词：低氧，团头鲂，浦江 2 号，肝脏，硼替佐米，转录组

The Transcriptomic Responses of Blunt snout bream (*Megalobrama amblycephala*) to Acute hypoxia alone, and in combination with bortezomib

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Abstract: Blunt snout bream (*Megalobrama amblycephala*) is sensitive to hypoxia. A new blunt snout bream strain, ‘Pujiang No.2’, was developed to overcome this shortcoming. As a proteasome inhibitor, bortezomib (PS-341) has been shown to affect the adaptation of cells to a hypoxic environment. In the present study, we examined how acute hypoxia alone (hypoxia-treated, HN), and in combination with bortezomib (hypoxia-bortezomib-treated, HB), impacted the hepatic ultrastructure and transcriptome expression compared to control fish (normoxia-treated, NN). The activities of alanine aminotransferase and aspartate aminotransferase in the HB group were significantly ($p < 0.01$) higher than those in the HN group. In addition, more severe liver damage such as vacuoles, nuclear atrophy, and nuclear lysis were observed in the HB group. RNA-seq was performed on livers from the HN, HB and NN groups. KEGG pathway analysis disclosed that many DEGs (differently expressed genes) were enriched in the FOXO, AMPK, PI3K-Akt and MAPK signaling pathway. We explored the adaptation mechanism of ‘Pujiang No.2’ to hypoxia stress by using bortezomib, and combined with transcriptome analysis, accurately captured the genes related to hypoxia tolerance advantage.

Keywords: Hypoxia, *Megalobrama amblycephala*, Pujiang No.2, Liver, Bortezomib, Transcriptome

基于血液转录组研究野外和迁地保护区两种生活环境对长江江豚听觉的影响

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摘要：为深入探究不同生活环境对长江江豚听觉功能的影响，本研究采集生活于野外(CJ)和迁地保护区(XJ)的长江江豚血液样本进行转录组学分析。结果表明，在CJ组和XJ组共鉴定出4613个差异表达基因，进一步筛选了81个与听觉相关的基因。其中，绝大多数抗氧化基因和热休克蛋白基因在CJ组上调表达，抗氧化通路FOXO pathway和骨发育相关通路TGF-beta pathway、NF-kappa B pathway在该组激活。本研究为探究长江江豚听觉系统应对环境胁迫的分子机制提供了新视角，同时为合理保护濒危珍稀物种长江江豚提供了重要的理论参考。

关键词：长江江豚；血液转录组；听觉；环境胁迫；噪声

Effects of different living environments on hearing of the Yangtze finless porpoise based on blood transcriptome method: wild and ex situ reserve

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Abstract: In order to explore the effects of different living environments on the auditory function of the Yangtze finless porpoise, we collected blood samples of the Yangtze finless porpoise living in wild (CJ) and ex situ reserve (XJ) for transcriptome analysis. The results showed that 4613 differentially expressed genes were identified in the CJ and XJ groups, and 81 genes related to hearing were further screened. Most of the antioxidant genes and heat shock protein genes were up-regulated in the CJ group, and the antioxidant FOXO Pathway, bone developing-related TGF- Beta pathway and NF-Kappa B pathway were activated in the CJ group. This study provides a new perspective for exploring the molecular mechanism of the auditory system of the Yangtze finless porpoise in response to environmental stress, and provides an important theoretical reference for rational protection of the endangered and rare species of Yangtze finless porpoise.

Key words: Yangtze finless porpoise; blood transcriptome; hearing; environmental stress; noise

金色品系三角帆蚌内壳色和光泽度遗传参数及基因型与环境互作效应分析

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摘要：本文利用微卫星标记对上海崇明和金华武义两个养殖地点的19个母系半同胞家系共570只19月龄金色品系三角帆蚌进行亲子鉴定分析得到41个全同胞家系，研究其内壳颜色和光泽度遗传参数及基因型与环境互作效应。本研究表明，通过选育是可以改良内壳颜色和内壳光泽度的，且需要考虑到基因与环境互作效应对金色品系三角帆蚌内壳颜色和内壳光泽度的影响。

关键词：三角帆蚌；内壳颜色；内壳光泽；遗传参数；基因与环境互作效应

Estimates of the genetic parameters and genotype for inner shell color and inner shell luster and the impact of environmental influences in the golden strain of *Hyriopsis cumingii*

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Abstract: In this study, we investigated the effects of the environment on the genetic parameters and their genotypes, on the inner shell color and luster of F1 golden strain *H. cumingii*, reared at two sites (Chongming and Wuyi). Inner shell color parameters and inner shell luster were recorded in 570 19-month-old individuals. Microsatellite-based DNA parentage analysis was used to assign the mussels to 19 maternal half-sib families, including 41 full-sib families. This study demonstrated that inner shell color parameters and inner shell luster could be improved by selective breeding. Environmental influences on genotype for inner shell color and inner shell luster should be taken into account in future selective breeding programs in golden strain *H. cumingii*.

Keywords: *Hyriopsis cumingii*; Inner shell color; Inner shell luster; Genetic parameters; Environment influences on genotype

缢蛏在氨氮诱导的氧化应激下抗氧化系统及细胞凋亡的变化

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摘要：近年来，氨氮对海洋贝类的养殖造成了一定的威胁。为了探究氨氮对缢蛏的氧化应激以及细胞凋亡的影响，本研究将缢蛏放置于两种浓度的非离子氨中(0.25mg/L, 2.5mg/L)暴露 72h 并恢复 72h。结果表明，高浓度组缢蛏活性氧(O_2^-, H_20_2)的含量及抗氧化酶(SOD, CAT, GPX)的活性在胁迫后较初始值均显著上升且无法恢复到正常值（$p<0.05$）,线粒体凋亡途径上的四个关键基因(Bcl-2, Bax, Cyt-C, Caspase 7)均在氨氮胁迫后发生差异表达（$p<0.05$）。同时实验采用 TUNEL 法对肝胰腺、鳃的细胞凋亡进行了原位观察，结果表明细胞凋亡与氨氮浓度和暴露时间存在线性关系且鳃的细胞凋亡更加明显。本实验为进一步深入探究氨氮对海洋贝类的毒性作用机制提供了丰富的参考资料。

关键词：缢蛏；活性氧；氧化应激；细胞凋亡

Alternation of antioxidant system and apoptosis of *Sinonovacula contricta* under oxidative stress induced by ammonia

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Abstract: In recent years, ammonia has posed a certain threat to the culture of marine shellfish. In order to investigate the effects of ammonia on *Sinonovacula contricta* at the level of oxidative stress and apoptosis, in this study, clams were exposed to two concentrations of non-ion ammonia (0.25mg/L,2.5mg/L) for 72h and recovered for 72h. The results showed that the levels of reactive oxygen species (O_2^-, H_20_2) and the activities of antioxidant enzymes (SOD, CAT, GPX) were significantly increased in the high concentration group compared to the initial values and unable to return to normal values ($p<0.05$). Four key genes(Bcl-2, Bax, Cyt-C, Caspase 7) in the mitochondrial apoptosis pathway were found to be differentially expressed after ammonia stress ($p<0.05$). In situ observation of apoptosis by TUNEL showed that apoptosis was linearly related to dose and time and was more pronounced in the gills. The experiment provides rich reference for further in-depth investigation into the mechanism of toxic effects of ammonia on marine shellfish.

Key words: *Sinonovacula contricta*, ROS, oxidative stress, apoptosis

不同生长速率的黑鲷混合组织的转录组分析

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摘要：为探究黑鲷生长性状的主要调控基因及通路，本实验利用 Nlumica 高通量测序技术对 4 月龄黑鲷不同生长速度个体的脑、肝脏、肌肉组织混合样本进行转录组测序及生物信息学分析，并通过 GO 功能富集分析和 KEGG Pathway 分析，寻找参与黑鲷肌肉生长、物质代谢等过程的相关调控通路。结果表明：转录组共筛选出 3104 个差异表达基因，包括 1129 个上调基因，1975 个下调基因，其中包括 MYH4、IGF-1、IGF-2、 Myl3、MYH6、Mb、GHR1 等参与肌肉生长调控的关键基因。在 GO 和 KEGG 富集分析中， 我们筛选到与生长相关的显著富集 GO 条目 25 条、KEGG 通路 39 条，如代谢途径、甲状腺信号通路、PPAR 信号通路等。这些差异基因与信号通路可能在黑鲷生长过程中起到关键调控作用，为进一步探究黑鲷生长发育关键分子调控机制及培育优良品种黑鲷提供理论基础。

关键词： 黑鲷， 转录组， 生长性状， 调控通路

Comparative transcriptome analysis of mixed tissues of black porgy (*Acanthopagrus schlegelii*) with differing growth rates

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Abstract: In order to explore the main regulatory genes and pathways of growth traits in black porgy, Illumina high-throughput sequencing technology was used to perform transcriptome sequencing of mixed samples of brain, liver, and muscle tissues of 4-month-old black porgy individuals with different growth rates, followed by bioinformatics analyses. Using GO function enrichment analysis and KEGG Pathway analysis, relevant regulatory pathways involved in the process of muscle growth and material metabolism of black porgy were found. The results showed that 3104 DEGs were screened out in the transcriptome, of which 1129 were up-regulated genes and 1975 were down-regulated genes, including MYH4, IGF-1, IGF-2, Myl3, MYH6, Mb, GHR1 and other key genes involved in the regulation of muscle growth. Through GO and KEGG enrichment analysis, we found 25 significantly enriched GO entries and 39 KEGG pathways related to growth, such as metabolic pathways, thyroid signaling pathways, and PPAR signaling pathways. These differential genes and signaling pathways may play a key role in regulating growth of black porgy, and provide a theoretical basis for further exploration of the key molecular mechanisms regulating growth and development of black porgy, ultimately contributing to the development of unique breeding strains of this species.

Key words: black porgy, transcriptome, growth traits, regulatory pathway

尼罗罗非鱼对碳酸盐碱度耐受性的研究

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摘要：该研究以两种规格[大:(21.56±0.27) g，小:(5.92±0.03) g]的尼罗罗非鱼(*Oreochromis niloticus*) 幼鱼作为研究对象，配制不同浓度的碳酸盐（$NaHCO_3$）碱水体展开高浓度胁迫致死、96 h 急性胁迫和慢性驯化实验，探究罗非鱼对碳酸盐碱的耐受性。结果表明：尼罗罗非鱼 96 h 的半致死碱度为 6.25 $g·L^{-1}$ ~ 9.01 $g·L^{-1}$，其耐碱能力虽弱于青海湖裸鲤等耐高碱鱼类，但其仍强于大多淡水养殖鱼类；在幼鱼阶段，体质量增加 3 倍以上的尼罗罗非鱼对碳酸盐碱胁迫的耐受性显著增强；养殖中可通过 2 $g·(L·d)^{-1}$ 的每日碱增加对罗非鱼进行碱驯化养殖；急性碱胁迫下“时间-碱度-死亡率”间关系可用互补重对数模型较好地拟合。

关键词：碱胁迫；耐受性；尼罗罗非鱼；规格；互补重对数模型；

Study on the carbonate alkalinity tolerance of Nile tilapia

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Abstract: In this study, we examined two sizes of Nile tilapia (*Oreochromis niloticus*) [large: (21.56±0.27) g, small: (5.92±0.03) g] to explore their tolerance to carbonate alkalinity. Different carbonate-alkalinity solutions were prepared with $NaHCO_3$ to carry out the following experiments: high concentration lethal experiments, acute alkaline stress experiments and chronic alkaline acclimation experiments.The results show that the half lethal alkalinities of Nile tilapia upon acute stress for 96 h range from 6.25 $g·L^{-1}$ to 9.01 $g·L^{-1}$; The alkaline tolerance of tilapia is weaker than that of fishes which adapted to extreme alkaline environment (*e.g. Gymnocyprinus przewalskii*), but it is still stronger than that of most freshwater cultured fishes; At the juvenile stage, three times or more weight gain increases the alkaline tolerance of tilapia significantly; Tilapia can be acclimated by daily alkaline increment of 2 $g·L^{-1}$ in production; And the relationship of "time-alkalinity-mortality" upon acute alkaline stress can be well fitted by the complementary log-log model.

Key words: alkaline stress; tolerance; Nile tilapia; size; complementary log-log model;

GABA 受体在厚壳贻贝变态发育过程中的作用研究

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摘要：γ-氨基丁酸(Gamma-aminobutyric acid, GABA)在哺乳动物中是一种重要的中枢神经抑制性神经递质，GABA 可以调控许多无脊椎动物变态发育。通过分析厚壳贻贝不同发育阶段幼体转录组数据发现，GABA $_{B2}$ 受体在变态前的眼点幼虫阶段高表达，同时采用实时荧光定量 PCR 实验验证了该基因的表达模式，表明 GABA $_{B2}$受体可能参与调控厚壳贻贝幼虫变态发育。为研究 GABA 受体在厚壳贻贝幼虫变态过程中的作用，本实验利用 GABA 及其受体抑制剂（Bicuculline、CGP52432 和 Pimozide）研究其对厚壳贻贝幼虫变态发育的作用，实验结果显示 10^{-4}M GABA 对厚壳贻贝幼虫的变态具有诱导活性，而 3 种 GABA 受体抑制剂（10^{-4}M ~ 10^{-6}M）均显著抑制了厚壳贻贝幼虫变态（$p < 0.05$），且 10^{-4}M Bicuculline、10^{-4}M CGP52432 和 10^{-5}M Pimozide 抑制效果更明显。本研究表明厚壳贻贝 GABA 受体可能参与调控幼虫的变态发育，为解析厚壳贻贝变态发育的神经内分泌调控机制提供理论依据。

关键词：厚壳贻贝；GABA 受体；拮抗剂；幼虫变态

Effect of GABA receptor on larval metamorphosis of the mussel *Mytilus coruscus*

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Abstract: Gamma-aminobutyric acid (GABA) is an important inhibitory neurotransmitter in the central nervous system in mammals. In marine invertebrates, GABA has been reported to induce larval settlement and metamorphosis in many species. In this study, a GABA$_{B2}$ receptor gene has been found in the transcriptome data of *Mytilus coruscus*. The GABA$_{B2}$ receptor gene was highly significantly expressed in the pediveliger stage than other development stages using the real-time fluorescent quantitative PCR experiment ($p < 0.05$), which suggests that the GABA$_{B2}$ receptor gene may regulate the larval metamorphosis. The pharmacological experiment was conducted to study the effects of GABA and its receptor inhibitors (Bicuculline, CGP52432 and Pimozide) on larval metamorphosis of *M. coruscus*. The results showed that 10^{-4}M GABA induced 27±3% of the pediveliger larvae metamorphosis. All three GABA receptor inhibitors (10^{-4}M to 10^{-6}M) significantly inhibited larval metamorphosis compared to the control larvae($p < 0.05$). This study indicated that the GABA receptor may participate in the regulation of larval metamorphosis of *M. coruscus*, and provides a theoretical basis for studying the regulatory mechanism of larval metamorphosis.

Keywords: *Mytilus coruscus*; GABA receptor; antagonist; larval metamorphosis

利用常压室温等离子诱变技术(ARTP)选育耐缺氧兼具生长优势团头鲂

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摘要：利用新型常压和室温等离子体(ARTP)诱变工具，首次成功诱变对团头鲂进行诱变(*Megalobrama amblycephalala*)，获得团头鲂 HS (Hypoxia tolerance+ supergrowth)突变体。我们筛选出了受精卵和精子 ARTP 处理的最佳诱变参数。随机抽取两个对照组(每组 3 尾鱼)和两个 HS 组(每组 3 尾鱼)，包括 3132418～3223481SNPs 和 912886～934664 InDels，共获得 93.2GB 的测序数据。基因组水平平均突变率约为 0.30%，筛选出 3651 个 HS 组特有非同义 SNP 突变位于 1223 个基因中。结合 KEGG 和 Go terms，我们筛选了 4 个低氧相关基因 (Epo X1, VEGFR1、HO-1a LPAR6)和 5 与生长有关的基因(FAS、6-PFK somatostatin-1A,锌转运体 ZIP4,载脂蛋白 Eb)，这些基因都存在一个或多个非同义突变位点，其中 HO-1a 的突变位点为纯合。研究结果对团头鲂耐低氧和生长性状的遗传育种具有指导意义。

关键词：ARTP；突变；团头鲂；耐低氧；生长；重测序

Mutation breeding of hypoxia tolerance and super growth *Megalobrama amblycephala* by a novel mutagenesis with atmospheric and room temperature plasma

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Abstract: We used a novel atmospheric and room temperature plasma (ARTP) mutagenesis tool to successfully mutagen blunt-snout bream (Megalobrama amblycephala) for the first time and obtain HS (Hypoxia tolerance+ Super growth) mutants of blunt-snout bream. The optimal parameters for ARTP processing of fertilized eggs and sperm were screened out. The morphological measurement of the selected hs population is significantly different from that of the control group. A total of 93.2GB clean data were received from two control groups (3 fish in each group) and two HS groups (3 fish in each group) randomly selected, including 3132418 to 3223481SNPs and 912886 to 934664 InDels. The average mutation rate at the genome level is about 0.30%. 3651 HS group special non-synonymous SNP mutations are located in 1223 genes. Combining kegg and go terms, we screened out 4 hypoxia-related (Epo X1, VEGFR1, HO-1a, LPAR6) genes and 5 growth-related genes (FAS, 6-PFK, somatostatin-1A, zinc transporter ZIP4, Apolipoprotein Eb), which were non-synonymous mutations at one or more sites, and there is also a homozygous HO-1a. The result of these revelation will be useful in future selections of genetic breeding for hypoxia-tolerance and growth traits in blunt-snout bream.

Key words: ARTP; mutation; Megalobrama amblycephala; hypoxia tolerance; growth; re-sequencing

催乳素基因的分离及在牙鲆变态眼睛移动过程中的差异表达分析

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摘要：比目鱼变态过程中眼睛的移动是由不对称的细胞分裂驱动的。为了研究催乳素(PRL)在这一过程中的作用，本研究从牙鲆(*Paralichthys olivaceus*)中克隆了 *prl* 的全长 cDNA，推导出的 PRL 蛋白与其他硬骨鱼相比具有高度保守的序列，但与两栖动物、爬行动物、鸟类和哺乳类等高等脊椎动物相比，有一些氨基酸丢失。*prl* 基因的时空表达分析显示其在发育早期广泛表达，而在成体中仅在垂体、大脑和肠道中表达量相对较高。原位杂交显示 *prl* 基因在变态过程中在眼眶周围不对称分布，并且与细胞分裂信号一致。秋水仙素抑制细胞增殖，能够降低 *prl* 基因表达，提示 *prl* 参与移动眼眶下方细胞分裂。甲巯咪唑和 9-顺视黄酸处理都会导致分裂细胞数量减少和 *prl* 表达下调，提示 *prl* 受甲状腺激素信号通路和视黄酸相关信号通路的调控。研究结果使我们对 PRL 在比目鱼变态过程中的作用有了基本的认识。

关键词：催乳素；催乳素；细胞分裂；变态; 眼睛移动

Isolation of *prolactin* gene and its differential expression during metamorphosis involving eye migration of Japanese flounder *Paralichthys olivaceus*

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Abstract: Eye migration during flatfish metamorphosis is driven by asymmetrical cell proliferation. To figure out Prolactin (PRL) function in this process, the full-length cDNA of *prl* was cloned from Japanese flounder (*Paralichthys olivaceus*) in our study. The deduced PRL protein shares highly conserved sequence with other teleosts, but has several amino acids loss compared with higher vertebrates, including amphibians, reptiles, avian and mammals. Spatio-temporal expression of *prl* gene displayed its extensive expression in the early development stages, while the limited expression of *prl* was observed in the pituitary, brain, and intestine of adult fish. In situ hybridization showed the asymmetrical distribution patterns of *prl* gene around the eyes during metamorphosis, which was coincident with the cell proliferation signals. Colchicine inhibited cell proliferation and reduced the *prl* gene expression, which indicates that PRL was involved in cell proliferation in the suborbital area of the migrating eye. The treatment of methimazole and 9-cis-retinoic acid respectively led to a reduction in the number of proliferating cells and the downregulation of *prl* expression, suggesting PRL was regulated by thyroid hormone signaling pathway and retinoic acid related signaling pathways. The results gave us a basic understanding of PRL function during flatfish metamorphosis.

Key words: Prolactin, Flatfish, Cell proliferation, Metamorphosis, Eye migration

东北七鳃鳗(*Lethenteron morii*)TLR3 信号通路相关分子的鉴定、组织表达分析及初步功能研究

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摘要：为完善水生脊椎动物先天免疫系统的研究，并为先天免疫系统中 TLR 信号通路在脊椎动物中的起源和进化提供依据，本研究在圆口纲物种东北七鳃鳗中鉴定得到了 TLR3 及 TLR3 衔接分子 TRIF，分别命名为 LmTLR3 和 LmTRIF，并利用生物信息学方法分析了两个免疫分子的结构域特征，利用荧光定量 PCR 和免疫学方法初步探究了 LmTLR3 和 LmTRIF 的组织分布与蛋白功能。

关键词：先天免疫；东北七鳃鳗；TLR3；衔接分子

Identification, expression and functional characterization of TLR 3 Signaling Pathway in Northeast Chinese lamprey (*Lethenteron morii*)

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Abstract: In order to improve the research on the innate immune system of aquatic vertebrates and provide the basis for the origin and evolution of TLR signaling pathway in the innate immune system in vertebrates. In this study, TLR3 and TLR3 adaptor molecule TRIF, named as LmTLR3 and LmTRIF, were identified in Northeast Chinese lamprey (*Lethenteron morii*). The structural domain characteristics of two immune molecules were analyzed by bioinformatics methods, and the tissue distribution and protein function of LmTLR3 and LmTRIF were preliminarily explored by fluorescent quantitative PCR and immunology methods.

Key words: innate immune system; Northeast Chinese lamprey; Toll-like receptor 3; adaptor molecule

甲基法尼酯介导 Met-Kr-h1 信号通路参与中华绒螯蟹卵黄发生的调控机制

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摘要： 为探究甲基法尼酯(MF)在中华绒螯蟹卵黄发生过程中的分子调控机制，本研究利用 RACE 技术克隆并获得了中华绒螯蟹 *Es-Met* 和 *Es-Kr-h1* 的 cDNA 全长，采用 qPCR 技术分析了 *Es-Met* 和 *Es-Kr-h1* 在不同发育时期以及不同组织中的表达模式，GC/MS 方法检测不同发育时期时血淋巴中 MF 滴度，并且对中华绒螯蟹进行外源添加 MF 和去眼柄处理，检测了 *Es-Met*、*Es-Kr-h1* 和 *Es-Vg* 基因表达模式的变化；此外，利用 RNAi 探索 Es-Met 和 Es-Kr-h1 在中华绒螯蟹卵黄发生过程中的功能作用。主要结果如下：中华绒螯蟹 *Es-Met* 和 *Es-Kr-h1* 基因均在肝胰腺组织中表达量最高，且 *Es-Met*、*Es-Kr-h1* 和 *Es-Vg* 基因在卵巢发育过程中的表达量变化趋势与血淋巴 MF 滴度之间呈极强的正相关性，其中，*Es-Met* 和 *Es-Kr-h1* 表达量变化趋势完全一致；此外，在外源添加 MF 和 ESA 处理后，检测到 *Es-Met*、*Es-Kr-h1* 和 *Es-Vg* 基因表达量同步显著上调，而干扰 *Es-Met* 后，*Es-Vg* 表达量显著降低。综上所述，*Es-Met* 和 *Es-Kr-h1* 基因参与了中华绒螯蟹外源性卵黄发生的过程。

关键词： 甲基法尼酯；*Met*；*Kr-h1*；qPCR；RNAi；卵黄合成

The regulatory mechanism of *Met-Kr-h1* signal transduction pathway mediated Methyl farnesate involve in vitellogenesis from Chinese mitten crabs, *Eriocheir sinensis*

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Abstract: To explore the regulation mechanism of methyl farnesate (MF) in the vitellogenesis in Chinese mitten crabs *Eriocheir sinensis,* RACE technology was used to cloning the full-length cDNA of *Es-Met* and *Es-Kr-h1*. QPCR assay was used to determine gene expression in different developmental stages and different tissues, and GC/MS method was used to detect the hemolymph MF titer. In the present study, to explore the potential functional role of *Es-Met* and *Es-Kr-h1* in vitellogenesis, the expression patterns of *Es-Met, Es-Kr-h1* and *Es-Vg* genes were detected after MF treatment, ESA surgery, and RNAi. The main results are as follows: The *Es-Met* and *Es-Kr-h1* genes are both highest expressed in hepatopancreas. QPCR and GC/MS results showed that the expression pattern of *Es-Met*, *Es-Kr-h1* and *Es-Vg* in the hepatopancreas was strongly positively correlated with the hemolymph MF titer during ovarian development. Further more, the trends of *Es-Met* and *Es-Kr-h1* expression are completely consistent. The expression of *Es-Met*, *Es-Kr-h1* and *Es-Vg* in hepatopancreas can be simultaneously and significantly increased with the addition of higher concentrations of MF *in vitro, in vivo* and ESA surgery. To further investigate the functional role of *Es-Met* in vitellogenesis, RNA interference-mediated gene silencing was carried out both *in vitro* and *in vivo*. Results showed that injection of *EsMet* double-stranded RNA (dsRNA) led to a significant decrease in *EsVg* expression levels. Taken together, our results suggest that *Es-Met* and *Es-Kr-h1* are involved in vitellogenin biosynthesis in *E. sinensis*.

Key words: Methyl farnesate, *Met, Kr-h1*, qPCR, RNAi, vitellogenesis

斑马鱼 ***deltaD*** 基因对血管内皮生长因子家族基因(***vegfaa*** 和 ***flt4***)的调控

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摘要：为探究斑马鱼(*Danio rerio*)Notch 信号通路的配体 *deltaD* 基因对血管内皮生长因子(vascular endothelial growth factor, VEGF)家族中的 *vegfaa* 配体和 *flt4* 受体基因调控作用，本实验构建了 *deltaD* 真核表达载体及 *vegfaa* 和 *flt4* 报告基因载体,利用双荧光素酶报告基因实验，明确了 *deltaD* 基因可以通过调控 *vegfaa* 和 *flt4* 基因从而影响血管发育。

关键词:斑马鱼；*deltaD*；*vgefaa*；*flt4*；双荧光素酶报告基因

Regulation of deltaD Gene on Vascular Endothelial Growth Factor Family Genes (vegfaa and flt4) in Zebrafish (Danio rerio)

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Abstract: In order to explore the regulatory effect of *deltaD* gene, a ligand of zebrafish Notch signaling pathway, on *vegfaa* ligand and *flt4* receptor gene in vascular endothelial growth factor (VEGF) family, *deltaD* eukaryotic expression vector and *vegfaa* and *flt4* reporter gene vector were constructed in this experiment,using double luciferase reporter gene experiment, it is clear that *deltaD* gene can affect vascular development by regulating *vegfaa* and *flt4* genes.

Keywords: Zebrafish (*Danio rerio*); *deltaD*; *vegfaa*; *flt4*; double luciferase reporter gene

斑马鱼 *notch3* 基因真核表达载体的构建及表达分析

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摘要：为研究 *notch3* 基因在斑马鱼中的功能，根据其基因序列克隆其胞内段（Notch intracellular domain, NICD），接着利用同源重组技术构建 pCMV-N3ICD 表达载体，最后在真核细胞中经细胞免疫荧光技术和蛋白质印迹法验证 N3ICD 的表达。双荧光素酶报告基因实验发现 pCMV-N3ICD 真核表达载体能够明显增强 NF-κB（nuclear factor-κB）家族中 *rela* 和 *nfκb1* 启动子的活性。

关键词：斑马鱼；*notch3*；N3ICD；免疫荧光；真核表达载体；NF-κB

Eukaryotic Expression Vector Construction of Zebrafish (*Danio rerio*) *notch3* Gene and Its Expression Analysis

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Abstract: In order to further study the function of *notch3* in zebrafish, according to its gene sequence, Notch intracellular domain (NICD) was cloned, and then the expression vector pCMV-N3ICD was constructed by homologous recombination. Finally, the expression of N3ICD was verified by immunofluorescence and Western blot. Double luciferase reporter gene assay found the eukaryotic expression vector pCMV-N3ICD could significantly enhance the activities of *rela* and *nfκb1* promoters in NF-κB family（nuclear factor-κB）.

Key words: zebrafish (*Danio rerio*), *notch3*, N3ICD, immunofluorescence, eukaryotic expression vector, NF-κB

雷公藤红素对斑马鱼胚胎发育、血管生成和心脏的影响

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摘要：为了获知雷公藤红素对斑马鱼胚胎及心血管发育的毒性影响，以便更好地研究其药效和机制，本实验观察并记录了不同浓度药物浸泡 12 h、24 h、36 h、48 h、60h、72h 后斑马鱼胚胎的发育情况、血管生成、心脏状态以及心率变化，实验结果为雷公藤红素的临床用药剂量提供了一定的参考价值。

关键词：雷公藤红素；斑马鱼；发育；血管；心脏

Effects of triptolide on embryonic development, angiogenesis and heart of zebrafish

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Abstract: In order to know the toxic effects of Tripterygium wilfordii on zebrafish embryos and cardiovascular development, and to better study its efficacy and mechanism, this experiment observed and recorded the development, angiogenesis, heart state and heart rate changes of zebrafish embryos after soaking with different concentrations of drugs for 12 h, 24 h, 36 h, 48 h, 60 h and 72 h, The experimental results provide a certain reference value for the clinical dosage of triptolide.

Key words: Triptolide, Zebrafish, development, blood vessel, heart

鳜嗅囊组织结构与早期发育研究

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摘要：本研究利用组织学、免疫组织化学、扫描电镜和透射电镜观察描述了鳜嗅囊结构组织学特征和早期发育过程。结果表明：鳜具有 2 对鼻孔，前后鼻孔紧密相连，具有皮瓣。嗅囊位于两侧嗅腔内，由 16-20 个初级嗅板构成，为 G 型嗅囊。初级嗅板通过褶皱产生次级嗅板。嗅板远端边缘为非感觉区，感觉区主要分布在次级嗅板上。感觉区含有 5 种细胞:纤毛非感觉细胞、纤毛感觉细胞、微绒毛感觉细胞、支持细胞、基细胞；非感觉区存在大量粘液细胞。从仔鱼到幼鱼阶段，1-7 日龄嗅基板较薄，嗅上皮表面已有少量纤毛，10 日龄嗅孔形成，26 日龄出现第 1 个初级嗅板，55 日龄出现 8 个初级嗅板。鳜早期初级嗅板侧向平行排列，表面较为光滑尚未形成次级嗅板。结果表明，鳜早期嗅囊发育较迟缓，未完全功能化。随着初级嗅板数量的增加和次级嗅板的形成，其嗅觉感受能力增强。

关键词：鳜、嗅囊、嗅上皮细胞、组织学、早期发育

Tissue structure and early development of olfactory sac in *Siniperca chuatsi*

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Abstract: In this study, histology, immunohistochemistry, scanning electron microscopy and transmission electron microscopy were used to describe the histological characteristics and early development of olfactory sac in *Siniperca chuatsi.* The results showed that *S.chuatsi* had two pairs of nostrils, and the anterior and posterior nostrils were closely connected with each other. The olfactory sac is located in the olfactory cavities on both sides, which is composed of 16–20 primary olfactory plates, and is G-type olfactory sac. The primary olfactory plate generates secondary olfactory plate through folds. The distal edge of olfactory plate is a non-sensory area, and the sensory area is mainly distributed on the secondary olfactory plate. Sensory region contains five kinds of cells : cilia non-sensory cells, cilia sensory cells, microvilli sensory cells, supporting cells, basal cells. There are lots of mucous cells in the non-sensory area. From larvae to young fish, the olfactory substrate was thin at 1–7 days old, and there were a small amount of cilia on the surface of olfactory epithelium. The olfactory orifice was formed at 10 days old, the first primary olfactory plate appeared at 26 days old, and eight primary olfactory plates appeared at 55 days old. Early mandarin fish primary olfactory plate laterally parallel arrangement, the surface is relatively smooth has not yet formed secondary olfactory plate. The results showed that the olfactory sac of *S.chuatsi* developed slowly in the early stage and was not fully functional. With the increase in the number of primary olfactory plates and the formation of secondary olfactory plates, their olfactory perception ability is enhanced

Keywords: *Siniperca chuatsi*, olfactory sac, olfactory epithelial cells, histology, early development

青鱼高密度遗传连锁图谱的构建及生长性状 QTL 定位

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摘要：由数量性状基因座(QTL)控制的生长相关性状是水产养殖鱼类的重要经济性状。本研究基于基因分型测序(GBS)使用一个包含 128 个后代的 F_1 家族构建了青鱼(*Mylopharyngodon piceus*)第一个高密度遗传连锁图。总共发现和基因分型了 10,390 个单核苷酸多态性(SNP)。将 4,108 个高质量 SNP 分配到 24 个连锁群(LG)，图谱总长度为 1,708.53cM，分辨率为 0.51cM。检测到高密度连锁图与斑马鱼染色体之间的保守同线关系。在三个连锁群(LG10、LG17、LG20)上鉴定出了 17 个 QTL：1 个体重，4 个体长，6 个体高，6 个体宽。这些 QTL 的表型变异解释(PVE)范围为 10.9%至 15.5%。高密度遗传连锁图是宝贵的基因组资源，不仅可以用于了解该鱼类经济重要性状的基因组基础，还可以用于比较基因组学和青鱼的进化研究。鉴定出的 QTL 对青鱼接下来的标记辅助选择(MAS)有重要价值。

关键词：青鱼；连锁图谱；生长性状；数量性状位点；单核苷酸多态性

Construction of a high-density genetic linkage map and mapping of QTL for growth in black carp

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Abstract: Growth related traits controlled by quantitative trait loci (QTL) are important economic traits in aquaculture fish species. In this study, the first high-density genetic linkage map of black carp (*Mylopharyngodon piceus*) was constructed using one F_1 family comprising of 128 progenies, based on genotyping-by-sequencing (GBS). A total of 10,390 single nucleotide polymorphisms (SNPs) were discovered and genotyped. A number of 4,108 high-quality SNPs were assigned to 24 linkage groups (LGs) and the total length of the map was 1,708.53cM with a resolution of 0.51cM. Conserved syntenic relationship between the high-density linkage map and the zebrafish chromosomes was detected. 17 suggestive QTL: one for body weight, four for body length, six for body height, and six for body wide, were identified on three linkage groups (LG10, LG17, LG20). The phenotypic variance explained (PVE) by these QTL ranged from 10.9 to 15.5%. The high-density genetic linkage map serves as valuable genomic resources not only for understanding the genomic basis of economically important traits in this fish species, but also for comparative genomics and evolutionary studies of black carp. The identified QTL provide important value for ongoing marker assisted selection (MAS) in this fish.

Keywords: Black carp, Linkage map, Growth-related trait, Quantitative trait loci, SNP

温度对鳜体表的粘液细胞分布类型及其粘液免疫因子的影响

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摘要：为了解不同温度条件（10、20、30 ℃）对鳜体表粘液细胞类型和免疫因子的影响，利用 AB-PAS 染色法观察了鳜体表粘液细胞分布与类型的变化。染色结果显示头部粘液细胞数量最多，其次是背腹部，尾部粘液细胞数量最少，而且相较于低温组（10 ℃），常温组（20 ℃）和高温组（30 ℃）的II型粘液细胞增幅最大，IV型次之，I型略微减少，III型变化无规律。通过 qPCR 和双抗体夹心酶联免疫法分别检测了体表免疫因子（lgM、IL-1β、Hepcidin）基因表达量变化和 AKP、SOD、ACP、LYS 酶活活性变化，结果显示 lgM、Hepcidin 基因的表达量随温度升高而上调。而四种酶活力在低温组和常温组时变化趋势不明显，但在高温组的 36 h 时升高至峰值，在 72 h 又基本恢复至 0 h 水平。这些结果显示出粘液免疫随着温度的改变有着显著的差异。

关键词：鳜；体表粘液细胞；免疫因子；温度

Temperature Effects on DistributionType of Skin Mucus Cells and Mucus Immune Factors of *Siniperca chuatsi*

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Abstract: In order to understand the effects of different temperature conditions on the mucus cell types and immune factors on the surface of siniperca chuatsi, the distribution and types of mucus cells on the surface of *siniperca chuatsi* were observed by AB-PAS staining.The staining results showed that the number of mucous cells in the head was the largest, followed by the dorsal abdomen, and the number of mucous cells in the tail was the least. Compared with the low temperature group (10 ℃), the increase of type II mucous cells in the normal temperature group (20 ℃) and high temperature group (30 ℃) was the largest, followed by type IV mucous cells, type I decreased slightly, and the change of type III was irregular. QPCR and Elisa were used to detect the changes of expression levels of body surface immune factors (lgM, IL-1β, Hepcidin, AKP, SOD, ACP and LYS). The results showed that the gene expression levels of lgM and Hepcidin increased with the increase of temperature, compared with the low temperature group.The changes of the four enzyme activities were not obvious in the low temperature group and the normal temperature group, but increased to the peak at 36 h in the high temperature group, and basically recovered to the level of 0 h at 72 h.These results show that mucilage immunity varies significantly with temperature.

Key words: *Siniperca chuatsi,* skin mucous cells, Immune factors, temperature

鳜胰腺发育的组织学研究

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摘要：为了解鳜胰腺组织发育变化，以加深对其分布和细胞组成的认识，本实验利用解剖观察、苏木精-伊红（HE）染色和免疫组织化学的方法研究了鳜仔稚鱼（孵化后 1-30 天）胰腺的分布及成鱼胰腺细胞组成特点。孵化后 1 天在前肠背侧出现胰腺，11 天时在胰腺组织内观察到胰岛，前 16 天分布在肝、胃、前肠间系膜处，18 天后发育出的幽门盲囊系膜也存在胰腺组织，此后与成鱼分布一致。腺体成小叶状，内部存在胰岛，外分泌部与胰蛋白酶抗体呈阳性反应，胰岛内 B 细胞分布在中央区，A 细胞主要分布在边缘部分。鳜胰腺为内分泌和外分泌细胞组成的散布分布的致密型组织。

关键词：鳜；胰腺；发育

Histological study on pancreatic development of Mandarin fish (*Siniperca chuatsi*)

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Abstract: Ontogenetic changes in pancreas histological distribution and characteristics of endocrine and exocrine cells were investigated 1 to 30 dph (days post-hatch) and adult fish, used anatomy, hematoxylin-eosin staining and immunohistochemistry. On the 1 dph, developed a distinct pancreas on the dorsal side of intestinal tract, the cells of Langerhans' island was found on day 11. Before the 16 dph, pancreas distributed to liver, stomach, anterior intestine mesenteries and pyloric caecum when it appeared at day 18, thereafter, the distribution pattern was in accord with adult fish. The gland composed of many lobules, acinar cells had positive reaction with trypsin antibody, insulin-immunoreactive cells were located in the central region of the pancreatic islet, glucagon-immunoreactive cells were mainly restricted to the peripheral region. The results indicated of mandarin fish pancreas is disperse-dense type and composed of endocrine and exocrine cells.

Key words: *Siniperca chuatsi*, pancreas, development

鱼类补体 C8 进化、功能网络分析及 C8α 链与 CD59 之间的理论相互作用

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摘要：补体 C8 是膜攻击复合物的主要成分，目前仅在脊椎动物中发现。C8 包含三个亚基：C8a、C8b 和 C8g。在鱼类中关于 C8 研究还很有限。在本研究中系统发育分析表明 C8 基因在不同鱼类中完全不同。密码子使用偏差分析揭示了 C8 基因进化复杂性。选择压力分析发现 C8 基因在进化过程中受到负选择影响。基因共表达和蛋白质相互作用网络分析揭示了 C8 系统功能。蛋白质结构比较表明，人和草鱼 C8 亚基之间假定的功能残基和结构域是保守的。草鱼 C8a-CD59 蛋白复合物的模拟构象中缺少第一个功能相关位点。本研究结果对鱼类补体 C8 的进化和功能有了更深入的了解。

关键词：补体系统 基因网络 草鱼 免疫 潜在治疗靶点

Fish complement C8 evolution, functional network analyses, and theoretical interaction between C8 alpha chain and CD59

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Abstract: Complement C8, as a main component of the membrane attack complex, has only been identified in vertebrates. C8 comprises three subunits: C8a, C8b, and C8g. In fish, there have been limited studies of C8. In the present study, phylogenetic analysis indicated the complete divergence of C8 genes in different fish species. Codon usage bias analysis revealed the evolutionary complexity of C8 genes. Selective pressure analysis found that C8 genes have been affected by negative selection during evolution. The systematic functions of C8 were revealed by gene co-expression and protein-protein interaction network analyses. Protein structural comparisons showed that putative functional residues and domains were conserved between the C8 subunits of human and grass carp. The first functionally-related site was absent in the simulated conformation of the grass carp C8a-CD59 protein complex. The results of the present study provide a deeper understanding of the evolution and function of fish complement C8.

Key words: *Complement system Gene network Grass carp Immunity Potential therapeutic target*

脊尾白虾 CDK2 基因的克隆及其功能分析

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摘要：为了研究 CDK2 在卵巢发育过程中的分子调节机制，本研究克隆得到 CDK2 基因全长 cDNA 序列，并进行了相关研究，结果如下：脊尾白虾（*Exopalaemon carinicauda*）CDK2 全长 cDNA 长度为 1722bp，开放阅读框 918bp，编码着 305 个氨基酸。在进化上与同为十足目的日本沼虾和罗氏沼虾亲缘关系最近。Ec-CDK2 在卵巢中表达最高，随着卵巢的发育 Ec-CDK2 的表达量逐渐增加，并在III期到到顶峰。RNAi 结果显示，注射 dsRNA 可以明显延缓卵巢发育周期。这些结果表明，Ec-CDK2 在脊尾白虾外源性卵黄物质的积累中发挥了关键的作用，为进一步研究脊尾白虾卵巢发育的分子调控机制提供理论基础。

关键词：脊尾白虾；CDK2；表达分析；RNA 干扰

Cloning and functional analysis of CDK2 gene from Exopalaemon carinicauda

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Abstract: In order to study the molecular regulation mechanism of CDK2 during ovarian development, the full-length cDNA sequence of CDK2 gene was cloned and studied. The results are as follows: the full-length cDNA length of CDK2 of *Exopalaemon carinicauda* is 1722bp, 918bp open reading frame, encoding 305 amino acids. Evolutionarily, it is closest to *Macrobrachium nipponense* and *Macrobrachium rosenbergii*, which are of the same decapod order. The expression of ec-cdk2 was the highest in ovary.With the development of ovary, the expression of Ec-CDK2 gradually increased and peaked in phase III. RNAi results showed that injection of dsRNA could significantly delay the ovarian development cycle. These results show that Ec-CDK2 plays a key role in the the accumulation of exogenous yolk substances, which provides a theoretical basis for the further study of the molecular regulation mechanism of ovarian development of *Exopalaemon carinicauda*.

Key words: *Exopalaemon carinicauda*; CDK2; expression analysis; RNA interference

昼夜节律性缺氧和盐度变化胁迫下香港牡蛎血淋巴细胞变化

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摘要：几十年来，近岸海域水体营养物富集引起的海洋缺氧已成为全球性问题，尤其是夏季频繁发生的昼夜节律性缺氧。另一方面，突降暴雨和淡水排放使河口和海岸生态系统的盐度发生变化，这种变化往往伴随着缺氧发生。为了探讨昼夜节律性缺氧和盐度变化对贝类血细胞免疫功能的影响。香港牡蛎被暴露于两个溶解氧浓度（24 小时正常氧 6 mg / L, 12 h 正常氧 6 mg / L 和 12 h 缺氧 2 mg / L)和三个盐度(10、25 和 35‰)14 天。随后，将所有处理恢复到恒定的正常氧(6 mg/L)和 25‰的盐度下 3 天，研究联合应激对血淋巴免疫功能的恢复情况。结果表明，昼夜节律性缺氧和盐度变化可能影响香港牡蛎的健康和生存，这可能是导致香港牡蛎大量死亡的关键因素。

关键词：血淋巴；免疫反应；牡蛎；流式细胞术；缺氧；盐度

Hemocyte responses of the oyster *Crassostrea hongkongensis* exposed to diel-cycling hypoxia and salinity change

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Abstract: Marine hypoxia caused by nutrient enrichment in coastal waters has become a global problem for decades, especially diel-cycling hypoxia occurs frequently in summer season. On the other hand, sudden rainstorms and freshwater discharge make salinity in estuarine and coastal ecosystems variable, which often occurs with hypoxia. To investigate the effects of diel-cycling hypoxia and salinity changes on hemocyte immune function of *C. Hongkongensis*, oysters were exposed to a combination of two dissolved oxygen (DO) concentrations (24h normal oxygen 6 mg/L,12h normal oxygen 6 mg/L and 12h hypoxia 2 mg/L) and three salinities (10, 25 and 35‰) for 14 days. Subsequently, all treatments were restored to constant normal oxygen (6 mg/L) and salinity under 25‰ for 3 days to study the recovery of hemocyte immune function from the combined stress. Our results find that diel-cycling hypoxia and salinity change may impair the health and survival of the Hong Kong oyster *C. hongkongensis* and may be the key factors for the mass mortality of this oyster in the field.

Key words: Hemocyte, Immune response; Oyster; Flow cytometry; Hypoxia; Salinity

黄颡鱼 Bcl-2 和 Cycs 启动子功能及锌对其转录调控的研究

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摘要：为了探究锌调控凋亡相关基因（Bcl-2/Cycs）的分子机制，本实验克隆了这两种基因的启动子并且验证了其启动子区域中 MRE 和 HNF-α 转录结合位点。此外，我们还通过实时荧光定量和蛋白质印迹法测定了锌对黄颡鱼原代肝细胞 Bcl-2/Cycs 的 mRNA 和蛋白表达，并且使用 Annexin V-FITC/PI 双染验证了锌对凋亡的抑制作用。

关键词：细胞凋亡；启动子分析；转录调控；锌；脊椎动物

Functions analysis of Bcl-2 and Cycs promoters and their transcriptional regulation by Zinc in Yellow Catfish

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Abstract: In order to investigate the molecular mechanism of Zinc-regulated apoptosis-related genes (Bcl-2/Cycs), we cloned the promoters of these two genes and verified the MRE and HNF-α transcription binding sites in the promoter region. In addition, the mRNA and protein expressions of Zinc on Bcl-2/Cycs in primary hepatocytes of yellow catfish were determined by real-time fluorescence quantification and western blot, and the inhibitory effect of Zinc on apoptosis was confirmed by Annexin V-FITC/PI double staining.

Key words: apoptosis, promoter analysis, transcriptional regulation, Zinc, vertebrates

安徽地区克氏原螯虾群体的遗传多样性和遗传结构分析

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摘要：本文以芜湖（WH）、宣城（XC）、合肥（HF）3 个安徽地区克氏原螯虾人工养殖群体为研究对象，分别以铜陵（TL）、马鞍山（MAS）2 个安徽野生群体和监利（JL）、建湖（JH）、滆湖（GH）、兴化（XH）4 个人工养殖群体作为对照，选用 10 对克氏原螯虾微卫星引物对其进行微卫星遗传多样性和遗传结构研究。结果显示：安徽地区人工养殖克氏原螯虾群体的平均遗传多样性均高于 2 个野生群体和江苏、湖北 4 个地区的人工养殖群体，其中 XC 群体的遗传多样性最高。9 个群体全部 10 个位点经 Bonferroni 法校正后均显著偏离 Hardy-Weinberg 平衡且绝大多数位点显示杂合不足。AMOVA 分析表明遗传变异是由群体内部决定的；大多数组的 F_{st} 表现出中度分化（$0.05 < F_{st} < 0.15$）。基因流表明不同群体之间存在着广泛的基因交换，尤其是 GH 和 JH 群体之间。基于群体间 Nei's 遗传距离及 UPGMA 聚类树结果显示，WU 群体、GH 群体、MAS 群体和 JL 群体聚为一组，XC 群体和 HF 群体同属于一组，而 JH 群体、TL 群体、XH 群体分别自成一组。STRUCTUR 结果显示，XC 群体和 HF 群体的大多数个体被分配到相同的遗传群中，说明它们可能具有相同的起源。研究表明安徽地区克氏原螯虾人工养殖群体具有较高的遗传多样性，结果为安徽地区克氏原螯虾种质资源的保护和改良，提供了参考资料。

关键词：克氏原螯虾; 遗传多样性; 遗传结构; 微卫星

Genetic diversity and structure analysis of *Procambarus clarkii* stocks in Anhui Province

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Abstract： Based on three artificial cultured populations of *P. clarkii* in Anhui (WH, XC and HF) as the research object, on two wild population of *P. clarkii* in Anhui Province (TL and MAS) and four artificial cultured populations (JL, JH, GH and XH) as a contrast. Ten pairs of *procambarus clarkii* microsatellite primers were selected to study the microsatellite genetic diversity and genetic structure. The results revealed that the genetic diversity of *P. clarkii* artificial cultured in Anhui was higher than wild population and four artificial cultured populations (JL, JH, GH and XH), and the XC population had the highest genetic diversity. Tests of departures from Hardy-Weinberg equilibrium indicated all 10 loci in 9 stocks were significantly deviated from Hardy-Weinberg equilibrium after Bonferroni correction and most of them have significant heterozygosity deficiency． AMOVA analysis showed that genetic variation was determined within the population. Fst in most groups showed moderate differentiation ($0.05 < Fst < 0.15$). The gene flow demonstrated there had extensive gene exchanges between different populations, particularly between GH and JH. UPGMA tree revealed that XC and HF belonged to the same clade, and WU、GH、MAS and JL were in the other clade, whereas the remaining populations formed their own clade. STRUCTUR results showed that most individuals in XC and HF populations were assigned to the same genetic population, suggesting that they may have the same origin. The results showed that the cultured population of *P. clarkii* in Anhui Province had high genetic diversity, which provided reference for the protection and improvement of *procambarus clarkii* germplasm resources in Anhui Province.

Keywords: *P. clarkii*; genetic diversity; genetic structure; microsatellites

四种模式鱼类左右眼中央角膜厚度差异比较分析

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摘要：为开发人类角膜疾病的低成本模型，本实验以模式鱼角膜为实验对象，通过光学相干断层扫描仪（OCT）对四种模式鱼类的左右眼中央角膜厚度进行测量和比较分析发现，在同物种内左右眼中央角膜厚度存在稳定的显著差异。

关键词：弓背青鳉；斑马鱼；日本青鳉；海水青鳉；中央角膜厚度

Comparative analysis of central corneal thickness between left and right eyes of four fish models

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Abstract: In order to develop a low-cost model of human corneal diseases, the model fish cornea was used as the experimental object. The central corneal thickness of the left and right eyes of four model fish was measured and compared by optical coherence tomography (OCT). It was found that there were stable and significant differences in the central corneal thickness of the left and right eyes in the same species.

Key words: *Oryzias curvinotus*; *Zebrafish*; *Oryzias latipes*; *Oryzias melastigma*; Central corneal thickness

鲍环境适应性测评体系的构建及在分子辅助育种中的应用

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摘要：鲍是我国重要的经济贝类，现有的养殖模式下，鲍面临着严峻的环境压力，再加上全球气候变暖，来自环境的挑战将愈发激烈，培育抗逆品种的需求也愈发迫切。对性状的精准测定是实现抗逆育种的第一步，本研究以鲍的心率和附着力变化为研究对象，开发了相应的性状测评系统，并结合基础组重测序，开展全基因组关联分析，对影响鲍耐高温等性状的关键位点进行了筛查，向实现鲍抗逆性状的分子育种迈出了坚实一步。

关键词：鲍；抗逆性状；心率；附着力；全基因组关联分析

The indicators of environmental stresses tolerance in abalone and application to genome-wide association study

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Abstract: China is the largest producer and consumer of abalone worldwide. However, abalone is facing severe environmental pressure within the existing culture pattern. In addition, global warming exacerbates environmental challenges. Therefore, it is important to accelerate genetic improvements in abalone tolerance to environmental stresses. It is problematic to evaluate stress tolerance in abalone. In this study, the fluctuations of heart rate and attachment duration were hired to distinguish the different tolerances. Combined with genome resequencing, the genome-wide association studies of stress tolerance were conducted in abalone, which made a great step towards molecular assisted breeding.

Key words: abalone, stresses tolerance, heart rate, attachment duration, GWAS

大黄鱼 NEMO 基因通过促进 p65 入核正调控 NF-κB 通路

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摘要：核因子 κB (nuclear factor-κB, NF-κB) 诱导表达的基因广泛参与各种生命活动在免疫应答中起着非常重要的调节作用。NEMO 是 NF-κB 重要调控蛋白。本研究从大黄鱼（*Larimichthys crocea*）中克隆了 NEMO 基因，研究在大黄鱼组织中的分布情况以及在 NF-κB 信号通路中的作用。结果显示 ORF 为 1698bp，共编码 565 个氨基酸，预测分子量 64.70kDa。*Lc*NEMO 在所检测的所有组织中均有表达,在血中表达量最高。此外，*Lc*NEMO 可显著激活 NF-κB 及 TNF-α 的启动子。同时亚细胞定位结果显示 *Lc*NEMO 可导致 NF-κB 亚基 p65 入核。本研究为阐述 *Lc*NEMO 在 NF-κB 信号中的作用，探究大黄鱼 NF-κB 信号通路参与免疫应答奠定了基础。

关键词：大黄鱼；核因子 κB；p65；NEMO

The NEMO positively regulates the NF-κB pathway by promoting p65 to enter the nucleus, *Larimichthys crocea*

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Abstract: Nuclear factor κB (NF-κB), as a multifunctional transcription factor, is involved in various physiological and pathological processes. The regulatory IKK-subunit NF-κB essential modulator (NEMO) plays an important role in NF - κ B signaling pathway. In the present study, NEMO gene was cloned from *Larimichthys crocea*. The tissue expression profiles of *Lc*NEMO, were analyzed and its role in the NF-κB signaling pathway. The open reading frame (ORF) of *Lc*NEMO was 1704bp in length, encoding 567 amino acids with predicted molecular weight (Mw) of 64.85 kDa and theoretical isoelectric point (pI) of 5.40. The expression of *Lc*NEMO were widely distributed in all determined tissues, with the most predominant expression in brain. In addition, The NF-κB and TNF-α promoter activation of large yellow croaker could be significantly activate by overexpression of *Lc*NEMO alone. The subcellular localization showed that *Lc*NEMO could induce NF - κ B subunit p65 into nucleus. This finding provides supporting data that *Lc*NEMO plays an important role in NF - κ B signaling in *Larimichthys crocea*, as well as exploring the involvement of NF-κB signaling pathway in immune response laid the foundation.

Key words: *Larimichthys crocea*, nuclear factor-κB, p65, NEMO

不同纬度生境生长的弓背青鳉的群体遗传结构研究

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摘要：为探究不同纬度生长弓背青鳉（*Oryzias curvinotus*）的群体结构，本实验对四个地理位置的弓背青鳉进行群体全基因组重测序，通过 SNP 位点和线粒体数据进行系统发育、群体遗传结构和遗传多样性分析，综合结果发现栖息地越接近赤道，弓背青鳉受到的自然选择压力越大。

关键词：弓背青鳉；SNP；全基因组重测序；群体遗传；自然选择压力

Study on population genetic structure of bowback medaka growing in different latitudes

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Abstract： In order to explore the population structure of *Oryzias curvinotus* growing in mangroves at different latitudes, so as to better understand and protect mangrove biodiversity.In this experiment, the whole-genome resequencing of medaka from four geographical locations was re sequenced.Phylogenetic analysis, population genetic structure analysis and genetic diversity analysis were carried out by identifying SNP loci and mining mitochondrial data.The results showed that the closer the habitat was to the equator, the greater the selection pressure on medaka species.

Key words： *Oryzias curvinotus*, SNP, Whole-genome resequencing, Population genetics, natural selection pressure

基于 COI 基因分析十种石珊瑚系统发育关系

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摘要：通过 COI 基因特异扩增序列，对徐闻地区 10 种石珊瑚进行 COI 基因片段比较分析，采用临位连接（NJ）、最小进化（ME）构建系统进化树。结果表明，序列中 G+C 比例为 42.4%，颠换和转换发生在第 3 位，比例 82.61%和 71.43%；徐闻珊瑚较传统分类几乎一致，菊花珊瑚属存在并系发育。

关键词：石珊瑚；COI 基因；系统发育树；

Phylogenetic analysis of five hermatypic based on COI gene

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Abstract: The COI gene fragments of 10 hard corals in XuWen area were compared and analyzed by specific amplification sequences of COI gene, and phylogenetic trees were constructed by NJ and ME. The results showed that the proportion of G+C in the sequence was 42.4%, and the transposition and transformation occurred in the third place (82.61% and 71.43%). Compared with the traditional classification of XuWen coral, the genus Chrysanthemum coral existed and developed.

Key words: Coral, COI genes, Pylogenetic tree

基于 COI 基因探讨湛江海域网箱污损生物钩虾种群的分子生物学鉴定

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摘要：利用 DNA 条形码技术与形态学相结合鉴定网箱污损生物钩虾，为开展污损生物分子物种鉴定研究提供参考。通过形态和分子遗传特性分析发现，NJ 系统发育树及 ABDG 分类法均支持将本次 28 个样本分为 4 个群体，其中指拟钩虾 *Gammaropsis digitata* 为本次鉴定的优势种。

关键词：钩虾亚目；COI 序列；遗传结构；物种多样性

Molecular identification of *Gammaridea* samples in cage fouling organism in the sea area of Zhanjiang based on COI gene

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Abstract: DNA barcoding and morphology were used to identify the fouling organisms of macrobrachium unguiculatus in the cage, which provided a reference for molecular species identification. The results of morphological and molecular genetic analysis show that both NJ phylogenetic tree and ABDG classification support the classification of 28 samples into 4 populations, of which the dominant species was *Gammaropsis digitata*.

Key words: *Gammaridea*, COI sequences, Genetic structure, Species diversity

聚肌胞苷酸刺激鳜血细胞形态大小及其炎性免疫因子的应答

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摘要：传染性脾肾坏死病是鳜养殖危害严重的主要病毒性疾病。探究在聚肌胞苷酸（Poly I:C）刺激后不同时序下鳜血细胞形态大小和免疫因子产生的变化。比较不同时序(3h,6h,24h,36h,48h,72h,96h)下鳜血细胞差异，染色结果显示白细胞中单核细胞、淋巴细胞数量显著增多，36h 时恢复正常水平。血涂片姬姆萨(Giemsa)染色，光学显微镜观察对红细胞长、短径测量，结果显示，在 6h 有明显下降趋势，其中 48h 红细胞、单核细胞、嗜中性粒细胞数量 Poly（I:C）组大于对照组。通过双抗体夹心酶联免疫法检测血清免疫因子（补体 3（C3））、补体 4（C4））反应活性，结果显示 C3 中 6h、24h 时的处理组>对照组，差异显著($p<0.05$)，C4 中于 96h 时处理组>对照组，差异显著($p<0.05$)。结果表明，Poly（I:C）刺激后不同时序下鳜血细胞形态大小和免疫因子有明显影响。

关键词：鳜；聚肌胞苷酸；血细胞；炎性免疫

Polyinosinic acid Effects on Stimulates Blood Cell Size of Morphology and its Inflammatory Immune Factors of *Siniperca chuatsi*

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Abstract: *Infectious spleen and kidney necrosis is a major viral disease that seriously harms Siniperca chuatsi. Explor*e the changes in the morphology and size of blood cells and the production of immune factors in *Siniperca chuatsi* under different time sequence after *polyinosinic acid* (Poly I:C) stimulation. Comparing the differences in blood cells of *Siniperca chuatsi* at different time sequences (3h, 6h, 24h, 36h, 48h, 72h, 96h), the staining results showed that the number of monocytes and lymphocytes in white blood cells increased significantly, and the levels returned to normal at 36h. Blood smears were stained with Giemsa, and the long and short diameters of red blood cells were measured by optical microscope observation. The results showed that there was a significant downward trend at 6h, and the number of red blood cells, monocytes, and neutrophils at 48h Poly (I: C) The group is larger than the control group. The reactivity of serum immune factors (complement 3 (C3)) and complement 4 (C4)) was detected by double antibody sandwich enzyme-linked immunoassay. The results showed that the treatment group at 6h and 24h in C3>control group, the difference was significant ($p<0.05$)), the treatment group>control group in C4 at 96h, the difference was significant ($p<0.05$). The results showed that after Poly (I:C) stimulation, the morphology and size of blood cells and immune factors of *Siniperca chuatsi* were significantly affected at different timings.

Key words: *Siniperca chuatsi,* Polyinosinic acid,Blood Cell, Inflammatory Immune

海带配子体磷酸烯醇式丙酮酸羧激酶(PEPCK)的基因克隆与功能鉴定研究

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摘要：磷酸烯醇式丙酮酸羧激酶(PEPCK)广泛存在于高等植物、藻类和真菌中，催化磷酸烯醇式丙酮酸和 CO_2 形成草酰乙酸（OAA）。推测位于海带细胞质中的 PEPCK 参与将进入细胞的 CO_2 转换为 OAA 以储存。为验证胞质 PEPCK 的功能，本文通过 PCR 方法获得海带配 *PEPCK* 基因的 cDNA 全长序列，共 1734bp，编码一个含 577 个氨基酸残基的蛋白，生物信息学预测发现该蛋白位于细胞质中。构建原核表达载体 pET32a-PEPCK，并将其转化至大肠杆菌 BL21，诱导表达获得 PEPCK 重组蛋白，聚丙烯凝胶电泳显示其相对分子质量为 63 kDa。利用实时荧光定量 PCR(qPCR)方法分析海带 PEPCK 基因在不同 CO_2 浓度条件下的表达情况，结果显示与低 CO_2 浓度条件下的表达量相比，在高 CO_2 浓度下，PEPCK 基因的表达量显著升高，推测其参与了海带细胞质中 CO_2 的储存，为海带无机碳浓缩机制的重要组件。

关键词：海带；磷酸烯醇式丙酮酸羧激酶(PEPCK)；无机碳浓缩机制；基因表达；原核表达

Gene cloning and functional characterization of Phosphoenolpyruvate Carboxylase (PEPCK) in the gametophytes of *Saccharina japonica*

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Abstract: Phosphoenolpyruvate Carboxylase (PEPCK) exists in higher plants, catalyzes phosphoenolpyruvate and CO_2 to form oxaloacetate (OAA). It was speculated that PEPCK located in the cytoplast of S. japonica, and involved in convert intracellular CO_2 into OAA for storage. In this paper, the full-length cDNA of PEPCK was cloned by PCR from the gametophytes of *S. japonica*, constituted of 1734bp, encoded a 577-amino acids protein to verify the function of PEPCK in the cytoplast. Bioinformatics predicted that the protein was located in the cytoplast. The prokaryotic expression vector pET32a-PEPCK was constructed and transformed into *Escherichia coli* BL21. The recombinant protein of PEPCK was obtained by induced expression, polyacrylamide gel electrophoresis showed the molecular weight was about 63 kDa. Real-time fluorescent quantitative PCR (qPCR) was used to analyze the expression of PEPCK gene in *S. japonica* under different CO_2 concentrations, compared with low CO_2 concentrations, the result proved that expression of gene was significantly increased under high CO_2 concentrations to speculated that PEPCK was an important component of inorganic carbon concentration mechanism of *S. japonica*, and involved in CO_2 storage in cytoplast.

Key words：*Saccharina japonica*; Phosphoenolpyruvate Carboxylase (PEPCK); inorganic carbon concentration mechanism; gene expression; prokaryotic expression

基于几何形态测量法的剑尖枪乌贼角质颚形态变化研究

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摘要：为探究剑尖枪乌贼角质颚的生长变化规律，本研究使用几何形态测量学方法分析了不同发育阶段角质颚大小和形态差异。研究结果表明在发育过程中剑尖枪乌贼角质颚形态呈现渐变规律，同时存在异速生长现象，可能与剑尖枪乌贼发育过程中摄食和环境变化有关。

关键词：剑尖枪乌贼；角质颚；几何形态测量学；个体发育

Beak morphology variation of *Uroteuthis edulis* based on geometric morphometrics

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Abstract: In order to explore the pattern of growth change of Swordtip squid (*Uroteuthis edulis*) beak, this study use geometric morphometric methods to analyze the differences in beak size and morphology in different ontogenetic stages. The results show that the beaks pattern of *U. edulis* shows gradient law during development, meanwhile beak also showed an allometric growth, this may be related to the feeding and environment change during ontogenetic stage of *U. edulis*.

Key words: *Uroteuthis edulis*, beak, geometric morphometrics, ontogenetic

胶原特征性氨基酸对应激中华鳖裙边细胞生长的影响

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摘要：为了探讨胶原特征性氨基酸对中华鳖裙边细胞氧化损伤的可能缓解作用，本试验建立中华鳖胚胎期裙边成纤维细胞的培养方法和脂多糖（LPS）应激模型，通过裙边成纤维细胞原代培养和 MTT 及 HE 染色法研究胶原蛋白三大典型氨基酸（甘氨酸、羟脯氨酸和脯氨酸）对中华鳖裙边细胞增殖的影响。

关键词：中华鳖；裙边；甘氨酸；羟脯氨酸；脯氨酸; 胶原蛋白

Effects of characteristic amino acids of collagen on the growth of LPS-treated cell from the calipash of Chinese soft-shelled turtle *Pelodiscus sinensis*

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Abstract: The objective of this study was to investigate the mitigative effects of three typical amino acids of collagen (glycine, hydroproline and proline) on the oxidative stress of calipash from Chinese soft-shelled turtle *Pelodiscus sinensis*. The primary fibroblast cell culture method and lipopolysaccharide (LPS)-treated model of the embryonic calipash were established. The growth and proliferation of cells were studied by MTT and hematoxylin-eosin (HE) staining.

Key words: *Pelodiscus sinensis,* calipash, glycine, hydroproline, proline, collagen

葡萄糖诱导的 ROS 通过 AKT1-Beclin1 通路激活脂噬参与脂肪代谢的调控

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摘要：为探究脂噬在黄颡鱼葡萄糖诱导脂肪代谢中的发生机制及作用,本试验采用活体和离体的方式通过组织切片、酶活测定、实时荧光定量以及蛋白质免疫印迹、荧光染色、免疫荧光、免疫共沉淀等方法研究了不同碳水化合物和高糖作用下诱导的脂噬在脂肪代谢中的作用。并探索在高糖下脂噬的发生机制。

关键词：葡萄糖；脂噬；脂肪代谢;分子机制

Lipophagy mediated glucose-induced lipid metabolism via ROS/AKT/Beclin1 pathway

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Abstract: To explore the mechanism and role of lipophagy in the glucose-induced lipid metabolism, We demonstrated the role of lipophagy induced by different levels carbohydrates and high glucose in lipid metabolism using the histological assessment, Transmission Electron Microscope, enzyme activity determination, QPCR, Western blotting, immunofluorescence, and immunoprecipitation. And explored the mechanism of lipophagy in different levels carbohydrates and high glucose in yellow catfish (*P. fulvidraco*).

Key words: glucose, lipophagy, lipid metabolism; Molecular mechanism

基于 SMRT 测序技术的西施舌全长转录组分析

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摘要：西施舌是一种具有高药用价值的重要水产经济贝类。在本研究中， 我们使用 PacBio 单分子实时(SMRT)测序技术首次获得了西施舌的全长转录组，共鉴定了 39,209 条 unigenes 序列，同时对这些序列进行了结构分析和功能注释，可为后续的分子生物学相关研究提供参考。

关键词：西施舌；全长转录组；单分子实时测序；RNA 测序; 功能注释

SMRT sequencing of the full-length transcriptome of the *Coelomactra antiquata*

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Abstract: *Coelomactra antiquata* is an important aquatic economic shellfish with high medicinal value. In the present study, we conducted the first full-length transcriptome analysis of *C. antiquata* by using PacBio single-molecule real-time (SMRT) sequencing technology, and identified 39,209 unigenes sequences. At the same time, we carried out structural analysis and functional annotations on these sequences, which can provide reference for subsequent molecular biology related research.

Key words: *Coelomactra antiquata*; Full-length transcriptome; SMRT sequencing; RNA-seq; Function annotation

三角帆蚌 *CDK6* 基因克隆及功能分析

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摘要：为了探究 *CDK6* 序列特征、组织表达情况及其在细胞周期中的作用，本实验利用 RACE 技术克隆了三角帆蚌 *CDK6* 基因的 cDNA 全长，运用 qPCR 和原位杂交技术研究了 *CDK6* 在三角帆蚌外套膜组织的表达及定位，通过 RNAi 技术干扰 *CDK6* 的表达并探究了干扰后细胞周期调控通路相关下游基因的表达以及外套膜细胞分期的变化。

关键词：*CDK6*；三角帆蚌；qPCR；细胞周期调控；RNAi

Molecular cloning and functional characterization of *CDK6* gene in freshwater pearl mussel,*Hyriopsis cumingii*

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Abstract: To study *CDK6* sequence characteristics, tissue expression and its role in the cell cycle. In this study, the full-length cDNA was cloned by RACE technique, and the expression and localization of *CDK6* in the mantle tissues of *Hyriopsis cumingii*, were investigated by qPCR and in situ hybridization. After the interference of *CDK6* by RNAi technology, the expression of downstream genes related to the cell cycle regulatory pathway and the change of mantle cell cycle phase were investigated after the interference.

Key words: *CDK6*, *Hyriopsis cumingii*, qPCR, Cell cycle regulation, RNAi

鲤 *IL-17B* 基因序列特征、表达模式、原核重组蛋白的获得及其促炎作用

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摘要：白细胞介素 17（Interleukin-17，IL-17）是一类重要的炎症因子。本实验使用同源搜索和基因克隆在鲤中挖掘到了 2 个 *IL-17B* 基因（*CcIL-17B1* 和 *CcIL-17B2*），进行了鲤 *IL-17Bs* 基因序列特征和鱼类 *IL-17B* 的共线性分析；qPCR 揭示鲤 *IL-17Bs* 的表达模式；使用大肠杆菌表达系统，获得了 NusA-17B 重组蛋白；体内肛灌鲤肠道组织、体外孵育肾组织，通过切片和定量 PCR 测定炎症因子的表达，在体内和体外确定鲤 IL-17B 的促炎作用。

关键词：关键词：鲤；*IL-17B*；基因表达；重组蛋白；炎症反应

Sequence analysis, expression, acuquisition of prokaryotic recombinant protein and pro-inflammatory effect of Interleukin-17B in *Cyprinus carpio*

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Abstract: Interleukin-17 (IL-17) is an important inflammatory factor. In this study, two *IL-17B* genes (*CcIL-17B1* and *CcIL-17B2*) were excavated in carp by using homology search and gene cloning, and the sequence characteristics of carp *IL-17Bs* gene sequence and collinearity analysis were performed. The expression pattern of carp *IL-17Bs* were revealed by qPCR. Used *E.coli* expression system to obtain NusA-17B recombinant protein. Injected NusA-17B through the carp intestine in vivo and incubated kidney tissue using NusA-17B in vitro, the expression of inflammatory factors was determined by sectioning and quantitative PCR, and the pro-inflammatory effect of carp IL-17B was determined in vivo and in vitro.

Keyword: *Cyprinus carpio*; *IL-17B*; gene expression; recombinant protein; inflammatory response.

中华绒螯蟹肌质网钙泵 SERCA 基因的克隆与功能研究

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摘要：钙离子在信号转导中起重要作用，调节细胞的各种生理功能。钙离子从胞浆到肌浆或内质网腔的主动转运是通过肌质网钙泵(sarco/endoplasmic reticulum Ca2+ATPase, SERCA)实现的。在本研究中，我们从中华绒螯蟹的 Y 器官中克隆了 SERCA 基因的 cDNA 全长序列。qPCR 分析结果显示, Es-SERCA 在眼柄、肌肉、鳃、肝胰腺、肠、心脏、Y 器官中均有表达，不同组织中 Es-SERCA 表达的阶段性变化表明 SERCA 在钙稳态中起着重要的调节作用。蜕皮周期中 Y 器官中 ES-SERCA 的相对表达量与血淋巴中蜕皮激素含量的变化规律相似，表明钙离子信号刺激 Y 器官蜕皮激素的合成。本研究为进一步研究中华绒螯蟹蜕皮的分子机制提供了参考。

关键词：中华绒螯蟹；SERCA；蜕壳; 钙离子信号

Molecular cloning and functional characterization of sarco/endoplasmic reticulum Ca^{2+}ATPase from Chinese mitten crab (*Eriocheir sinensis*)

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Abstract: Ca^{2+} ion plays an important role in Ca^{2+} signaling and regulates various physiological functions of cells. The active transport of Ca^{2+} from the cytosol to the lumen of the sarcoplasmic or endoplasmic reticulum is achieved by sarco-endoplasmic Ca^{2+}-ATPases (SERCA). In this study, we cloned a full-length cDNA encoding a putative SERCA protein from the Y-organs in Chinese mitten crabs. qPCR indicated that *Es-SERCA* was widely expressed in eyestalk, muscle, gill, hepatopancreas, intestine, heart and Y-organ tissues, and the stage-specific changes among different tissues indicated a functional role of Es-SERCA in calcium homeostasis. The relative expression of the *Es-SERCA* in Y-organs during the molting cycle was similar to the change pattern of ecdysone concentration in hemolymph, indicating Ca^{2+} signaling stimulated ecdysone synthesis in Y-organs. Our study provides a reference for further research on the molecular mechanisms of the molting of Chinese mitten crabs.

Key words: *Eriocheir sinensis*; SERCA; Molting; Calcium signaling

三角帆蚌 Cu/Zn SOD2 基因的重组表达与纯化

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摘要：为了获得大量纯度较高的 Cu/Zn SOD2 重组蛋白，本研究在构建 Cu/Zn SOD2 原核表达载体，优化表达条件，进行可溶性诱导表达，并对其进行纯化和酶活测定。结果表明，成功构建了重组表达 pET32a-Cu/Zn SOD2，表达产物经 SDS-PAGE 电泳，在近 20-25KDa 之间有一条明显条带；经纯化的 Cu/Zn SOD2 重组蛋白,经 WST-8 法测定具较高酶活。本研究为进一步分析 Cu/Zn SOD 重组蛋白的功能提供了基础材料。

关键词：三角帆蚌；超氧化物歧化酶；重组表达；纯化

Cloning and Expression of a novel SOD gene from mussel *Hyriopsis cumingii*

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Abstract: In order to obtain a large amount of high-purity Cu/Zn SOD2 recombinant protein, in the present study, a Cu/Zn SOD2 prokaryotic expression vector was constructed, the expression conditions were optimized, the soluble induction expression, purification and enzyme activity measuring were carried out . The results showed that, the recombinant expression pET32a-Cu/Zn SOD2 was successfully constructed. The expression products were electrophoresed by SDS-PAGE, and there was a clear band between approximately 20-25KDa; the purified Cu/Zn SOD2 recombinant protein was subjected to WST-8 Method for determination of higher enzyme activity. This study provides a basic material for further analysis of the function of Cu/Zn SOD recombinant protein.

Key words: *Hyriopsis cumingii*; Superoxide dismutase; Recombinant expression; Purification

17β-雌二醇诱导斑点叉尾鮰雌性化研究

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摘要：为建立斑点叉尾鮰遗传性别鉴定方法及探究全雌化培育方法，研究采用基于性别连锁 SNP 特异性引物延伸反应的方法，并应用基于免疫胶体金技术的核酸检测试纸检测性别连锁 SNP，从而实现遗传性别分子水平的可视化鉴定。以卤虫-人工配合饲料为 17β-雌二醇(17β-estradiol, 17β-E2)载体,通过采集生长数据、存活率、解剖观察和组织切片观察性腺结构,结合遗传性别鉴定结果计算性逆转率并检测试验鱼各组织中 17β-E2 含量。建立一种准确、快速的基于性别连锁 SNP 特异性引物延伸反应的斑点叉尾鮰遗传性别鉴定方法，以及 17β-E2 诱导 XY 雄性斑点叉尾鮰雌性化方法,为后续全雄斑点叉尾鮰新品种的培育奠定了坚实的基础。

关键字：斑点叉尾鮰；遗传性别鉴定；性别连锁 SNP；17β-雌二醇；雌性化; 性逆转

STUDY ON FEMINIZATION OF CHANNEL CATFISH INDUCED BY 17β-ESTRADIOL

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Abstract: In order to establish an accurate and rapid method to identify the genetic sex of channel catfish and explore the appropriate method of feminization and 17β-estradiol doses for male channel catfish. The product of sex-linked SNP specific primer extension reaction was hybridized with DNA probe, and then detected by nucleic acid test paper based on immune colloidal gold technology. artemia and artificial compound feed were used as 17β-E2 vector to feed catfish larvae continuously for 27 days. The growth data and survival rate of catfish in each group were measured and counted at 60 dahs, the sex reversal rate also was calculated in combination with the genetic sex identification results. Furthermore, the ovarian development of XX and XY females in each group was compared and analyzed based on the H&E staining of ovary tissue paraffin sections. Finally, 17β-E2 contents in tissues of sex XY females in each group were detected and compared with control females at 270 dahs. This study revealed that the specific primer extension reaction of sex-linked SNP combined with nucleic acid test paper based on immune colloidal gold technology could accurately and quickly identify the genetic sex of channel catfish and established 17β-E_2 induced feminization of XY male channel catfish, and laid a solid foundation for the subsequent cultivation of new male channel catfish varieties.

Key words: channel catfish; genetic sex; sex-linked SNP, 17β-estradiol, feminization, sexual reversal

斑点叉尾鮰盐度胁迫应答基因的鉴定与分析

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摘要：本试验主要通过盐度半致死试验、盐度胁迫试验、MAPK 基因家族的鉴定与分析，采用比较转录组学的方法检测不同盐度胁迫下的转录水平变化，以揭示斑点叉尾鮰（*Ictalurus punctatus*）响应盐度胁迫的基因表达调控网络，鉴定差异表达的功能基因及其参与的生物学过程。鉴定并分析 MAPK 基因家族，基于转录组测序数据计算家族成员在不用盐浓度下的 RPKM （Reads Per Kilobase per Million mapped reads）值，筛选差异表达的基因家族成员，探索 MAPK 家族成员在机体应对盐度胁迫时所扮演的角色。试验的顺利开展有助于斑点叉尾鮰在盐度胁迫下生长性状、应对盐度胁迫机制的遗传解析，为其耐盐性育种提供新的方向和理论基础。

关键词：斑点叉尾鮰; 盐度; 半致死; 胁迫; 转录组学; MAPK 基因

Identification and analysis of salinity stress response genes in Channel Catfish (Ictalurus punctatus)

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Abstract: In this study, through salinity half-lethal test, salinity stress test and identification analysis of MAPK gene family, the changes of transcription level under different salinity stress were detected by comparative transcriptomics, so as to reveal the gene expression regulation network of channel catfish (*Ictalurus punctatus*) in response to salinity stress, identify differentially expressed functional genes and their biological processes. Identify and analyze MAPK gene family, calculate RPKM (reads per kilobase per million mapped reads) of family members without salt concentration based on transcriptome sequencing data, screen differentially expressed gene family members, and explore the role of MAPK family members in response to salinity stress. The successful development of the experiment is helpful to the genetic analysis of the growth characteristics of channel catfish under salinity stress and the mechanism of coping with salinity stress, and provides a new direction and theoretical basis for its salt tolerance breeding.

Key words: channel catfish, salinity, half-lethal, stress, transcriptomics, Mapk gene

单细胞测序解析刺参不同部位体腔细胞对排脏的生物学响应

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摘要：刺参具有复杂的水管系统，其内悬浮有大量体腔细胞，其种类与体腔中体腔细胞相同，但不同亚群细胞比例存在显著差异。波里氏囊作为水管系统的附属物，是刺参排脏后除体壁外唯一保留的器官，可能在刺参体腔细胞恢复和组织再生中发挥重要的作用。为了获知波里氏囊在排脏后体腔细胞再生中的作用，本实验借助单细胞 RNA 测序技术对排脏前及排脏后 6h 的体腔细胞和波里氏囊腔细胞分别进行测序，通过转录组文库数据的挖掘和分析以及后续的实验论证，初步明晰体腔细胞和波里氏囊腔细胞在分子水平上的异同，及排脏后两者在体腔细胞快速恢复中的生物学作用。

关键词：水管系统；波里氏囊；体腔细胞；单细胞测序；排脏；细胞再生

Analysis of biological response of coelomocytes from different parts after evisceration by single cell sequencing in *Apostichopus japonicus*

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Abstract: There is a complex water-vascular system in sea cucumber, *Apostichopus japonicus*, which contains a large number of coelomic cells and these cells are same in type. However, both of coelomic cells differ significantly in the proportion of subpopulations. As an appendage of the water-vascular system, polian vesicle is the only organ retained except the body wall after evisceration. So it is considered to play an important role in the recovery of coelomocytes and tissue regeneration of *Apostichopus japonicus*. In order to address the role of polian vesicle in the recovery of coelomocytes after evisceration, the coelomocytes from polian vesicle and coelom before evisceration and at 6 h after evisceration were sampled and sequenced by single-cell RNA sequencing technology. Through the mining and analysis of transcriptome library data and subsequent experimental demonstration, the similarities and differences between coelomocytes from coelom and coelomocytes from polian vesicle in the molecular level were preliminarily clarified, and furthermore, their biological roles in the rapid recovery of coelomocytes will also be investigated.

Key words: water-vascular system, polian vesicle, coelomocytes, single-cell RNA sequence, evisceration, regeneration

养殖密度对缢蛏生长、抗氧化水平和代谢水平的影响

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摘要：以缢蛏（*Sinonovacula constricta*）为研究对象，设置三个养殖密度组分别为 30 粒/箱（G30）、60 粒/箱（G60）、90 粒/箱（G90），养殖周期为 60d，每 15d 挖出测定其生长数据并在 0、60d 取样，测定不同密度对缢蛏生长和存活率、肝胰腺组织抗氧化酶和代谢酶的影响。结果表明，低密度组 G30 存活率最高，且壳长、壳宽、壳高和体质量特定生长率均显著高于 G60 组和 G90 组（$P<0.05$）；抗氧化物酶 GSH-Px 的活性 G90 组显著高于 G30 组和 G60 组（$P<0.05$），SOD 活性与 T-AOC 相比初始值都产生了一定程度的下降；代谢酶 PFK 的活性 G60 组显著低于 G30 组与 G90 组（$P<0.05$），G60 组的 SDH 活性显著高于 G30 组与 G90 组（$P<0.05$）。综上所述，高密度养殖会使缢蛏的抗氧化水平有所下降，同时在合理的养殖密度下缢蛏的有氧代谢比较旺盛，为探究缢蛏的适宜养殖密度提供了参考资料。

关键词：缢蛏；养殖密度；生长；抗氧化；代谢

Effects of culture density on growth, antioxidant and metabolism of *Sinonovacula constricta*

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Abstract: *Sinonovacula constricta* was selected as the research object. Three culture density groups were set up, respectively 30, 60 and 90 grains/box (G30, G60 and G90), with a culture cycle of 60 days. The effects of different density on growth and survival rate of *Sinonovacula constricta*, antioxidant enzyme and metabolic enzyme in hepatopancreas were determined. The results showed that the survival rate of G30 in low density group was the highest, and the specific growth rates of shell length, shell width, shell height and body weight in low density group were significantly higher than those in G60 and G90 groups ($P<0.05$). The activity of antioxidant enzyme GSH-Px in G90 group was significantly higher than that in G30 and G60 groups ($P<0.05$), and the initial value of SOD activity decreased to a certain extent compared with t-AOC. The activity of metabolic enzyme PFK in G60 group was significantly lower than that in G30 and G90 groups ($P<0.05$), and the ACTIVITY of SDH in G60 group was significantly higher than that in G30 and G90 groups ($P<0.05$). In conclusion, high density culture would reduce the antioxidant level of *Sinonovacula constricta*, and at the same time, the aerobic metabolism of *Sinonovacula constricta* was relatively strong under reasonable culture density, which provided reference for the exploration of the appropriate culture density of *Sinonovacula constricta*.

Key words: *Sinonovacula constricta*, breeding density, growth, antioxidant, metabolism

黄条鰤 leptin 及受体基因的克隆与表达分析

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摘要：本研究用 RACE 法获得了黄条鰤两种 leptin 配体（*lepa* 和 *lepb*）与两种受体基因（*lepr, leport*）的 cDNA 序列，*lepa* 基因含有 486bp 的 ORF,编码 161 个氨基酸，*lepb* 基因含有 471bp 的 ORF，编码 156 个氨基酸，*lepr* 基因含 3498bp 的 ORF,编码 1165 个氨基酸，*leport* 基因含有 ORF396bp,编码 131 个氨基酸。荧光定量 PCR 检测发现黄条鰤 leptin 及其受体基因在各组织中均有表达，*lepa* mRNA 在脑、肌肉、卵巢中表达水平较高，*lepb* mRNA 在脑、鳃、肌肉中高度表达，*lepr* mRNA 在鳃、肾、卵巢中表达量较高，*leprot* mRNA 在脑和卵巢中显著性表达。在胚胎发育过程中，*lepa*、*lepb*、*lepr* 和 *leprot* 均可检测到表达，*lepa* mRNA、*lepb* mRNA 表达水平随着胚胎发育整体趋于上升趋势。*lepr* mRNA 表达趋势呈现钟形曲线，在 64 细胞期达到表达水平巅峰。*leport* mRNA 在受精卵时表达水平达到巅峰。在黄条鰤仔稚鱼时期发现 *lepa* mRNA、*lepr* mRNA 和 *leport* mRNA 表达水平逐渐升高并在黄条鰤快速生长时期显著降低，表明 *lep/lepr* 系统对于黄条鰤仔稚鱼的摄食转换策略、生长发育具有一定的调控作用。

关键词：黄条鰤、leptin、瘦素受体、克隆、组织表达分析

Cloning and expression analysis of leptin and receptor genes in *Seriola aureovittata*

Abstract: In this study, two leptin ligands (*lepa* and *lepb*) and two receptor genes (*lepr, leport*) were obtained by RACE method. *lepa* gene contains 486bp ORF encoding 161 amino acids, *lepb* gene contains 471bp ORF encoding 156 amino acids, *lepr* gene contains 3498bp ORF encoding 1165 amino acids, *leport* gene contains 396bp ORF encoding 161 amino acids, edited code 131. Fluorescence quantitative PCR detection showed that *Seriola aureovittata* leptin and its receptor genes were expressed in various tissues. *lepa* mRNA was highly expressed in brain muscle and ovary, *lepb* mRNA was highly expressed in brain muscle and *lepr* mRNA was highly expressed in gill, kidney and ovary. The *leprot* mRNA is significant in the brain and ovary . The *leprot* mRNA is significantly expressed in the brain and ovary. During embryonic development, *lepa, lepb* and *leprot* can be detected. *lepa* mRNA, *lepb* mRNA expression level tends to rise with embryonic development as a whole. *lepr* mRNA expression trend presents a bell-shaped curve and reaches the peak. *leport* at 64 cell stage mRNA levels peak when the egg is fertilized. The *lepa* mRNA, *lepr* mRNA and *leport* mRNA expression levels of *Seriola aureovittata* are gradually increased in the epidemiological stage, and significantly decreased in the epidemiological stage, indicating that *lep/lepr* system has significant effects on the feeding transformation strategy, growth and development of young and infected *Seriola aureovittata.*

Keywords: *Seriola aureovittata*, leptin, leptin receptor, cloning, tissue table

中华绒螯蟹羧酸酯酶（*Es-CXE6*）基因的克隆、表达及其与甲基法尼酯的关联性

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摘要：甲基法尼酯（MF）是一种重要的倍半萜类物质，其参与调节甲壳类动物中许多重要的生理过程，包括卵巢发育和生殖过程。本实验采用RACE技术从中华绒螯蟹中肝胰腺组织克隆出了羧酸酯酶（*Es-CXE6*）cDNA，全长1919bp，序列结果分析表明*Es-CXE6*属于CXE多功能酶家族。此外，本实验运用了QPCR技术对MF添加和ESA处理后组织进行相对定量分析，结果表明*Es-CXE6*在卵巢发育中与血淋巴MF滴度具有一定的负相关性，且MF滴度增加或ESA处理均可显著上调*ES-CXE6* 基因表达量。综上所述，本次实验结果表明*Es-CXE6*基因与中华绒螯蟹MF滴度相关。

关键词：中华绒螯蟹；*Es-CXE6*；甲基法尼酯；基因表达

Cloning and expression of carboxylesterase (*Es-CXE6*) gene from *Eriocheir sinensis* and its association with methyl farnesoate

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Abstract: Methyl farnesate (MF) is an important sesquiterpenoid regulating many crustaceans important physiological processes, including ovarian development and reproduction. In the present study, RACE technology was used to clone the full-length (1919 bp) cDNA of carboxylesterase (*Es-CXE6*) from the hepatopancreatic of the *Eriocheir sinensis*. Sequence analysis showed that *Es-CXE6* belongs to the Carboxylesterase superfamily. QPCR technology was performed to detect the relative expression of *Es-CXE6* after MF treatment and ESA surgery. QPCR results showed that *Es-CXE6* has a negative correlation with hemolymph MF titer during ovarian development. IN addition, *ES-CXE6* gene expression was significantly increased after MF treatment and ESA surgery. In summary, the results of this study showed the relation of *Es-CXE6* with MF titer in *E. sinensis*.

Key words: *Eriocheir sinensis*, *Es-CXE6*, methyl farnesoate, gene expression

中华绒螯蟹二龄早熟和晚熟品系选育第 5 代生长性能和性腺发育的比较

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摘要：为研究中华绒螯蟹二龄早熟和晚熟群体在第 5 代的选育情况，对两选育群体进行养殖实验。结果显示：（1）扣蟹养殖阶段，两选育群体的最终体质量与增重率均高于对照组；对照组 4.50-5.99g 和≥6.00g 规格的比例显著低于早熟群体。（3）成蟹养殖阶段，2 选育品系的最终体质量高于对照组；早熟组的生殖蜕壳时间早于其余两组，其在 8 月 15 日的生殖蜕壳比例显著高于晚熟组；早熟组性腺指数 GSI 始终较高，晚熟组始终较低;晚熟雌体＞140g 规格所占的比例显著高于对照组。综上，经过多代连续选育后，中华绒螯蟹在扣蟹和成蟹阶段的生长性能均有较大的提升，性腺发育速度得到有效控制，为新品种的申报和后续的大规模推广提供数据参考。

关键词：中华绒螯蟹；群体选育；生长性能；生殖蜕壳；性腺发育

Growth performance and gonadal development of the second-year early-maturing and late-maturing strains of the fifth selective generation of *Eriocheir sinensis*

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Abstract: This study was aimed to evaluate the growth and gonad development of selected strains of *Eriocheir sinensis*: early-maturing strain (EM) and late-maturing strain (LM). The results showed that: (1) The final body weight and WGR of the breeding strains were higher than the control group during the juvenile culture stage. (2) During the adult culture stage, the final body weight of two strains was higher than that of the control group; The puberty molting time of EM was earlier than the other two groups, and the proportion of puberty molting in August 15 was significantly higher than LM; The GSI of the EM was always higher than the LM; The proportion of female LM>140g was significantly higher than that of the control group. The results showed that selective breeding is an effective means to regulate growth performance and gonad development of *E. sinensis*.

Key words: Chinese mitten crab; selective breeding; growth performance; puberty moulting; gonad development

低氧胁迫下瓦氏黄颡鱼（*Pelteobagrus vachelli*）肌肉组织中转录组、miRNA 组、蛋白组、代谢组联合分析

李杰 [b]，张国松 [a,b*]，尹绍武 [b*]等

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摘要：为了揭示鱼类低氧适应的分子调控机制，便于研究人员找到环境应激中的低氧标志物。本实验运用多组学（转录组、miRNA 组、蛋白组和代谢组）联合分析方法，鉴定了低氧胁迫下瓦氏黄颡鱼肌肉组织中涉及不同生物途径的几个缺氧相关的 miRNA-mRNA-蛋白质-代谢物 pairs。这些 pairs 有助于深入了解鱼类低氧的分子调控机制，其研究方法和实验设计可用于不同鱼类。

关键词:多组学；低氧；瓦氏黄颡鱼

Integrated application of multi-omics strategies provides insights into the environmental hypoxia response in *Pelteobagrus vachelli* muscles

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Abstract: Revealing the molecular mechanism of fish hypoxia adaptation will help researchers to find hypoxic markers for hypoxia induced by environmental stress. Here, we used a multi-omics approach to identify several hypoxia-associated miRNAs, mRNAs, proteins, and metabolites involved in diverse biological pathways in the muscles of Pelteobagrus vachelli. Our findings contribute meaningful insights into the molecular mechanisms of hypoxia, and the methods and study design can be utilized across different fish species.

Keywords: Multi-omics; Hypoxia; *Pelteobagrus vachelli*; muscle

三角帆蚌细胞的培养与鉴定

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摘要：细胞培养在现代生物领域广泛应用，是生物高技术产业的重要部分，但是目前贝类细胞系很少，仅见左旋淡水蜗牛（*Biomphalaria glabrata*），三角帆蚌（*Hyriopsis cumingii*）作为特有的淡水贝类具有极高研究意义。本研究采用胰蛋白酶消化法分离原代细胞，通过改良细胞培养基，培养色线组织、外套膜组织、鳃组织原代细胞并成功传代，其中外套膜组织细胞传至 11 代，并鉴定细胞特征。结果显示，在三角帆蚌细胞培养中添加 10%的自制蚌血清对培养基进行改良，为细胞生长发育提供了一个良好的微环境。用倒置显微镜观细胞形态及生长情况，发现三角帆蚌细胞增殖迅速,聚集成团、连接成片,呈现旺盛的分泌功能。用线粒体基因 *COI* 对原代和传代细胞进行验证，成功证实为三角帆蚌细胞。采用 Label-free 方法对三角帆蚌血清和胎牛血清进行了蛋白组学分析，筛选出差异蛋白并验证。

关键词：细胞培养；Label-free；三角帆蚌；血清；细胞验证

Culture and identification of *Hyriopsis cumingii* cells

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Abstract: Cell culture is widely used in modern biological field and is an important part of biological high-tech industry, but there are few cell lines in shellfish at present, only *Biomphalaria glabrata*.*Hyriopsis cumingii* as a unique freshwater shellfish has high research significance. In this study, the trypsin digestion method was used to isolate the primary cells, and the primary cells of pallial line , mantle and gill tissue were cultured and successfully passed on through the improved cell culture medium, among which the mantle tissue cells were passed on to the 11th generation, and the cell characteristics were identified. The results showed that adding 10% homemade serum in the cell culture of *Hyriopsis cumingii* improved the culture medium and provided a good microenvironment for cell growth and development. The cell morphology and growth of *Hyriopsis cumingii* were observed under an inverted microscope. It was found that the cells proliferated rapidly, clustered and joined into slices, and showed vigorous secretory function. The primary and passage cells were confirmed to be *Hyriopsis cumingii* cells by mitochondrial gene *COI*.The label-free method was used for proteomic analysis of *Hyriopsis cumingii* serum and fetal bovine serum, and the differential proteins were screened and verified.

Key words: Cell culture, Label-free, *Hyriopsis cumingii,* serum, Cells validation

坛紫菜响应高光胁迫分子机制的初步研究

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摘要：坛紫菜（*Neoporphyra haitanensis*）生活于中高潮区，退潮后会遭受到周期性和连续性的强光胁迫，但高潮复水后坛紫菜叶状体能快速恢复正常生长，表明坛紫菜具有极强的耐高光能力。然而，其耐高光机制尚不明确。因此，本研究挑选了两个耐高光能力具有显著差异的坛紫菜新品系作为研究对象，测定了高光胁迫下两个品系藻体光合速率、抗氧化酶活性等生理指标，构建了两个品系的差异转录表达谱，并结合荧光定量分析技术获得了调控坛紫菜耐高光的关键通路和基因。具体结果如下，在高光胁迫下，两种坛紫菜品系叶状体的丙二醛含量均显著上升，光系统部分基因表达量显著降低，藻体光合能力显著下降，表明藻体受到了氧化损伤。但藻体可以通过非光化学淬灭机制，抗氧化系统，调节色素组分和捕光蛋白基因表达等方式来应对高光胁迫。本研究结果为阐明紫菜的耐高光机理提供了理论参考。

关键词：坛紫菜；高光胁迫；抗氧化系统；非光化学淬灭；捕光蛋白

A preliminary study on the molecular mechanism of Neoporphyra haitanensis in response to high light stress

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Abstract: *Neoporphyra haitanensis* lives in the mid-to-high tide area and will be subjected to periodic and continuous strong light stress after low tide. *N. haitanensis* can quickly return to normal growth after rehydration at high tide, indicating that *N. haitanensis* is highly resistant to high light ability. However, the mechanism of its resistance to high light is still unclear. For this reason, this study selected two new strains of *N. haitanensis* with significant differences in high light tolerance. The photosynthetic rate, antioxidant enzyme activity and other physiological indicators of the two strains under high light stress were measured, and the differential transcription expression profiles of the two strains were constructed to provide a theoretical basis for the analysis of the high light tolerance mechanism of *N. haitanensis* fronds. The results showed that under high light stress, the malondialdehyde content of the fronds of the two *N. haitanensis* strains increased significantly, the expression of some genes in the photosystem was significantly reduced, and the photosynthetic capacity of the algae was significantly decreased, indicating that the algae was oxidatively damaged. However, the algae can respond to high light stress through non-photochemical quenching mechanisms, antioxidant systems, regulation of pigment components and light-harvesting protein gene expression. The results of this study provide a theoretical reference for elucidating the mechanism of high light tolerance of laver.

Keywords: *Neoporphyra haitanensis*, High light stress, Antioxidant systems, Non-photochemical quenching, Light harvesting protein

鲂鲌 ELOVL1 与 ELOVL6 基因的组织胚胎表达及饥饿应答研究

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摘要：本研究克隆了鲂鲌回交种的长链脂肪酸延长酶（*elovl1* 和 *elovl6*)基因，进行了同源性比对分析。并对鲂鲌成鱼的组织表达和胚胎表达进行了分析，阐明了该基因在鲂鲌的肝脏、脑、鳃、肾脏、心脏等组织及不同胚胎发育时期的表达特性；另外，通过饥饿实验处理，对鲂鲌幼鱼进行了生物学的表达差异分析。本研究为鲂鲌杂交种及其它杂交鱼类的脂肪酸合成研究提供了重要理论依据。

关键词：回交种；ELOVL；基因表达；饥饿应答

Expression of *elovl1* and *elovl6* genes in tissues and embryos and starvation response of *Megalobrama amblycephala*♀×(*M. amblycephala*×*Culter alburnus*)♂

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Abstract: In this study, the *elovl1* and *elovl6* genes of backcross line [*Megalobrama amblycephala*♀×(*M. amblycephala*×*Culter alburnus*)♂] were cloned and compared. The adult tissue expression and embryonic expression of backcross line were analyzed, and the expression characteristics of the gene in liver, brain, gill, kidney, heart and different embryonic development stages of backcross line were clarified; In addition, the biological expression difference of juvenile backcross line was analyzed through starvation experiment. This study provides an important theoretical basis for the study of fatty acid synthesis of backcross line and other hybrid fish.

Key words: backcross, ELOVL, gene expression, starvation responds

中华绒螯蟹“长荡湖 1 号”奇数年子一代的成蟹养殖性能评估

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摘要：成活率和成蟹体质量是中华绒螯蟹（*Eriocheir sinensis*）遗传选育的重要指标，“长荡湖 1 号”A 系和 B 系分为以成活率和大规格为主要选育指标。本研究在实际池塘养殖条件下评估“长荡湖 1 号”奇数年选育子一代的成蟹养殖性能。

关键词：中华绒螯蟹；长荡湖 1 号；配套系选育；池塘养殖；养殖性能；性腺发育

The evaluation on culture performance of the first generation of odd year Chinese mitten crab (*Eriocheir sinensis*) “Changdang Lake 1” during the adult culture stage

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Abstract: The survival rate and body weight of adult crabs are important indexes for genetic selection of Chinese mitten crab (*Eriocheir sinensis*). Survival rate and large size were the main breeding indexes for strain A and strain of " Changdang Lake 1". In order to explore the difference in growth performance and culture effect of Chinese mitten crab "Changdang Lake 1" in odd year generation, the juveniles were reared to adult in 9 similar ponds close to production conditions in Changdang Lake area.

Key words：*Eriocheir sinensis*; Changdang Lake 1; Complete set line breeding; Pond-culture; Culture performance; Gonadal development

生长快与生长慢黄姑鱼肌肉、肝脏转录组的比较分析

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摘要：黄姑鱼(*Nibea albiflora*)是一种具有重要经济价值的海产鱼类。本研究利用 Illumina HiSeq 测序平台对同一养殖群体中 124 尾生长快（均重 181.05±28.33g）和 118 尾生长慢（均重 103.77±27.16g）的黄姑鱼肌肉和肝脏组织进行高通量测序比较，每尾测序量为 4Gb。经拼接组装，最终获得 25,326 个转录本，其中 3,481 个转录本是之前黄姑鱼转录组测序数据中所未见。生长快和生长慢个体进行差异表达基因分析的结果表明，在筛选条件为 padj 值为 0.5,log2FoldChange 值为 0.5 情况下，肝脏组织共有 548（297 个上调/241 个下调）个差异表达基因被检测到，肌肉组织共有 183（41 个上调/142 个下调）个差异表达基因被检测到。根据 padj 值，在肝脏中筛选出 *apoa4*、*kcng2*、*ptpru*、*gtr1* 基因和肌肉中筛选出 *f13a*、*snx13*、*dpp10*、*syt10* 等作为黄姑鱼生长性状的差异基因，其中 *snx13* 可能在黄姑鱼生长发育中有重要功能。本研究中所获得的转录本信息，不但丰富了数据库中黄姑鱼的转录组资源，为后续黄姑鱼基础研究提供了参考，还为功能基因的挖掘、基因组学研究提供了有效的数据支撑。

关键词：黄姑鱼；转录组；生长差异；差异基因

Comparative analysis of the muscle and liver transcriptomes of fast-growing and slow-growing yellow drum

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Abstract: Nibea albiflora is a marine fish with important economic value. In this study, 124 fast-growing (average weight 181.05±28.33g) and 118 slow-growing (average weight 103.77±27.16g) Nibe albiflora muscle and liver tissues from the same culture population were sequenced at 4Gb each using the Illumina HiSeq sequencing platform. 25,326 transcripts were obtained after splicing and assembly. Of these, 3,481 transcripts were not seen in previous transcriptome sequencing data. The results of differentially expressed gene analysis in fast and slow growing individuals showed that a total of 548 (297 up/241 down) differentially expressed genes were detected in liver tissue and 183 (41 up/142 down) differentially expressed genes were detected in muscle tissue under the screening conditions of padj value of 0.5 and log2FoldChange value of 0.5 were detected. Based on padj values, *apoa4, kcng2, ptpru, gtr1* genes were screened in liver and *f13a, snx13, dpp10, syt10* in muscle as differentially expressed genes for growth traits in yellow drum, among which snx13 may have important functions in growth and development of yellow drum. The transcript information obtained in this study not only enriched the transcriptome resources of yellow drum in the database and provided reference for the subsequent basic research of yellow drum, but also provided effective data support for the mining of functional genes and genomics research.

Key words: *Yellow drum, transcriptome, growth difference, differential gene*

影响大黄鱼肌肉 DHA 与 EPA 含量的功能基因挖掘

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摘要：大黄鱼是我国重要的海水养殖鱼类，HUFA（主要是 DHA 与 EPA）含量是鱼类肌肉品质评价的重要指标，与鱼类本身生长发育等也密切相关，开展 DHA 和 EPA 含量相关基因挖掘研究可以为遗传改良提供基础资料。本研究对 676 尾养殖大黄鱼进行全基因组重测序(6X)，再通过 Agilent7890B 气相色谱仪对 206 尾大黄鱼肌肉组织样品 HUFA 含量进行测定，然后通过 GWAS 技术获取基因组中相关的 SNP 标记信息，在显著的 SNP 周边挖掘影响大黄鱼 DHA 与 EPA 含量的功能基因。初步发现亚麻酸含量和 EPA（－0.81），DHA（－0.61）含量负相关，DHA 含量和 EPA 含量正相关，相关系数 0.79。GWAS 分析初步发现了与亚麻酸合成 DHA 能力及 DHA 含量相关的遗传位点及功能基因，发现了至少 3 个显著的 GWAS 位点，其中 7 号染色体上的位点内部包含 *elovl1* 基因（脂肪酸延长酶基因）、15 号染色体上的位点包含 *elovl6* 基因，其他位点内不包含酶基因；初步发现了由亚麻酸合成 EPA 能力及 EPA 含量的遗传位点或基因，比如信号最强的 15 号染色体上检测的位点内部包含 *fads6* 基因。本研究通过在大黄鱼上开展基因组选择育种的研究，以期望为大黄鱼品质的遗传改良提供遗传背景知识、开发辅助育种的分子标记和遗传操作的目标基因。同时对大黄鱼营养学及其他鱼类同类研究也有应用与借鉴价值。

关键词：大黄鱼；HUFA；GWAS；WGS

Mining of functional genes affecting DHA and EPA content in muscle of Large yellow croaker

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Abstract: Large yellow croaker (*Larimichthys crocea*) is an important mariculture fish in China. The content of HUFA (mainly DHA and EPA) is an important index to evaluate the muscle quality of fish, and it is also closely related to the growth and development of fish. Mining genes related to DHA and EPA content can provide basic data for genetic improvement. In this study, the whole genome of 676 cultured large yellow croaker was re-sequenced (6X). The HUFA content of muscle tissue samples of large yellow croaker was determined by Agilent7890B gas chromatograph, and then the relevant SNP marker information in the genome was obtained by GWAS technique. The functional genes affecting DHA and EPA content of large yellow croaker were mined around the significant SNP. It was found that the content of linolenic acid was negatively correlated with the content of EPA(-0.81) and DHA(-0.61), while the content of DHA was positively correlated with the content of EPA(0.79). GWAS analysis preliminarily found genetic loci and functional genes related to linolenic acid synthesis DHA ability and DHA content, and found at least three significant GWAS loci, of which the loci on chromosome 7 contained the *elovl1* gene (fatty acid elongase gene), the loci on chromosome 15 contained the *elovl6* gene, and the other loci did not contain the enzyme gene. The genetic loci or genes of the ability to synthesize EPA and EPA content from linolenic acid have been preliminarily found. for example, the loci detected on chromosome 15 with the strongest signal contain *fads6* gene. In this study, genomic selection breeding was carried out on large yellow croaker, in order to provide genetic background knowledge for genetic improvement of large yellow croaker quality, develop molecular markers for auxiliary breeding and target genes for genetic operation. At the same time, it also has application and reference value to the nutrition of large yellow croaker and other fish similar research.

Key words: Large yellow croaker (*Larimichthys crocea*),HUFA , GWAS, WGS

Hc-MPPED2 基因对紫色三角帆蚌黑色素代谢通路的影响作用

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摘要：为了探究 MPPED2 基因对紫色三角帆蚌黑色素代谢的影响，完善珍珠颜色遗传的分子机制，为三角帆蚌分子育种提供理论基础，本实验从三角帆蚌珍珠囊转录组获取基因序列，获取序列共 1234bp，其中包括开放阅读框（ORF）909bp，利用实时荧光定量、原位杂交、dsRNA 干扰验证其对紫色三角帆蚌黑色素代谢的影响，实验结果表明 *Hc-MPPED2* 对三角帆蚌黑色素代谢通路起抑制作用。

关键词：MPPED2；紫色三角帆蚌；黑色素；珍珠颜色

Effects of *Hc-MPPED2* gene on melanin metabolism pathway in purple *Hyriopsis cumingii*

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Abstract: In order to explore the effect of MPPED2 gene on melanin metabolism of *Hyriopsis cumingii*, improve the molecular mechanism of pearl color inheritance, and provide a theoretical basis for molecular breeding of *H. cumingii*, gene sequences were obtained from the pearl capsule transcriptome of *H. Cumingii*, with a total of 1234bp, including open reading frame (ORF) of 909bp. Quantitative Real time PCR, In situ hybridization and dsRNA interference were used to verify the effects of *Hc-MPPED2* on melanin met m abolism of *H. cumingii*. The experimental results showed that *Hc-MPPED2* inhibited melanin metabolism pathway of *H. cumingii*.

Key words: MPPED2, melanin, pearl color, *Hyriopsis cumingii*

大黄鱼生长快与生长慢个体肝脏、脾脏组织的转录组比较分析

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摘要：为了探究大黄鱼生长性状的分子调控机制，本研究从同一个养殖群体中选取生长快个体 182 尾（体重均值为 527.1 ± 83.6 g）、生长慢个体 230 尾（体重均值为 238.4 ± 52.3 g）、合计 412 尾，对其肝脏、脾脏组织进行 RNA 提取和转录组测序，根据测序数据进行基因表达差异的比较分析，以 $\text{padj} < 0.05$、$\text{abs}(\log_2\text{FoldChange}) > 1$ 为标准筛选差异表达基因。筛选到的差异表达基因数量分别为肝脏：共 295 个，其中生长快组上调 99 个、下调 196 个；脾脏：共 149 个，其中生长快组上调 67 个、下调 82 个；差异表达基因在 NR 和 Swiss-Prot 数据库的注释率分别为肝脏 98.98 %、82.37 %，脾脏 99.33 %、81.88 %。通过对所有差异表达基因进行 GO 和 KEGG 功能富集分析，并结合功能注释结果筛选相关功能基因，初步筛选出了与脂肪酸合成和能量相关的基因，如 *fasn*、*g6pd*、*acaca*、*acly*、*fads2* 和 *aacs* 等；与免疫相关的基因，如 *mrc1*、*pol*、*cdh12*、*igdcc4*、*nlrc3* 和 *sbk1* 等。研究结果为后续相关基因功能的深度挖掘鉴定以及大黄鱼生长性状的分子调控机制解析提供了重要参考。

关键词：大黄鱼；转录组；生长性状；差异表达基因

Comparative analysis of transcriptome of liver and spleen in fast-growing and slow-growing individuals of *Larimichthys crocea*

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Abstract: In order to explore the molecular regulation mechanism of growth traits of *Larimichthys crocea*, 182 fast-growing individuals (average body weight 527.1 ± 83.6 g) and 230 slow-growing individuals (average body weight 238.4 ± 52.3 g) were selected from the same culture population. RNA extraction and transcriptome sequencing were performed on their liver and spleen tissues, and the differences of gene expression were compared and analyzed according to the sequencing data. $\text{Padj} < 0.05$ and $\text{abs}(\log_2\text{FoldChange}) > 1$ were used as criteria to screen differentially expressed genes. The number of differentially expressed genes screened were: liver: a total of 295, of which 99 were up-regulated and 196 down-regulated in the fast-growing group; spleen: a total of 149, of which 67 were up-regulated and 82 down-regulated in the fast-growing group; the annotation rates of differentially expressed genes in the NR and Swiss-Prot databases were 98.98 % and 82.37 % in the liver and 99.33 % and 81.88 % in the spleen, respectively. Through GO and KEGG functional enrichment analysis of all differentially expressed genes, and combined with the results of functional annotation, we screened out the genes related to fatty acid synthesis and energy, such as *fasn*, *g6pd*, *acaca*, *acly*, *fads2* and *aacs*, and immune-related genes, such as *mrc1*, *pol*, *cdh12*, *igdcc4*, *nlrc3* and *sbk1*. The results provide an important reference for the further identification of the function of related genes and the analysis of the molecular regulation mechanism of the growth traits of *Larimichthys crocea*.

Key words: *Larimichthys crocea*; transcriptome; growth traits; differentially expressed genes

牙鲆性腺发育中 miR-200 家族靶向调节 *amh* 表达的研究

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摘要: 为了探究 miR-200 家族与抗缪勒氏管激素（AMH）在牙鲆性腺发育中的调控作用，本实验利用双荧光素酶报告基因与绿色荧光蛋白报告基因检测系统分别验证了 miR-200 家族 4 个 miRNA 与 *amh* 之间的靶向关系，结果表明 *amh* 是 miR-200a 和 miR-200b 的直接靶基因。并在牙鲆精巢原代培养的支持细胞中将 miR-200a 过表达，采用 real-time PCR 检测了其过表达后 *amh* 及雄性性别相关基因 *dmrt1* 和 *gsdf* 的表达变化。

关键词: 牙鲆；性腺发育；miR-200 家族；*amh*

The research on miR-200 family targeting *amh* in gonadal development of Japanese flounder

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Abstract: To explore the regulatory role of miR-200 family and anti-muiller tube hormone (AMH) in Japanese flounder（*Paralichthys olivaceus*）gonad, the target relationship between four miRNAs of miR-200 family and *amh* was analyzed by double luciferin reporter gene and green fluorescent protein reporter assay. These results showed that *amh* is a direct target gene of miR-200a and miR-200b. After miR-200a was overexpressed in primary Sertoli cells from testes, the expression changes of *amh* and *dmrt1* and *gsdf* were determined by real-time PCR.

Keywords: Japanese flounder; gonadal development; miR-200 family; *amh*

牙鲆性腺发育中 *Cbx2* 与 *let-7* 家族的靶向关系研究

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摘要：*Cbx2* 在哺乳动物性腺发育中起着重要作用，为深入研究 *let-7* 家族和 *cbx2* 在牙鲆性腺发育中的作用机制，我们预测并验证了 *let-7* 家族与 *cbx2* 之间的靶向关系，检测了不同发育阶段牙鲆性腺中 *let-7g* 和 *cbx2* 的表达，并进一步探讨了 *let-7g* 与 *cbx2* 的作用关系以及 *let-7g* 在牙鲆性腺发育中的调节作用。证明了 *cbx2* 是 *let-7b*、*let-7d*、*let-7e*、*let-7g* 和 *let-7j* 的靶基因；*let-7g* 在精巢不同发育阶段的表达显著高于卵巢，而 *cbx2* 在精巢中的表达显著低于卵巢；*let-7g* 在原代精巢细胞中负调节 *cbx2* 的表达，但在 siRNA 干扰后，*sf1* 的表达也显著降低，为阐明 *let-7g* 在牙鲆性腺中的作用提供了依据。

关键词：*cbx2*，*let-7* 家族，*sf1*，性腺发育，牙鲆

Cbx2 is a functional target of the *let-7* family in the gonads of Japanese flounder (*Paralichthys olivaceus*)

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Abstract: Chromobox homolog 2 (*cbx2*) plays an important role in gonadal development in mammals. In order to further study the mechanism of *let-7* family and *cbx2* in the gonadal development of Japanese flounder（*Paralichthys olivaceus*）, we predicted and verified the targeted relationship between *let-7* family and *cbx2*. Furthermore, we detected the expression of *let-7g* and *cbx2* in the gonads of Japanese flounder at different developmental stages. Finally, the relationship between *let-7g* and *cbx2* and the regulatory role of *let-7g* in the gonad of Japanese flounder were further explored. The results showed that *cbx2* was the target gene of l*et-7b, let-7d, let-7e, let-7g* and *let-7j*. let-7g was significantly higher in the different developmental stages of the testis than in the ovary, while the expression of *cbx2* in testis was significantly lower than that in ovary. *let-7g* can negatively regulate *cbx2* at the level of primary testicular cells, however the expression of *sf1* (steroid producing factor 1) was also significantly decreased after the interference of *cbx2* siRNA, which provides a basis for clarifying the function of *let-7g* and *cbx2* in the gonad of Japanese flounder.

Keywords: *cbx2, let-7* family, *sf1*, gonadal development, *Paralichthys olivaceus*

中华绒螯蟹溶血磷脂酰甘油酰基转移酶的基因克隆及在卵巢发育过程中的表达特征

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摘要：为探究溶血磷脂酰甘油酰基转移酶(LPGAT)在中华绒螯蟹(*Eriocheir sinensis*)卵巢发育过程中的表达调控特征，本研究采用实时荧光定量、原位杂交和 RNA 干扰分析其在卵巢发育过程中的时空表达模式。结果表明: (1) qPCR 显示 *Es-lpgat1* 在中华绒螯蟹卵巢发育期的多种组织中均有表达。(2)卵巢发育过程中, II 期卵巢和肝胰腺中 *Es-lpgat1* 表达量最高($P<0.05$)。(3)原位杂交结果显示，在卵巢发育 II 期, *Es-lpgat1*-mRNA 定位于卵黄发生前卵母细胞(PRO)和内源性卵黄合成期卵母细胞(EN)的细胞质中;在肝胰腺中，*Es-lpgat1*-mRNA 均主要定位于成纤维细胞(F)和吸收细胞(R)中。(4)干扰 *Es-lpgat1* 后, *Es-gpat2* 和 *Es-dgat2* 的表达水平显著上调。综上所述, *Es-lpgat1* 主要在中华绒螯蟹卵巢和肝胰腺中表达，可能参与卵巢发育期间的磷脂代谢。

关键词：中华绒螯蟹；卵巢发育；荧光定量；原位杂交; RNA 干扰

Cloning and expression characteristics analysis of lysophosphatidylglycerol acyltransferase in ovarian development of *Eriocheir sinensis*

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Abstract: To investigate the regulation of lysophosphatidylglycerol acyltransferase (LPGAT) expression in the ovarian development of *Eriocheir sinensis*, this study used real-time quantitative PCR, in situ hybridization and RNA interference to analyze its temporal and spatial expression patterns during ovarian development. The results showed that: (1) The qRT-PCR results showed that *Es-lpgat1* was expressed in different tissues during the ovarian development of *E. sinensis*. (2) During ovarian development cycle, both hepatopancreas and ovary at ovarian stage II had the significantly highest expression levels of *Es-lpgat1*-mRNA ($P<0.05$). (3) The results of ISH showed that in ovarian stage II, the strong signal of *Es-lpgat1*-mRNA was localized in the cytoplasm of PRO and EN of the ovary. However, the strong signal of *Es-lpgat1*-mRNA was localized in F cells and R cells of hepatopancreas. (4) After knockdown of *Es-lpgat1*, the expression levels of *Es-gpat2* and *Es-dgat2* were significantly up-regulated. In summary, *Es-lpgat1*-mRNA is mainly expressed in the ovary and hepatopancreas of *E. sinensis*, which was significantly related to their ovarian stages; these results suggested *Es-lpgat1* may be involved in phospholipid metabolism during ovarian development of *E. sinensis*.

Key words: *Eriocheir sinensis*; ovarian development; qPCR; *in situ* hybridization; RNA interference

两种来源虾青素对 HepG2 细胞氧化损伤的保护作用

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摘要：研究旨在明确两种来源虾青素预处理对 HepG2 细胞抗氧化应激损伤的影响，利用叔丁基过氧化氢（t-BHP 400μM，2h ）建立 HepG2 细胞氧化损伤模型，实验分为空白对照组、氧化损伤模型组、雨生红球藻源虾青素酯处理组（5μM）、人工合成虾青素处理组（5μM），通过检测细胞内活性氧（ROS）水平、细胞内抗氧化活性（CAA）、丙二醛（MDA）、谷胱甘肽（GSH）以及谷胱甘肽过氧化物酶（GPx）水平的变化，探究虾青素对 HepG2 细胞氧化损伤的保护作用。结果显示，经两种来源虾青素预处理 24h 后，与氧化损伤模型组相比细胞内活性氧水平、MDA 及 GPx 活性显著性降低（$P<0.05$），GSH 含量显著性升高（$P<0.05$）。以上结果说明两种来源虾青素对 t-BHP 诱导的 HepG2 细胞氧化损伤具有一定的保护作用。

关键词：虾青素；HepG2 细胞；叔丁基过氧化氢；氧化应激

Protective effects of two different sources of astaxanthin on t-BHP-induced oxidative stress damage in HepG2 cells

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Abstract: The aim of the present study was to explore the effect of astaxanthin on antioxidative stress injury of HepG2 cells.The injury model of HepG2 cells was established by t-BHP(400μM,2h).The cells were divided into 4 groups:Blank control group,model group, Astaxanthin ester from Haematococcus pluvialis , Synthetic Astaxanthin. The protective effect of astaxanthin on oxidative damage of HepG2 cells was explored by detecting the ROS levels, intracellular antioxidant activity (CAA), malondialdehyde (MDA), glutathione (GSH) and glutathione peroxidase (GPx). The results showed that after pretreatment with two sources astaxanthin for 24 hours, compared with the model group, the ROS levels, MDA and GPX decreased significantly ($P < 0.05$), and the content of GSH increased significantly ($P < 0.05$).The results above indicate that two sources of astaxanthin have a certain protective effect on oxidative damage of HepG2 cells induced by t-BHP.

Key words: Astaxanthin, HepG2 cells, t-BHP, oxidative damage

中华绒螯蟹骨形态发生蛋白（BMPs）在不同蜕皮时期的表达

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摘要：为研究骨形成蛋白(Bone morphogenetic proteins，BMPs)在中华绒螯蟹蜕皮时期的功能，本文以不同蜕皮时期的中华绒螯蟹为研究对象，运用 qPCR 方法分析了 *BMP*1b、*BMP*2、*BMP*7 基因在蜕皮不同时期眼柄、肌肉、鳃、肝胰腺、肠道、Y-O、心脏中的表达水平变化。结果表明，BMPs 在不同蜕皮时期不同组织的表达趋势存在时空差异。*BMP*1b、*BMP*2 *和 BMP*7 在蜕皮后期的鳃、肌肉、肝胰腺中表达较高，推测可能参与甲壳硬化。

关键词：中华绒螯蟹；骨形态发生蛋白；蜕皮周期

Expression of bone morphogenetic proteins (*BMPs*) in *Eriocheir sinensis* at different molting stages

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Abstract: In order to study the function of bone morphogenetic proteins (BMPs) in the molting periods of *Eriocheir sinensis*, the expression levels of *BMP*1b, *BMP*2 and *BMP*7 genes in eyestalk, muscle, gill, hepatopancreas, intestine, Y-O and heart were analyzed by qPCR. The results showed that there were temporal and spatial differences in the expression trend of BMPs in different tissues at different molting stages. *BMP*1b, *BMP*2 and *BMP*7 are highly expressed in gills, muscles, and hepatopancreas at the late molting stage, which is speculated to be involved in crustacean sclerosis.

Key words: *Eriocheir sinensis*; bone morphogenetic protein; molting

秦岭细鳞鲑鳃和肝脏组织对温度胁迫的转录组反应

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摘要：随着全球变暖对鱼类的影响，特别是像秦岭细鳞鲑这种冷水性鱼类。因为持续升高的气温影响了生物多样性的良性循环，甚至影响了生物的生存和繁殖能力，引起生物适应性困难甚至死亡。秦岭细鳞鲑属于濒危保护鱼类，其栖息水温最高 21℃，属于典型的冷水性鱼类。为了更好地保护和促进其种群恢复，本研究以人工繁育的子一代鱼作为研究对象，通过温度胁迫实验，研究其分子层面对温度胁迫的反应，找到与温度相关的分子标记。实验随机选取 200 尾当年鱼苗，其中 60 尾作为对照组，其余从自然水温开始升温，每小时升高 1℃，观察鱼对温度的反应，升温到 24.5℃后停止，选取最先死亡的 60 尾作为热不耐受组，最后死亡的 60 尾作为热耐受组。样本采集后进行转录组测序分析。结果显示，对照组和耐受组的转录组模式相似，不耐受组表达差异性大于耐受组，说明耐受组的基因表达可能随着暴雷时间的增加而进行了自我修复。组织不同是基因表达差异化的主要因素，它们对热胁迫表现出不同的生理生化反应。与其他研究结果类似，鱼体在高温环境下，会发生热休克反应、免疫反应、代谢调节和离子转运等。这将有助于更好地理解秦岭细鳞鲑对温度的响应机制，为种质资源保护提供分子标记等数据参考。

关键词:冷水鱼；种质资源；热耐受性；温度限制；热胁迫

Transcriptomic responses to heat stress in gill and liver of endangered *Brachymystax lenok tsinlingensis*

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Abstract：Global warming significantly affects fish, particularly cold-water fish, because increased temperature adversely impacts their abilities to grow or reproduce, and eventually influences their fitness or even causes death. To survive, fish may alter their distribution or behavior to avoid the stress, and perhaps acclimate or evolve resistance to the elevated temperature. Brachymystax lenok tsinlingensis is an endangered cold-water species in China, and it has been found to alter the altitudinal distribution, decrease swimming efficiency and develop resistance under heat exposure, which badly impact the continuing conservation work. To better protect them, it is essential to understand how they respond to thermal stress behaviorally and physiologically. Therefore, the fish were exposed to 24.5 ◦C and based on the time taken for them to lose equilibrium, they were separately sampled as sensitive and tolerant groups. Both gill and liver tissues were collected from both groups for transcriptome sequencing. Sequencing results demonstrated that control and tolerant groups were similar in transcriptomic patterns and sensitive groups differentially expressed more genes than tolerant ones, suggesting the gene expression of tolerant groups may return to base levels as exposure time increased. Tissue differences were the major factor affecting gene expression, and they also displayed different physiological responses to heat stress. Consistent with other studies, heat shock response, immune response, metabolic adjustment and ion transport were found to be triggered after exposed to elevated temperature. The findings would contribute to a better understanding of responding mechanisms of fish to thermal stress and provide guidance for future conservation programs.

Key words：Cold-water fish; Conservation; Heat tolerance; Thermal limit; Thermal stress

不同类胡萝卜萝卜素对三角帆蚌内壳色、组织总类胡萝卜素含量及珍珠质量的影响

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摘要：设置补充 β-胡萝卜素和虾青素的投喂处理组，饲喂白色和紫色 2 种色系插核三角帆蚌 120 天。探究不同类胡萝卜素对三角帆蚌内壳色、各组织内总类胡萝卜素含量的影响，以及对所育珍珠圆度、色泽和光泽的影响。

关键词：三角帆蚌；β-胡萝卜素；虾青素；内壳色；珍珠

Effects of different carotenoids on inner shell color, tissue total carotenoids content and pearl quality in *Hyriopsis cumingii*

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Abstract: To study the effects of different carotenoids on inner shell color, tissue total carotenoids content and the roundness, color, luster of pearls in *Hyriopsis cumingii*, two stains of *Hyriopsis cumingii* in white and purple were fed for 120 days by setting up feeding treatment groups supplemented with β-carotene and astaxanthin.

Key words: *Hyriopsis cumingiiy*, β-carotene, astaxanthin, inner shell color, pearl

三角帆蚌数量性状与所育有核珍珠光泽度相关性分析

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摘要：为了研究三角帆蚌对有核珍珠光泽度的影响，用 8 组不同选择顺序的白色三角帆蚌为材料，进行一对多的插核实验。记录了供片蚌和育珠蚌的壳长、壳高、壳宽、体质量、外壳色、内壳光泽度等数量性状以及相关珍珠光泽度性状参数。对供片蚌和育珠蚌各数量性状与珍珠光泽度性状参数进行相关性分析和回归分析。

关键词：三角帆蚌；光泽度；数量性状；相关分析

Correlation analysis of nucleated luster with quantitative traits of Hyriopsis cumingi

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Abstract: In order to study the effect of *Hyriopsis cumingii* on the luster of nucleated pearls, 8 groups of white H.cumingii with different selection sequences were used as materials for one-to-many nucleation experiments. The quantitative characters such as shell length, shell height, shell width, body weight, shell color, inner shell luster and related pearl luster were recorded. Correlation analysis and regression analysis were carried out on the quantitative characters and pearl luster parameters of donor mussels and host mussels.

Key words: *Hyriopsis cumingii*, luster, quanitiative trait, correlation analysis

高温胁迫对坛紫菜“申福 2 号”氮磷吸收的影响

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摘要：全球变暖背景下，栽培紫菜种质退化和人为因素导致的高温胁迫，对坛紫菜的健康养殖造成了严重影响。本文以坛紫菜野生栽培品系为对照，研究了高温胁迫对国审坛紫菜新品种“申福 2 号”氮磷吸收的影响，并对两者氮磷吸收差异的机制进行了探讨。研究发现相比于正常培养温度（23℃），高温胁迫（30℃）严重抑制了两个品系（种）的氮磷吸收，且对氮素吸收的影响更大。此外，高温胁迫对两个品系（种）氮磷吸收的影响也存在差异，高温对野生栽培品系氮磷吸收的影响更明显。转录组测序和 q-PCR 的结果印证了这一现象，相较于野生栽培品系，“申福 2 号”的氮素吸收相关基因在高温胁迫下均显示出较高的表达量或在胁迫后期恢复更快；3 个磷转运蛋白基因也显示同样的趋势。综上表明 “申福 2 号”在应对高温胁迫时表现出更高的氮磷吸收效率，推测其为“申福 2 号”更耐高温的原因之一。

关键词：申福 2 号；高温胁迫；氮磷吸收；转录组测序

Effects of high temperature stress on nitrogen and phosphorus absorption of *Pyropia haitanensis* strain "Shenfu 2"

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Abstract: In this paper, the effects of high temperature stress on the nitrogen and phosphorus absorption of the new *Pyropia haitanensis* strain "Shenfu 2" were studied, and the mechanism of the difference of nitrogen and phosphorus absorption between them was also discussed. It was found that compared with normal culture temperature (23℃), high temperature stress (30℃) had a serious inhibition on nitrogen and phosphorus absorption of the two strains, especially on nitrogen absorption, and the effects of high temperature stress on nitrogen and phosphorus absorption of the wild cultivar were more obvious. RNA sequencing and q-PCR results also confirmed this phenomenon, under high temperature stress, the gene involved in nitrogen absorption of new strain "ShenFu 2" are displayed higher expression or in the late stress recovery faster compared with wild cultivars. Three phosphorus transporter genes involved in phosphorus uptake showed the same trend. The new strain "Shenfu 2" showed higher nitrogen and phosphorus absorption efficiency in coping with high temperature stress, which was speculated to be one of the reasons for new strain "Shenfu 2" to be more resistant to high temperature.

Key words: Shenfu 2；high temperature stress；nitrogen and phosphorus absorption；RNA seq

基于环境 DNA 技术和传统捕捞方法对淡水湖泊鱼类群落研究的比较：一套新的环境 DNA 通用 PCR 引物

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摘要：由于气候变化、生境退化、生物入侵和过度捕捞等因素影响，淡水鱼类多样性正在迅速减少。直接从环境样品中获得的环境 DNA（Environmental DNA，eDNA）可用于评价水生物种的分布。我们开发了一套新的鉴定淡水鱼类物种的 PCR 引物（16s 200），用于鱼类线粒体 DNA 序列的 eDNA 代谢编码。利用 16s 200 引物，检测到分布在中国江苏省滆湖的 27 种鱼类。通过比较刺网和地笼的鱼类捕获数据，利用 eDNA 技术的监测结果与刺网数据相似性更高。环境 DNA 监测技术因其分子生物学手段的鉴定准确、对目标生物不造成干扰和样品采集的便利等优势，可与传统的鱼类群落分析方法相结合，为鱼类分类学研究及其多样性保护提供有效的技术支撑。

关键词：环境 DNA；PCR 引物；鱼类群落；生物多样性；传统捕捞

Comparison of fish communities using environmental DNA metabarcoding and capture methods in a freshwater lake: a new set of universal PCR primers

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Abstract: Freshwater biodiversity is under pressure from the detrimental effects of climate change, habitat degradation, biological invasion, and overfishing. Environmental DNA (eDNA) obtained directly from environmental samples can be used to evaluate the distribution of aquatic species. We developed a new set of universal PCR primers (16S 200) for eDNA metabarcoding from mitochondrial DNA sequences. Using the new 16S 200 primers, we detected the presence of 27 fish species distributed across four families in Lake Gehu, in southeastern China. Data from eDNA metabarcoding were more consistent with results from gill net capture methods than from ground cage capture. The eDNA metabarcoding is an efficient and cost-effective method that can be used in conjunction with traditional survey methods for analyzing fish communities; therefore, eDNA metabarcoding may be useful for analyzing fish communities in future studies.

Key words: environmental DNA; PCR primers; fish communities; biodiversity; capture methods

噬藻体 PaV-LD 内肽酶和穿孔素的功能分析

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摘要：PaV-LD 是一种从有害的丝状蓝细菌 *Planktothrix agardhii* 中分离的噬藻体，其中 ORF123 和 ORF124 的共同表达对聚球藻 PCC6803 具有生长抑制和溶解作用。然而，它们是否单独具有该功能仍有待阐明。在本研究中，我们旨在研究 ORF123 和 ORF124 在大肠杆菌和聚球藻 PCC6803 中各自的功能。结果表明，ORF123 编码一种内肽酶，含有一个 M23 家族肽酶结构域和一个跨膜区。在大肠杆菌（*E.coli*）中单独表达内肽酶时，观察到 *E.coli* 生长受到抑制、细胞膜损伤和胞内酶泄漏等现象，证明该蛋白具有出显著的溶菌活性。同样，由 ORF124 编码的穿孔素也显示出对 *E.coli* 的溶菌作用。此外，缺失突变分析结果表明内肽酶和穿孔素的跨膜区对于它们的溶菌功能是必不可少的。同时，内肽酶和穿孔素在聚球藻 PCC6803 中的表达证实了它们对蓝藻细胞也具有溶解作用。总之，我们的研究揭示了内肽酶和穿孔素各自的功能，这将有助于我们更好地理解 PaV-LD 的裂解机制。

关键词：PaV-LD；内肽酶；穿孔素；聚球藻 PCC6803

Functional analysis of the endopeptidase and holin from cyanophage PaV-LD

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Abstract: PaV-LD, a cyanophage isolated from harmful filamentous cyanobacterium *Planktothrix agardhii*, and co-expression of its ORF123 and ORF124, showed the growth inhibitory and lytic effects on the *Synechocystis* sp. PCC6803. However, whether they work individually for the above functions remains to be elucidated. In this study, we aimed to study their individual function of ORF123 and ORF124 in *E. coli* and *Synechocystis* sp. PCC6803. Results showed that the ORF123 encoded an endopeptidase, which harbored an M23 family peptidase domain and a transmembrane region. Expression of the endopeptidase in *E. coli* alone revealed that the protein exhibited remarkable bacteriolytic activity, as evidenced by observation of growth inhibition, membrane damage and leakage of intracellular enzyme. Similarly, the holin, a membrane-associated protein encoded by the ORF124, also displayed the comparative bacteriolytic effect to the endopeptidase in the same manner. Moreover, deletion mutations indicated that the transmembrane domains of the endopeptidase and holin were indispensable for their bacteriolytic activity. Meanwhile, the bacteriolytic functions of the endopeptidase and holin on algae cells were confirmed by expressing them in the *Synechocystis* sp. PCC6803. Collectively, our study revealed the individual role of endopeptidase and holin, which will contribute to better understand the lytic mechanism of PaV-LD.

Key words: PaV-LD*;* endopeptidase; holin; *Synechocystis sp. PCC6803*

第三专题：水产营养与饲料

山区鲟鱼早期培育与消化酶相关性研究

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摘要：为分析发育早期消化酶活性情况及不同饵料开口对山区鲟鱼苗种生长发育的影响，对山区养殖培育的鲟鱼亲本（史氏鲟 *Acipenser schrenckii* ♀×西伯利　亚鲟 *Acipenser baeri* ♂）进行了全人工繁殖，测定了由胚胎到仔鱼不同发育时期消化酶活性，并分别以人工配合饲料、水蚯蚓、轮虫、熟蛋黄为开口饵料，对仔鱼进行了养殖试验。结果表明，孵化初期，胃蛋白酶、胰蛋白酶、脂肪酶和淀粉酶活性均较低，随着不断生长发育，四种消化酶活性逐渐升高；同一发育期，脂肪酶活性均显著低于其他三种消化酶（$p<0.05$），蛋白酶（胃蛋白酶和胰蛋白酶）活性显著高于脂肪酶和淀粉酶活性（$p<0.05$）；水蚯蚓养殖试验组生长指标优于其他试验组（$p<0.05$）。

关键词：鲟鱼；仔鱼；早期培育；消化酶

The association between larval rearing and the activity of digestive enzyme in sturgeon in Mountains Area

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Abstract: This experiment analyzed the activity of digestive enzyme and the effects of different initial feeding diets on growth and development. The activity of digestive in different development period were analyzed in complete artificial propagation of Acipenser schrenckii ♀×Acipenser baeri♂ larvae in mountains area. Artificial commercial diet, water earthworm, rotifer and cooked egg yolk were fed as initial feeding diets, to investigate the effects of different initial feeding diets on the survival rate and growth situation. The results showed that the activity of pepsase, trypsin, lipase and amylase were low in the beginning of incubation, and the activity of the four digestive enzymes activity gradually increased with the growth and development.The activity of lipase were significantly lower, the activity of pepsase and trypsin were significantly highter than the activity of lipase and amylase in the same period.The statistical index of final weight, final length, Specific growth rates(SGR), Weight gain rates(WGR) and Survival rate(SR) were significantly highter in the four groups fed with water earthworm than the other groups.

Key words: Hybrid Sturgeon, larva , larval rearing, Digestive enzyme

饲料中乙酸钠对卵形鲳鲹生长性能、肉质、血清生化和免疫功能的影响

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摘要：乙酸是一种主要的短链脂肪酸，在调节鱼类生长、免疫方面起着十分重要的作用。本实验制做 6 种含有不同乙酸钠水平的等氮等脂饲料，饲喂卵形鲳鲹幼鱼（初始均重：6.06±0.02g）8 周。结果显示：饲料中添加乙酸钠可显著提升卵形鲳鲹的增重率、特定生长率、摄食量、肌肉的脂肪含量和黏性。添加乙酸钠的饲料显著增加卵形鲳鲹血浆中高密度脂蛋白胆固醇含量，同时降低血浆中甘油三酯、葡萄糖的含量；此外，饲料中添加乙酸钠可调控卵形鲳鲹 Keap1, IL-8, TNF-α, NF-κB, Nrf2 和 TGF-β 基因的表达水平，增强其抗氧化和免疫功能；饲料中过量的乙酸钠会对卵形鲳鲹的生长和免疫功能产生不利影响。以卵形鲳鲹的增重率为指标，通过二次回归分析得出乙酸钠的最适添加量为 1423.67mg/kg。

关键词：卵形鲳鲹；乙酸钠；生长性能；肉质；血清生化；免疫功能

Effects of dietary sodium acetate on growth performance, fillet quality, plasma biochemistry and immune function of juvenile golden pompano (*Trachinotus ovatus*)

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Abstract: Six isonitrongenous and isolipidic diets were formulated with graded level of sodium acetate (SA) to feed 360 fish (mean initial body weight: 6.06 ± 0.02 g) for 8 weeks. The results showed that dietary SA level significantly improved weight gain rate, specific growth rate, feed intake and lipid contents and gumminess of dorsal muscle of golden pompano. Diets supplemented with SA significantly increased high density lipoprotein cholesterol contents and decreased triglyceride and glucose contents of plasma. Furthermore, dietary SA level promoted antioxidative ability and immune function of golden pompano by upregulating expression levels of related genes. Excess SA caused negative effects on the growth and immune function of juvenile golden pompano. The optimum SA supplement level for juvenile golden pompano was evaluated to be 1423.67 mg/kg based on a quadratic regression model of weight gain rate.

Key words: *Trachinotus ovatus*; sodium acetate; growth performance; fillet quality; plasma biochemistry; immune function

胆碱对幼草鱼生长和肠道免疫功能的影响和机制

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摘要：本研究旨在探究胆碱对幼草鱼生长和肠道免疫功能的影响和机制，并确定需要量。试验选取1440尾健康草鱼（9.29±0.02 g），分为6个处理，饲喂不同胆碱水平的饲粮（0、400、800、1200、1600和2000 mg/kg）60天。结果表明：适宜的胆碱可促进幼草鱼的生长性能，提高肠道消化吸收能力；能提高肠道免疫功能，从而提高肠炎抵抗能力。进一步研究发现：胆碱进入细胞后通过磷酸化代谢途径调控JAK1、JAK2/STAT3、炎症因子mRNA水平以及P-STAT3Y705核转位，从而提高草鱼肠道上皮细胞(IECs)免疫功能；同时，胆碱也能调控肠道巨噬细胞的免疫能力，通过磷酸化途径和氧化途径分别激活JAK2和JAK2/TYK2调控炎症因子的基因表达，两种途径均不影响P-STAT3Y705核转位，且其对线粒体功能的调控与线粒体P-STAT3S727磷酸化有关。以增重百分比、饲料效率以及肠炎发病率为标识，确定幼草鱼对胆碱的需要量分别为1330.7、1283.4以及1581.1 mg/kg。

关键词：胆碱；草鱼；肠道免疫功能；上皮细胞；巨噬细胞；JAK/STAT3

Effect of choline on growth and intestinal immune function of juvenile grass carp (*Ctenopharyngodon idella*) and involved mechanism

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Abstract: The purpose of this study was to explore the effects of choline on the growth and intestinal immune function of juvenile grass carp. 1440 grass carps were divided into 6 treatments and fed diets with different choline levels for 60 days. Results: suitable choline could promote the growth performance of juvenile grass carp, and improve the intestinal digestion and absorption capacity; It improved intestinal immune function to improved enteritis resistance. Further studies showed that choline regulated JAK1, JAK2/STAT3, inflammatory factor mRNA levels and P-STAT3S727 nuclear translocation with phosphorylation pathway to improve the immune function of IECs of grass carp; Choline could also regulate the immune function of macrophages, which activate JAK2 and JAK2/TYK2 respectively through phosphorylation and oxidation. Both pathways didn’t affect the nuclear translocation of P-STAT3S727, and its regulation of mitochondrial function was related to the phosphorylation of P-STAT3S727. Based on the weight gain rate, feed efficiency and incidence rate of enteritis, the requirement for choline in juvenile grass carp were 1330.7, 1283.4 and 1581.1 mg/kg, respectively.

Key words: choline, grass carp, immune function, macrophages, JAK/STAT3

不同水平的共轭亚油酸对生长后期草鱼生产性能和肌肉品质的影响及机制

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摘要： 本研究旨在探索共轭亚油酸（CLA）对生长后期草鱼生产性能和肌肉品质的影响及机制，并确定最适添加量。试验选择初重为 663.33±1.08 g 的健康草鱼 450 尾，分为 6 个处理，饲喂含 CLA（0、3、6、9、12、15 g/kg）的饲粮 60 天。结果表明：适宜水平的 CLA 提高了生长后期草鱼的生产性能和肌肉品质；同时提高了肌肉的抗氧化能力。进一步研究发现：CLA 可降低肌肉的粗脂肪含量，增加蛋白质含量，提高 pH；并通过 TGF-β/Smads 和 TOR 信号途径促进肌肉中胶原蛋白的合成，并调控 p38MAPK 途径和抑制 MSTN 途径从而增加肌纤维的密度；此外，CLA 可激活 Nrf2 信号途径上调抗氧化酶及其亚型基因表达进而增强抗氧化酶活性，提高肌肉的抗氧化能力；最后，以 PWG、EPA、胶原蛋白含量、肌纤维密度以及 MDA 含量为标识，确定生长后期草鱼 CLA 最适添加量分别为 6.41、7.00、7.74、7.31、7.04 g/kg 饲粮。

关键词：共轭亚油酸；生长后期草鱼；生产性能；肉质；胶原蛋白

Effects of different levels of conjugated linoleic acid on growth performance and flesh quality as well as the mechanisms in sub-adult grass carp (*Ctenopharyngodon idella*)

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Abstract: This study explored the effects of conjugated linoleic acid (CLA) on the growth performance and flesh quality as well as further probed involved mechanisms in sub-adult grass carp. 450 grass carps with an weight of 663.33±1.08 g were randomly divided into 6 treatments , which were fed diets at 0, 3, 6, 9, 12, and 15 g/kg diets for 60 days, respectively. The appropriate level of CLA improved the production performance and muscle quality of grass carp; and it improved the antioxidant capacity of muscle. Further studies showed CLA could reduce the crude fat content of muscle, increase protein content and pH; through TGF-β/Smads pathway and TOR pathway the synthesis of collagen were promoted, regulating p38MAPK pathway and inhibiting MSTN pathway increased the density of muscle fibers; it also activated Nrf2 signaling pathway and up-regulated the gene expression of antioxidant enzymes and their subtypes to improve the antioxidant capacity of muscle; finally, the diets of grass carp are 6.41, 7.00, 7.74, 7.31 and 7.04 g/kg based on the contents of PWG, EPA, collagen, muscle fiber density and MDA.

Key words: Conjugated linoleic acid, Sub-adult grass carp, Growth performance, Flesh quality, Collagen

酶解鸡浆对黄颡鱼幼鱼生长性能和消化吸收能力的影响

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摘要： 本试验旨在研究酶解鸡浆(EC)对黄颡鱼幼鱼生长性能和消化吸收能力的影响，并确定最适添加量。本试验选取 1080 尾（6.73±0.01g）健康黄颡鱼，分为 6 个处理，饲喂添加 EC（0%、1%、2%、3%、4%、5%）的饲粮 60 天。结果表明：在黄颡鱼幼鱼饲粮中添加适量的 EC 改善了鱼体组分、提高了氨基酸代谢；并且提升肠道发育及消化吸收。进一步研究发现，适量 EC 通过降低 MDA 和 PC 含量以及提高抗氧化酶活性，进而显著提高肠道抗氧化能力；并通过上调紧密连接和粘附连接相关蛋白的 mRNA 水平，下调 claudin-12、ROCK 的 mRNA 水平以及 GTP-RhoA 蛋白表达，从而增强肠道结构的完整性。综上，适宜水平 EC 能提高肠道的消化吸收能力，因此能替代饲粮中部分鱼粉。根据最佳生长性能确定黄颡鱼幼鱼饲粮中 EC 的适宜添加比例为 3%。

关键词：酶解鸡浆；生产性能；黄颡鱼幼鱼；消化吸收

Effects of enzymatic chicken mash on growth performance, digestion and absorption of juvenile yellow catfish (*Pelteobagrus fulvidraco*)

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Abstract: This experiment was aimed to study the effects of enzymatic chicken mash (EC) on the growth performance, digestion and absorption capacity of juvenile yellow catfish, and to determine the optimal dosage. 1080 yellow catfish (6.73±0.01 g) were divided into 6 treatments and fed with EC (0%, 1%, 2%, 3%, 4%, 5%) for 60 days. The results showed an appropriate level of EC improved the composition of fish body and amino acid metabolism; it also Improve intestinal development, digestion and absorption. Further studies showed an appropriate amount of EC improved antioxidant capacity by reducing the contents of MDA and PC and increasing the activity of antioxidant enzymes; The integrity of intestinal structure was enhanced by up regulating the mRNA levels of tight junction and adhesion junction proteins, down regulating the mRNA levels of claudin-12 and ROCK and the expression of GTP-RhoA protein. In conclusion, the appropriate level of EC can improve the intestinal digestion and absorption capacity, so it can replace some fish meal in the diet. According to the best growth performance, the appropriate proportion of EC in the diet of juvenile *Pelteobagrus fulvidraco* was 3%.

Key words: Enzymatic chicken mash, Growth performance, Juvenile yellow catfish, Digestion and absorption

野生鱼群肠道中微生物的外源引入与定殖选择的量化研究

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摘要：肠道菌群随着个体发育而演变，并受环境影响而呈现出动态过程。为了量化研究鱼类肠道中微生物的外源引入与定殖选择，本研究通过对长江武汉段的水体环境微生物和 10 种鱼类肠道微生物的 16S rRNA 扩增子测序分析，确定了鱼类肠道微生物与水体环境微生物相一致的占比，并初步量化了水体环境微生物引入鱼类肠道的能力，以及肠道环境对外源引入微生物定殖选择的能力。

关键词：长江；自然水体；野生鱼类；环境微生物；肠道微生物；引入；选择

The quantification of the introduction and selection of environmental microbes in fish gut: A case study for wild fish populations

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Abstract: Gut microbial communities shift with host development, and have a dynamic equilibrium driven by environment. To quantify the introduction and selection of environmental microbes in fish gut, the current study used 16S rRNA gene amplicon sequencing to get the structure of the environmental microbial community and the gut microbial community in 10 fish species from Wuhan section of Yangtze River. The results identified that more than half of gut microbial community was common with water environmental microbial community. And then, we preliminarily quantifying the capacity of water environmental microbial community were introduced into fish gut and the capacity of these microbial community were selected by fish gut environments.

Key words: Yangtze River, natural water, wild fish population, environmental microbiota, gut microbiota, introduction, selection

苏南溪流司氏鉠(*Liobagrus styani*)食性和营养级分析

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摘要： 司氏鉠（*Liobagrus styani*）是一种分布范围较小的淡水小型鱼类，已被《中国脊椎动物红色名录》列为极危物种（Critically Endangered，CR）。目前与其相关的研究较为缺乏，特别是对其食物组成和生态功能定位尚不清晰。本研究在苏南溪流水域首次发现司氏鉠，于 2017 年至 2019 年分季节采集司氏鉠央样本 16 尾，通过高通量测序技术和碳、氮稳定同位素等分析了其食物组成及营养级，了解司氏鉠食物来源及其在生态系统中的功能地位。研究结果显示，司氏鉠摄食的食物种类有 21 属种，分属于节肢动物门、脊索动物门和环节动物门等。同位素结果显示其营养级为 3.30±0.07。上述结果表明司氏鉠以脊索动物门中的真热带鲶属和半鲿属为主要食物来源的肉食性鱼类，为深入揭示司氏鉠在溪流生态系统物质与能量传递过程的作用机制提供重要基础资料。

关键词：司氏鉠；食性；摄食策略；高通量测序；稳定同位素；营养级

Diet and trophic level analysis of the *Liobagrus styani* in Streams in southern Jiangsu

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Abstract: As a small-bodied freshwater fish, *Liobagrus styani* is listed as an endangered species in the “Red List” of Chinese vertebrates. Currently, there is a lack of research focusing on it, especially the food composition and ecological function have rarely been reported. In this study, *Liobagrus styani* was first found in the stream of Southern Jiangsu. In order to understand its food source and ecological niche, 16 samples of *Liobagrus styani* were collected seasonally to analyze the food composition and nutritional level by high-throughput sequencing technology and carbon and nitrogen stable isotopes from 2017 to 2019. The results showed, 21 species were identified as the food consumed of *Liobagrus styani*, belonging to Arthropoda, Chordata and Annelida. And the trophic level was 3.30±0.07. All these showed that *Liobagrus styani* is a carnivorous fish with Eutropiichthys and Hemibagrus as the main food source. This study will provide an important basic data to study the material and energy transfer process mechanism of *Liobagrus styani*.

Key words: *Liobagrus styani*; Feeding habits; High-throughput sequencing; Stable isotope; Trophic level

大口黑鲈幼鱼转食配合饲料相关 SNPs 标记挖掘及初步验证

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摘要：课题组前期利用高通量测序技术初步挖掘一批与大口黑鲈幼鱼转食性状相关的分子标记，为研究这些转食相关标记在大样本中的多态性和普适性，本研究随机挑选 8 个可用 PCR-RFLP 的 SNPs 位点在 192 尾幼鱼中进行分型，并通过关联分析研究 8 个 SNPs 多态性与幼鱼转食和生长性状的相关性。

关键词：大口黑鲈；转食配合饲料；SNP 标记；关联分析

Excavation and preliminary validation of SNPs related to switching to formulated feed of largemouth bass, *Micropterus salmoides*

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Abstract: In our previous study, high-throughput sequencing technology was used to preliminarily excavate a number of molecular markers related to switching to formulated feed in largemouth bass juveniles. In order to study the polymorphism and universality of these markers related to switching to formulated feed in large samples, 8 SNPs for PCR-RFLP genotyping were randomly selected in this study, and 192 juvenile fishes were genotyped and analyzed by PCR-RFLP typing technique, and the correlation between polymorphism and feeding transformation and growth traits was analyzed by association analysis.

Key words: *Micropterus salmoides*; switch to formulated feed; SNP; association analysis

不同水温下花鲈对饲料精氨酸需求量的研究

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摘要：为了探究不同水温(27℃和 33℃)下花鲈对饲料精氨酸的需求量，本实验配置精氨酸水平为 1.16%、1.65%、2.04%、2.44%、2.98%和 3.36%的 6 种等氮等脂实验饲料，饲喂初始体重为(2.90±0.05)g 的花鲈。结果表明，33℃组花鲈生长性能显著高于 27℃组。在 27℃或 33℃水温下，2.04%精氨酸组花鲈幼鱼增重率达到最大值。27℃组花鲈鳃组织 GPx 和 SOD 酶活力、*ZO-1*、*Occludin* 和 *Claudin b* 基因相对表达量、血清 iNOS 和溶菌酶活力、NO、补体 3 和补体 4 含量显著高于 33℃组。在所有处理组中，27℃水温下花鲈鳃组织 GPx 和 SOD 酶活力、*ZO-1*、*Occludin* 和 *Claudin b* 基因、血清 TNOS、iNOS 和溶菌酶活力在 2.04%或 2.44%精氨酸组达到最大值。研究表明，33℃会降低花鲈生长，鳃组织免疫功能和血清免疫生化指标。在 27℃或 33℃水温下，以花鲈增重率和溶菌酶为评价指标，通过二次曲线模型分析得出花鲈幼鱼对饲料精氨酸的需要量为 2.37-2.53%(5.27%-5.62%饲料蛋白)。

关键词：精氨酸；水温；花鲈；需求量

Dietary arginine requirement of spotted seabass (*Lateolabrax maculatus*) reared at different water temperatures

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Abstract: A growth experiment was conducted to investigate dietary arginine requirement of spotted seabass (*Lateolabrax maculatus*) reared at different water temperatures (27°C and 33°C). Six iso-nitrogenous and iso-lipid diets with different arginine levels (1.16%, 1.65%, 2.04%, 2.44%, 2.98% and 3.36%) were prepared to fed fish with an initial body weight of 2.90±0.05 g. Growth of fish reared at 27°C was significantly higher than that of fish reared at 33°C ($P < 0.05$). The maximum value of weight gain rate was obtained in fish fed the diet with 2.04% arginine at 27°C or 33°C. Furthermore, activities of GPx and SOD, the mRNA expression of *ZO-1*, *Occludin* and *Claudin b* in the gills, activities of iNOS and lysozyme as well as contents of NO, complements 3 and 4 in the serum of fish reared at 27°C were significantly higher than those of fish reared at 33°C ($P < 0.05$). Furthermore, activities of GPx and SOD, the mRNA expression of *ZO-1*, *Occludin* and *Claudin b* in the gills, activities of TNOS, iNOS and lysozyme in the serum reached the maximum values in fish fed the diet with 2.44% or 2.04% arginine at 27°C among all treatments. These results showed that a temperature of 33°C decreased growth, immune function of the gills and serum parameters of fish. At 27°C or 33°C, second-order polynomial regression of WG and lysozyme against arginine levels showed that the arginine requirement of spotted seabass was in the range of 2.37%-2.53% of the dry diet, corresponding to 5.27%-5.62% of dietary protein.

Key words: arginine, water temperatures, spotted seabass, requirement

不同饲料脂肪水平下肌醇对中华绒螯蟹幼蟹的生长及对脂肪代谢的调节作用研究

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摘要：本研究旨在评估饲料肌醇（MI）对不同饲料脂肪水平下中华绒螯蟹幼蟹的生长性能、体营养组成、抗氧化能力及脂肪代谢的影响。试验共设计四组饲料分别包含：7%脂肪和 0 mg/kg 肌醇（N），7%脂肪和 1600 mg/kg 肌醇（N+MI），13%脂肪和 0 mg/kg 肌醇（H），以及 13%脂肪和 1600 mg/kg 肌醇（H+MI），分别投喂初始体重为 4.58±0.05 g 的中华绒螯蟹 8 周。试验结果表明：H+MI 组的增重率和特定生长率显著高于 H 组（$P<0.05$）。饲料中补充肌醇可有效改善由于饲喂饲料 13%脂肪所导致的肝胰腺中肌醇含量的减少，以及全蟹、肝胰腺和肌肉中脂肪的沉积。与 H 组相比，饲喂 H+MI 饲料可上调中华绒螯蟹肝胰腺的抗氧化酶的活力，且肝胰腺中的丙二醛含量降低（$P<0.05$）。此外，饲料中补充肌醇上调肝胰腺脂肪分解与转运相关基因的表达，而下调脂肪合成与吸收相关基因的表达，这可能与 IP3R/CaMKKβ/AMPK 信号途径的激活有关。综上，饲料中补充肌醇可以提高高脂饲料下中华绒螯蟹对脂肪的利用能力，减少肝胰腺脂肪沉积。本研究工作为甲壳动物饲料中肌醇的生理功能提供了新的见解。

关键词：肌醇；中华绒螯蟹；脂肪代谢；调控途径; 高脂饲料

Myo-inositol improves growth performance and regulates lipid metabolism of juvenile Chinese mitten crab (*Eriocheir sinensis*) fed different percentage of lipid

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Abstract: This study evaluated the effects of dietary myo-inositol (MI) on growth performance, body composition, antioxidant status and lipid metabolism of juvenile Chinese mitten crab (*Eriocheir sinensis*) fed different percentage of lipid. Crabs (4.58 ± 0.05 g) were fed four diets including a normal lipid diet (N, containing 7% lipid and 0 mg/kg MI), N with MI supplementation (N+MI, containing 7% lipid and 1600 mg/kg MI), a high lipid diet (H, containing 13% lipid and 0 mg/kg MI) and H with MI supplementation (H+MI, containing 13% lipid and 1600 mg/kg MI) for 8 weeks. The H+MI group showed higher weight gain and specific growth rate than those in the H group. The dietary MI could improve the reduction of MI content in the hepatopancreas, and lipid accumulations in the whole-body, hepatopancreas and muscle as a result of feeding on the high dietary lipid (13%) in crabs. Besides, the crabs fed the H+MI diets increased the activities of antioxidant enzymes, but reduced the malondialdehyde content in hepatopancreas compared with those fed the H diets. Moreover, dietary MI enhanced the expression of genes involved in lipid oxidation and exportation, yet reduced lipid absorption and synthesis genes expression in the hepatopancreas of crabs fed the H diet, which might be related to the activation of IP3R/CaMKKβ/AMPK signalling pathway. This study demonstrates that MI could increase lipid utilization and reduce lipid deposition in the hepatopancreas of *E. sinensis* fed a high lipid diet. This work provides new insights into the function of MI in the diet of crustaceans.

Key words: Myo-inositol, *Eriocheir sinensis*, Lipid metabolism, Regulatory pathways, High lipid diet

二氯乙酸钠通过调控 PDK2/4-PDHE1α 轴和改善胰岛素敏感性提高罗非鱼糖利用能力

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摘要：鱼类不能有效利用糖类作为能量物质，究其原因目前研究仍不清晰。研究发现，PDKs-PDHE1α 轴在机体葡萄糖氧化分解过程中发挥重要调控作用。因此，本研究旨在探究二氯乙酸钠（DCA）调控 PDKs-PDHE1α 轴是否能够提高罗非鱼对葡萄糖氧化利用效率。本实验将罗非鱼幼鱼（1.90 ± 0.11g）随机分成四组，分别投喂高糖组（HC，45%玉米淀粉）和高糖添加不同浓度 DCA（DCA1，HC+3.75g/kg DCA；DCA2，HC+7.5g/kg DCA；DCA3，HC+11.25g/kg DCA）四组饲料，进行为期 6 周的养殖实验。结果显示：与 HC 组相比，DCA 处理显著提高摄食高糖饲料罗非鱼增重率、饲料蛋白质效率和躯体比，而显著降低饲料系数。此外，DCA 处理显著降低罗非鱼腹腔脂肪含量、血清和肝脏中甘油三酯及全鱼总脂含量；同时，DCA 处理显著下调脂肪合成相关基因的表达。14C 标记葡萄糖注射及糖原染色实验发现，DCA 显著提高罗非鱼肝脏葡萄糖氧化分解和糖原合成能力，而显著降低葡萄糖向脂肪的转化。与 HC 组相比，DCA 处理显著降低 PDK2/4 基因及蛋白表达，同时降低 PDHE1α 蛋白的磷酸化水平。此外，DCA 处理显著提高胰岛素信号通路关键蛋白和糖原合成酶激酶 β 的磷酸化水平。本研究表明，DCA 通过抑制 PDK2/4，激活 PDHE1α 并改善胰岛素敏感性及糖原合成能力提高罗非鱼对高糖饲料的利用率。

关键词：尼罗罗非鱼；二氯乙酸钠；葡萄糖利用；PDK2/4-PDHE1α；胰岛素敏感性；糖原合成

Dichloroacetate increases the utilization of high-carbohydrate diet in Nile tilapia (*Oreochromis niloticus*) by regulating the PDK2/4-PDHE1α axis and improving insulin sensitivity

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Abstract: Fish are poor users of dietary carbohydrates for energy source, and the reasons for which are still unclear. It was found that the PDKs-PDHE1α axis plays an important regulatory role in the oxidative glucose catabolism of the organism. Therefore, the aim of this study was to investigate whether regulation of the PDKs-PDHE1α axis by dichloroacetate (DCA) could improve the efficiency of glucose oxidation and utilization in Nile tilapia. In this experiment, Nile tilapia juveniles (1.90 ± 0.11 g) were randomly divided into four groups and fed four diets with high carbohydrate group (HC) and high carbohydrate supplemented with different concentrations of DCA (DCA1, DCA2 and DCA3) for 6 weeks. The results showed that the DCA treatment significantly increased the weight gain, protein efficiency ratio and carcass ratio of Nile tilapia, while significantly decreased the feed conversion ratio. In addition, DCA treatment significantly reduced the mesenteric fat index, serum and liver triglyceride concentration and the total lipid content of whole fish; meanwhile, DCA treatment significantly down-regulated the expression of genes related to lipid synthesis. 14C-labeled glucose injection and glycogen staining experiments revealed that DCA treatment significantly improved the oxidative glucose catabolism and glycogen synthesis in the liver, while significantly reduced the conversion of glucose to lipid. Compared with the HC group, DCA treatment significantly decreased PDK2/4 gene and protein expression, while decreasing the phosphorylation level of PDHE1α protein. In addition, DCA treatment significantly increased the phosphorylation levels of key proteins of insulin signaling pathway and glycogen synthase kinase β. This study demonstrates that DCA promotes glucose utilization in Nile tilapia fed on high-carbohydrate diet by inhibiting PDK2/4, activating PDHE1α and improving insulin sensitivity and glycogen synthesis.

Key words: Nile tilapia; Dichloroacetate; glucose utilization; PDK2/4-PDHE1α axis; insulin sensitivity

维生素 D_3 通过其代谢物及 VDR 调控中华绒螯蟹幼蟹生长、蜕壳及免疫力

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摘要：维生素 D_3（VD_3）是一种不可或缺的脂溶性维生素，其与动物骨骼矿化以及生长密切相关。然而在具有重要经济意义的甲壳类动物中，这种联系尚未得到深入研究。本研究配制六种不同 VD_3 水平（0、3000、6000、9000、12000 和 18000 IU/kg）的等氮等能饲料，分别饲喂幼蟹（0.29 ± 0.01 g）56 天。基于生长结果的 VD_3 最适添加范围为 5685.43-10000 IU/kg。饲喂 9000 IU/kg VD_3 组的幼蟹具有最佳的生长性能。9000 IU/kg VD_3 可以显著提高幼蟹肝胰腺和肠道的抗氧化能力，同时实时荧光定量 PCR 结果表明可以显著提高蜕壳相关基因和免疫相关基因的表达水平。转录组结果表明添加 9000 IU/kg VD_3 可以改变内质网的蛋白质加工，类固醇生物合成以及抗原加工呈递。酶联免疫吸附试验结果表明 9000 IU/kg VD_3 可提高维生素 D 受体（VDR）、维甲酸 X 受体（RxR）和 C 型凝集素（CTL）蛋白浓度。血清中 1α,25-二羟基 VD_3 浓度在 3000-9000 IU/kg VD_3 组显著提高。本研究揭示膳食 VD_3 及其代谢物可以调控幼蟹的蜕壳和先天免疫。

关键词：中华绒螯蟹；维生素 D_3；蜕壳；先天免疫; 肝胰腺；肠道

Impact of dietary vitamin D_3 supplementation on growth, molting, antioxidant capability and immunity of juvenile *Eriocheir sinensis* by metabolites and vitamin D receptor

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Abstract: Vitamin D_3 (VD_3), as an indispensable and fat-soluble nutrient, is associated with skeletal mineralization and health in animals. However, such associations have not been well studied in economically important crustaceans. Six levels (0, 3000, 6000, 9000, 12000 and 18000 IU/kg) of VD_3 with isonitrogenous and isolipidic diets to fed *Eriocheir sinensis* (0.29 ± 0.01 g) for 56 days. The range of optimal VD_3 requirements is 5685.43-10000 IU/kg based on growth. The crab fed 9000 IU/kg VD_3 had the best growth performance. This VD_3 dose significantly increased antioxidant capacity in the hepatopancreas and intestine and was optimal for molting and innate immunity via quantitative PCR analysis. Transcriptomics analyses indicate that VD_3 could alter protein processing in the endoplasmic reticulum, steroid biosynthesis, antigen processing and presentation. As shown by the enzyme-linked immunosorbent assay, VD_3 could improve VDR, RxR and CTL concentrations. The 1α,25-dihydroxy VD_3 content in serum was significantly higher in 3000-9000 IU/kg VD_3. The study suggests that dietary VD_3 and its metabolites can regulate molting and innate immunity in crab.

Key words: *Eriocheir sinensis*, vitamin D_3, molting, innate immunity, hepatopancreas, intestine

混合植物蛋白在黄颡鱼配合饲料中的应用研究

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摘要：为减少黄颡鱼饲料鱼粉使用量以降低养殖成本, 本试验通过组织切片、酶活测定、实时荧光定量以及蛋白质免疫印迹等方法研究了不同水平混合植物蛋白（棉粕:菜粕=2：3）替代鱼粉后对黄颡鱼幼鱼生长性能、肠道健康和肝脏蛋白代谢的影响。

关键词：黄颡鱼；鱼粉替代；植物蛋白

Application of mixed plant protein in compound feed of Yellow catfish

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Abstract: In order to lower the cost of breeding by reducing the use of fish meal in diet of yellow catfish, the histological assessment, qPCR, and western blotting were applied. This study was carried out to investigate the influences of replacing fish meal with different levels of mixed plant protein (cotton meal: rapeseed meal = 2:3) on growth performance, intestinal health, and liver protein metabolism of juvenile yellow catfish.

Key words: yellow catfish, replacing fish meal, plant protein

葡聚糖作为饲料添加剂对中华绒螯蟹的生长及生化指标的影响

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摘要：试验以室外稻渔综合种养模式下养殖中华绒螯蟹作为研究对象,在基础饲料中按 1：100 添加葡聚糖,并监测其生长性能及部分生化指标。经过 28 天室外池塘养殖，实验组中华绒螯蟹增重率 180%±5.6%，高于对照组中华绒螯蟹增重率 99.2%±7.2%；实验组中华绒螯蟹的超氧化物歧化酶（SOD）值为 162.9±3.4U/mg,高于对照池 93.5±2.6U/mg；实验组中华绒螯蟹的溶菌酶（LZM）值为 14.8±2.2U/mg，高于对照组 6.7±1.6U/mg;室外养殖实验结束时，实验组中华绒螯蟹成活率为 97%，高于对照组中华绒螯蟹成活率 90%。结果表明:室外池塘投喂按 1:100 添加葡聚糖的饲料可以有效的提升中华绒螯蟹生长性能及非特异性免疫力。

关键词：中华绒螯蟹；葡聚糖；生长指标；生理指标

Effects of dextran as feed additive on growth and Biochemical Indices of Eriocheir sinensis

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Abstract: The experiment took the Chinese mitten crab (*Eriocheir sinensis*) as the research object, Glucan was added to the basal diet at a ratio of 1:100.Its growth performance and some biochemical indexes were monitored。After 28 days of outdoor pond farming, The weight gain rate of the experimental group was 180%±5.6%, which was higher than 99.2%±7.2% of the control group. The superoxide dismutase (*SOD*) value of the experimental group was 162.9±3.4U/mg, which was higher than that of the control group 93.5±2.6U/mg. The lysozyme (*LZM*) value of the experimental group was 14.8±2.2U/mg, which was higher than that of the control group 6.7±1.6U/mg. At the end of the outdoor farming experiment, The survival rate of Chinese mitten crab in the experimental group was 97%, which was higher than that in the control group 90%.The results show that: Outdoor pond feeding with 1:100 dextran can effectively improve the growth performance and non-specific immunity of Eriocheir Sinensis.

Key words: Chinese mitten crab, glucan, Growth indicators, Physiological indexes

第四专题：疾病防控与质量安全

罗非鱼无乳链球菌 FbsA 蛋白乳酸菌口服疫苗制备及其免疫效果的研究

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摘要：无乳链球菌（*Streptococcus agalactiae*）是威胁中国罗非鱼养殖发展的重要病害。为了研制免疫高效、操作简单的无乳链球菌疫苗，该研究利用同源重组法构建表达无乳链球菌 FbsA 蛋白的 pNZ8148-fbsA 质粒，通过电转化乳酸乳球菌（Lactococcus lactis）NZ9000 中获得 L.lactis NZ9000 pNZ8148-fbsA 重组乳酸菌，使用 nisin 诱导表达并进行 Western blot 鉴定，L.lactis NZ9000 pNZ8148-fbsA 和佐剂与饲料混匀制备口服疫苗。免疫结束后的第 18 天通过腹腔注射无乳链球菌攻毒获得相对免疫保护率。结果显示，蛋白印迹的分子量为 34.5kDa，与目的蛋白大小一致。与对照组比较，L.lactis NZ9000 pNZ8148-fbsA 的血清抗体水平显著提高，其相对免疫保护率为 53.38%。该研究为进一步的罗非鱼链球菌口服疫苗研究奠定了基础，具有广泛的应用价值和前景。

关键词：无乳链球菌；口服疫苗；乳酸菌疫苗；FbsA 蛋白；免疫；罗非鱼

Live recombinant Lactococcus lactis vaccine expressing FbsA for protection against *Streptococcus agalactiae* in tilapia

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Abstract: *Streptococcosis* is a serious disease that threatens the development of *Oreochromis niloticus* industry in China. In order to make a vaccine of *Streptococcus agalactiae* with high immune efficiency and simple operation, we constructed a recombinant plasmid pNZ8148-fbsA which could express FbsA protein of S. agalactiae by using homologous recombination. The recombinant plasmid was electro-transferred into L.lactis NZ9000. The FbsA protein was induced by nisin and tested by Western blot. L.lactis NZ9000 pNZ8148-fbsA were thoroughly mixed with Oral adjuvant and fish feed as oral vaccine. After immunization for 18 days, the relative immune protective (RPS) rate was obtained by intraperitoneal injection with S.agalactiae. The Western blot analysis showed that the molecular weight of expressed protein was 34.5 kDa, which is equal to the expected protein size. Oral immunization showed that the serum antibody of L.lactis NZ9000 pNZ8148-fbsA significantly higher than those of the other groups. RPS of fish from group L.lactis NZ9000 pNZ8148-fbsA was the highest(53.58%). This study lays a foundation for further study on oral vaccine of tilapia against S. agalactiae and has wide application value and prospect.

Key words: *Streptococcus agalactiae*; oral vaccine; Lactococcus lactis vaccine; FbsA protein; immune; tilapia

盐度和碱度对中华绒螯蟹毒性作用研究

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摘要：为探究中华绒螯蟹对盐碱水环境的生理耐受性，以便指导中华绒螯蟹的盐碱水养殖，本实验采用单因子静态急性毒性实验法和均匀正交设计法开展了中华绒螯蟹对盐度、碱度以及盐碱交互作用的耐受性研究，确定了盐度和碱度对中华绒螯蟹作用 24 h、48 h、72 h 和 96 h 时的半致死浓度和安全浓度。

关键词: 中华绒螯蟹; 盐度; 碱度; 毒性作用

Study on toxicity of salinity and alkalinity on *Eriocheir sinensis*

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Abstract: In order to investigate the physiological tolerance of Chinese mitten crab (*Eriocheir sinensis*) to saline-alkali water environment, and to guide the saline-alkali aquaculture of Eriocheir sinensis, The tolerance of Chinese mitten crab to salinity, alkalinity and saline-alkali interaction was studied by one-way acute toxicity tests and a uniform orthogonal test, The semi-lethal concentration and safe concentration of salinity and basicity for 24 h, 48 h, 72 h and 96 h were determined.

Key words: Chinese mitten crab, salinity, alkalinity, toxic effect

碱度适应性驯化对大鳞鲃（*Luciobarbus capito*）幼鱼血液生理生化及肝脏抗氧化系统的影响

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摘要： 为了从血液生理生化、肝脏抗氧化应激等方面研究大鳞鲃对碱度驯化的生理适应性变化，选择体质量为(13.66±1.26)g 的大鳞鲃幼鱼开展 NaHCO3 碱度适应性驯化实验，空白组一直处于淡水中养殖，驯化组经 20mol/L 的碱度适应性驯养 7d 后再放入 40mmol/L 的碱度水体中，未驯化组直接放入 40mmol/L 的碱度水体中，测定比较在鱼体放入 40mmol/L 碱度水体中第 0h、6h、12h、24h、48h、96h、7d 幼鱼血液生理生化指标和肝组织抗氧化系统相关指标变化。

关键词：大鳞鲃；碱度；生理生化；抗氧化酶

Effects of alkalinity adaptive acclimation on blood physiology and biochemistry and liver antioxidant system of juvenile *Luciobarbus capito*

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Abstract: In order to study the physiological adaptability of *Luciobarbus capito* to alkalinity acclimation from the aspects of blood physiology, biochemistry and antioxidant stress, the juvenile *Luciobarbus capito* with body weight of (13.66 ± 1.26) g was selected to carry out the experiment of $NaHCO_3$ alkalinity acclimation. The blank group was cultured in fresh water all the time. The acclimation group was acclimated to 20 mmol/L alkalinity for 7 days and then put into 40 mmol/L alkalinity water. The non-acclimation group was directly put into 40 mmol/L alkalinity water. The changes indexes of blood physiological and biochemical and related indexes of liver antioxidant system of juvenile fish in 40 mmol/L alkalinity water for 0 h, 6 h, 12 h, 24 h, 48 h, 96 h and 7 d were compared.

Key words: *Luciobarbus capito*; alkalinity; physiological biochemical; antioxidant enzymes

珠三角地区池塘养殖大口黑鲈病毒病和诺卡氏菌病流行病学调查与分析

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摘要：在建立 real-time Q-PCR（qPCR）检测技术基础上，2020 年 6 月 1 日到 2021 年 7 月 31 日，共 14 个月，检查珠三角地区养殖池塘的大口黑鲈样品共 901 个，检出蛙病毒属虹彩病毒（MRV）阳性样品 331 个，阳性率为 36.67%，其中南海区阳性检出率为 19.22%，顺德区阳性样品检出率为 39.48%。共检出弹状病毒（SCRV）阳性样品 130 个，阳性率为 14.28%，其中苗种检出率为 63.08%，养殖鱼阳性样品检出率为 36.92%。检出的肿大细胞病毒属虹彩病毒（ISKNV）阳性样品 10 个，都与 MRV 混合感染。共检出诺卡氏菌（NS）阳性样品 69 个，阳性率为 7.66%，其中与 MRV 混合感染 20 个，检出率为 2.22%。从目前的调查数据显示，珠三角大口黑鲈虹彩病毒的感染以 MRV 为主，该病毒可在鱼体内呈隐性带毒状态。多种细菌和寄生虫皆可导致大口黑鲈发病，也存在病毒混合感染现象，导致疾病发生，多病原在此过程中或互为诱因。

关键词：大口黑鲈；流行病学调查；大口黑鲈虹彩病毒；鳜弹状病毒；鰤诺卡氏菌；qPCR

Epidemiological investigation and analysis of viral disease and Nocardia disease of largemouth bass(*Micropterus salmoides*) cultured in pond in pearl River Delta

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Abstract: Based on the establishment of real-time Q-PCR (qPCR) detection technology, there were a total of 901 largemouth bass(Micropterus salmoides) samples of Pearl River Delta region examined from June 1, 2020 to July 31, 2021, and 331 positive samples of Ranovirus belonging to iridum iridum virus (MRV) were detected, with a positive rate of 36.67%. The positive rate was 19.22% in Nanhai district and 39.48% in Shunde District. A total of 130 SCRV positive samples were detected, with a positive rate of 14.28%, among which the positive rate of seedling was 63.08% and that of cultured fish was 36.92%. Ten ISKNV positive samples were detected, all of which were mixed with MRV. A total of 69 nocardia (NS) positive samples were detected, with a positive rate of 7.66%, and 20 of them were mixed with MRV, with a positive rate of 2.22%. According to the current investigation data, the iridovirus infection of largemouth bass in pearl River Delta is mainly ranaviruses, which can be detected in normal fish, indicating that the virus can be recessive and virulent in fish. According to the disease investigation and virus detection, a variety of bacteria and parasites can cause the disease of largemouth bass, and there is also the phenomenon of mixed virus infection, which leads to the disease. Multiple pathogens may be inducements of each other in this process.

Key words: Largemouth bass (*Micropterus salmoides*); Epidemiological investigation; Largemouth bass ranavirus, MRV; Siniperca chuatsi rhabdovirus SCRV; Nocardia Seriolae, NS; qPCR

IHNV 与 IPNV 的分离鉴定及病毒混合感染对虹鳟致病性的影响

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摘要：为研究 IHNV 和 IPNV 病毒在鱼类体内的相互作用关系及其对宿主的致病性的影响，本研究通过 RT-PCR 方法检测甘肃某鱼场患病的虹鳟幼鱼存在 IHNV 和 IPNV 混合感染，利用空斑纯化病毒技术分离获得了 IHNV GS17 株和 IPNV GS17 株。通过动物攻毒试验并利用实时荧光定量 PCR 方法检测试验鱼肝脏中 IHNV、IPNV 载量和脾脏中 IFN1、MX-1 的表达水平，利用间接 ELISA 检测血液特异性抗体 IgM 水平。结果显示 IPNV 和 IHNV 混合感染虹鳟幼鱼，IPNV 对 IHNV 增殖存在抑制作用，抑制作用与病毒在宿主体内的相对载量有关。混合感染会使宿主体内干扰素水平增强，但 IPNV 对宿主体内干扰素的抑制作用提高了病毒混合感染对虹鳟幼鱼的致病性。对两种疾病的诊断和科学防治具有重要指导意义。

关键词：传染性造血器官坏死病毒（IHNV）；传染性胰腺坏死病毒（IPNV）；混合感染；病毒载量；致病性

Isolation and Identification of IHNV and IPNV and the Effect of Mixed Virus Infection on the Pathogenicity of Rainbow Trout

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Abstract: In order to study the interaction between IHNV and IPNV virus in fish and its effect on the pathogenicity of the host, this study used RT-PCR to detect the mixed infection of IHNV and IPNV in diseased rainbow trout juveniles from a fish farm in Gansu. IHNV GS17 strain and IPNV GS17 strain were isolated using plaque purification virus technology. Through the animal challenge test and real-time fluorescence quantitative PCR method, the IHNV and IPNV load in the liver of the test fish and the expression levels of IFN1 and MX-1 in the spleen were detected, and the blood specific antibody IgM level was detected by indirect ELISA. The results showed that IPNV and IHNV mixed infection of rainbow trout juveniles. IPNV has an inhibitory effect on the proliferation of IHNV, and the inhibitory effect is related to the relative load of the virus in the host. Mixed infection can increase the level of interferon in the host, but the inhibitory effect of IPNV on the interferon in the host increases the pathogenicity of mixed infection of the virus to the juvenile rainbow trout. It has important guiding significance for the diagnosis and scientific prevention of the two diseases.

Key words: Infectious hematopoietic organ necrosis virus (IHNV); Infectious pancreatic necrosis virus (IPNV); Mixed infection; Viral load; Pathogenicity

鲤鱼浮肿病毒 L3 株的分离与鉴定

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摘要：由于 CEV 没有合适的易感细胞，病毒体外分离培养困难，在一定程度上制约 CEV 分子生物学的研究发展，严重阻碍 CEVD 的防治。筛选 CEV 的易感细胞，建立 CEV 体外分离培养方法，对该病毒的基础生物学特性研究及疫苗的研发具有重要的理论与实践意义。本研究利用组织切片技术对患病鱼组织病理进行观察，建立进化树将获得的病原的基因片段进行分子系统进化树的分析，利用 SYBR Real-time PCR 方法对病原的靶器官进行检测；筛选 CEV 的易感细胞，将体外培养和分离的病毒进行动物攻毒回归试验。本研究通过制备的鲤肾脏原代细胞分离获得 CEV-L3 株，为 CEV 易感细胞系的建立和病毒的生物学特性的进一步研究奠定了重要的物质基础，为鲤浮肿病的流行病学、临床诊断、免疫防治及选育抗 CEV 鲤品系的研究具有重要意义。

关键词：鲤鱼浮肿病毒；分离；鉴定；原代细胞

Isolation and Identification of Carp EdemaVirus L3 Strain

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Abstract: Because CEV does not have suitable susceptible cells, it is difficult to isolate and culture the virus in vitro, which restricts the research and development of CEV molecular biology to a certain extent, and seriously hinders the prevention and treatment of CEVD. The screening of CEV susceptible cells and the establishment of CEV in vitro isolation and culture methods have important theoretical and practical significance for the study of the basic biological characteristics of the virus and the development of vaccines. In this study, tissue sectioning technology was used to observe the histopathology of diseased fish. The phylogenetic tree was established to analyze the molecular phylogenetic tree of the obtained pathogenic gene fragments. The SYBR Real-time PCR method was used to detect the target organs of the pathogen; CEV was screened. Susceptible cells, the virus cultured and isolated in vitro is subjected to the animal challenge regression test. In this study, the CEV-L3 strain was obtained by isolation of primary carp kidney cells, which laid an important material foundation for the establishment of CEV susceptible cell lines and the further study of the biological characteristics of the virus, and contributed to the epidemiology of carp edema The research on clinical diagnosis, immune control and breeding of anti-CEV carp line is of great significance.

Key words: Carp edema virus; isolation; identification; primary cell

激活 NF-κB 信号通路鲑甲病毒蛋白的筛选及作用机制的研究

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摘要：为探究鲑甲病毒（Salmonid Alphavirus）感染鲑科鱼类能否激活 NF-κB 信号通路。本研究将探究 SAV 激活 NF-κB 信号通路的分子机制，及其介导炎症反应的关键蛋白，并对其作用位点进行确定，分析 SAV 蛋白激活 NF-κB 信号通路介导炎症反应的分子机制，进一步分析 SAV 激活蛋白与 CHSE-214 宿主细胞蛋白之间的相互作用。通过 SAV 感染 CHSE-214 细胞，利用双荧光素酶报告系统验证 SAV 激活 NF-κB 的能力，同时筛选激活 NF-κB 的 SAV 蛋白及其关键功能域，及上游模式识别受体，验证筛选出的蛋白对 NF-κB 信号通路的激活作用及其产生的下游相关炎症因子；通过质谱筛选与 SAV 关键蛋白相互作用的 CHSE-214 宿主细胞蛋白，并采用 CO-IP 技术、激光共聚焦共定位、双荧光素酶报告系统验证病毒与宿主细胞之间的互作，分析 SAV 蛋白激活 NF-κB 通路的分子机制及其对病毒复制的影响。

关键词：鲑甲病毒；NF-κB；Nsp2；炎症反应；致病机制

Screening of salmon alpha virus protein that activates NF-κB signaling pathway and study of its pathogenic mechanism

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Abstract: To explore whether Salmonid Alphavirus infected salmonids can activate the NF-κB signaling pathway. This study will explore the molecular mechanism of SAV activating the NF-κB signaling pathway, and its key proteins that mediate the inflammatory response, and determine its site of action, and analyze the molecular mechanism of SAV protein activating the NF-κB signaling pathway to mediate inflammation. Further analyze the interaction between SAV activator protein and CHSE-214 host cell protein. Infect CHSE-214 cells with SAV, use the dual luciferase reporter system to verify the ability of SAV to activate NF-κB, and screen the SAV protein that activates NF-κB and its key functional domains, as well as upstream pattern recognition receptors, to verify the screened The activation of the NF-κB signaling pathway and the downstream related inflammatory factors produced by the protein; the CHSE-214 host cell protein that interacts with SAV key proteins is screened by mass spectrometry, and CO-IP technology, laser confocal colocalization, dual The luciferase reporter system verifies the interaction between the virus and the host cell, and analyzes the molecular mechanism of the SAV protein activating the NF-κB pathway and its effect on virus replication.

Key words: Salmon alpha virus; NF-κB; Nsp2; inflammatory response; pathogenic mechanism

核酸适体在抗水生病毒研究中的应用

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摘要：近年来我国水产养殖业发展迅速，养殖规模不断扩大。然而当前高密度、集约化的养殖模式易导致养殖病害频繁爆发，造成了巨大的经济损失。因此应着力开展水产病害快速检测技术与高效防控技术的研究，以实现对水产病害的快速诊断、实时监控和有效预防治疗。核酸适体是利用指数富集的配基系统进化技术(Systematic Evolution of Ligands by Exponential Enrichment, SELEX)筛选获得的、能够高特异性识别并检测靶物质的单链寡核苷酸，它们可以特异性识别和结合靶标物质。本研究对核酸适体在抗水生病毒研究中的应用进行了综述和讨论。首先，利用核酸适体能够高特异性识别病原微生物的特性，核酸适体已经用于构建高灵敏的生物传感器用于病原的快速检测、疾病的实时监测，具有特异性高、操作方便的特点。其次，基于核酸适体的抗病毒能力，它们在开发靶向抗病毒药物方面具有巨大的应用潜力。此外，核酸适体还可用于构建高特异性荧光分子探针，通过将核酸适体识别靶标的高灵敏、高特异性转换为强荧光信号的发生，用于病毒侵染宿主机制的研究。

关键词：核酸适体；水生病毒；快速检测技术；抗病毒治疗；侵染机制研究

Aptamers applications in anti-aquatic virus researches

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Abstract: The rapid development of aquaculture has caused frequent various viral pathogens outbreaks, which results in great economic losses. The development of rapid detection assays and effective agents help fight against these pathogens. Aptamers are single-stranded oligonucleotides, they could specially recognize and bind to the targets. In this study, we reviewed and discussed the applications of aptamers in anti-aquatic virus researches. As aptamers could highly specially recognize and monitor virus infection, aptamers are used as molecular probes to establish novel detective assays to identify aquatic virus, which are characterized of high specificity and convenient operation. Based on some aptamers' antiviral abilities, they have great potentials in developing antiviral drugs. Furthermore, aptamers serve as high specific molecular probes for virus pathogenesis researches. Aptamers have great potentials in various science fields, including pathogen sensitive detection, effective therapies, pathogenesis researches and so on.

Key words: Aptamers, aquatic virus, rapid detection assay, anti-virus therapies, pathogenesis researches

对虾急性肝胰腺坏死病 (AHPND) 毒力基因 ***pir*AB** 的进化研究

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摘要：本研究分离得到一株能够导致对下急性肝胰腺坏死病（Acute hepatopancreas necrosis disease, AHPND）的 *Vibrio owensii* 菌株（strain SH-14），其中包含与 *Vibrio parahaemolyticus* 病原菌相同的、编码 PirAB 毒蛋白的致病质粒（pVH）。进一步分析表明：该质粒目前分布于 3 个种、11 株 AHPND 病原弧菌（Vibrio）中。此外，发现 13 个与之序列高度相似，但不编码 PirAB 毒蛋白的质粒（pVH-r）分布于多种不同的的弧菌中。多方面证据表明，毒力基因 pirAB 可能是在强力转座子介导下，由宽宿主范围、转移能力强、可在宿主菌中稳定存在的质粒散播至各种不同种类的宿主菌中，暗示自然界中可能存在更多不同的 AHPND 病原微生物。

关键词：对下急性肝胰腺坏死病, 质粒, 转座子, IS903, Tn903

Shrimp AHPND-causing plasmids encoding the PirAB toxins as mediated by ***pirAB*-Tn903** are prevalent in various ***Vibrio*** species

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Abstract: Here, we report the complete sequences of the AHPND-causing plasmid isolated from *V. owensii*, as well as those of its 11 siblings (pVH family). In addition, we also included 13 related plasmids (pVH-r family) without the *pirAB* genes isolated from a variety of species within the Vibrio Harveyi clade. Furthermore, the homologue counterparts of *pirAB* genes were also detected in a non-pVH plasmid in *V. campbellii*. Taken together, our results provide novel insights into the acquisition and evolution of *pirAB* as well as related plasmids in the Vibrio Harveyi clade.

Key words: Acute hepatopancreatic necrosis disease, plasmid, transposon, IS903, Tn903

一氧化氮对感染虾肝肠胞虫脊尾白虾的影响

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摘要：为了增加虾体免疫力，抵御虾肝肠胞虫（*Enterocytozoon hepatopenaei*，EHP）感染，本实验通过向感染肝肠胞虫的脊尾白虾围心腔注射 10 μL 浓度为 0 μg/L、0.3 μg/L、0.6 μg/L、0.9 μg/L 的一氧化氮，检测肝胰腺中相关非特异免疫酶的活力，以及血液中一氧化氮含量，探讨注射一氧化氮对 EHP 阳性脊尾白虾的影响。研究表明，病虾肝胰腺中总一氧化氮合酶（TNOS）、诱导型一氧化氮合酶（iNOS）、酸性磷酸酶以及碱性磷酸酶的活力均高于健康虾，72 h 内病虾 TNOS 活力先升高再降低，iNOS 活力单调递增。注射 NO 浓度为 0.3 μg/L、0.6 μg/L，24 h 后病虾血液中 NO 含量最高，本实验对于虾体抵御 EHP，降低 EHP 造成的经济损失有一定的参考价值。

关键词：虾肝肠胞虫；脊尾白虾；一氧化氮；

Effect of Nitric Oxide on *Exopalaemon carinicauda* Infected with *Enterocytozoon hepatopenaei*

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Abstract: In order to increase the immunity of *Exopalaemon carinicauda* and resist *Enterocytozoon hepatopenaei* (EHP) infection, this experiment was performed by injecting 10 microliters into the pericardial cavity of EHP at a concentration of 0 μg/L、0.3 μg/L、0.6 μg/L、0.9 μg/L nitric oxide were used to detect the activity of related non-specific immune enzymes in the hepatopancreas and the content of nitric oxide in the blood to explore the effect of injection of nitric oxide on EHP-positive *Exopalaemon carinicauda*. Studies have shown that the total nitric oxide synthase (TNOS) activity, inducible nitric oxide synthase (iNOS) activity, acid phosphatase activity and alkaline phosphatase activity in the hepatopancreas of diseased shrimp are higher than those of healthy shrimp, and diseased shrimp within 72 h TNOS activity first increased and then decreased, iNOS activity increased monotonously. When the NO concentration was 0.3μg/L and 0.6μg/L, the NO content in the blood of sick shrimp peaked after 24 hours. This experiment has certain reference value for shrimps to resist EHP and reduce the economic loss caused by EHP.

Key words: *Enterocytozoon hepatopenaei*; *Exopalaemon carinicauda*; Nitric Oxide;

弧菌减毒菌株的构建及生物安全性评估

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摘要：前期构建鳗弧菌减毒菌株，通过感染南美白对虾来评估减毒菌株的毒力下降大小，以及通过一些生物学分析实验，对毒减菌株进行一些生物学验证其表征变化情况。

关键词：弧菌;缺失；减毒菌株

Construction of attenuated strains of Vibrio and its biosafety assessment

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Abstract: The attenuated strain of Vibrio anguilla was constructed in the early stage, and the virulence decrease of the attenuated strain was evaluated by infection with Penaeus vannamei, and some biological analysis experiments were carried out on the attenuated strain to verify its characterization changes.

Keywords: Vibrio; deletion; attenuated strain

福建霞浦患病仿刺参病理组织观察与分析

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摘要：2020 年 11 月下旬，福建霞浦海区仿刺参出现患病症状，为探究患病仿刺参病因，对病参进行组织病理观察与分析。体表观察结果显示，患病仿刺参体壁出现大面积溃烂；解剖后镜检发现呼吸树上寄生有大量后口虫。取患病仿刺参体壁、肠道、呼吸树等组织进行组织病理切片分析，发现患病仿刺参肠道组织萎缩、肠壁变薄、环形皱襞变少、体壁和呼吸树结构破坏，同时呼吸树上发现有量寄生虫体。结果表明，后口虫在仿刺参呼吸树上的大量寄生可能是引起此次仿刺参患病的主要因素之一。

关键词：仿刺参；后口虫；组织切片

Observation and analysis of pathological tissue of Xiapu Apostichopus japonicus in Fujian Province

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Abstract: In late November 2020, the sick symptoms of *Apostichopus japonicus* appeared in Xiapu sea area, Fujian Province. In order to explore the etiology of the sick *Apostichopus japonicus*, histopathological observation and analysis were carried out. The results of body surface observation showed that the body wall of sick *Apostichopus japonicus* appeared large-area ulceration; Microscopic examination after dissection showed that there were a large number of post-mouth bugs insects parasitic on respiratory trees. The diseased tissues such as body wall, intestine and respiratory tree of *Apostichopus japonicus* were taken for histopathological section analysis. It was found that the diseased *Apostichopus japonicus* intestinal tissue atrophied, the intestinal wall became thinner, the circular folds became less, the structure of body wall and respiratory tree was damaged, and a large number of parasites were found on the respiratory tree. The results showed that a large number of parasites on the respiratory tree of *Apostichopus japonicus* may be one of the main factors causing the disease of *Apostichopus japonicus*.

Key words: *Apostichopus japonicus*, post-mouth bugs, tissue slice

仿刺参源美人鱼发光杆菌的分离鉴定及致病研究初探

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摘要：为了探究引起霞浦海参发病死亡的原因及其病原菌的药物敏感性，于 2020 年从福建霞浦海区患病仿刺参中分离得到优势菌株 XP-11，回归感染实验证实其具有致病性；在 TCBS 固体培养基上培养 24 h 后观察，菌落呈中央隆起、边缘光滑、圆形、透明或者橘色；经 Biolog 自动微生物鉴定系统、16S rRNA 和 gyrB 管家基因鉴定该菌株为美人鱼发光杆菌；毒力基因分析结果显示，菌株 XP-11 含有溶血素 hlyAch 基因以及磷脂酶活性 pIpA 基因、霍乱弧菌溶血素 hlyA 基因；药物敏感性分析结果显示，菌株 XP-11 对四环素、恩诺沙星、环丙沙星、头孢曲松、氧氟沙星、诺氟沙星、头孢拉定、复方新诺明等 8 种药物敏感；其对恩诺沙星、硫酸新霉素、甲砜霉素、氟苯尼考、盐酸多西环素、氟甲喹、磺胺间甲嘧啶钠、磺胺甲噁唑+甲氧苄啶的最小抑菌浓度(ug/ml)分别为 0.08、2、1、1、0.06、0.125、4、1.2/0.06。本研究为仿刺参养殖过程中由美人鱼发光杆菌引起的疾病防控提供参考依据。

关键词：仿刺参；美人鱼发光杆菌；鉴定；药物敏感性

Isolation and Identification of *Photobacterium damselae* sea cucumber and Evaluation of Its Pathogenicity

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Abstract: In order to explore the causes of morbidity and mortality of Xiapu sea cucumber and the drug sensitivity of its pathogens, the dominant strain xp-11 was isolated from sick *Apostichopus japonicus* in Xiapu sea area, Fujian Province in 2020. The regression infection experiment confirmed its pathogenicity; After cultured on TCBS solid medium for 24 hours, the colonies showed central bulge, smooth edge, round, transparent or orange; The strain was identified as luminous Mermaid by Biolog automatic microbial identification system, 16S rRNA and gyrB housekeeping gene; Virulence gene analysis showed that strain xp-11 contained hemolysin *hly*A$_{ch}$ gene, phospholipase activity *pip*V gene and Vibrio cholerae hemolysin *hly*A gene; The results of drug sensitivity analysis showed that strain xp-11 was sensitive to 8 drugs, such as tetracycline, enrofloxacin, ciprofloxacin, ceftriaxone, ofloxacin, norfloxacin, Cefradine and compound xinnomine; The minimum inhibitory concentrations (ug / ml) of enrofloxacin, neomycin sulfate, thiamphenicol, florfenicol, doxycycline hydrochloride, fluoromequine, sulfamethoxazole sodium and sulfamethoxazole + trimethoprim were 0.08, 2, 1, 1, 0.06, 0.125, 4 and 1.2/0.06, respectively. This study provides a reference basis for disease prevention and control caused by photobacterium Mermaid in the process of sea cucumber culture.

Key words: *Apostichopus japonicus*, *Photobacterium damselae*, appraisal,drug sensitivity

三疣梭子蟹寄生纤毛虫-异阿脑虫的分离鉴定、人工培养及综合防控效果研究

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摘要：自 2017 年以来，浙江省宁波市奉化某养殖场的养殖三疣梭子蟹大量死亡，死亡率高达 80%。对病蟹现场临床检测发现，其血液异常澄清透明，显微镜检发现新死和濒死蟹血淋巴中大量存在一种纤毛虫。首先，本研究将分子生物学和生物信息学分析结果与显微和超微结构特征相结合，以探明其生物学特征，确定该虫为异阿脑虫属一未知种的纤毛虫；另外，通过回感实验证明该虫为引起三疣梭子蟹死亡的真正病原。为了找到有效的抗虫药物和建立安全高效的防治方法，本研究筛选到了硫酸奎宁等，并分别开展体外杀虫实验和养殖蟹异阿脑虫病的药物防、治实验，并证明效果显著。

关键词：三疣梭子蟹；异阿脑虫；奎宁；防控

Isolation, characterization and virulence of *Mesanophrys* sp. (*Ciliophora: Orchitophryidae*) in farmed swimming crab (*Portunus trituberculatus*) and anti-parasitic effects of quinine sulfate

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Abstract: A disease outbreak occurred in swimming crab (*Portunus trituberculatus*) farmed in eastern China, with a mortality rate of more than 80%. To further investigate the characteristics and pathogenesis, we reported isolation, characterization and virulence of the causative agent of this disease from 10 sick crabs. The results of the morphological study confirmed that the ciliate was similar to *Mesanophrys* ciliates and *O. stellarum* cultured in supportive media, but different from *O. stellarum* cultured in living sperm cells of starfish (*Leptasterias* spp.). Also, the growth of the ciliate did not interfere with light, which was different from *O. stellarum*. Accordingly, the ciliate was classified as genus *Mesanophrys* and temporarily named as *Mesanophrys* sp. In addition, experimental infection confirmed that *Mesanophrys* sp. was the pathogen that infected farmed crabs. The anti-parasitic effects and toxicity of quinine sulfate on *Mesanophrys* sp. were investigated. Quinine sulfate can kill *Mesanophrys* sp. by interacting with the DNA, mitochondria and cell membrane of parasites. Also, quinine sulfate can prevent the infection of crabs and treat the *Mesanophrys* sp. disease in aquaculture. It is possible, therefore, to combine the prevention and treatment in production, kill pathogens by drugs in the water during the high incidence of the disease and maintain a suitable environment for preventing the spread and infection of pathogens. In addition, early detection and treatment of the diseased crabs reduced the death of crabs and inhibited the spread of the diseases.

Key words: *Portunus trituberculatus; Mesanophrys* sp.; Quinine sulfate; Prevention Treatment

脂质和氨基酸：虾肝肠胞虫胞内寄生的重要物质依赖

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摘要：本研究利用 4D label-free 蛋白质组和乙酰化修饰组学技术，从蛋白水平分析虾肝肠胞虫（EHP）感染对凡纳滨对虾初级代谢通路的影响，同时通过鉴定的病原蛋白信息，初步探究病原与宿主间的相互作用关系。我们发现初级代谢缺陷的 EHP 为维持胞内寄生劫持了大量宿主的能量和代谢底物，扰乱了宿主的能量生成以及脂质和氨基酸代谢，蜕皮生长所需的有机物质储备不足和保幼激素的持续高水平阻滞了对虾的生长发育。

关键词：虾肝肠胞虫，凡纳滨对虾，脂质和氨基酸代谢紊乱

Lipid and amino acid: an important substance dependence for parasitic life of *Enterocytozoon hepatopenaei*

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Abstract: In this study, 4D label-free proteomics and acetylation modification omics were used to analyze the primary metabolism change of *Litopenaeus vannamei* after challenged by *Enterocytozoon hepatopenaei*, and to explore the interaction between pathogens and hosts. We found that EHP stole vast energy and metabolic substrates of host cells to maintain its intracellular parasitic life, and disrupted host energy generation, lipid and amino acid metabolism. Therefore the insufficient reserve of organic materials required for molting growth and the continuous high level of juvenile hormone hindered the growth and development of shrimp.

Key words: *Enterocytozoon hepatopenaei, Litopenaeus vannamei*, lipid and amino acid metabolism disorder

传染性早熟病毒的发现及其致病性研究

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摘要：自 2010 年以来，我国养殖罗氏沼虾中出现了以性早熟为主要特征的铁虾综合征（iron prawn syndrome, IPS），导致罗氏沼虾养殖产量损失严重。然而 IPS 的成因一直不明，严重制约了罗氏沼虾养殖业的绿色高质量发展。本团队利用甲壳动物新病原鉴定平台，通过病毒宏转录组、组织病理学和透射电镜等技术从患 IPS 的罗氏沼虾中发现一种新病毒。病毒粒子为球形，大小在 40—60 nm 之间；基因组全长 12630 nt，为单股正链 RNA 病毒；病毒通过水体浸浴能感染正常罗氏沼虾并导致罗氏沼虾出现 IPS。系统发育分析表明，该病毒属于荆门病毒和黄病毒属之间的一个新属。结合病毒组学、感染实验和原位杂交发现该病毒与罗氏沼虾性早熟具有很强相关性，因此暂将该病毒命名为传染性早熟病毒（infectious precocious virus, IPV）。我们还建立了 IPV 的套式 RT-PCR 和实时荧光定量 PCR 方法，进一步确认了流行病学样品中 IPV 感染与 IPS 的相关性。综上所述，本研究从养殖罗氏沼虾中发现了一种新病毒，并报道了该病毒与罗氏沼虾的性早熟有关的证据。

关键词：罗氏沼虾，性早熟，黄病毒，致病性

Discovery and pathogenicity of infectious precocious virus

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Abstract: Since 2010, the iron prawn syndrome (IPS) characterized by sexual precocity has appeared in the farmed *Macrobrachium rosenbergii*, which has led to substantial production losses. However, the cause of IPS was not clear, which seriously restricts the green development of *M. rosenbergii* industry. We used the identification platform of emerging pathogen in crustacean to discover a novel virus from the IPS-affected *M. rosenbergii* through viral metatranscriptomic sequencing, histopathological examination and transmission electron microscopy. Putative virus particles showed as spherical with a diameter of 40—60 nm. The virus contains a positive-sense, single-stranded RNA genome of 12,630 nucleotides. A subsequent immersion challenge study with viral extracts of IPS-affected samples reproduced the gross signs of IPS. Phylogenetic analysis indicated that it may belong to a new genus between Jingmenvirus and *Flavivirus*. Studies from viral metatranscriptome, bioassay and *in situ* hybridization showed that infection with IPV has a strong correlation with IPS. We provisionally name this virus infectious precocity virus (IPV). We developed nested reverse transcription-PCR and real-time PCR methods and confirmed that all IPS-affected prawns tested IPV positive but normal prawns tested negative. Collectively, our study revealed a novel virus of *Flaviviridae* associated with sexual precocity in *M. rosenbergii*.

Key words: *Macrobrachium rosenbergii*, sexual precocity, *Flaviviridae*, pathogenicity

基于 SCoT 分子标记的黄河鲤抗嗜水气单胞菌群体遗传多样性分析

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摘要：为揭示黄河鲤抗嗜水气单胞菌不同群体遗传多样性的差异，本研究通过对 300 尾黄河鲤人工注射嗜水气单胞菌进行感染，死亡率为 40%。利用 SCoT 对最先死亡的 30 尾（the first dead population, FP）、最后死亡的 30 尾（the last dead population, LP）和存活群体中的 30 尾（survival population, SP）进行了遗传多样性和群体遗传结构分析。结果显示：3 个群体的平均有效等位基因数（N_e）为 1.3828～1.4029，平均 Nei’s 基因多样性指数（H）为 0.2258～0.2467，平均 Shannon’s 信息指数（I）为 0.3453～0.3804，其中 SP 的 Ne、H、I 最高。聚类分析和主坐标分析显示，FP 和 LP 聚成一支，SP 为独立一支。遗传结构分析显示，所有样品被分为 2 个理论群体（K=2）,与聚类分析结果一致。研究表明，抗嗜水气单胞菌群体具有较高的遗传多样性，本研究为黄河鲤抗嗜水气单胞菌分子育种提供理论依据。

关键词：黄河鲤（*Cyprinus carpio haematopterus*）；嗜水气单胞菌（*Aeromonas hydrophila*）；SCoT；遗传多样性；

Analysis of genetic diversity of the yellow river carp anti-hydrophilic monocytobacteria group based on SCoT molecular markers

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Abstract: In order to reveal the difference of genetic diversity of different populations of Yellow River carp against *Aeromonas hydrophila*, 300 Yellow River carp were artificially infected with *A.hydrophila*, and the mortality rate was 40%. SCoT was used for the first 30 dead population (FP), the last 30 dead population (LP) and the 30 survival population (SP), Genetic diversity and population genetic structure were analyzed. The results showed that the average number of effective alleles (N_e) in the three populations ranged from 1.3828 to 1.4029, the average Nei's gene diversity index (H) ranged from 0.2258 to 0.2467, and the average Shannon's information index (I) ranged from 0.3453 to 0.3804. Cluster analysis and principal coordinate analysis showed that FP and LP clustered into one branch, and SP was independent. Genetic structure analysis showed that all samples were divided into two theoretical populations (K=2), which was consistent with cluster analysis results. This study provided a theoretical basis for the molecular breeding of *A. hydrophila* resistance in Yellow River carp.

Key words: Yellow River carp(*Cyprinus carpio haematopterus)*; *Aeromonas hydrophila*; SCoT; genetic diversity

灭多威在小球藻-大型溞-斑马鱼食物链中的传递特征

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摘要：为研究灭多威（Methomyl）在水生生物的富集传递效应，选择普通小球藻（*Chlorella vulgaris*）、大型溞（*Daphnia magna*）和斑马鱼（*Brachydanio rerio*）为研究对象，开展普通小球藻对灭多威的富集效应和灭多威在普通小球藻、大型溞以及斑马鱼体内的传递效应试验。普通藻对灭多威具有较强的富集能力，通过摄食过程将灭多威传递到大型溞，再通过摄食过程大型溞传递到斑马鱼，经传递的灭多威能够抑制摄食，代谢等生命活动。

关键词：灭多威；食物链；富集传递效应

Methomyl on *Chlorella vulgaris- Daphnia magna- Brachydanio rerio* through its food chain

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Abstract: To study the bioaccumulation and transfer the effect of Methomyl in aquatic organisms, Chlorella vulgaris (Chlorella vulgaris), Daphnia magna (Daphnia magna) and Brach-ydanio rerio (Brachydanio rerio) were selected as the research objects. We carried out ex-periments on the bioaccumulation effect of chlorella vulgaris on methomyl and the trans-mission effect of methomyl in chlorella vulgaris, Daphnia magna and Brachydanio rerio. Chlorella vulgaris had a strong ability to accumulate methomyl.Methomyl was passed to t-he Daphnia magna through the feeding process, and then passed to the Brachydanio r-erio by the Daphnia magna through the feeding process. The passed methomyl could inh-ibit life activities such as food intake and metabolism.

Key words: methomyl; food chain; bioaccumulation

牙鲆抗菌免疫相关 lncRNA 及 lncRNA-miRNA-mRNA 调控网络的鉴定和特征分析

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摘要：为解析非编码 RNA-编码 RNA 互作的抗菌免疫调控机制，以便应用于鱼类病害防控，本研究系统地鉴定了响应鳗弧菌感染的牙鲆长链非编码 RNA（lncRNA）及其调控通路，并通过多组学联合分析对免疫相关 lncRNA-miRNA-mRNA 调控网络进行了构建和特征分析。

关键词：LncRNA；牙鲆；鳗弧菌；免疫通路; ceRNA 网络

Identification and characterization of immune-related lncRNAs and lncRNA-miRNA-mRNA networks of *Paralichthys olivaceus*

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Abstract: In order to uncover the anti-bacterial immune mechanism of interaction between non-coding RNA and protein coding RNA, by which facilitates disease control in fish, in this study, we systematically identified the lncRNAs and their regulatory pathways of *Paralichthys olivaceus* in response to *Vibrio anguillarum* infection. We also constructed and characterized the immune-related lncRNA-miRNA-mRNA regulatory networks based on integrated analyses of multiple omics.

Key words: LncRNA, CNS, *Paralichthys olivaceus*, *Vibrio anguillarum*, immune pathway, ceRNA network

木犀草素对感染致 AHPND 副溶血性弧菌南美白对虾的保护作用

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摘要：为了获知凡纳滨对虾感染致肝胰腺坏死综合征副溶血性弧菌（VP_{AHPND}）后木犀草素的保护作用，以便在实际对虾养殖生产中更好的防控疾病，本实验测定了 VP_{AHPND} 攻击后，对虾喂食木犀草素后的保护率、免疫参数和肝胰腺组织病理变化，分析了木犀草素对凡纳滨对虾生存性能、抗病力和免疫力的影响。

关键词：木犀草素；凡纳滨对虾；副溶血性弧菌；AHPND；免疫调节；抗病力

Luteolin protects against acute hepatopancreatic necrosis disease-causing strain of *Vibrio parahaemolyticus* in *Litopenaeus vannamei*

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Abstract: The effects of oral administration of luteolin, on the survival performance, disease resistance, and immunity of VP_{AHPND} infected *Litopenaeus vannamei* were investigated. Compared with the infected only group, the shrimps in the luteolin groups showed significantly lower cumulative mortality over 5 days after infection ($p < 0.05$). In the luteolin groups, the vibrio density were consistently lower and the immune parameters were consistently higher than those in infected only group ($p < 0.05$). In the luteolin groups, the hepatopancreatic tubule structure and integrity were better than those in the infected only group. Moreover, with the dose of luteolin increased, the therapeutic effect was also enhanced.

Key words: Luteolin; *Litopenaeus vannamei*; *Vibrio parahaemolyticus*; AHPND; Immunomodulation; Disease resistance

鲤疱疹病毒 2 型保护抗原的筛选及 DNA 疫苗的构建

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摘要：近年来，由鲤疱疹病毒 2 型 (CyHV-2)感染引起的鲫造血器官坏死病给鲫鱼养殖业造成巨大的经济损失。本研究对 CyHV-2 膜蛋白进行抗原表位分析，筛选出 8 个富含抗原表位的肽段，原核表达，并对重组蛋白的免疫原性进行分析。在此基础上，构建 CyHV-2 DNA 疫苗，并进行 DNA 疫苗对异育银鲫的免疫效果评价。

关键词：鲤疱疹病毒2型；抗原表位；DNA疫苗；免疫效果

Screening for protective antigens of *Cyprinid herpesvirus 2* and construction of DNA vaccines

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Abstract： In recent years, crucian carp hematopoietic necrosis caused by *Cyprinid herpesvirus 2* (CyHV-2) infection has caused an enormous economic loss to the aquaculture industry. In this study, antigenic epitope analysis was performed on the membrane proteins of CyHV-2, and 8 antigen-rich peptide fragments were selected for prokaryotic expression. Then, the immunogenicity of the recombinant proteins was analyzed. On this basis, DNA vaccines were constructed for immunization of hybridized Prussian carps. The protective effect of DNA vaccines against challenge in hybridized Prussian carps was evaluated.

Key words： *Cyprinid herpesvirus 2*(CyHV-2), antigenic epitope, DNA vaccine, immune effect

体外消化模拟法评价中华绒螯蟹体内恩诺沙星、环丙沙星的生物可利用性

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摘要：我国作为水产大国，一些抗生素如恩诺沙星的不合理使用已经影响到了水产品的质量和人类自身的安全，本文对安徽、江苏、辽宁三省 92 份养殖中华绒螯蟹样品中 27 种抗生素的发生情况进行了调查，发现主要残留的抗生素为恩诺沙星和环丙沙星。进一步采用体外消化模拟法对中华绒螯蟹体内的恩诺沙星、环丙沙星的生物可利用性进行评估。

关键词：中华绒螯蟹；恩诺沙星；环丙沙星；生物可利用性

Bioavailability of enrofloxacin and ciprofloxacin in Chinese mitten crab (*Eriocheir sinensis*) was evaluated by in vitro digestion simulation

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Abstract:As aquaculture power in our country, some antibiotics such as well, the unreasonable use of has affected the quality of aquatic products and human security, in this paper, the three provinces of anhui, jiangsu, liaoning, 92 breeding in eriocheir sinensis samples has investigated the occurrence of 27 kinds of antibiotics, found that the main residual antibiotics for grace and ciprofloxacin. The bioavailability of enrofloxacin and ciprofloxacin in Chinese mitten crab was evaluated by in vitro digestion simulation.

Key words: chinese mitten crab; Enrofloxacin; Ciprofloxacin; Bioavailability

灭多威对斑马鱼胚胎抗氧化防御系统的影响

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摘要：探究灭多威对斑马鱼胚胎抗氧化防御系统的影响，以便为斑马鱼作为污染检测指示生物提供理论依据。将斑马鱼胚胎暴露于0、2、20、200 μg/L灭多威中，在24、48、72、96 h时测定鱼体内超氧化物歧化酶(SOD)、过氧化氢酶(CAT)、谷胱甘肽还原酶(GR)、还原型谷胱甘肽(GSH)、氧化型谷胱甘肽(GSSG)活性及丙二醛(MDA)含量的变化。

关键词：灭多威；斑马鱼；胚胎；抗氧化防御因子；氧化损伤

Effects of methomyl on antioxidant defense system of zebrafish embryos

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Abstract: To explore the effects of methomyl on the antioxidant defense system, so as to provide theoretical basis for zebrafish as a pollution detection indicator. Zebrafish embryos were exposed to 0, 2, 20, 200 μg/L methomyl. The activities of superoxide dismutase (SOD), catalase (CAT), glutathione reductase (GR), reduced glutathione (GSH), oxidized glutathione (GSSG) and the content of malondialdehyde (MDA) in zebrafish were measured at 24, 48, 72 and 96 h.

Key words: methomyl; zebrafish; embryo; antioxidant defense factor; oxidative damage

改性生物炭对水体中磺胺二甲嘧啶的吸附性能

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摘要：当前，随着抗生素在农牧渔业等领域的大量使用，水体中残留的抗生素愈加威胁着环境与人类的健康发展，生物炭被认为是去除这类新型污染物的理想材料。制备 3 种纳米改性生物炭并研究吸附特性，通过对磺胺二甲嘧啶的吸附作用，为其在水产养殖尾水处理中的应用奠定基础。

关键词：改性生物炭 磺胺二甲嘧啶 吸附 养殖尾水

Adsorption properties of modified biochane on sulfameldimidine in the water

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Abstract: At present, with the large number of antibiotics in the fields of agriculture, the antibiotics remaining in the water threatens the healthy development of the environment and humans, and biocompanies are considered to remove the ideal materials for such new pollutants. Three nano-modified biochacha were prepared and studied the adsorption characteristics, and the application of the sulfamer dimethylpyrimidine was used to lay the foundation for its application in aquaculture tail water treatment.

Key words: Modified biocompatible; Sulfamethylimidine; Adsorption; Tail water

白藜芦醇对红罗非鱼肠道组织结构及炎症因子含量的影响

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摘要：为了获知日粮白藜芦醇（RES）对高脂摄食红罗非鱼肠道组织结构及炎症因子含量的影响。本试验设置 8%脂肪、10%脂肪、10%脂肪+RES 以及 10%脂肪+RES+EX527 4 组，测定了红罗非鱼生长性能指标、腹脂沉积、肠道组织结构及炎症因子含量。

关键词：白藜芦醇；肠道炎症因子；肠道显微结构

Effects of resveratrol on intestinal histology and expression of inflammatory factors in red tilapia *Oreochromis mossambicus* ♀×*O.niloticus* ♂

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Abstract: In order to know the effects of dietary resveratrol (RES) on intestinal tissue structure and inflammatory factor content of high-fat feeding red tilapia. In this experiment, 8% fat, 10% fat, 10% fat+RES and 10% fat+RES+Ex527 groups were set up to determine the growth performance index, abdominal fat deposition, intestinal tissue structure and inflammatory factor content of red tilapia.

Key words: resveratrol; intestinal inflammatory factors; intestinal microstructure

饵料饲喂差异对大口黑鲈(*Micropterus Salmoides*)膳食消费引起人体潜在神经发育效应的风险与收益评估

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摘要：为评估饵料饲喂差异对大口黑鲈(*Micropterus Salmoides*)膳食消费引起人体潜在神经发育效应的风险与收益。本研究采集人工配合饲料、冰鲜鱼和冰鲜鱼转饲料饲喂的鲈鱼共 181 条。以 FAO/WHO 的确定性方法和概率评估计算净智商点增益值(net IQ)。

关键词：大口黑鲈(*Micropterus Salmoides*)；n-3 长链多不饱和脂肪酸；汞；智商点；风险效益评估

Risk and benefit assessment of potential neurodevelopmental effects of feed consumption on largemouth bass (*Micropterus Salmoides*)

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Abstract: The purpose of this study was to evaluate the potential neurodevelopmental effects of different feeds on largemouth bass (*Micropterus Salmoides*). A total of 181 perch were collected from formulated feed, iced trash fish feed and iced trash fish to feed. Net IQ was calculated using deterministic methods and probabilistic assessments from FAO and WHO.

Key words: *Micropterus Salmoides*; n-3LCPUFA; Mercury; IQ points; Risk and benefit assessment

水产养殖水体中土腥味物质的快速前处理方法的建立

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摘要：为了实现节约成本、快速简易和批量化的检测水体中土腥味物质（主要包括土臭素、2-甲基异莰醇）。我们利用磁性吸附与分散式液相萃取相结合方法，用合适的分散式液相作为萃取剂，实现水产养殖水体中土臭味物质的净化、提取和浓缩。

关键词：土臭素；2-甲基异莰醇；分散式固相萃取法；分散式液相萃取

Establishment of a rapid pretreatment method for earthy smelling substances in aquaculture water

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Abstract: In order to achieve cost-saving, rapid, simple, and mass detection of earthiness smell substances in water (mainly geosmin, 2-methylisoborneol). The purification, extraction, and concentration of soil odor substances in aquaculture water were realized by combining magnetic adsorption and dispersed liquid phase extraction with appropriate dispersed liquid phase as extraction agent.

Key words: Geosmin, 2-methylisoborneol, Dispersed solid phase extraction, Dispersive liquid phase extraction

利用多介质环境逸度模型比较典型抗生素磺胺甲噁唑和恩诺沙星在水产养殖中的环境归趋

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摘要：磺胺甲噁唑和恩诺沙星是我国水产养殖过程中 2 种常用的抗生素,但两者在罗非鱼养殖环境中的归趋行为尚不明确。通过野外养殖研究 2 种药物在罗非鱼养殖环境中的分配规律,应用多介质环境逸度模型模拟药物在养殖环境中的归趋行为。该研究对保护渔业生态环境、保障罗非鱼水产品的质量安全具有重要意义。

关键词：磺胺甲噁唑；恩诺沙星；罗非鱼；多介质环境逸度模型；归趋

Comparing the environmental fate of typical antibiotics sulfamethoxazole and enrofloxacin in aquaculture using a multi-media environmental fugacity model

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Abstract: Sulfamethoxazole and enrofloxacin are two commonly used antibiotics in aquaculture in China, but their fate in tilapia culture environment is not clear. The distribution of two drugs in tilapia culture environment was studied through field culture experiments, and the multi-medium environmental fugacity model was used to simulate the fate behavior of drugs in culture environment. This study is of great significance to protect the fishery ecological environment and ensure the quality and safety of tilapia aquatic products.

Key words: sulfamethoxazole; enrofloxacin; multimedia environment fugacity model; fate

白鲢(*Hypophthalmichthys molitrix*)腐败希瓦氏菌(*Shewanella putrefaciens*)的 16S rRNA 鉴定

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摘要：从患病白鲢(*Hypophthalmichthys molitrix*)体表分离获得 1 株革兰氏阴性细菌，菌株编号为 BD1-5，通过多种实验室分析方法进行鉴定研究。结果表明，患病白鲢体表皮肤溃烂，尤其尾部溃烂严重；对该病例主要组织进行镜检未见明显寄生虫；鲤春病毒血症病毒(Spring viremia of carp virus, SVCV)、鲤疱疹病毒 II 型(Cyprinid herpesvirus II, CyHV-II)和锦鲤疱疹病毒(Koi herpesvirus, KHV)均为阴性；采用 PCR 方法获得该分离菌株 16S rRNA 序列大小为 1416bp，与 *Shewanella putrefaciens* (GenBank NO.: KX185698)序列相似性为 99.72%；系统发育树分析显示该菌株与 *Shewanella putrefaciens* (GenBank NO.: KY817253)等自然聚为一枝。综合菌株形态及 16S rRNA 序列分析结果，最终判定该分离株为腐败希瓦氏菌(*S. putrefaciens*)，属于革兰氏阴性杆菌。本研究结果为腐败希瓦氏菌(*S. putrefaciens*)作为白鲢养殖过程中一种潜在致病原提供了理论依据和参考。

关键词：白鲢；腐败希瓦氏菌；16S rRNA

16S rRNA identification of *Shewanella putrefaciens* from the sliver carp *Hypophthalmichthys molitrix*

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Abstract: A bacterial strain was isolated from *Hypophthalmichthys molitrix*, and named BD1-5, physiological, gram stain examination, sequencing of 16S rRNA and phylogenetic tree analysis were carried out in the study. Results showed that the skin of sliver carp festered, especially the severe tail. There were no obvious parasites in the main tissues of the case. Molecular biology tests showed SVCV, CyHV-II and KHV were all negative. The 16S rRNA PCR method was used to obtain a fragment sequence of 1416bp, shown 99.72% similarity with *Shewanella putrefaciens* (GenBank NO.: KX185698). The phylogenetic analysis of the target sequence showed that the sample formed a dependent brach on the phylogenetic tree with *Shewanella putrefaciens* (GenBank NO.: KY817253). According to the results of the morphology of the strain and the sequence of 16S rRNA, the strain was proved to be *Shewanella putrefaciens*, which was gram-negative rod bacterium. The result revealed that *S. putrefaciens* as a potential new pathogen may pose a threat to the culture of *H. molitrix*.

Key words: *Hypophthalmichthys molitrix*; *Shewanella putrefaciens*; 16S rRNA

天然产物芍药苷抗对虾白斑病毒活性研究

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摘要：为了解决白斑病毒（WSSV）大规模爆发给对虾水产养殖业造成的损失难题，本实验利用对虾为模型，通过存活率和实时定量荧光（RT-qPCR）检测了 8 中天然小分子化合物抗 WSSV 的活性，结果表明芍药苷具有良好的抗 WSSV 活性,并且其可以通过提高对虾先天免疫反应抗菌肽等的表达来抑制 WSSV。

关键词：对虾；白斑病毒；芍药苷；天然产物

Study on the activity of natural product paeoniflorin against shrimp white spot virus

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Abstract: In order to solve the problem of the large-scale outbreak of white spot virus (WSSV) causing losses in shrimp aquaculture, this experiment used shrimp as a model to detect the anti-WSSV activity of eight natural small molecules by survival rate and RT-qPCR, and the results showed that paeoniflorin had significant anti-WSSV activity, and it could inhibit WSSV by increasing the expression of antimicrobial peptides in the innate immune response of shrimp.

Key words: shrimp, WSSV, paeoniflorin, natural products

嘧菌酯潜在的水环境风险：通过 Nrf2 信号通路增加鱼类病毒易感性

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摘要：水生生态系统中存在的长期污染会对水生环境以及水生生物产生多种不利影响，其中包括提高水生生物对病原体的敏感性。嘧菌酯（AZ）是一种在亚洲广泛用于防治大豆锈病的甲氧基丙烯酸酯类农药。然而，在长期使用的过程中它有可能进入并污染水生生态系统导致鱼类对病毒抵抗力降低。为了研究 AZ 潜在的水环境风险，作者检测了长期暴露于 AZ 的宿主在鲤春病毒血症病毒（spring viraemia of carp virus，SVCV）感染下抗病能力的变化。实验结果表明，尽管环境浓度 50 μg/L 暴露下的 AZ 对细胞和斑马鱼没有明显毒性，但 SVCV 增殖却随着药物暴露时间的增长显著增加，最高病毒载量甚至超过对照组 100 倍。相关机制结果表明，AZ 在 5 和 50 μg/L 浓度下抑制抗病毒 Nrf2 信号通路的激活，其相关变化包括 Nrf2 表达、蛋白磷酸化水平和下游 HO-1 含量的降低。另外，Nrf2 信号通路上游调控信号结果显示出 MAPK 信号通路中 P38 磷酸化显著减少，与 Nrf2 变化正相关，说明 AZ 主要通过 P38 调控 Nrf2 磷酸化入核，从而最终导致干扰素表达量下降，促进病毒在细胞和鱼体内增殖。综上所述，作者提出 AZ 对非靶标水生生物致毒机制的新见解，提醒研究学者应关注甲氧基类农药在水环境中蓄积可能会诱发鱼类病毒病暴发，危及生态环境的安全。

关键词：嘧菌酯；Nrf2；鲤春病毒血症病毒；易感性

Potential aquatic environmental risks: Exposure to azoxystrobin increases virus susceptibility in fish cells and zebrafish

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Abstract: High residue of azoxystrobin (AZ) has been found in some water environments, suggesting that AZ has entered aquatic ecosystems and produced serious damages to fish associated with potentially increasing the susceptibility to pathogens. This study aims to characterize the defense abilities of epithelioma papulosum cyprini (EPC) cells and zebrafish, which were exposed to AZ at concentrations of 5 and 50 μg/L in environmentally-relevant exposure concentration range (34~215 μg/L) in China, and subsequently, challenged these with spring viraemia of carp virus (SVCV). Negative effects of AZ on cytotoxicity were not observed less than 500 μg/L during 4 d exposure period before viral infection. For the viral challenges, SVCV replication increased significantly in EPC cells and zebrafish that were exposed to up to 50 μg/L of AZ at 3, 5 and 7 d, thus exhibiting an obvious increase of greater replication rate in zebrafish than that of the control at 14 d. Further data from intracellular biochemical assays indicated that AZ at 5 and 50 μg/L inhibited the activation of the nuclear factor erythroid 2-related factor 2 (Nrf2) pathway, and the associated changes included a decrease in Nrf2 expression, Nrf2 phosphorylation, heme oxygenase-1 (HO-1) content, and antioxidant activities (including total antioxidant, reduced glutathione, and catalase). While no significant differences in extracellular signal-regulated kinase 1/2 (ERK1/2) and c-Jun NH 2-terminal kinase (JNK) mitogen-activated protein kinases (MAPKs) in zebrafish were observed, P38 phosphorylation was significantly decreased at 7 and 14 d, and the changes in MAPKs were more evident in EPC cells previously exposed to AZ at 7 d. These results revealed that AZ initially induced low phosphorylation of MAPKs, triggering the attenuation of Nrf2 phosphorylation to weaken Nrf2 translocation into the nucleus in a longer exposure period (more than 5 d). The data in the cells and fish also showed that antioxidant activities were decreased to some extent at 5~7 d for the cells and 7~14 d for the fish. Furthermore, interferon-related factors were decreased in AZ-exposed zebrafish, explaining why fish can't resist the virus infection. These results indicate a new adverse threat of AZ pollution that may amplify viral outbreaks and endanger ecological safety.

Key words: Azoxystrobin; Spring viraemia of carp virus; Nuclear factor erythroid 2-related factor 2; Virus susceptibility

新型香豆素类衍生物抗对虾白斑综合症防治研究

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摘要：白斑综合症病毒（White spot syndrome virus，WSSV）是迄今对虾养殖业危害最大的一种病毒，其宿主极为广泛，包括世界上所有人工养殖对虾种类、野生虾类和大部分蟹类。该病毒病被世界动物卫生组织（Office international des épizooties，OIE）列为必须上报的动物疾病，而我国农业部所发布的《一、二、三类动物疫病病种名录》也将其列为 A 类动物疫病。目前为止，尚无任何有效措施对该病进行防治，只能实行较为严格的卫生管理和控制。因此，作者设计合成并鉴定了一系列香豆素衍生物，利用南美白对虾仔虾模型评价其抗 WSSV 活性。结果表明，香豆素衍生物 C2 和 C7 的最大抗病毒效率均超过了 95%，其半数有效浓度（EC_{50}）分别为 5.993 和 5.727 mg/L。通过化合物的前处理和后处理，香豆素衍生物 C2 和 C7 均能显著降低仔虾体内 WSSV 的含量，可见其具有一定的预防和治疗作用。感染 WSSV 的仔虾浸泡 C2 和 C7 后，在 3 d 内的存活率均超过 50%，并且每天连续更换 C2 和 C7 后，在 5 d 内的存活率仍超过 50%。此外，C2 和 C7 还能在一定程度上抑制 WSSV 的水平传播。综上所述，作者认为香豆素类衍生物 C2 和 C7 具有开发成抗 WSSV 的特异性药物的潜力，而且为其他水产病毒病害新药的研发提供参考和借鉴。

关键词：香豆素类衍生物；白斑综合症病毒；药物抗病毒；新药研发

Study on prevention and treatment of novel coumarin derivatives against white spot syndrome virus

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Abstract: White spot syndrome virus (WSSV) is the most damaging virus in shrimp farming and its hosts are extremely widespread, including all cultivated shrimp species, wild shrimp and most crab species in the world. The virus is listed as a notifiable animal disease by the World Organisation for Animal Health (Office international des épizooties, OIE), and it is also listed as a category A animal disease in the List of Animal Disease Categories I, II and III issued by the Ministry of Agriculture in China. To date, there are no effective measures to combat the disease and only relatively strict hygiene management and control can be implemented. Therefore, authors designed, synthesized and characterized a series of coumarin derivatives and evaluated their anti-WSSV activity using a model of Pacific white shrimp (*Litopenaeus vannamei*) larvae. The results showed that the maximum antiviral efficiency of coumarin derivatives C2 and C7 exceeded 95%, with EC_{50} of 5.993 and 5.727 mg/L, respectively. Both coumarin derivatives C2 and C7 significantly reduced the WSSV levels in the larvae by pre-treatment and post-treatment of compounds, which shows that they have preventive and therapeutic effects. The survival rate of WSSV-infected larvae was more than 50% within 3 days after immersion in C2 and C7, and still more than 50% within 5 days after continuous replacement of C2 and C7. In addition, C2 and C7 inhibited the horizontal spread of WSSV to some extent. In summary, authors concluded that coumarin derivatives C2 and C7 have the potential to be developed into specific drugs against WSSV, and that they provide references and lessons for the development of new drugs for other aquatic viral diseases.

Key words: Coumarin derivatives; White spot syndrome virus; Antiviral drugs; New drug development

香鱼 C 型凝集素的分子鉴定、表达及功能初探

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摘要：为了获知鱼类 C 型凝集素(CTL)的生物学功能及免疫调控机制，以便为香鱼病害的免疫防控提供新思路，本研究从香鱼转录组中获得了 CTL(PaCTL)基因 cDNA 序列。首先通过序列分析及系统进化树构建确定其序列特征及系统发育关系，然后采用实时荧光定量 PCR 测定其组织表达分布及其在鳗弧菌感染下的表达变化，进一步通过原核表达、尿素梯度复性得到 PaCTL 重组蛋白(rPaCTL)。在此基础上，测定了 rPaCTL 的细菌凝集活性及糖结合特性，并在整体上探究了 rPaCTL 对感染鳗弧菌香鱼存活率及组织载菌量的影响，最后在细胞水平上探究了 rPaCTL 的调理作用及其对香鱼单核/巨噬细胞的杀菌能力、呼吸爆发功能及炎性因子表达的影响。研究结果将初步解析 CTL 在鱼类抵抗病原菌感染中的免疫调控机制。

关键词：香鱼； C 型凝集素；单核/巨噬细胞；凝集活性；免疫调节

Molecular identification, expression and function analysis of C-type lectin in ayu, *Plecoglossus altivelis*

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Abstract: In order to understand the biological function and immune regulation mechanism of fish C-type lectin (CTL), and provide new entry piont for the diseases immune prevention and control in ayu (*Plecoglossus altivelis*), the cDNA sequence of ayu CTL (PaCTL) gene was obtained from ayu transcriptome. Firstly, the sequence characteristics and phylogenetic relationship of PaCTL were determined by sequence analysis and phylogenetic tree construction. Then, the tissue expression distribution of the PaCTL and its expression changes under the infection after *Vibrio anguillarum* infection were determined by real-time quantitative PCR. Further, the recombinant PaCTL protein (rPaCTL) was obtained by prokaryotic expression and urea gradient renaturation. On this basis, the bacterial agglutination activity and sugar-binding properties of rPaCTL were measured, and the effects of rPaCTL on survival rate and tissue load of *V. anguillarum*-infected ayu were investigated. Finally, the effects of rPaCTL on the bactericidal ability, respiratory burst function and the expression of inflammatory cytokines of monocytes/macrophages were investigated at the cellular level. The results will preliminarily explain the immune regulation mechanism of CTL resistance to pathogen infection in fish .

Key words: *Plecoglossus altivelis*, C-type lectin, Monocyte/macrophage, Agglutinating activity; immunomodulation

水产/水源性致病微生物等温扩增微流控芯片检测平台的开发

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摘要：将环介导等温扩增技术与微流控芯片技术联合应用，开发了水产/水源性致病微生物快检平台，针对弧菌、WSSV、沙门氏菌等 28 种水产致病微生物或水源性致病菌开展快速筛查和鉴定，并个性化组装试剂盒 4 个。该平台检测通量高、操作便捷（一次性加样）、检测快速（<60 min），在水产品及其养殖环境的生物危害因子的筛查和监测中取得了良好应用。

关键词：致病微生物；环介导等温扩增；微流体芯片；实时检测

A real-time LAMP-based microfluidic chip platform for detecting of aquatic/waterborne pathogenic microorganisms

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Abstract: A platform for rapid detection of aquatic/waterborne pathogenic microorganisms was developed by combining a loop mediated isothermal amplification (LAMP) assay on a microfluidic chip. It can screen and identify 28 aquatic pathogenic microorganisms/waterborne pathogens such as *Vibrio* spp., white spot syndrome virus, *Salmonella enterica* and et al. Four detection kits were custom assembled. This platform with high throughput, convenient operation (one-step loading) and rapid detection (<60 min) is applicable in the screening and monitoring of biological hazard factors in aquatic products and aquaculture environment.

Key words: pathogenic microorganisms, loop-mediated isothermal amplification, microfluidic chip, real-time detection

鲤疱疹病毒II型编码的 microRNA (CyHV-2-KT-635)通过靶向 ORF23 调控病毒复制

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摘要：据有关报道，疱疹病毒家族能够编码和表达靶向病毒和细胞转录产物的 microRNA。在我们前期的研究发现，一种新的 microRNA CyHV-2-KT-635 被证明可以靶向功能未知的病毒基因。本研究证明了 CyHV-2-KT-635 可靶向调控病毒基因 ORF23，验证 OR23F 基因序列上的相关靶点，并鉴了 CyHV-2-KT-635 对 ORF23 表达的影响。我们发现在异育银鲫尾鳍细胞系 GiCF 中沉默病毒 ORF23 和转染 CyHV-2-KT-635 模拟物均能显著抑制病毒的增殖，降低病毒滴度，表明 CyHV-2-KT-635 可下调 ORF23 基因。并且通过生物信息学分析，ORF23 蛋白序列中的 tRNA 结构域与宿主编码的核糖核苷酸还原酶小亚基（将 NTP 转化为 dNTP）R2i 和 P53R2i 具有较高的同源性。以上发现有助于理解病毒编码的 microRNA 对鲤疱疹病毒II型复制的影响。

关键词：鲤疱疹病毒II型；CyHV-2-KT-635；核糖核苷酸还原酶；病毒复制

Cyprinid herpesvirus 2 encoded microRNA (CyHV-2-KT-635) regulates viral replication by targeting the ORF23

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Abstract: Herpesvirus family have been reported to be able to encode and express functional viral microRNAs that target both viral and cellular transcripts. With previous studies, a novel miRNA CyHV-2-KT-635 has been proved to target the viral genes with unknown functions. In this study, the target gene of CyHV-2-KT-635 regulated was proved to the viral gene ORF23 directly, the target point on gene sequence was verified and CyHV-2-KT-635 was identified to influence the expression of ORF23. According to the bioinformatics analysis, the tRNA domain and ribosome domain in the protein sequence of ORF23 were found to share lots of homology with R2i and P53R2i, which are related to the ribonucleotide reductase small subunit in the host (transform NTP to dNTP). Within expectations, silencing of viral ORF23 or transfecting CyHV-2-KT-635 mimics in GiCF could suppress viral propagation significantly. These findings are helpful to understand the effect of virus encoded microRNA on the replication of Cyprinid herpesvirus 2.

Key Words: Cyprinid herpesvirus 2, CyHV-2-KT-635, ribonucleotide reductase, Viral replication

一种鲤疱疹病毒II型弱毒株及其在预防鲫造血器官坏死病中的应用

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摘要：疫苗为病毒病防治最有效的手段。本研究通过浸润免疫和注射免疫的方式，对一株鲤疱疹病毒II型弱毒株作为疫苗防治鲫造血器官坏死病的安全性、保护性进行评价。结果表明该弱毒株对被免疫异育银鲫无致病性，其安全性为100%；在对应的免疫浓度下，对病毒感染的保护率为90%以上。此外，体外、体内传代表明该弱毒株未出现毒力返强且具有稳定的保护性。

关键词：鲤疱疹病毒II型；弱毒疫苗；保护率；　安全性

Attenuated strain of Cyprinid herpesvirus 2（C_1P_2) as vaccine candidate against herpesviral hematopoietic necrosis disease in silver crucian carp, *Carassius auratus gibelio*

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Abstract: Vaccine is widely accepted as an effective control against viral diseases. In this study, the safety and protection rate of an attenuated cyprinid herpesvirus 2 (CyHV-2) were evaluated as the vaccine against to herpesviral hematopoietic necrosis disease of Gibel carp (*Carassius auratus gibelio*). The results indicated that the attenuated CyHV-2 was non-pathogenic and the protection rate of the attenuated strain against CyHV-2 infection of Gibel carp was more than 90%. In addition, there is no virulence reversion of the attenuated CyHV-2 propagated *in vivo* and passaged on RyuF-2 cell.

Key words: Cyprinid herpesvirus 2, Attenuated vaccine, Protection rate, Safety

抗甲状腺药物甲巯咪唑和丙基硫氧嘧啶抑制厚壳贻贝幼虫变态的作用研究

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摘要：附着变态是双壳贝类幼虫从浮游转变为底栖生活的重要过程。 本研究在厚壳贻贝转录组数据中筛选得到两个甲腺原氨酸脱碘酶基因的部分序列，通过 RACE 技术克隆得到 cDNA 全长序列。 多重序列比对发现甲腺原氨酸脱碘酶的核心催化中心位于一段 15 个氨基酸的保守区域，其中包含一个必须的 Sec（U）残基。系统发育分析显示，软体动物厚壳贻贝(McDy)和太平洋牡蛎（CgDx 和 CgDy） 聚为一支，并与脊椎动物(D2 和 D3)的脱碘酶共享一个代表共同祖先的节点。本研究选取了抗甲状腺药物甲巯咪唑(Methimazole,MMI)和甲腺原氨酸脱碘酶抑制剂丙基硫氧嘧啶(Propylthiouracil, PTU)，研究其对厚壳贻贝幼虫变态的作用。两种拮抗剂均显著抑制了眼点幼虫的变态过程($P<0.05$)， 且两种拮抗剂暴露过程中眼点幼虫的存活无显著差异($P>0.05$)。为研究 MMI 和 PTU 对厚壳贻贝稚贝生长的影响，本研究对稚贝进行了 28 天的暴露实验。MMI 在 10-3M 和 10-4M 浓度显著抑制了稚贝壳长生长($P<0.05$)，而 PTU 对稚贝壳长生长无影响。 研究结果表明 MMI 和 PTU 干扰了肾上腺素诱导厚壳贻贝眼点幼虫的变态过程，MMI 和 PTU 对贻贝幼虫变态和发育的影响很可能是通过一种内分泌信号， 这对探索变态的起源和进化提供了理论依据。

关键词： 厚壳贻贝；甲腺原氨酸脱碘酶；幼虫变态；甲巯咪唑； 丙基硫氧嘧啶

Larval metamorphosis is inhibited by methimazole and propylthiouracil that reveals possible hormonal action in the mussel *Mytilus coruscus*

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Abstract： Larval metamorphosis in bivalves is a key event for the larva-to-juvenile transformation. In the present study, we molecularly characterized the full-length of two iodothyronine deiodinase genes (McDx and McDy) based on *Mytilus coruscus* transcriptome. Both McDx and McDy contain a Sec residue in their active catalytic center. Phylogenetic analysis revealed that deiodinases of molluscs (McDy, CgDx and CgDy) and vertebrates (D2 and D3) shared a node representing an immediate common ancestor, which resembled vertebrates D1 and might suggest that McDy acquired specialized function from vertebrates D1. Anti-thyroid compounds, methimazole (MMI) and propylthiouracil (PTU), were used to investigate their effects on larval metamorphosis and juvenile development in *M. coruscus*. Both MMI and PTU significantly inhibited the larval metamorphosis ($P < 0.05$), and there was no significant effect on the larval survival ($P >0.05$). The juveniles of *M. coruscus* were exposed four weeks to MMI and PTU for investigating the effect on growth. Shell length of *M. coruscus* juveniles was significantly decreased in 10-3 and 10-4 M MMI treatment groups compared to the control group ($P < 0.05$), whereas PTU had no effect on juvenile growth. Our findings suggest that both MMI and PTU reduced larval metamorphosis in response to the metamorphosis inducer epinephrine. The effect of MMI and PTU on larval metamorphosis and development is most likely through a hormonal signal in the mussel *M. coruscus*, with the implications for exploring the origins and evolution of metamorphosis.

Keywords: *Mytilus coruscus*; iodothyronine deiodinase; larval metamorphosis; methimazole; propylthiouracil

罗氏沼虾野田村病毒感染过程中罗氏沼虾 microRNA 表达谱的初步研究

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摘要：为分析罗氏沼虾野田村病毒（*Macrobrachium rosenbergii* nodavirus,MrNV）感染罗氏沼虾幼体过程中 microRNA (miRNA)的表达谱,寻找罗氏沼虾抗病毒的潜在生物标志物，本实验利用高通量测序技术分析了罗氏沼虾幼体在病毒感染过程中 miRNA 的表达情况，并对显著差异表达的 miRNA 进行了靶基因预测以及注释分析。结果表明，罗氏沼虾幼体感染病毒组文库中存在 62 个 miRNA，未感染对照组文库中存在 67 个 miRNA。文库间显著差异表达的 miRNA 共有 20 个，对应的靶基因共有 880 个，靶基因主要富集于硫代谢、泛素化介导的蛋白水解、核糖体、ECM 受体互作和刺激神经组织的配体受体互作等途径。本研究不仅为 miRNA 的调控机理研究提供了丰富的数据资源，也为挖掘病毒感染相关差异表达的 miRNA 及其功能研究奠定基础，为进一步开发免疫调节药物及病害的防治提供新途径。

关键词：罗氏沼虾；野田村病毒；miRNA 筛选；功能研究

Study on the microRNA expression profile of *Macrobrachium rosenbergii* infected with *Macrobrachium rosenbergii* virus

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Abstract: In order to analyze the microRNA (miRNA) expression profile of *Macrobrachium rosenbergii* infected with *Macrobrachium rosenbergii* nodavirus (MrNV) and find the potential antiviral biomarkers of *Macrobrachium rosenbergii*, the high-throughput sequencing technology was used to analyze miRNA expression in *Macrobrachium rosenbergii* larvae during virusl infection, and the prediction of target gene and annotated analysis of miRNA with significant differential expression were performed in this study. The results showed that there were 62 miRNAs in the library of the infected group and 67 miRNAs in the uninfected control group. The expression level of 20 miRNAs were significantly different, corresponding to a total of 880 target genes. These miRNAs were mainly enriched in sulfur metabolism, ubiquitin mediated proteolysis, ribosome, ECM-receptor interaction, Neuroactive ligand-receptor interaction and so on. This study not only provides a wealth of data resources for miRNA regulation mechanism, but also lays a foundation for the study of differentially expressed miRNAs related to viral infections and provides a new way for the further development of immunomodulatory drugs and disease prevention and treatment.

Key words: *Macrobrachium rosenbergii* virus; miRNA; expression profile

铜绿微囊藻和微囊藻毒素-LR 对凡纳滨对虾肠道组织、免疫指标及微生物菌群的影响

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摘要：研究了铜绿微囊藻（MA）和微囊藻毒素-LR（MC-LR）对凡纳滨对虾肠道组织形态、免疫应答及微生物菌群的影响。结果显示，MA 和 MC-LR 胁迫：1）导致对虾肠道黏膜脱落以及明显的细胞凋亡特征；2）诱导肠道氧化应激反应，其中超氧阴离子生成能力、脂质过氧化物和丙二醛含量均有所增加，而抗氧化酶 T-AOC、SOD 和 GST 活性紊乱。3）降低抗菌肽（ALF、Crus 和 Pen-3）基因相对表达量，增加炎症相关基因（MyD88、Rel、TNF-a）、模式识别受体（TLR4）和细胞凋亡因子（Casp-3）相对表达量。4）降低肠道菌群多样性，优势菌群丰度发生明显波动。结果表明，MA 和 MC-LR 胁迫可通过诱导凡纳滨对虾肠道组织结构改变、氧化应激、免疫应答以及微生物菌群变化等途径影响其肠道生理功能。

关键词：对虾；铜绿微囊藻；微囊藻毒素；肠道免疫；肠道菌群

Effects of *Microcystis aeruginosa* and microcystin-LR on intestinal histology, immune response, and microbial community in *Litopenaeus vannamei*

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Abstract: Shrimp were experimentally exposed to *Microcystis aeruginosa* (MA) and microcystin-LR (MC-LR) for 72 h. The results showed that both MA and MC-LR exposure caused marked histological variation and apoptosis characteristics and increased oxidative stress in the intestine. The relative expression levels of antimicrobial peptide genes (ALF, Crus, Pen-3) decreased, while those of pro-inflammatory cytokines (MyD88, Rel, TNF-a), a pattern-recognition receptor (TLR4) and a mediator of apoptosis (Casp-3) increased. MA and MC-LR exposure also caused intestinal microbiota variation, including decreasing microbial diversity and disturbing microbial composition. Our results indicate that MA and MC-LR exposure causes intestinal histopathological and microbiota variations and induces oxidative stress and immune responses in *L. vannamei*.

Key words: Cyanobacteria, Intestinal immunity, Microbiota, Microcystins, Shrimp

亚硝酸盐对虾肝肠胞虫感染脊尾白虾的影响

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摘要：为探究亚硝酸盐胁迫对脊尾白虾生长状况及体内肝肠胞虫携带量的影响，设置 5 个不同亚硝酸盐氮浓度（0.008、3.0、6.0、9.0 mg/L 和 12.0 mg/L）试验组，跟踪测定三周内脊尾白虾的生长指标和肝肠胞虫载量的变化。结果显示，6 mg/L 的亚硝酸盐氮可抑制肝肠胞虫的传播，进而对脊尾白虾生长有一定的促进作用。本研究有助于在养殖生产过程中通过合理控制亚硝酸盐浓度以抑制肝肠胞虫的传播，从而提高感染虾肝肠胞虫的脊尾白虾的存活率和养殖产量。

关键词：脊尾白虾；虾肝肠胞虫；亚硝酸盐；生长状况；载量

Effect of nitrite on the infection of *Enterocytozoon hepatopenaei* in *Exopalaemon carinicauda*

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Abstract: In order to investigate the effects of nitrite stress on the growth status and the carrying capacity of *Enterocytozoon hepatopenaei* in *Exopalaemon carinicauda*, five experimental groups with different nitrite concentrations (0.008, 3.0, 6.0, 9.0 and 12.0 mg/L) were set up to determine the changes of growth indexes and EHP load of E. carinicauda within three weeks. The results showed that 6 mg/L nitrite could inhibit the transmission of EHP and promote the growth of white shrimp. This study was helpful to control the concentration of nitrite reasonably in order to inhibit the spread of EHP, so as to improve the survival rate and breeding yield of E. carinicauda; infected with *Enterocytozoon hepatopenaei*.

Key words: *Exopalaemon carinicauda; Enterocytozoon hepatopenaei;* nitrite; growth status; capacity

藕虾模式水质与产品重金属含量关联分析

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摘要：为了解决目前养殖水体富营养化等问题，提出藕虾养殖模式，研究不同密度(藕、虾)水质与重金属关联，结果发现当小龙虾养殖密度为 50 斤/亩时，藕产量能达到 1927.2 斤/亩，且水质基本符合地表水环境质量标准规定的III类水标准，水质与重金属间存在一定关系，但需要跟踪监测多年。

关键词：荷藕；克氏原螯虾；水质；重金属；藕虾模式；关联分析

Correlation analysis between water quality and heavy metal content of lotus shrimp model products

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Abstract: In order to solve the problem such as aquaculture water body eutrophication, it puts forward the model of lotus root shrimp farming, the study of different density (lotus root, shrimp) water quality associated with heavy metals, the results showed that when the lobster breeding density of 50 kg/mu, lotus root yield can reach 1927.2 kg/mu, quality meet the requirements of surface water environment quality standards and III class water standard, There is a certain relationship between water quality and heavy metals, but it needs to be monitored for many years.

Key words: Lotus root; *Procambarus clarkii*; Water quality; Heavy metals; Lotus root shrimp pattern; Correlation analysis

乌鳢体重、全长增长率及抗诺卡氏菌病的全基因组关联分析

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摘要：本研究利用简化基因组测序技术(Super-GBS)发掘 SNP 标记，采用混合线性模型(EMMAX)对不同家系标记混养的 405 个乌鳢个体 12 月龄-15 月龄期间的体重、全长增长率和抗诺卡氏菌病性状进行全基因组关联分析(Genome-wide association study, GWAS)，以筛选目标性状显著关联数量性状核苷酸（Quantitative trait nucleotides, QTNs）遗传位点，并发掘候选基因。结果共获得多态性位点 54433 个，包括 SNP 位点 47536 个，INDEL 位点 6897 个；关联分析共得到目标性状显著关联 QTNs 位点 32 个。以这些 QTNs 位点为探针，在乌鳢全基因组上找到了距离其最近的 8 个候选基因，它们可能是影响乌鳢生长速度和抗诺卡氏菌病的重要候选基因，这为乌鳢速生、抗病性状的分子标记辅助育种提供了理论素材和参考。

关键词：乌鳢；体重增长率；全长增长率；抗诺卡氏菌病；全基因组关联分析；简化基因组测序

Genome-wide association study of body weight growth rate, total length growth rate and nocardiosis resistance traits in *Channa Argus*

Abstract: The Northern snakehead (*Channa argus*) is a special snakehead fish cultivated mainly in Asia for food. In this study, we conducted a genome-wide association study (GWAS) using 405 individuals and simplified genome sequencing (super-GBS) technology to identify quantitative trait nucleotides (QTNs) and candidate genes potentially associated with the growth rate of body weight (BW) and total length (TL) and nocardiosis resistance traits during the culture period of 12-15 months of age. Results a total of 54433 polymorphic loci were obtained, including 47536 SNP loci and 6897 INDEL loci, and 32 significant QTNs loci associated with the target traits were detected. Furthermore, 8 candidate genes were found by searching the nearest gene to each detected QTN in the whole genome of *C. argus*. All of them might be important candidate markers and functional genes, which could influence the growth rate and nocardiosis resistance traits in *C. argus.* Our study also provided a potential useful tool and a reference for marker-assisted selection of growth rate and nocardiosis resistance traits in *C. argus.*

Key words: *Channa argus,* body weight growth rate, total length growth rate, GWAS, super-GBS

长江江豚健康评价体系的研究

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摘要：长江江豚（*Neophocaena phocaenoides asiaeorientalis*）是目前生活在我国长江中仅有的珍稀濒危鲸类动物，了解其野生种群的生理和健康状况对于该物种的保护具有重要指导意义。本研究利用 2002-2015 年湖北长江天鹅洲白鱀豚国家级自然保护区与江西鄱阳湖长江江豚省级保护区共计 136 头次的长江江豚体检数据，统计分析了包括血液学和血液生化 54 个临床指标的生理参数区间，并结合行为学指标，构建基于行为与生理健康两个维度的长江江豚健康评价体系。结果表明长江江豚的白细胞计数（WBC）、血小板计数（PLT）以及谷草转氨酶（AST）等多个临床指标的生理参数区间同陆生哺乳动物及其他近缘种存在较大差别，显示长江江豚物种的特异性。本次研究结果为长江江豚的健康状况评估和养护提供了科学依据。

关键词：长江江豚；血液学；血液生化；健康评价体系

Study on the health evaluation system of Yangtze finless porpoise (*Neophocaena asiaeorientalis asiaeorientalis*)

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Abstract: The Yangtze finless porpoise (*Neophocaena asiaeorientalis asiaeorientalis*) is the only cetaceans that lives in the Yangtze River. Understanding the physiology and health of Yangtze finless porpoise may provide important information for the protection of this species. In this study, we statistically analyzed 54 hematology parameters and blood chemistry parameters from total of 136 Yangtze finless porpoises in the Tian-e-zhou Baiji National. Nature Reserve in Hubei Province and the Poyang Lake Provincial Reserve in Jiangxi Province. The health evaluation system of Yangtze finless porpoise was constructed based on the behavioral and physiological health. The results showed that the blood parameters of WBC, Blood platelet (PLT), and aspartate aminotransferase (AST) of Yangtze finless porpoise were significantly different from those of terrestrial mammals and other related species. These results provide scientific basis for assessment and conservation of Yangtze finless porpoise.

Keywords: Yangtze finless porpoise; hematologic test; blood biochemical indices; health evaluation system

CAFS clean-up 净化柱结合超高效液相色谱—三重四极杆串联质谱法测定水产品中磺胺类药物残留

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摘要：为实现水产品中磺胺类药物残留更加快速高效的检测，本实验在样品经提取后，采用 CAFS clean-up 净化柱净化，结合超高效液相色谱—三重四级杆串联质谱法，运用基质加标法定量分析，实现了水产品中 21 种磺胺类药物残留的快速检测。实验表明，目标化合物在 1～100 μg/kg 浓度范围内线性良好，标准曲线的相关系数均在 0.99 以上，回收率在 64.57%-137.19%之间，方法定量限（LOQ）为 0.5-5.0 μg/kg。

关键词：磺胺类、水产品、CAFS clean-up 净化柱、高效液相色谱-三重四极杆串联质谱

CAFS clean-up purification column combined with ultra performance liquid chromatography-triple quadrupole tandem mass spectrometry for the determination of sulfonamide residues in aquatic products

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Abstract: In order to achieve a more rapid and efficient detection of sulfa drug residues in aquatic products, this experiment uses CAFS clean-up purification column to purify the sample after extraction, combined with ultra-high performance liquid chromatography-triple quadrupole tandem mass spectrometry, and uses matrix Adding standard method for quantitative analysis, achieved rapid detection of 21 sulfa drug residues in aquatic products. The experimental show that the target compound has a good linearity in the concentration range of 1-100 μg/kg, and the correlation coefficients of the standard curves are all above 0.99; the recovery rate is between 64.57% and 137.19%; the limit of quantification (LOQ) of the method is 0.5-5.0 μg/kg.

Key words: Sulfonamides, aquatic products, CAFS clean-up purification column, UPLC-MS/MS

半滑舌鳎苗种肠积水病的病原分离、鉴定及快速检测方法的建立

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摘要：利用 BHI 和 TSA 培养基，从患病半滑舌鳎苗种分离病原菌，通过 16S rDNA 序列扩增和比对，发现主要细菌性病原为大菱鲆弧菌，其次是哈维弧菌和溶藻弧菌。根据回感试验推测引起半滑舌鳎肠积液病的主要致病菌为大菱鲆弧菌。根据大菱鲆弧菌 luxr 基因序列，设计筛选出特异引物，并建立 PCR 检测方法，其灵敏度为 10^4 CFU/mL。

关键词：半滑舌鳎；肠积水；大菱鲆弧菌；PCR

Isolation, identification and rapid detection of terohydrosis in *Cynoglossus semilaevis*

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Abstract: Using BHI and TSA medium, the pathogens were isolated from the seedlings of sick tongue sole. Through 16S rDNA sequence amplification and comparison, it was found that the main bacterial pathogens were *Vibrio scophalmi*, followed by *Vibrio harveyi* and *Vibrio alginolyticus*. According to the allelopathy test, it is speculated that the main pathogen causing intestinal effusion of *Cynoglossus semilaevis* is *Vibrio scophalmi*. According to the LuxR gene sequence of *Vibrio scophalmi*, specific primers were designed and screened, and a PCR detection method was established with a sensitivity of 10^4 CFU / ml.

Key words: *Cynoglossus semilaevis*, hydrosalgia, *Vibrio scophalmi*, PCR

扑草净在罗非鱼(*Oreochromis niloticus*)体内的急性毒性、生物富集与消解

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摘要：将平均体重为 50.00 ± 10.00 g 的罗非鱼幼鱼（*Oreochromis niloticus*）暴露于不同浓度的除草剂扑草净水溶液种，以研究其急性毒性、生物富集和消除过程。首先，进行了 96 h 的的急性毒性实验。计算得出 96 h LC_{50} 是 5.49 mg/L，96 h LC_{10} 是 5.02 mg/L。然后将鱼暴露在 0.55 mg/L（1/10 96 h LC_{50}）和 0.055 mg/L （1/100 96 h LC_{50}）的扑草净溶液中 28 天，接着将鱼转入干净的地下水中进行 14 天的消除实验。结果表明，在暴露期间，水和组织中的扑草净保持波动水平。因此，浓度很难达到稳定状态。不同组织的生物富集能力为肝脏＞鳃＞肌肉＞血液。在高浓度暴露下，各组织的累积浓度水平始终高于低浓度暴露。1/100 96 h LC_{50} 暴露下各种组织的最高累积浓度为：肌肉：0.136 ± 0.0616 mg/kg（1d）；肝脏：3.74 ± 2.95 mg/kg（7d）； 鳃：0.971 ± 1.45 mg/kg（1d）和血液： 0.0716 ± 0.0669 mg/kg（22d）。在 1/10 96 h LC_{50} 暴露下，最高水平为：肌肉：1.27 ± 0.284 mg/kg （1d）；肝脏：16.9 ± 12.7 mg/kg（7d）；鳃：8.11 ± 3.02 mg/kg（1d）和血液：0.751 ± 0.0775 mg/kg （22d）。当暴露于低浓度时，在肝脏中观察到最高的生物浓缩因子 (BCF)，达到 93.1。这也表明肝脏可能是解毒的关键器官之一。此外，对于其他组织，最高的 BCF 为：肌肉：6.03（1/10 96 h LC_{50}）； 鳃 32.3（1/10 96 h LC_{50}）和血液： 2.91（1/10 96 h LC_{50}）。此外，观察到扑草净从生物体中消除迅速。转移至干净的水后，所有组织中积累的大部分扑草净在 24 h 内都被消除。但是，应加强对扑草净应用的监督，以防止可能的生态毒理风险，并确保食品安全。

关键词: 扑草净, 急性毒性, 生物富集, 消除, 生物浓缩, 罗非鱼

Acute toxicity, bioaccumulation and Elimination of Prometryn in Tilapia (*Oreochromis niloticus*)

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Abstract:Tilapia juvenile (*Oreochromis niloticus*) (mean weight 50.00 ± 10.00 g) were aqueous exposed to different concentrations of herbicide prometryn to investigate the acute toxicity, bioaccumulation and elimination process. First, a 96 h acute toxicity test was carried out. The 96 h LC_{50} was calculated as 5.49 mg/L, and the 96 h LC_{10} was 5.02 mg/L. Then, fish were exposed to 0.55 mg/L (1/10 96 h LC50) and 0.055 mg/L (1/100 96 h LC_{50}) of prometryn solution for 28 days, followed by 14 days of elimination in clean groundwater. The result shows that in both water and tissues, the prometryn level kept fluctuating during the exposure period. Thus, it is hard for the concentration to reach a steady state. The bioaccumulation ability of different tissues is liver > gill > muscle > blood. Under the high concentration exposure, the accumulated concentration levels in various tissues were always higher than those exposed to low concentration. The highest accumulated concentration of various tissue under the 1/100 96 h LC_{50} exposure were: muscle: 0.136 ± 0.0616 mg/kg (1d); liver: 3.74 ± 2.95 mg/kg (7d); gill: 0.971 ± 1.45 mg/kg (1d) and blood: 0.0716 ± 0.0669 mg/kg (22d). Under the 1/10 96 h LC_{50} exposure, the highest levels were: muscle: 1.27 ± 0.284 mg/kg (1d); liver: 16.9 ± 12.7 mg/kg (7d); gill: 8.11 ± 3.02 mg/kg (1d) and blood: 0.751 ± 0.0775 mg/kg (22d). The highest bioconcentration factor (BCF) was observed in the liver when exposed to the low concentration, reaching 93.1. That also indicates the liver could be one of the key organs for detoxification. Besides, for other tissues, the highest BCFs were: muscle: 6.03 (1/10 96 h LC_{50}); gill: 32.3 (1/10 96 h LC_{50}), and blood: 2.91 (1/10 96 h LC_{50}). Furthermore, prometryn was observed eliminated from the organism rapidly. Most of the accumulated prometryn was removed within 24h after being transferred to clean water for all the tissues. However, supervision of prometryn application should be improved to prevent the possible ecotoxicological risk and ensure food safety.

Keywords: Prometryn, Acute toxicity, Bioaccumulation, Elimination, Bioconcentration, Tilapia

IolR 下调 RmpA 蛋白抑制嗜水气单胞菌自凝集和生物被膜的形成

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摘要：病原菌的特定代谢能力被视为一种新型毒力相关因子-营养毒力(ntritional vrulence)。将病原菌的代谢能力放到与经典毒力因子同样重要的位置上去研究，才能真正破解病原菌的致病机制。本实验采用转录组测序结合凝胶阻滞试验探究肌醇代谢调控因子 IolR 调控嗜水气单胞菌自凝集和生物被膜形成的分子机制。研究结果将有助于阐明肌醇代谢与细菌毒力的关系，为解析细菌致病机制提供新的视角。

关键词：嗜水气单胞菌；生物被膜；自凝集；IolR；代谢

IolR inhibits cell autoaggregation and biofilm formation by downregulating RpmA in *Aeromonas hydrophila*

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Abstract: The specific metabolic capacity of pathogens is regarded as a new virulence related factor-trophic virulence. Only by putting the metabolic capacity of pathogens into the same important position as the classical virulence factors can we really crack the pathogenesis of pathogens. In this study, mRNA-seq and EMSA were used to explore the molecular mechanism of inositol metabolic regulatory factor IolR in regulating the autoagglutination and biofilm formation of *Aeromonas hydrophila*. The results of this study will help to clarify the relationship between inositol metabolism and bacterial virulence, and provide a new perspective for analyzing the pathogenesis of bacteria.

Key words: Aeromonas hydrophila; Biofilm; agglutination; IolR; metabolism

斑马鱼 SETD3 通过降解 SVCV-P 蛋白来正调控抗病毒反应

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摘要：SETD3 是蛋白赖氨酸甲基转移酶(PKMT)家族的成员，催化赖氨酸残基上添加甲基基团。然而，SETD3 参与的蛋白质网络和信号通路仍未被广泛研究。我们的数据表明，过表达 SETD3 导致 SVCV 感染后 SVCV- N 和 SVCV- G mRNA 显著抑制。我们的结果表明，正调控独立于其甲基化活性。我们提出了一个在 SETD3 和 SVCV 的 P 蛋白(SVCV-P)之间的蛋白互作。有趣的是, SETD3 通过蛋白酶体途径导致 SVCV-P 蛋白的降解。综上所述, 我们的数据揭示了 PKMT SETD3 在病毒磷蛋白响应 SVCV 感染的调节中的一种新的固有免疫因子。

关键词：SETD3；SVCV-P；SVCV；蛋白互作

Zebrafish SETD3 positively regulates the antiviral responses by degrading SVCV-P protein

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Abstract: SETD3 is a member of the protein lysine methyltransferase (PKMT) family, which catalyzes the addition of methyl group to lysine residues. However, the protein network and the signaling pathways in which SETD3 is involved remain largely unexplored. Our data indicate that overexpression of SETD3 results in a significant inhibition of SVCV-N and SVCV-G mRNA after SVCV infection. Our results imply that the positive regulation independent of its methylation activity. We present a functional cross-talk between SETD3 and a P protein of SVCV (SVCV-P). Interestingly, SETD3 leads to the degradation of SVCV-P through the proteasomal pathway. Together, our data uncover a new intrinsic immune factor of the PKMT SETD3 in the regulation of the viral phosphoprotein in response to SVCV infection.

Keywords: SETD3；SVCV-P；SVCV；Co-Immunoprecipitation

斑马鱼 IRF2a 负调控宿 SVCV 病毒天然免疫反应

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摘要：IRF2 属于 IRF1 家族，N 端 DBD 结构域和 C 端 IAD2 结构域。斑马鱼基因组上 IRF2 有 2 个拷贝，分别是 IRF2a 和 IRF2b。利用 IRF2a 敲除系的斑马鱼尾鳍原代细胞研究该基因在 SVCV 病毒感染过程中的调控作用，发现相较于野生型尾鳍细胞，IRF2a$^{-/-}$细胞系对 SVCV 感染不敏感，表现出抗病毒作用。通过双荧光素报告系统发现，过表达 IRF2a 能够显著抑制 IFNφ1, IFNφ3 和 ISRE 的活性，因此 IRF2a 可能通过抑制细胞的天然免疫应答进而促进病毒的增殖。SVCV 病毒蛋白与 IRF2a 蛋白互作实验证明，IRF2a 与 SVCV P 蛋白存在互作，并依赖于 IRF2a C 末端 IAD 结构域。P 蛋白通过减少 IRF2a-K48 泛素修饰稳定蛋白并促进 IRF2a 入核实现病毒逃逸。

关键词：IRF2；SVCV；泛素化；入核；病毒逃逸

Zebrafish IRF2a negatively regulates innate antiviral immunity

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Abstract: IFN regulatory factor (IRF) 2 belongs to the IRF1 family with a DNA binding domain (DBD) at the N terminus and an IRF association domain (IAD) at the C terminus and contains two copies in zebrafish genome. In this study, luciferase reporter assay showed that IRF2a inhibited promoter activities of IFNφ1, IFNφ3 and ISRE induced by SVCV and Poly(I:C), which demonstrated that IRF2a may facilitate the immune evasion of SVCV by inhibiting cellular innate immune response. Furthermore, we found SVCV P protein interacted with IRF2a and promoted nuclear translocation and stability of IRF2a by suppressing the K48-linked ubiquitination .

Key words: IRF2a, SVCV, nuclear translocation, ubiquitination, immune evasion

花鲈 Pannexin1、connexin32 和 connexin43 基因鉴定、表达分析及其在炎症诱导 ATP 释放中的作用

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摘要：在损伤、病原体感染等病理生理条件下，活化的免疫细胞可通过连接蛋白 Pannexin（Panx）和 connexin（Cx）通道将 ATP 释放到细胞外。胞外 ATP 是一种重要的损伤相关分子模式分子，在机体天然免疫的激活过程中起重要作用。本研究克隆鉴定了花鲈（*Lateolabrax maculatus*）Panx1、Cx43 和 3 个 Cx32 基因（*Lm*Panx1、*Lm*Cx43、*Lm*Cx32.2、*Lm*Cx32.2x 和 *Lm*Cx32.7），通过体内和体外实验，分析了它们在 LPS、poly(I:C)或迟缓爱德华氏菌（*Edwardsiella tarda*）等不同的免疫刺激后，这些基因 mRNA 水平的表达模式变化。还通过构建真核表达质粒分析了它们的亚细胞定位。此外，我们还研究了它们在炎症诱导细胞释放 ATP 过程中的作用。

关键词：ATP；Panx1；Cx32；Cx43；花鲈；天然免疫；

Identification and expression analysis of Pannexin1, connexin32 and connexin43 genes and their role in their role in inflammation-induced ATP release in the spotted sea bass (*Lateolabrax maculatus*)

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Abstract: ATP is released by activated immune cells through the Pannexin (Panx) and connexin (Cx) channels under injury, pathogen infection or other pathophysiological conditions. Extracellular ATPs are the important damage-associated molecular patterns (DAMPs), which played an important role in activation of host innate immunity. In the study, Panx1, Cx43 and three Cx32 genes (namely *Lm*Panx1, *Lm*Cx43, *Lm*Cx32.2, *LmCx*32.2x and *Lm*Cx32.7) were identified and characterized from the spotted sea bass (*Lateolabrax maculatus*). Through the experiments in vivo and/or in vitro , we analyzed their expression patterns after different immune stimulations such as by LPS, poly(I:C) and *Edwardsiella tarda* infection; By constructing the eukaryotic expression plasmids, we analyzed their subcellular localizations. In addition, their roles in the inflammation-induced ATP release were investigated.

Key words: ATP, Panx1, Cx32, Cx43, *Lateolabrax maculatus*, innate immunity

哈维氏弧菌浸泡感染下泥蚶(*Tegillarca granosa*)不同组织弧菌载量的变化规律分析

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摘要：为明确哈维氏弧菌感染下，泥蚶(*Tegillarca granosa*)不同组织弧菌载量的变化规律，通过哈维氏弧菌浸泡感染泥蚶的方法，建立弧菌浓度计数标准曲线，记录攻毒水体和泥蚶组织中的哈维氏弧菌含量的动态变化及相关关系。研究结果为泥蚶感染弧菌发病过程中，免疫识别及免疫响应机制的研究提供了参考。

关键词：泥蚶; 哈维氏弧菌; 弧菌载量; 免疫抗性

LOAD VARIATION OF VIBRIO HARVEYI IN THE BLOOD CLAM TEGILLARCA GRANOSA

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Abstract：To understand the variation detail of bacterial load in different tissues of the blood clam *Tegillarca granosa* (including gill, mantle, adductor, hepatopancreas, and blood) under *Vibrio harveyi* challenge, a *V. harveyi* immersion experiment was conducted and the standard curve of *V. harveyi* concentration was established by turbidimetric method, from which the dynamic relationship between the bacterial growth and reproduction in seawater under *Vibrio* challenge in 24 h was described, the bacterial load of the blood clam tissues was calculated, and the relationship between the *Vibrio* load in hepatopancreas and the immersion different concentrations (1×10^{5}, 1×10^{6}, 1×10^{7}, 5×10^{7} CFU/mL) of *Vibrio* in seawater was specified. This study provided a reference for the immune recognition and response during pathogenesis by *Vibrio* infection in *T. granosa*.

Key words : *Tegillarca granosa*; *Vibrio harveyi*; *Vibrio* load; immune resistance

金鱼对鲫源 II 型鲤疱疹病毒(CyHV-2) SH01 株的敏感性研究

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摘要：II 型鲤疱疹病毒(CyHV-2)是疱疹病毒科(Alloherpesviridae)鲤疱疹病毒属(*Cyprinivirus*)的成员，是一种致命的水生动物传染性病原，感染金鱼(*Carassius auratus*)和鲫 (*Carassius Carassius*)。虽然金鱼和鲫同属鲫属(*Carassius*)，但尚不清楚它们是否对同一株 CyHV-2 分离株敏感。CyHV-2 SH01 株是在上海附近一家养殖场的鲫发生疱疹病毒性造血器官坏死病(herpesviral haematopoietic necrosis，HVHN)时分离到的。用 CyHV-2 SH01 攻击金鱼和鲫，我们发现注射感染 24 h 的金鱼和鲫的病毒感染进程是迅速而致命的。注射感染的金鱼的肾组织中病毒的平均拷贝数为 $10^{3.47}$-$10^{3.59}$ copies/mg。CyHV-2 SH01 注射感染的金鱼和鲫的肝、脾、肾和鳃组织中出现显著的组织病理学变化(细胞皱缩、细胞质空泡化、鳃丝融合、肝脏充血)。综上，金鱼和鲫对由 CyHV-2 SH01 株引起的 HVHN 表现出较高的敏感性。

关键词：II 型鲤疱疹病毒(CyHV-2)；鲫；金鱼；敏感性；病理学；观赏鱼

Susceptibility of Goldfish to Cyprinid Herpesvirus 2 (CyHV-2) SH01 Isolated from Cultured Crucian Carp

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Abstract: Cyprinid herpesvirus 2 (CyHV-2), a member of the Alloherpesviridae family belonging to the genus *Cyprinivirus*, is a fatal contagious aquatic pathogen that affects goldfish (*Carassius auratus*) and crucian carp (*Carassius carassius*). Although crucian carp and goldfish belong to the genus Carassius, it is unclear whether they are susceptible to the same CyHV-2 isolate. CyHV-2 SH01 was isolated during herpesviral hematopoietic necrosis disease (HVHN) outbreaks in crucian carp at a local fish farm near Shanghai. In this study, goldfish and crucian carp were challenged with CyHV-2 SH01. We found that CyHV-2 SH01 could cause rapid and fatal disease progression in goldfish and crucian carp 24 h post-injection. The average virus titer in the kidney tissue of injected goldfish was $10^{3.47}$-$10^{3.59}$ copies/mg. Histopathological changes (cellular wrinkling and shrinkage, cytoplasmic vacuolation, fusion of the gill lamellae, and hepatic congestion) in liver, spleen, kidney and gill tissues of infected goldfish and crucian carp after CyHV-2 SH01 injection. Thus, crucian carp and goldfish showed a high sensitivity to HVHN disease caused by CyHV-2 SH01.

Key words: CyHV-2, crucian carp, goldfish, sensitivity, pathology, ornamental fish

CyHV-2 SH01 毒株全基因组测序及注释

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摘要：鲤疱疹病毒II型（CyHV-2）是一种感染金鱼(*Carassius auratus*)和鲫(*Carassius Carassius*)的致病率较高的病毒，对我国养殖业造成了巨大的经济损失。CyHV-2 为疱疹病毒科（*Alloherpesviridae*）鲤疱疹病毒属（*Cyprinivirus*）的一种线性双链 DNA 病毒，其基因组结构与鲤疱疹病毒I型（CyHV-1）、鲤疱疹病毒III型（CyHV-3）、斑点叉尾鮰疱疹病毒I型（IcHV-1）及蛙疱疹病毒I型(RHV-1)相似。本研究对从中国上海附近一家养殖场患病鲫体内采集的 CyHV-2 毒株 CyHV-2 SH01 进行了基因组测序。将基因组测序得到的原始数据进行过滤、质控，然后对质控后的数据进行基因组组装，矫正以及优化，最终得到大小为 275,452bp 的基因组。通过对质控后数据比对到基因组，得到其测序深度为 614.62X，以及 3905 个完整的 CDS 并注释。据资料显示目前共有 7 株 CyHV-2 分离自金鱼和鲫的分离株，其全基因组同源性大约在 98%。我们将对 CyHV-2 SH01 株与其他株 CyHV-2 分离株进行分析和序列比较，通过基因测序和序列挖掘，为进一步了解 CyHV-2 基因组提供更多新的线索。

关键词：鲫；鲤疱疹病毒II型；基因组；基因测序；

Whole genome sequencing and annotation of CyHV-2 SH01 strain

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Abstract: Cyprinid herpesvirus 2 (CyHV-2) is a pathogen with a high mortality rate that infects goldfish (*Carassius auratus*), crucian carp (*Carassius auratus*) and has caused huge economic losses to the farming industry in China. CyHV-2 is a linear double-stranded DNA virus belonging to the genus Cyprinivirus in the family Alloherpesviridae, and its genome structure is similar to cyprinid herpesvirus 1, cyprinid herpesvirus 3, ictalurid herpesvirus-1 and ranid herpesvirus-1. In this study, the genome of CyHV-2 SH01, a CyHV-2 isolate collected from diseased crucian carp from a farm near Shanghai, China, was sequenced. The raw data from the genome sequencing was filtered and QC'd, then the QC'd data was assembled, corrected and optimised to obtain a genome of 275,452bp in size. By comparing the post-quality control data to the genome, its sequencing depth was obtained as 614.62X, as well as 3905 complete CDS and annotated. According to the data there are currently seven CyHV-2 isolates from goldfish and crucian carp with a genome-wide homology of approximately 98%. We will analyse and compare the sequence of CyHV-2 SH01 strain with other strains of CyHV-2 isolates to provide more new clues for further understanding of the CyHV-2 genome through gene sequencing and sequence mining.

Keywords: crucian carp；cyprinid herpesvirus 2；genome；gene sequencing

EGCG 衍生物体外抑制Ⅰ型草鱼呼肠孤病毒的研究

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摘要：表没食子儿茶素没食子酸酯（EGCG）是从茶叶中提取的重要成分，具有抗氧化、抗病毒与增强机体免疫等功能。为了提高 EGCG 在生产应用上的广泛性，对 EGCG 进行结构修饰，使其改性成脂溶性，本文开展了表没食子儿茶素没食子酸棕榈酸酯（EGCG-P）与乙酰化表没食子儿茶素没食子酸（ACEGCG）体外抗病毒方面的研究，结果显示，EGCG-P 与 ACEGCG 对 GCRV-JX01 感染细胞的抑制作用呈剂量依赖性，且 EGCG-P 相较于 ACEGCG 达到相同抑制效果所需药物剂量更低，EGCG-P 浓度为 10μg/ml 和 40μg/ml 时病毒表达量相对于对照组上清中病毒的滴度分别降低了 10^2 和 10^3 $TCID_{50}$，而 ACEGCG 浓度为 60μg/ml 和 120μg/ml 时才能达到相同抑制效果，结果表明 EGCG-P 和 ACEGCG 均能有效抑制 GCRV-JX01 的增殖。本研究为开发 EGCG 衍生物作为拮抗草鱼出血病的环保型药物奠定基础。

关键词：草鱼出血病；草鱼呼肠孤病毒；EGCG-P；ACEGCG

Study on the inhibition of genotypeIGCRV by EGCG derivatives in *vitro*

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Abstract: Epigallocatechin gallate (EGCG) is an important ingredient extracted from tea, which has antioxidative, antiviral and immunological functions. In order to improve the wide application of EGCG in production, the structure of EGCG was modified to be fat-soluble. In this experiment, the antiviral effects of epigallocatechin gallate palmitate (EGCG-P) and acetylated epigallocatechin gallate (ACEGCG) were studied in vitro. The results showed that the inhibitory effect of EGCG-P and ACEGCG on GCRV-JX01-infected cells was dose-dependent, and that EGCG-P required a lower drug dose than ACEGCG to achieve the same inhibitory effect, relative to the control supernatant, viral expression was reduced by 10^2 and 10^3 $TCID_{50}$ at EGCG-P concentrations of 10μg/ml and 40 μg/ml, the same inhibitory effect was achieved with ACEGCG concentrations of 60 μg/ml and 120 μg/ml. The results showed that both EGCG-P and ACEGCG could effectively inhibit the proliferation of GCRV-JX01. This experiment demonstrates that EGCG derivatives antagonise grass carp hemorrhagic disease, laying the foundation for the development of environmentally friendly drugs.

Keywords: Grass carp hemorrhagic disease; Grass carp reovirus; EGCG-P; ACEGCG

鲤疱疹病毒 2 型 ORF55 蛋白的表达及其互作多肽筛选

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摘要：鲤疱疹病毒 2 型（Cyprinid herpesvirus 2，CyHV-2）属于双链 DNA 病毒，共编码 154 种开放阅读框（ORFs）。其中 ORF55 基因预测编码胸苷激酶（thymidine kinase，TK），参与核酸代谢。本实验针对 CyHV-2 病毒 ORF55 基因进行原核表达系统的构建，经诱导表达、超声破碎、洗脱后得到纯化的 ORF55 重组蛋白，SDS-PAGE 分析显示 ORF55 蛋白大小约为 75 kDa。运用噬菌体展示技术筛选 ORF55 特异性互作多肽。经过三轮淘选和序列测定，结果表明 ORF55 蛋白主要和 1 种多肽相互作用。与 NCBI 比对发现该多肽与金鱼基因组中 4 个基因具有同源性，提示其可能是 ORF55 互作蛋白。本研究为深入探索 ORF55 在病毒感染过程中的生物学功能奠定了重要基础。

关键词：鲤疱疹病毒 2 型；ORF55；原核表达，噬菌体展示技术

Expression of herpesvirus type 2 ORF55 protein and screening of its interacting peptides

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Abstract: Cyprinid herpesvirus 2 (CyHV-2) is a double-stranded DNA virus that encodes 154 open reading frames (ORFs). The ORF55 gene is predicted to encode thymidine kinase (TK), which is involved in nucleic acid metabolism. In this experiment, a prokaryotic expression system was constructed for the CyHV-2 virus ORF55 gene, and the purified ORF55 recombinant protein was obtained after induction of expression, ultrasonic fragmentation and elution, and the size of ORF55 protein was about 75 kDa by SDS-PAGE. After three rounds of panning and sequence determination, the results showed that the ORF55 protein interacted mainly with one peptide. The peptide was found to be homologous to four genes in the goldfish genome by comparison with NCBI, suggesting that it may be an ORF55-interacting protein. This study provides an important basis for exploring the biological functions of ORF55 during virus infection.

Keywords: Cyprinid herpesvirus 2, ORF55, prokaryotic expression, phage display technology

斑点叉尾鮰疱疹病毒糖蛋白 ORF59 的特性及其在病毒感染过程中的封闭作用分析

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摘要：斑点叉尾鮰疱疹病毒（CCV，*Ictalurid herpesvirus 1*）具有较强的传染性和致病性，对鱼业养殖造成了巨大的经济损失。本研究旨在表征 CCV 糖蛋白 ORF59 并探讨其对宿主细胞中病毒感染的影响。首先，通过 Western Blot 实验和亚细胞定位实验证实 CCV ORF59 是一种在感染后期表达的病毒膜蛋白。使用杆状病毒表达系统在 sf9 昆虫细胞中表达重组蛋白 ORF59 并进行蛋白封闭实验，实验结果表明重组 ORF59 蛋白对病毒入侵具有剂量依赖性抑制作用。使用 shRNA 敲降 ORF59，结果表明 ORF59 表达量降低同时减少了斑点叉尾鮰卵巢细胞中传染性病毒颗粒的产生。本研究结果表明，重组 ORF59 蛋白可能通过阻止宿主细胞表面的受体结合而抑制 CCV 的进入，并且表明 ORF59 的低表达可能对 CCV 子代的结构完整性产生负面影响。这些发现将促进对 CCV 感染期间糖蛋白 ORF59 关键功能的研究。

关键词：斑点叉尾鮰疱疹病毒；糖蛋白 59；杆状病毒表达系统；蛋白封闭；病毒复制

Characterization of *Ictalurid herpesvirus 1* glycoprotein ORF59 and its blocking role on viral infection in catfish cells

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Abstract: The channel catfish virus (CCV, *Ictalurid herpesvirus 1*) has caused sustained economic losses in the fish industry because of its strong infectivity and pathogenicity. Thus, it is necessary to determine the function of viral proteins in the CCV infection process. The present study aimed to characterize CCV glycoprotein ORF59 and explore its impact on virus infection in host cells. First, its exclusive presence in the membrane fraction of the cell lysate and subcellular localization verified that CCV ORF59 is a viral membrane protein expressed at late-stage infection. A protein blocking assay using purified His6 tagged ORF59, expressed in sf9 insect cells using a baculovirus expression system, indicated a dose-dependent inhibitory effect of recombinant ORF59 protein on virus invasion. Knockdown of the *ORF59* using a short hairpin shRNA showed that *ORF59* silencing decreased the production of infectious virus particles in channel catfish ovary cells. The results of this study suggested that recombinant ORF59 protein might inhibit CCV entry by abrogating cellular binding, and indicated that low expression of *ORF59* might have a negative impact on the structural integrity of CCV virus progeny. These findings will promote future studies of the key functions of glycoprotein ORF59 during CCV infection.

Key words: *Ictalurid herpesvirus 1*; glycoprotein ORF59; Baculovirus expression; Protein blocking; Virus replication

斑点叉尾鮰病毒 ORF25 和 ORF63 基因对病毒 DNA 复制和感染至关重要

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摘要：斑点叉尾鮰病毒(channel catfish virus, CCV)是鱼类养殖业中最重要的病毒性病原体之一，可导致幼年斑点叉尾鮰发生致命的出血性疾病。基因组 DNA 复制是 CCV 生命周期中不可或缺的关键事件，本研究在斑点叉尾鮰卵巢细胞(channel catfish ovary cells, CCO)中评估了假定的由病毒 ORF25 和 ORF63 编码的解旋酶和引发酶对 CCV 基因组复制和感染的影响。结果表明 RNA 干扰敲降 ORF25 和 ORF63 后，CCV 基因组拷贝数在病毒感染的 CCO 细胞中显著降低。相比之下过表达 ORF25 和 ORF6 导致病毒基因组拷贝数增加。与上述结果一致，在病毒感染的 CCO 细胞中，严格依赖病毒 DNA 复制的真晚期基因的表达在过表达或 RNA 干扰 ORF25 和 ORF63 基因后被显著增加或抑制。此外，敲降 ORF25 和 ORF63 基因显著抑制 CCV 诱导的细胞病变，降低 CCO 细胞中子代病毒滴度。通过透射电镜观察，CCV 感染 CCO 细胞后，敲降 ORF25 和 ORF63 基因导致病毒粒子显著减少。综上所述，结果表明 ORF25 和 ORF63 对于调控 CCV 基因组复制和 CCV 诱导感染至关重要。我们的研究结果将有助于了解 CCV 的复制机制，并有助于开发在斑点叉尾鮰养殖中控制 CCV 感染的抗病毒策略。

关键词：斑点叉尾鮰病毒；基因组复制；病毒感染；抗病毒

Channel catfish virus ORF25 and ORF63 genes are essential for viral DNA replication and infection

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Abstract: The channel catfish virus (CCV) is one of the most important viral pathogens in fish industry which can cause a lethal hemorrhagic disease in juvenile channel catfish. In spite of the CCV genome has been fully sequenced, Molecular mechanisms of CCV infection and pathogenesis are still less known. Genomic DNA replication is a necessary and key event for CCV life cycle. In this study, the impacts of putative helicase and primase encoded by viral ORF25 and ORF63 on the CCV genome replication and infection were evaluated in channel catfish ovary (CCO) cells. The results showed that the number of CCV genome copies was decreased significantly in virus-infected CCO cells after knockdown of the ORF25 and ORF63 using RNA interference. In contrast, the overexpression of ORF25 and ORF63 led to a slight increase in the number of virus genome copies. Consistent with above results, the expression of CCV true-late genes which strictly depends on viral DNA replication was significantly increased or repressed by overexpression or RNA interference targeted viral ORF25 and ORF63 genes in virus-infected CCO cells. In addition, knockdown of ORF25 and ORF63 remarkably inhibited CCV-induced cytopathic effects and decreased progeny virus titer in CCO cells. Moreover, transmission electron microscope observation of CCO cells infected with CCV accompanied by siRNA targeted viral ORF25 and ORF63 genes showed that the number of virus particles remarkably reduced. Taken together, these results indicated that ORF25 and ORF63 are essential for regulating CCV genome replication and CCV-induced infection. Our findings will provide benefit for understanding the replication mechanisms of CCV and contribute to the development of antiviral strategy for controlling CCV infection in channel catfish culture.

Key words: Channel catfish virus, Genome replication, Virus infection, Antiviral

鲫疱疹病毒（CyHV2）蛋白 KLP 利用宿主自噬降解 MITA 实现免疫逃逸

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摘要：关于病毒利用宿主自噬系统的机制研究已在多种陆生动物病毒中被报道，而对于水生生物病毒与宿主自噬之间的研究所知甚少。在此，我们发现鲫疱疹病毒（CyHV2）的激酶样蛋白（KLP）能够利用宿主细胞的自噬过程降解 MITA 进而阻断干扰素（IFN）的产生。首先，KLP 抑制外源 DNA 或 RNA 诱导的 IFN 激活，并且与 DNA 或 RNA 激活的信号通路的交汇分子 MITA 结合。这一相互作用基于 KLP 与 MITA-C 端的结合，同时亚细胞定位分析显示，MITA-C 能够被 KLP 招募。随后，我们发现 KLP 能够引起 MITA 发生自噬途径降解，且只有在 MITA 存在时，KLP 才能启动细胞的自噬流。进一步探究发现 KLP 与自噬分子 Beclin1 和 ATG14 结合，并通过增强 K63 连接的多聚泛素化来促进 Beclin1 的稳定。最后，KLP 能够明显减弱细胞本身或由 MITA 诱导的抗病毒能力。上述研究表明，只有在靶标分子 MITA 存在的情况下，鱼类病毒 CyHV2 才能够调节细胞的自噬过程，这揭示了一种崭新的水生病毒利用宿主自噬系统的免疫逃逸机制。

Abstract: Control of host autophagy acceleration or attenuation has been confirmed in multiple terrestrial animal viruses. Little is known about such mechanisms in aquatic viruses. Here, we report a selective and ingenious autophagy modulation regulated by kinase-like protein (KLP) of cyprinid herpesvirus 2 (CyHV2) to restrict interferon (IFN) production by degrading MITA. First, exogenous DNA or RNA-mediated IFN activation were both abrogated by CyHV2 KLP. The common intersection point of MITA with these two signaling pathways was the interaction with KLP. The C terminus of MITA was indispensable for the interaction and was recruited by KLP in subcellular colocalization analysis. Subsequently, we found that KLP degraded MITA in an autophagy-lysosome-dependent manner; interestingly, individual KLP could not launch host autophagic flow only if with MITA present. KLP was also colocalized with the autophagy components Beclin1 and ATG14 and enhanced Beclin1 stability through K63-linked polyubiquitination but not ATG14. Finally, KLP significantly decreased the normal state or MITA enhanced cellular antiviral capacity. These data demonstrated an elaborate autophagic process manipulated by a fish virus only in the presence of the host target, illuminating a mechanism of aquatic viral immune evasion.

第五专题：渔业资源与生态养护

基于耳石 Sr/Ca 探究黄海小黄鱼早期生活史和种群划分

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摘要：小黄鱼作为一种高度洄游性鱼类，其全生命周期的洄游较为清晰，但对其早期生活史的洄游机制鲜有研究，且在种群划分方面存在分歧，尤以黄海海域的种群争议居多。为此，本研究从连云港近海（Y1）、盐城近海（Y2）和黄海外海（Y3）采集 30 尾小黄鱼成鱼，分析其耳石 Sr/Ca 以探究其早期生活史和种群划分。根据小黄鱼耳石沉积特征和生长规律，以耳石核心为起点，将其早期生活史 Sr/Ca 元素变化阶段依次划分为胚胎期（N）、仔鱼期（L）、变态期（M）和稚鱼期（J）。结果显示：从 N 期至 J 期，三个群体小黄鱼的耳石 Sr/Ca 均呈显著下降趋势，表明其从 N 期到 J 期的早期生活史是从近海向近岸的洄游模式；以 N 期至 J 期的 Sr/Ca 进行典型判别分析，显示三个群体被明显地划分为两个种群，即黄渤海群（Y1）和黄海南部群（Y2 和 Y3），其差异主要为黄渤海群耳石 L 期和 J 期的 Sr/Ca 显低于于黄海南部群。由此可见，基于耳石 Sr/Ca 和个体发育阶段可以用以探究小黄鱼生活史和种群划分。

关键词：耳石微化学；小黄鱼；种群划分；早期生活史；黄海

Early life migration and population discrimination of the small yellow croaker *Larimichthys polyactis* from the Yellow Sea: Inferences from otolith Sr/Ca ratios

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Abstract: As a highly migratory species, the whole life migration of *L. polyactis* has been intensively studied. Nevertheless, knowledge about its early life migration is scarce, and population divisions are inconsistent. In the present study, otolith Sr/Ca was analysed to investigate the early migratory patterns and discriminate the populations of *L. polyactis* in the Yellow Sea, including two spawning groups and one overwintering group. The variation in Sr/Ca ratios of ontogenetic growth zones, including the nucleus (N), larval (L), metamorphosis (M), juvenile (J), and edge (E) zones, was measured by electron probe microanalysis. The variation in Sr/Ca ratios in early developmental growth zones was generally characterised by an evident downward trend from the N to J zone, which suggests that the early migratory pattern of *L. polyactis* might be from inshore to nearshore water. Canonical discriminant analysis, based on the otolith Sr/Ca ratios of the N, L, M, and J zones, allowed the successful discrimination of the two populations, namely, the northern and southern Yellow Sea groups, whose differences were mainly reflected in the L and J zones.

Key words: Otolith microchemistry, *Larimichthys polyactis*, population discrimination, early life migration, the Yellow Sea

基于北斗船位数据的渔业信息解译与应用研究——以中国毛虾限额捕捞管理为例

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摘要：本研究提取 62 艘毛虾网船在限额捕捞期间的 421700 条北斗船位数据经纬度、航速、航向等信息，运用缓冲区叠加分析法、DBSCAN 密度聚类算法、平均中心算法、核密度估计以及数据库查询对捕捞努力量等管控要素进行分析研究。结果显示，所有毛虾网船累计作业 239 个航次、1942 个网次，捕捞过程分为航行、抛锚布网、等待渔获、收渔获、停航等 5 个状态，中国毛虾捕捞状态船位点呈直线分布，总捕捞时长为 4413.73h，82.4%的单网次捕捞时长为 1.5—3.5 h，各网次捕捞产量呈现多核心空间分布模式，总捕捞努力量为 108106343 m2·h，计算 62 艘的捕捞总产量值约为 2328t，比上报产量高 12.6%；本文通过北斗船位数据解译和提取捕捞努力量以计算中国毛虾捕捞产量及资源空间分布情况，有效应用于中国毛虾限额捕捞，为解决我国单品种限额捕捞难点积累了宝贵经验。

关键词：渔船监控系统；毛虾网；捕捞努力量；产量计算；限额捕捞

Interpretation and Application of Fishery Information based on Beidou Position Data: A Case Study of TACs Pilot Project of *Acetes chinensis*

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Abstract: A total of 421 700 VMS (vessel monitoring system) data of Beidou satellite navigation from 62 stow net vessels during fishing period were used. The data including the time, position, speed, direction, etc., were mined and proceed for the extraction of fishing effort by buffer overlay analysis, the DBSCAN (Density-based Spatial Clustering of Application with Noise) algorithm, the mean center algorithm, kernel density estimation, and database querying. The results show that the stow net vessels performed 239 voyages with 1942 nets, the total fishing time was 4413.73 h, and the total fishing effort was 108106343 m2·h. The calculated yield was 2328 t, which is 12.6% higher than the reported yield. The fishing status was recognized and divided into five phases (cruising, casting, waiting, hauling, and suspending). The fishing routes of catching A. chinensis were strait lines, and the spatial distribution of fishing yield with stow nets featured multiple-centered pattern. At present, challenges remain in the implementation of TACs in China for targeted species stock survey and fishing log management. The method of interpreting the fishing behaviors, the extraction methods of voyages, nets, positions, and fishing effort, and the method of yield calculation in this study provided an effective way to implement TACs projects in fishery.

Key words: vessel monitoring system; Acetes chinensis stow net; fishing effort; yield calculation; total allowable catch system

杭州湾北部渔业资源群落结构分析

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摘要：根据 2016-2017 年嵊泗海域渔业资源 4 个航次的调查数据，运用 Bray-Curtis 相似性系数及多维尺度、ABC 曲线等方法，对该海域渔业资源进行物种群落结构聚集性分析。结果表明：1）调查海域共出现渔业资源 78 种，丰度和生物量均以鱼类最高，其次为蟹类和虾类；2）棘头梅童鱼、焦氏舌鳎、葛氏长臂虾和日本蟳为优势种；3）群落结构稳定性分析显示春季和秋季群落结构稳定性较好，夏季和冬季受干扰较严重。

关键词：杭州湾；渔业资源；优势种；群落聚类

Community structure analysis of fishery resources in northern of Hangzhou Bay

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Abstract: Based on the data of four seasons from 2016 to 2017 in northern of Hangzhou Bay, Bray-Curtis similarity matrix, ABC curves and other methods were used to analyze the community structure aggregation of species diversity. The results showed that: 1)78 species of fishery importance were collected from the surveyed waters, with the highest abundance and biomass of fish, followed by crab and shrimp; 2) *Collichthys lucidus*, *Cynoglossus joyner*, *Palaemon gravieri* and Charybdis japonica were the dominant species; 3) The cluster analysis of the community showed that the community structure stability in spring and autumn was better, but it was disturbed seriously in summer and winter.

Key words: Hangzhou Bay, fishery resources, species diversity, community structure

金湾风电海域渔业资源声学评估

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摘要：基于水声学技术与典范对应分析（CCA），本文研究了金湾风电海域的鱼类群落结构现状、空间分布及其环境响应机制。群落 H'指数为 1.74，表明鱼类群落受到一定的外部压力。鱼类资源具有明显的聚集分布特征，风电场南部鱼类资源多于北部。溶解氧、水深、pH、Chl-a、硝酸盐 (NO3−)、氨 (NH4+) 和磷 (PO4+) 等是影响鱼类分布的关键环境因子，但由于 CCA 分析仅占总变异的 45.49%，即还存在其他的外界压力，其中风电建设活动的影响尤为值得关注。未来通过设置对照研究区，研究风电运行期间对当地鱼类群落的长期影响，为进一步探究风电工程对海洋生态系统的整体影响奠定基础。

关键词：金湾海上风电场；渔业资源；声学评估；环境因子；CCA 分析

Acoustic assessment of fishery resources in Jinwan offshore wind farm area

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Abstract: In October 2019, an acoustic survey of fishery resources was conducted in Jinwan offshore wind farm area. The mean H' index was 1.74, indicated that the fish community diversity was moderate. The fishery resources had evident aggregate distribution patterns, and the southern part of the OWF area had more resources than the northern part, with a continuously decreasing trend in both densities from south to north. Seven environmental factors were selected by CCA analysis to reveal the correlation between fish assemblages and environmental factors, including nitrate (NO_3^-), ammonia (NH_4^+), DO, water depth, pH, Chl a, and phosphorus (PO_4^+). However, as the CCA analysis only accounted for 45.49% of the total variation, other stresses that affect the fish assemblages not included in the current survey should exist, and the future most noteworthy stress might be the OWF facilities. In future studies, control areas with more trawl samples can be set up to explore the long-term impact of OWF facilities on fish communities.

Key words: Jinwan offshore wind farm; Fishery resources； Acoustic assessment; Environmental factors; Canonical correspondence analysis

我国深远海大型围栏养殖发展现状与展望

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摘要：深远海大型围栏养殖是我国海水养殖业结构调整和产业升级中新兴的养殖模式之一，具有养殖面积大、鱼类活动空间大、养殖环境更近自然和养殖鱼类品质更近生态等特点。本文在介绍围网养殖发展概况、深远海养殖内涵的基础上，重点概述我国深远海大型围栏养殖发展现状及其研究进展，并对今后的发展方向加以展望，为我国深远海大型围栏智能化生态养殖模式的构建提供参考。

关键词：深远海养殖; 围栏养殖; 发展现状; 展望

Development status and prospect of deep-sea large-scale fence culture in China

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Abstract: The deep-sea large-scale fence culture is one of the emerging aquaculture models in the structural adjustment and industrial upgrading of mariculture in China. It has the characteristics of large breeding area, large fish activity space, closer to nature and closer to ecology. Based on the introduction of the development of enclosure culture and the connotation of deep-sea aquaculture, this paper focused on the development situation and research progress of Chinese deep-sea large-scale fence culture, and looks forward to the future development direction. This article provides a reference for the construction of intelligent ecological breeding mode of deep-sea large-scale fence in China.

Key words: Deep-sea mariculture; Fence culture; Development situation; Prospect

梁子湖枝角类生物种群的衰退与农药污染的关系研究

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摘要：自然水体是众多化学污染物的最终归宿地，而水体化学污染与水生生物的健康效应关系研究还现有报道。本研究以梁子湖为研究对象，调查了整个湖区的水质情况和浮游动植物的种群丰度，发现部分区域出现枝角类生物种群衰退现象。进一步的化学分析结果发现梁子湖部分区域枝角类生物种群衰退现象与农药的符合污染有关，并最终确认了主要致毒农药污染物，为梁子湖的污染管理提供了数据支撑。

关键词：梁子湖；种群衰退；化学污染物；分析化学；效应介导

The relationship between population decline of Cladocerans in Liangzihu lake and pesticide pollution

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Abstract: The natural water bodies are the destinations of chemical pollutants, but the relationships between aquatic chemical pollution and health effects of aquatic organisms have been rarely studied. In this study, we examined the population density of plankton and found that in some waters of Liangzihu lake, the population of Cladocerans was declined. Furthermore, using analysis chemical methods, we found that the pollution of pesticides were responsible for the decline of Cladoceran population. Lastly, the pesticides were identified, and these data are useful for pollution management of Liangzihu lake.

Key words: Liangzihu lake, population decline, chemical pollutants, analysis chemical, effect mediation

浙江地区野生及养殖大口黑鲈肌肉组织及生化组成特性分析

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摘要：为比较浙江地区水库野生鲈鱼和池塘养殖“优鲈1号”的形态学及肌肉营养成分差异，采用形态学、组织学和生化分析的方法进行差异比较研究。结果显示，野生鲈鱼体型较为瘦长，拥有更小的内脏团和更大的净肉率（净重/体重），且肌肉呈现丰富的结缔组织分布，肌纤维也更加细密；来自水库野生鲈鱼的粗蛋白含量（18.49%）显著高于池塘养殖“优鲈1号”（17.99%）（$P<0.05$），其粗脂肪含量（1.68%）显著低于“优鲈1号”（1.87%）（$P<0.05$），二者都属于低脂鱼类；在两个鲈鱼群体中共检测出17种氨基酸，除缬氨酸Val和天冬氨酸Asp，剩余的15种氨基酸均存在显著差异（$P<0.05$）；两个鲈鱼群体肌肉中均检测到15种相同的脂肪酸组分，除脂肪酸C16:1无显著差异（$P>0.05$）外，不同种群间脂肪酸种类组成和含量差异明显（$P<0.05$）。在矿物质含量检测中，K、Mg和Se在野生鲈鱼肌肉中的含量显著高于“优鲈1号”（$P<0.05$），而Na、Ga、P、Zn的含量则相反（$P<0.05$）。研究结果表明，来自浙江省衢州市步胜水库的野生鲈鱼具有更高的营养价值和食用价值，合理的开发利用能够增加现有大口黑鲈良种的多样性。

关键词：大口黑鲈；野生与池塘养殖；肌肉营养成分

Analysis of muscle tissue and biochemical composition characteristics of wild and cultured largemouth bass in Zhejiang Province

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Abstract: Analysis of morphology, histologic and biochemistry were used to compare the related differences of wild largemouth bass and YouLu 1 in Zhejiang province. The results showed that the wild bass were thinner and longer, owned smaller internal quality and much net meat percentage, had rich connective tissue in muscle and finer muscle fibers. The crude protein content of wild bass (18.49%) was significantly higher than that of YouLu 1 (17.99%) ($P < 0.05$), but its crude lipid content (1.68%) was significantly lower than that of YouLu 1 (1.87%) ($P < 0.05$), and they were all low fat fish. ***Furthermore***, 17 amino acids were detected between the two groups, except for Val and Asp, the remaining 15 amino acids were significantly different ($P < 0.05$). Moreover,15 identical fatty acid components were detected in the muscle of the two populations, there were significant differences in the composition and content of fatty acids among different populations ($P < 0.05$), except for C16:1 ($P > 0.05$).The content of K, Mg and Se in the muscle of wild bass were significantly higher than that of YouLu 1 ($P < 0.05$), while the contents of Na, Ga, P and Zn were significantly lower ($P < 0.05$).The results showed that the wild largemouth bass from Busheng Reservoir had higher nutritional value and edible value, reasonable development and utilization of the wild bass could increase the diversity of the existing superior largemouth bass population.

Key words: Largemouth bass, Wild and Pond cultured, Muscle nutritional composition

中东大西洋翼柄柔鱼年龄与生长的初步研究

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摘要：本文根据 2020 年 5 月我国鱿钓船在中东大西洋所采集的 682 尾翼柄柔鱼(*Sthenoteuthis pteropus*)样本，对其基础生物学数据进行了分析，并通过耳石微结构的观测对其年龄与生长进行了研究。结果表明，翼柄柔鱼的胴长为 124~580 mm；体质量为 80~6365 g。耳石生长纹数计数显示，翼柄柔鱼样本年龄为 105~365 d。根据耳石日龄及捕捞日期推算得出，翼柄柔鱼样本孵化日期为 2019 年 5 月—2020 年 2 月，主要为冬春生群体。翼柄柔鱼初次性成熟胴长为 404 mm，胴长生长符合 Logistic 模型。研究初步掌握了捕捞海渔翼柄柔鱼的基础生物学特性，为我国在该海渔合理开发其资源提供了基础资料。

关键词：翼柄柔鱼；耳石；年龄与生长；中东大西洋

A preliminary study on the age and growth of the orangeblack flying squid in the Middle East and Atlantic Ocean

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Abstract：The results showed that the mantle length of the orangeblack flying squid (*Sthenoteuthis pteropus*) was 124~580mm; the body weight was 80~6365g. The age of *S.pteropus* samples ranged from 105 to 365 days. According to the calculation of the age of otoliths and the date of fishing, the incubation date of the samples of *S.pteropus* is from May 2019 to February 2020, mainly for winter and spring populations; the mantle length growth conforms to the Logistic model. The basic biological characteristics of sea fish Pteropodidae provide basic data for our country to rationally develop its resources in this sea.

Key：*Sthenoteuthis pteropus*, otolith, age and growth, the Middle East Atlantic Ocean

东印度洋、南海海域鸢乌贼种群遗传结构研究

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摘要：为了解东印度洋赤道、南海海域鸢乌贼（*Sthenoteuthis oualaniensis*）种群遗传结构，更好地对鸢乌贼渔业资源进行合理的管理，本研究测定了鸢乌贼东印度洋赤道北部、南部和南海北部、南部四个群体共 120 尾个体线粒体 DNA 细胞色素 b 基因。结果显示，南海两个群体间不存在显著的遗传分化，东印度洋两个群体间遗传分化较小；其中，东印度洋赤道两侧频繁的洋流活动可能是导致赤道南北群体遗传分化的重要因素，而东印度洋与南海之间的地理隔离则导致两个地理群体间遗传分化显著。综上所述，东印度洋赤道、南海海域群体是两个独立的群体，在渔业管理上也应视为两个独立的管理单元。

关键词：鸢乌贼；种群遗传结构；细胞色素 b 基因；东印度洋；南海

Genetic structure of *Sthenoteuthis oualaniensis* population in the east Indian Ocean and South China Sea

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Abstract: This research was conducted to understand the population genetic structure of Purpleback flying squid from the East Indian Ocean and the South China Sea, to rationally manage the resources of Squid fishery. The cytochrome b (Cytb) sequences of 120 mitochondrial DNA from four subpopulations of Purpleback flying squid were measured. These results indicate that the indistinctive genetic differentiation existed between the two groups from north and south of the South China Sea, while the difference of the genetic differentiation between the two groups from north and south of the East Indian Ocean was small. The frequent ocean current activities on both sides of the East Indian Ocean could be the main factor leading to the genetic differentiation existing in the north and south of the East Indian Ocean. While the geographical isolation between the East Indian Ocean and the South China Sea might be the main reason causing to the prominently genetic differentiation between the two geographical groups. In conclusion, the two groups in the East Indian Ocean and the South China Sea were independent, therefore, they should be regarded as two independent units.

Keywords: East Indian Ocean; South China Sea; *Sthenoteuthis oualaniensis*; Cytochrome B Gene; population genetic structure

基于 Ecopath 模型的桑沟湾养殖生态系统食物网结构和生态系统特征研究

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摘要：桑沟湾是中国北方典型的海水养殖区，也是多营养层次综合养殖（Integrated Multi-Trophic Aquaculture，IMTA）的重要代表。本研究基于 Ecopath 模型来探究桑沟湾养殖生态系统的食物网结构和生态系统特征。研究表明，桑沟湾养殖生态系统的营养级介于 1.00-3.89 之间，主要以低营养级的养殖生物为主，海带、牡蛎、扇贝和鲍鱼贡献了整个生态系统 97.30%的生物量，生态系统转换效率为 10.85%。养殖收获对扇贝、牡蛎和海带有正向影响，对鲍鱼有负向影响，牡蛎、扇贝和鲍鱼相互之间存在显著的负向影响。从生态系统特征看，连接指数（Connectance Index，CI）、系统杂食性指数（System Omnivory Index，SOI）和总初级生产力与总呼吸量之比（Total primary production/total respiration，TPP/TR）分别为 0.26、0.08 和 3.57，显示桑沟湾养殖生态系统通过 IMTA 模式，将养殖活动的人为干扰降到最低，最大限度地保护生态系统和提高利益相关者的经济效益。本研究以期为海水养殖生态系统结构分析、养殖容量评估研究提供参考。

关键词：桑沟湾；Ecopath 模型；食物网结构；生态系统特征

Food web structure and ecosystem attributes of Sanggou Bay ecosystem based on Ecopath model

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Abstract: Sanggou Bay is well known as an exemplary coastal water of Integrated Multi-Trophic Aquaculture (IMTA). In this paper, Ecopath model was used to study the food web structure of Sanggou Bay ecosystem. According to the model, Sanggou Bay ecosystem ranged from 1.00 to 3.89 in trophic level. Sanggou Bay ecosystem was dominated by low trophic levels. Kelp, oyster, scallop and abalone were all in TL I and TL II, together accounted for 97.30% in biomass of all functional groups. Transfer efficiency was 10.85%. Aquaculture harvest had a positive influence on scallop, oyster and kelp, but had a negative influence on abalone. Oyster, scallop and abalone showed negative impacts on each other. From the system properties, connectance index (CI) was 0.26 and system omnivory index (SOI) was 0.08, the ratio of total primary production to total respiration (TPP/TR) was 3.57, these presented that IMTA in Sanggou Bay showed a way to minimize the disturbance of aquaculture to protect the ecosystem and improve economic benefits for stakeholders. This paper may provide reference for research and management of ecosystem structure of aquaculture waters.

Key words: Sanggou Bay, Ecopath, food web structure, ecosystem attributes

不同模型和空间分辨率对大西洋热带海域大眼金枪鱼渔场预报精度的影响

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摘要：为掌握不同模型和空间分辨率对大西洋热带海域大眼金枪鱼（*Thunnus obesus*）渔场预报精度的影响，选取 29 个海洋环境因子。基于 5 种模型(随机森林(RF)、梯度提升决策树(GBDT)、k 最近邻(KNN)、逻辑斯蒂回归(LR)和 stacking 集成(由 RF、GBDT 和 KNN 模型集成，STK)，以天为时间分辨率，4 种不同空间分辨率，利用 75%的数据训练得到模型，将 25%测试数据代入模型进行验证。根据预测准确率和综合评价指标 F1 分数对 5 种模型、4 种分辨率得到的结果进行了评价。结果表明：（1）STK 模型对大西洋大眼金枪鱼渔场的预报准确率和 F1 分数较高；（2）空间分辨率为 1°×1°时，STK 模型对大西洋大眼金枪鱼渔场的预报准确率和 F1 分数最高。

关键词：大眼金枪鱼；空间分辨率；渔情预报模型；大西洋热带海域

Effects of different models and spatial resolutions on prediction accuracy of bigeye tuna fishing ground in tropical waters of Atlantic Ocean

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Abstract: In order to understand the effects of different models and spatial resolutions on the prediction accuracy of bigeye tuna (Thunnus obesus) fishing ground in the tropical waters of Atlantic Ocean, and 29 marine environmental factors were selected. Based on five models (random forest (RF), gradient lifting decision tree (GBDT), k nearest neighbor (KNN), logistic regression (LR) and stacking ensemble learning (stacked by RF, GBDT and KNN models, STK), with day as the temporal resolution, with four different spatial resolutions, the models were trained using 75% data. Twenty five percent of the data were substituted into the models for verification. The results of 5 models and 4 resolutions were evaluated according to the prediction accuracy and the comprehensive evaluation index F1 score. The results showed that: (1) The prediction accuracy and F1 score of STK model for bigeye tuna fishing ground were the highest among 5 models; (2) When the spatial resolution was 1°× 1°, the prediction accuracy and F1 score of STK model for bigeye tuna fishing ground were the highest among 4 spatial resolutions.

Key words: Bigeye tuna; spatial resolution; fishing forecast model; tropical waters; Atlantic Ocean

基于体长股分析法的鲢、鳙资源量评估

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摘要：本文根据从滆湖渔业管理委员会获得的鲢、鳙渔获样本数据。运用国际粮食与农业组织(FAO)开发的渔业评估软件 FiSAT II对湖内鲢、鳙的种群资源量进行评估。通过软件下的体长变换渔获曲线法(Length-converted Catch Curve)对湖内鲢、鳙死亡系数进行估算，进而使用软件下的体长有效种群分析法(Length-Structured VPA)对湖内鲢、鳙种群资源量进行评估。结果表明：(1) 湖内鲢的最大体长组捕捞死亡系数 F=1.71，自然死亡系数 M=0.47，总死亡系数 Z=2.18，资源利用率 E=0.78; 湖内鳙的最大体长组捕捞死亡系数 F=1.62，自然死亡系数 M=0.27，总死亡系数 Z=1.89，资源利用率 E=0.86。(2) 随着鱼类体长的增长，滆湖鲢、鳙的自然死亡率逐渐降低，较小个体的死亡多为自然死亡。(3) 2017 年开捕前滆湖鲢资源量约为 1164.1096 万尾；鳙资源量约为 896.7694 万尾。本次实验为国内淡水渔业资源评估提供了有效的科研参考。

关键词：江苏省滆湖；FiSAT II软件；体长变换渔获曲线法；体长有效种群分析法

Population Estimation of Silver Carp and Bighead Carp Based on Body Length Analysis

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Abstract: Using the fishery assessment software FiSAT II to estimate the population of silver carp and bighead in Ge lake. Length-converted Catch Curve method and Length-Structured VPA method were used to estimate the mortality and fish population. Results showed that (1) For silver carp, the total mortality is 2.18, natural mortality is 0.47, exploitation ratio is 0.78 and mortality of the maximum body length group is 1.71; The total mortality of bighead carp is 1.89, natural mortality is 0.27, exploitation ratio is 0.86 and mortality of the maximum body length group is 1.62. (2) With increasing of the fish body length, natural mortality of silver carp and bighead carp decreased. The juvenile individuals almost died naturally. (3) There were 11.641 million silver carp and about 8.968 million bighead carp in Gehu lake in 2017. The research contribute to the fish population estimation.

Key words: Gehu Lake, Jiangsu Province; FiSAT II software; Length-converted Catch Curve; Length-Structured VPA

基于问卷调查的我国中西太平洋金枪鱼围网渔业影响因素分析

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摘要：为探讨我国中西太平洋金枪鱼围网渔业的高质量可持续发展，本文通过调查问卷的形式，从资源环境、市场、技术、政策和保障等 5 个方面向我国金枪鱼围网渔业企业及行业协会了解资源量、市场分布及需求、捕捞技术能力、国家远洋渔业扶持力度、物流保障能力等 13 个具体因素对我国中西太平洋金枪鱼围网渔业发展的可能影响，并采用主成分分析方法分析了各因素对金枪鱼围网渔业的影响程度。结果表明：（1）通过观测各成分特征值，选取 4 个主成分即可基本反映影响发展我国中西太平洋金枪鱼围网渔业的情况。（2）主成分特征值分别为 3.65、2.73、3.04 和 1.75，方差贡献率分别为 28%、21%、23%和 13%，总方差贡献率为 86%。（3）综合分析得出渔获物国际市场价格对我国中西太平洋金枪鱼围网渔业影响最大，其次为渔获物加工及产品开发能力和生产成本。中西太平洋渔业委员会的管理制度、渔场作业环境和资源的调查与评估能力影响最小。本研究结果可为我国中西太平洋金枪鱼围网渔业进一步提升发展水平和市场竞争力，促进围网渔业的可持续发展提供参考。

关键词：中西太平洋；金枪鱼围网渔业；主成分分析；影响因素；问卷调查

Analysis of factors influencing China tuna purse seine fishery in the Western and Central Pacific Ocean (WCPO) Based on questionnaire survey

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Abstract: This paper, by questionnaire, investigated the possible effect of 13 specific factors from five aspects, such as tuna stocks, the market distribution and the demand of catch, fishing technology capacity, national support policies of pelagic fisheries, logistics support capacity and so on, on the development of China tuna purse seine fisheries in the WCPFC, analyzed the influence degree of various factors on the tuna purse fishery by principal component analysis method. The results show that :(1) By observing the characteristic values of each component, selecting four principal components can basically reflect the influence of all factors on the development of tuna purse seine fishery in in the WCPO of China. (2) The characteristic values of principal components were 3.65, 2.73, 3.04 and 1.75, respectively; The variance contribution rates of the four principal components were 28%, 21%, 23% and 13% respectively, and the total variance contribution rate was 86%. (3) Comprehensive analysis shows that the international market price of catch has the greatest influence on China's tuna purse seine fishery in the WCPO waters, followed by catch processing and product development capability and production cost. The management system of the Western and Central Pacific Fisheries Commission, operational environment of fishing grounds and resources survey and assessment capacity had the least impact. The results of this study can provide reference for further improving the development level and market competitiveness of China's tuna purse seine fishery in the WCPO and promoting the sustainable development of purse seine fishery.

Keyword: Western and Central Pacific Ocean; Tuna Purse Seine Fishery; Principal Component Analysis (PCA); influencing factors; Questionnaire Survey

大型海藻坛紫菜、龙须菜和海带的栽培对近岸海域微生物群落的影响

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摘要：大型经济红藻坛紫菜、龙须菜和褐藻海带的大规模栽培不仅带来经济效益，还具有一定的环境修复作用。然而，尚不清楚栽培区微生物群落对不同的大型海藻和季节的响应，以及微生物与大型海藻的相互作用。为此，4 次采集了坛紫菜(*Pyropia haitanensis*)养殖区(P)、龙须菜(*Gracilaria lemaneiformis*)、海带（*Saccharina japonica*）混养区(G)和对照区(C)的 52 份海水样品，然后通过 18S 和 16S rRNA 基因测序分析了真菌和细菌群落结构。结果表明，大规模海藻栽培主要增加溶解氧(DO)、降低无机营养物质，并释放大量有机物，这可能改变了真核和原核微生物群落的多样性。盐度和温度的季节变化与微生物群落组成和结构呈显著正相关。此外，本研究发现一些微生物，如 *Aurantivirga*、*Pseudomonas*、*Woeseia* 等会富集于大型海藻培养区，且不同海藻的富集微生物不同。这些研究结果有利于加深对大型海藻养殖的生态环境效果的认识。

关键词：微生物群落组成，龙须菜，坛紫菜，海带，18S/16S rRNA，环境因子

Effects of cultivation of macroalgae *Pyropia haitanensis* ,*Gracilaria lemaneiformi*s and *Saccharina japonica* on microbial community in coastal waters

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Abstract: The large-scale cultivation of *Pyropia haitanensis*, *Gracilaria lemaneiformis* and *Saccharina japonica* not only brings economic benefits, but also has some environmental restoration effects. However, it is not clear how microbial communities in cultivated zones respond to different macroalgae and seasons, as well as the interaction between microorganisms and macroalgae. For this purpose, a total of 52 seawater samples in different zones and growth times during four months were collected from the *Pyropia haitanensis*(P), *Gracilaria lemaneiformis*-*Saccharina japonica*(G) and control zones (C), respectively. These samples were then analyzed using 18S and 16S rRNA gene sequencing. Our results showed microbial communities were predominantly shifted by increased dissolved oxygen (DO), decreased inorganic nutrients and released organic matter duo to macroalgae cultivation. Also, seasonal changes in salinity and temperature are strongly correlated with microbial community composition and structure. In addition, certain microbial groups,such as *Aurantivirga*、*Pseudomonas*、*Woeseia* would be enriched in response to seaweed cultivation and the enriched microorganisms were different for different macroalgae. These findings contribute to a better understanding of the ecological effects of macroalgae culture.

Keywords: Microbial community composition, *Gracilaria lemaneiformis*, *Saccharina japonica, Pyropia haitanensis*, 18S/16S rRNA, Environmental properties

太湖鲤山湾水生植物修复区鱼类群落结构年际动态分析

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摘要：太湖鲤山湾作为国家水产种质资源保护区，其前身为中华绒螯蟹等水产品围网养殖区，导致区域内水生植物大量丧失。为恢复保护区内的生态功能和渔业资源，于2015年在该保护区内进行生态修复。为探究其修复效果，于2015、2021年调查该水域资源情况。结果显示：2年内共采集鱼类43种，其中2015、2021年分别采集27、37种，基于栖息水层、繁殖习性和摄食特征等生态类型划分：以栖息于中下层、喜水草上产卵的杂食性鱼类为主；保护区内单位努力捕获量CPUE由0.03上升为0.05；优势种中大鳍鱊、麦穗鱼、兴凯鱊等的年际相对生物量分别由0.24、0.24、0.26上升为2.03、1.12、0.47；其年际相对丰度升高比例均高达50%以上。以上结果表明，修复区内整体资源量呈上升趋势，同时偏好水草区域生活鱼类资源量升高，由此可见实施水生植物修复能够对鱼类资源养护起到良好的效果。

关键词：鱼类群落；时间格局；生态修复；生物多样性

Interannual dynamic analysis of fish community structure in aquatic plant restoration area in Lishan Bay of Taihu Lake

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Abstract: As a national aquatic germplasm resource protection zone, Lishan Bay in Taihu Lake was formerly known as a seine farming area for aquatic products such as Chinese mitten crabs, which led to the massive loss of aquatic plants in the area. In order to restore the ecological functions and fishery resources in the reserve, ecological restoration was carried out in the reserve in 2015. In order to explore the effect of restoration, the resource situation of the water area was investigated in 2015 and 2021. The results showed that a total of 43 species of fish were collected in 2 years, of which 27 and 37 were collected in 2015 and 2021 respectively, based on ecological types such as habitat water layer, reproductive habits and feeding characteristics: inhabiting in the middle and lower layers, spawning on aquatic plants The main omnivorous fishes in the reserve; the CPUE per unit effort in the reserve increased from 0.03 to 0.05; the interannual relative biomass of dominant species such as *Acheilognathus macropterus*, *Pseudorasbora parva*, and *Pseudorasbora parva* increased from 0.24, 0.24, 0.26, respectively The increase is 2.03, 1.12, 0.47; the increase in the relative abundance between the years is as high as more than 50%. The above results show that the resource amount is on the rise, and at the same time, the amount of living fish resources in the aquatic grass area is increasing. It can be seen that the implementation of aquatic plant restoration can have a good effect on the conservation of fish resources.

Key words: fish community; temporal pattern; biodiversity

2019 年 3 月西北太平洋亚热带海域浮游动物种类组成与分布

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摘要：根据 2019 年 3 月“淞航号”调查船在西北太平洋（28o－35oN，147o－154oE）进行渔业资源调查期间采集的浮游动物样本，分析了浮游动物的种类组成与分布。结果表明：该海域共鉴定出浮游动物 456 种（含浮游幼体和未定种）属于 14 个类群 8 个门类，其中桡足类 163 种为最优势类群。优势种包括 9 种暖水种以及 1 种温带种。暖流指示种六鳍箭虫和寒流指示种捷氏哲水蚤均是优势种并同时出现在亚热带海域，表明亲潮和黑潮对该海域浮游动物的多样性和时空分布起到了重要作用。单纯度指数（C）、均匀度指数（J'）、Shannon-Wiener 多样性指数（H'）、丰富度指数（d）均值分别为 0.09±0.10、0.76±0.10、4.88±0.71、23.53±8.08。四种指数空间分布不均匀，呈现斑块状。

关键词: 西北太平洋; 浮游动物; 种类组成; 生物多样性指数

Composition and distribution of zooplankton species in the subtropical waters of the Northwestern Pacific Ocean during March 2019

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Abstract: Based on the investigation data of 44 stations in the area 28^{o}－35^{o}N、147^{o}－154^{o}E of the Northwestern Pacific Ocean by the research ship “Songhang” in March 2019, we analyzed the species composition and distribution of zooplankton. The results showed that the composition of zooplankton in the surveyed area includes 8 categories, 14 groups, 456 species (including planktonic larvae and undetermined species). There were 163 species of copepods as the most dominant group. The dominant species included 9 warm-water species and one temperate species. Both the warm current indicator species S. hexaptera and the cold current indicator species C. jashnovi occurred simultaneously in the subtropical sea, indicating that the Kuroshio Current and the Oyashio Current had an important impact on the diversity and temporal-spatial distribution of marine zooplankton. The average values of purity index(C), eveness index(J'), Shannon-Wiener diversity index(H') and richness index(d) were 0.09±0.10, 0.76±0.10, 4.88±0.71 and 23.53±8.08, respectively. The spatial distribution of the four indexes were uneven and irregular.

Key Words: the northwestern Pacific Ocean; zooplankton; species composition; biodiversity index

基于几何形态测量学的 7 产地中华绒螯蟹背甲分析

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摘要：为有效了解长江中下游部分知名产地中华绒螯蟹的形态特征，本研究应用几何形态测量学方法对长江中下游湖南大通湖，安徽黄陂湖、沱湖、女山湖、无为长江江段，江苏溱湖、石臼湖等 7 个产地的中华绒螯蟹背甲形态进行了产地差异性的比较研究。基于 35 个地标点系统所进行的背甲形态特征归纳及相对扭曲得分判别分析的结果表明，上述 7 个产地的中华绒螯蟹背甲形态存在明显的差异，且对雌、雄个体的产地判别准确率均为 100％。背甲几何形态测量学比较法可为中华绒螯蟹原产地溯源及保护提供便捷及非致死的创新途径。

关键词：中华绒螯蟹；几何形态分析；地标点；产地；差异性

Comparison of Chinese mitten crabs *Eriocheir sinensis* carapaces from seven geographical origins based on geometric morphometric analysis

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Abstract: In order to effectively identify the morphological characteristics of Chinese mitten crabs *Eriocheir sinensis*, geometric morphology analysis was used to comparatively study the differences of the carapace morphology of the crabs from seven well-known geographical origins in the middle and lower reaches of the Yangtze River, i.e., the Datong Lake in Hunan Province; the Huangpi Lake, Tuo Lake, Nvshan Lake, and Wuwei section of the Yangtze River in Anhui Province, the Qinhu Lake, Shijiu Lake in Jiangsu Province. The analysis was carried out based on the carapace morphology characterized by a 35-landmark point system, and corresponding discriminant analysis was done to find the carapace variables based on the relative warps scores. The results showed that the carapace morphologies were significantly different among the crabs from the aforementioned origins. Moreover, the identification accuracies of both female and male crabs among the seven origins were 100%. Our study demonstrated that geometric morphometric analysis could provide a convenient, fast, nonlethal and innovative approach for geographical origin traceability and protection of *E. sinensis*.

Key words: *Eriocheir sinensis*, geometric morphometric analysis, landmark, geographical origin, traceability

阳澄湖中华绒螯蟹周年养殖期间矿质元素“指纹”的动态

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摘要：为有效掌握阳澄湖原产中华绒螯蟹在周年养殖期间矿质元素组成及含量的动态变化，本研究从 2018 年 3 月到 2019 年 2 月逐月对湖区围网中华绒螯蟹第三步足的 10 种矿质元素进行测定。主成分分析结果显示，在周年生长过程中，第三步足矿质元素微化学“指纹”在前三个月变化较大，之后的九个月养殖过程中相关“指纹”特征趋于稳定；线性判别分析与主成分分析有着相同的结果，微化学“指纹”特征在经历三个月的养殖后才较为稳定。上述基于第三步足规范性的研究首次证明，阳澄湖原产中华绒螯蟹中矿质元素微化学“指纹”特征至少需要在湖区养殖三个月后才能定型。

关键词：阳澄湖；中华绒螯蟹；矿质元素；第三步足；微化学“指纹”；周年养殖

Dynamics of element microchemistry "fingerprints" in the Yangcheng Lake originated Chinese mitten crabs *Eriocheir sinensis* during year-round culture period

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Abstract: In order to effectively grasp the dynamic changes of the mineral element composition and content of the originated Chinese mitten crab (*Eriocheir sinensis*) in Yangcheng Lake during the year-round culture period. This study conducted monthly determinations of 10 mineral elements in the third pereiopods of the crabs in the lake from March 2018 to February 2019. The results of principal component analysis showed that during year-round culture period, the microchemistry “fingerprint” of mineral elements in the third pereiopod changed greatly in the first three-month culture period. In contrast, the “fingerprint” characteristics tended to be stable during the next nine-month period. Linear discriminant analysis obtained similar results, i.e., the "fingerprint" profiles of mineral elements stabilized after three months of culture. In this study, the analysis by the third pereiopod samples effectively demonstrated, for the first time, that it required at least three-month culture period for stereotype of the element "fingerprint" profiles for the Yangcheng originated *E. sinensis* crabs during year-round culture in the lake water environment.

Key words: Yangcheng Lake; *Eriocheir sinensis*; mineral element; third pereiopod; microchemistry “fingerprint”; year-round culture period

茜素络合物对青鱼幼鱼耳石的标记效果

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摘要： 放流标记技术研究是支撑增殖放流效果评估的重要内容。本研究用浓度为 100 mg·L^{-1} 的茜素络合物（ALC）对约 2 月龄的青鱼（*Mylopharyngodon piceus*）幼鱼进行了 48 h 标记浸泡，再将其移入正常水体中恢复续养 20 d。在可见光和不同的激发光下对其矢耳石、星耳石和微耳石耳进行确认，荧光标记率均达 100%。对比研究发现，蓝色激发光为相关标记的最佳检测光源，绿色激发光次之。微耳石是用于荧光标记观察和标记时滞检测的最适耳石类型，星耳石次之。将鱼体浸泡入 ALC 溶液中至其在耳石上形成标记沉积，以及将鱼体移出 ALC 溶液至其耳石上标记区域结束，均存在 1 d 时滞。

关键词： 青鱼；耳石；荧光标记；茜素络合物；增殖放流

Otolith marking effect on juvenile black carp (*Mylopharyngodon piceus*) by alizarin complexone

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Abstract: Investigation on artificial marking technology is very important supporting work for national fish mark release recapture and effectiveness tracing evaluation issues. In this study, two-month old juvenile black carps (*Mylopharyngodon piceus*) had been immersed in an alizarin complexone (ALC) solution of 100 mg·L^{-1} for 48 h, and then transferred to normal water for a 20-d recovery culture. Three pairs of otoliths (i.e., sagitta, lapillus and asteriscus) were observed under visible light and different excitation light. All of them achieved 100% mark success. Moreover, the optimum light source for marking observation was blue excitation light, followed by green excitation light. The lapillus was the optimal otolith type for ALC marking determination and judgment of time lag among the three pairs of otoliths, followed by asteriscus. There was a time lag of 1 day between the carps immersed into ALC solution and ALC deposition into otolith, as well as between removing immersed carps from ALC solution and ending of ALC mark in otolith.

Key words: *Mylopharyngodon piceus*, Otolith, Fluorescent marking, Alizarin complexone, Enhancement release

应用稳定同位素技术研究江苏近海食物网营养结构的季节性变化

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摘要：本研究基于稳定同位 s 素技术对江苏近海春、夏、秋季采集的不同生物类群（鱼类、甲壳类、头足类和底栖动物等）进行稳定同位素的分析，利用 SIBER 模型计算不同季节消费者的营养生态位，并计算出 6 种营养结构的量化指标。结果表明：三个季节的 $\delta^{13}C$、$\delta^{15}N$ 值均差异不显著（$P>0.05$）。春季 $\delta^{13}C$ 值范围是-24.47‰～-14.50‰，$\delta^{15}N$ 值范围是 6.86‰～（14.98±0.49）‰，营养级范围是 1.52~4.28±0.17；夏季 $\delta^{13}C$ 值的范围是-19.86‰～-14.44‰，营养级范围是 1.25～3.52；$\delta^{15}N$ 值范围是 5.79‰～(12.54±3.50)‰；秋季 $\delta^{13}C$ 值的范围是(-22.17±4.90)‰～(-14.21±0.36)‰；$\delta^{15}N$ 值范围是 6.30‰～（14.60±0.51）‰，营养级范围 1.34~4.15±0.14。各个季节的食物网结构稳定，一些消费者的营养生态位出现不同程度的重叠现象。其中，春季的食物来源较为广泛，生物营养层次和群落多样性更高；夏季消费者的食物来源更加丰富，但生态位分化程度较低；秋季的食物网结构比较单一，但营养生态位分布较广。

关键词：稳定同位素，江苏近海，营养结构，生态位，季节性变化

Seasonal variation in the trophic structure of food webs in coastal waters of Jiangsu Province based on stable isotope techniques

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Abstract: In this study, we used stable isotope technology to analyze different species (fish, crustaceans, cephalopods, benthos, etc.) collected in spring, summer and autumn in the coastal area of Jiangsu Province. We used SIBER model to calculate the trophic niche of consumers, and calculated the quantitative indicators of six metrics in different seasons. The results showed that there were no significant differences in $\delta^{13}C$ and nitrogen $\delta^{15}N$ values among three seasons ($P > 0.05$). In spring, the $\delta^{13}C$ values ranged from -24.47‰ to -14.50‰, the $\delta^{15}N$ values ranged from 6.86‰ to (14.98±0.49) ‰, and the trophic levels ranged from 1.52 to 4.28±0.17. In summer, the $\delta^{13}C$ values ranged from -19.86‰ to -14.44‰, the $\delta^{15}N$ values range from 5.79‰ to (12.54±3.50) ‰, and the trophic level ranged from 1.25 to 3.52. In autumn, the $\delta^{13}C$ values range from (-22.17±4.90) ‰ to (-14.21±0.36) ‰, the $\delta^{15}N$ values ranged from 6.30‰ to (14.60±0.51) ‰, and the trophic levels ranged from 1.34 to 4.15±0.14. The structure of food web was stable in each season, and the trophic niche of some species overlaps in different degrees. In addition, the food sources are more extensive, and the trophic level and community diversity are higher in spring, the food sources of consumers are more abundant, but the degree of trophic niche differentiation is lower in summer, while in autumn, the structure of food web is relatively simple, but the distribution of trophic niche is wider.

Key words: stable isotopes, coastal waters of Jiangsu Province, trophic structure, trophic niche, seasonal variation

个体差异对西北印度洋鸢乌贼角质颚外部形态变化的影响

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摘要：根据 2019 年冬春季(2—5 月)中国灯光罩网渔船在西北印度洋生产调查期间采集的 1009 尾鸢乌贼样本，分析了其角质颚外部形态变化的影响因素。结果表明：角质颚外形特征参数在不同性别、不同胴长组和不同性腺成熟度间均存在显著差异。各特征参数与脊突长的比值在不同性腺成熟度、不同胴长组间也无显著差异，比值保持稳定，表明角质颚各区域生长保持一致。研究表明，201～250mm 可能是西北印度洋鸢乌贼角质颚外部形态在胴长上的生长拐点，雌性个体性腺成熟度II期和雄性个体性腺成熟度III期可能对应角质颚外部形态在性腺成熟度上的生长拐点。

关键词：鸢乌贼；角质颚；个体生长；外部形态；西北印度洋

Effects of individual differences on beak morphology of *Sthenoteuthis oualaniensis* in the northwest Indian Ocean

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Abstract: With 1009 *Sthenoteuthis oualaniensis* samples collected by Chinese light falling-net fishery during February to May in the northwest Indian Ocean, we analyzed the influencing factors of the morphology change of the beak. There were significant differences in the morphologic growth between genders, different gonad maturity stages, and different mantle length. The ratio of each characteristic parameter to CL was nearly stable with the change of sex, gonad maturity and mantle length, suggesting consistent growth of each dome of beak. Our results suggested the mantle length of 201 mm to 250 mm seemed to be the threshold for the morphologic growth of beak on the body size, while the gonad maturity ofIIandIIIstages seemed to be the threshold for the morphologic growth of beak on the gonad maturity.

Key words: *Sthenoteuthis oualaniensis*, beak, individual growth, morphology, the northwest Indian Ocean

性成熟和个体大小对西北印度洋鸢乌贼耳石形态的影响

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摘要：根据 2019 年 2-5 月我国灯光罩网渔船在西北印度洋海域调查生产期间采集的 1009 尾鸢乌贼样本，利用方差分析(ANOVA) 和最小显著差异法(LSD)研究性别、性腺成熟度以及不同胴长范围对耳石形态变化和相对尺寸变化的影响。结果显示，不同性别间 TSL、LDL、WL 和 MW 的变化存在极显著性差异，雌、雄样本不同性腺成熟度和不同胴长组间 TSL、LDL、WL 和 MW 的变化也均存在极显著性差异；MW/TSL 的变化在不同性别间不存在显著性差异，但在不同性腺成熟度和不同胴长组间存在极显著性差异。研究表明，无论雌雄，性成熟和个体大小对西北印度洋海域鸢乌贼耳石的外形生长都会产生影响。性腺成熟度III期、胴长 300-500mm 是雌性鸢乌贼耳石外形的生长拐点，雄性耳石外形生长拐点不明显。

关键词：鸢乌贼；耳石形态；性别；性腺成熟度；个体大小

Effects of sexual maturity and body size on statolith shape of *Sthenoteuthis oualaniensis* in the Northwest Indian Ocean

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Abstract: According to the samples of *Sthenoteuthis oualaniensis* totaled 1009 in number collected in the northwest Indian Ocean from February to May of 2019 by the Chinese light falling-net fishery fleets. The external form growth and statolith shape changes affected by sex, gonad maturity and individual size are analyzed by the analysis of variance (ANOVA) and Least-significant difference (LSD). The results indicated that the changes of TSL, LDL, WL and MW between different sexes were statistically significant. For both female and male samples, the changes of TSL, LDL, WL and MW between different gonad maturity and different mantle length ranges were also statistically significant. However, changes of ratio of MW to TSL in different sexes showed no significant differences but changes in different gonad maturity and different mantle length ranges showed very significant differences. The study showed that sexual maturation and size of *S. oualaniensis* had an obvious effect on its statolith growth in both males and females. Stage lll gonadal maturity and 300-500 mm mantle length are the growth inflection points of statolith shape of female individuals, while there is no distinct inflection point in male individuals.

Key words: *Sthenoteuthis oualaniensis*, morphology characteristics of statolith, sex, gonad maturity, body size

基于碳氮稳定同位素的西北印度洋鸢乌贼摄食洄游研究

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摘要：为探索西北印度洋鸢乌贼生长发育过程中的食性和栖息地变化情况，本研究通过测定西北印度洋鸢乌贼内壳叶轴切割后各片段的碳、氮稳定同位素比值，分析了个体间的营养生态位关系以及内壳片段稳定同位素比值连续序列的变化规律。

关键词：内壳；稳定同位素；鸢乌贼；洄游

A study on feeding ecology and migration patterns of *Sthenoteuthis oualaniensis* off the northwest Indian Ocean using stable isotope analysis

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Abstract: In order to explore the food and habitat changes in the growth and development of the northwest Indian Ocean squid（*Sthenoteuthis oualaniensis*）, this study analyzed the nutritional ecological niche relationship between different individuals, and the change law of the continuous sequence of Carbon and Nitrogen stable isotope ratios in gladius after cutting the proostracum of gladius.

Key words: gladius, stable isotope, *Sthenoteuthis oualaniensis*, migration

太平洋褶柔鱼个体摄食洄游的稳定同位素研究

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摘要：太平洋褶柔鱼是具有高度洄游性的中上层头足类，是生态系统中的关键物种，也是我国远洋渔业重要捕捞对象之一。了解掌握太平洋褶柔鱼摄食及洄游信息有助于对其资源进行合理利用。头足类内壳是一良好的信息载体，其生长发育具有不可逆性且生长贯穿整个生活史过程，包含了头足类生活史过程中的全部信息。本研究通过对太平洋褶柔鱼内壳按生长方向进行 20mm 的连续切割，测定其碳、氮稳定同位素比值，并初步分析了其在生长发育过程中的食性转换和洄游习性。

关键词：稳定同位素; 内壳; 太平洋褶柔鱼; 洄游路径; 食性

Stable isotope study on feeding and migration of *Todarodes pacificus*

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Abstract: *Todarodes pacificus* is a highly migratory pelagic cephalopod, a key species in the ecosystem, and one of the important fishing objects in China's pelagic fishery. Understanding the feeding and migration information of *Todarodes pacificus* is helpful for rational utilization of its resources. The gladius of *Todarodes pacificus* is a good information carrier, and its growth and development are irreversible and run through the whole life history process, including all the information in the life history.In this study, the carbon and nitrogen stable isotope ratios of the gladius of the *Todarodes pacificus* were measured by continuous 20mm cutting according to the growth direction, and the feeding habits and migration habits of the *Todarodes pacificus* during its growth and development were analyzed.

Key words: stable isotope, gladius, *Todarodes pacificus*, migration path, diets

不同年间中国南海鸢乌贼角质颚生长特性研究

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摘要：为了获知不同年间角质颚外部形态存在的差异，以便了解海洋环境对鸢乌贼生长的影响，本实验通过单方差分析和线性函数拟合得出两个年份(2016、2017)的样本胴长、体重、净重与鸢乌贼角质颚外部形态参数存在的差异，可能与厄尔尼诺事件和拉尼娜事件有关。

关键词：鸢乌贼；角质颚；年间比较；厄尔尼诺；拉尼娜；南海

Growth characteristics of beak of *Sthenoteuthis oualaniensis* from south China Sea in different years

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Abstract: The Marine environment plays an important role in the variation of external morphological parameters of *Sthenoteuthis oualaniensis* from different years.In this study, the differences in mantle length, body weight, somatic weight and external morphological parameters of *Sthenoteuthis oualaniensis* beak in 2016 and 2017 were obtained through one-way difference analysis and linear function fitting, which may be related to El Niño events and La Niña events.

Key words: *Sthenoteuthis oualaniensis*, beak;inter-annual variations, the El Niño, the La Niña, the south China sea

西北太平洋北方拟黵乌贼角质颚色素沉积特性分析

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摘要：角质颚是头足类重要的摄食器官。本文研究了北方拟黵乌贼（*Gonatopsis borealis*）角质颚色素沉积特性。根据2018年9—11月中国鱿钓船在西北太平洋生产调查期间采集的268尾北方拟黵乌贼样本，对其渔业生物学数据进行测定，对其角质颚色素沉积等级进行划分，研究色素沉积等级是否存在性别间差异，并拟合色素沉积等级与胴长、体质量和角质颚外形参数的关系。

关键词：北方拟黵乌贼；角质颚；色素沉积；外部形态参数；西北太平洋

Analysis of pigmentation characteristics on beak for *Gonatopsis borealis* in the Northwest Pacific Ocean

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Abstract: The beak was an important feeding organ of cephalopods. We matched the relationships between the beak pigmentation and mantle length (ML), body weight (BW), sexual maturity and the external morphological parameters of 268 beaks of *Gonatopsis borealis* collected in the Northwest Pacific Ocean from September to November of 2018 by Chinese jigging fishing fleets. This study provides a basis for the fishery ecology research of *Gonatopsis borealis* resource based on the beaks.

Key words: *Gonatopsis borealis*, Beak, Pigmentation stage, morphological parameters, Northwest Pacific Ocean

基于食物网拓扑结构的鱼类关键种识别——以竺山湖为例

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摘要：关键种对维持湖泊生态系统稳定（湖泊生态系统稳定）有重要意义，但识别关键种存在一定的困难（识别困难）。为识别湖泊生态系统中的关键种，本文以竺山湖为例，于 2019 年 11 月至 2020 年 10 月每月对该水域进行了鱼类样本采集，共采集鱼类种类 48 种，并基于食性划分出 39 个功能群。以摄食关系为基础构建了竺山湖食物网拓扑结构图，并利用网络分析法计算该食物网 39 个功能群的网络指数，结合 Key Player Problem 运算的结果进行了分析。研究结果显示，蒙古鲌（*Culter mongolicus*）、翘嘴鲌（*Culter alburnus*）、大银鱼（*Protosalanx hyalocranius*）和陈氏短吻银鱼(*Salangichthys tangkahkeii*)在食物网的网络分析结构中处于最高位置，与其他功能群的联系密切，对食物网的控制能力最强，是竺山湖食物网的关键种。

关键词：关键种；食物网；拓扑结构；网络分析法；竺山湖

Identification of keystone species of fish based on food web topology: the case of Zhushan Lake

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Abstract: Keystone species are important for maintaining the stability of lake ecosystem.However, it is difficult to find keystone species accurately. In order to explore the keystone species in the lake ecosystem, we took Zhushan Lake for example, and collected monthly fishery sample in it from November 2019 to October 2020 to construct a topological structure of the food web of Zhushan Lake based on feeding relationships. 48 species of fish, which were divided into 39 functional groups, were collected. We calculated the network indices of these groups in this food web using network analysis method, and combined the results of Key Player Problem operation. The results showed that *Culter mongolicus*, *Culter alburnus*, *Protosalanx hyalocranius* and *Salangichthys tangkahkeii* were in the highest position in the network analysis structure of the food web. They had close connection with other functional groups, has the strongest control over the food web. So they were the keystone species in the food web of Zhushan Lake.

Key words: Keystonestone species; food network; topology; network analysis method; Zhushan Lake

连云港海域春季游泳生物群落结构及变化

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摘要：为了深入了解连云港近岸海域游泳生物群落结构组成及其年间变化，于2016-2020年连续5年春季在连云港海域开展了游泳生物调查。应用多元统计分析和结构冗余度分析方法，分析了连云港海域春季游泳生物群落组成、资源密度、多样性、优势种和冗余度等。结果显示，连云港海域资源密度在逐年增加，群落生物多样性水平中等且呈下降趋势。2016年和2019年春季群落响应单元均为2，其余年份均为1，群落结构冗余度水平较低；研究表明，连云港春季海域游泳生物空间结构动态变化由少数种类决定。2016-2020年连云港游泳生物种类在逐渐减少，资源量和资源密度呈上升趋势，决定连云港近岸海域游泳生物结构特征的可替代种类较少，当主要种资源受到损害时，游泳生物群落结构会发生较大的变化。

关键词：游泳生物；典型种；分歧种；响应单元；

Community structure and changes of swimming organisms in Lianyungang sea area in spring

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Abstract: In order to deeply understand the composition and annual changes of swimming biological community in Lianyungang Coastal Waters, a survey of swimming organisms was carried out in Lianyungang Coastal Waters in the spring of 2016-2020. The composition, resource density, diversity, dominant species and redundancy of swimming community in Lianyungang sea area in spring were analyzed by using multivariate statistical analysis and structural redundancy analysis. The results showed that the resource density in Lianyungang sea area was increasing year by year, and the community biodiversity level was medium and showed a downward trend. In the spring of 2016 and 2019, the community response unit was 2, and in other years it was 1, so the redundancy level of community structure was low; The results show that the dynamic change of spatial structure of swimming organisms in Lianyungang sea area in spring is determined by a few species. From 2016 to 2020, the species of swimming organisms in Lianyungang are gradually decreasing, and the resource quantity and resource density are increasing. There are few replaceable species that determine the structural characteristics of swimming organisms in Lianyungang Coastal Waters. When the main species resources are damaged, the community structure of swimming organisms will change greatly.

Key words: swimming organisms; Typical species; Divergent species; Response unit;

南海西沙群岛海域鸢乌贼 *Sthenoteuthis oualaniensis* 胃组织微塑料沉积特性研究*

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摘要：随着微塑料在全球海洋环境和鱼类中被发现，海洋微塑料污染越来越受到各界学者的关注。然而，头足类微塑料的研究甚少，南海鸢乌贼（*Sthenoteuthis oualaniensis*）对微塑料的摄取特性的研究更是未见报道。本文根据 2020 年 3-5 月中国生产调查船于南海西沙群岛海域采集的 36 尾鸢乌贼样本，对其胃组织微塑料沉积特性进行了研究。

关键词：鸢乌贼；南海；胃组织；微塑料

Study on characteristic of microplastic deposition in stomach tissues of *Sthenoteuthis oualaniensis* in the South China Sea

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Abstract: With the discovery of microplastics in the global marine environment and fishes, marine microplastics pollution has attracted more and more attention. However, little was known about the effects of microplastics on cephalopods, and the ingestion of microplastics by *Sthenoteuthis oualaniensis* in the South China Sea is unknown. In this study, the characteristic of microplastic deposition in the stomach tissues of 36 *S. oualaniensis* was analyzed by the samples collected from the South China Sea in March to May in 2020.

Key words: *Sthenoteuthis oualaniensis*; South China Sea; stomach tissue; microplastics

长荡湖鱼类群落结构多样性研究及其与环境因子的关系

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摘要：利用相对重要性指数(IRI)、ABC 曲线和冗余分析（RDA）等方法，对长荡湖鱼类群落结构特征及其与环境因子的关系进行了相关分析。鱼类结构结果表明：长荡湖优势种为刀鲚、鲫和鲢。ABC 曲线表明，长荡湖鱼类生物量和丰度曲线有不同程度的交叉重叠，W 值为- 0.005，故长荡湖鱼类群落处于中度干扰状态。冗余分析（RDA）表明，水深、叶绿素含量、浊度、Ph、亚硝酸盐浓度是目前影响长荡湖鱼类群落的主要环境因子。

关键词：长荡湖；鱼类群落结构；环境因子；冗余分析

Diversity of fish community structure and its relationship with environmental factors in Changdang Lake

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Abstract: Based on the relative importance index (IRI), ABC curve and redundancy analysis (RDA), the characteristics of fish community structure and its relationship with environmental factors in Changdang Lake were analyzed. The results of fish structure showed that the dominant species in Changdang Lake were coilia nasus, carassius carp and silver carp. ABC curve showed that the biomass and abundance curves of fish in Changdang Lake overlapped to varying degrees, and the W value was -0.005. Therefore, the fish community in Changdang Lake was in moderate disturbance state. Redundancy analysis (RDA) showed that water depth, chlorophyll content, turbidity, PH and nitrite concentration were the main environmental factors affecting the fish community in Changdang Lake.

Key words: Changdang lake, fish community structure, environmental factors, redundancy analysis

不同捕捞方式下印度洋北部鸢乌贼渔场时空分布差异

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摘要：为了解印度洋北部海域渔场的时空分布规律，对2017-2019年灯光敷网、灯光罩网和鱿钓3种捕捞方式的鸢乌贼作业次数、产量和捕捞努力量渔获量（CPUE）进行统计分析。通过产量重心分析、聚类分析和方差分析，对3种捕捞方式的渔场时空分布及其年间差异进行了分析比较。

关键词：印度洋北部；鸢乌贼；捕捞方式；中心渔场；时空分布

Spatial and temporal distribution of fishing ground of *Sthenoteuthis oualaniensis* in northern Indian Ocean under different fishing methods

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Abstract: The Indian Ocean are the main fishing grounds of *S.oualaniensis*, so exploring the spatial and temporal variation is the basis and precondition for fishing forecasting. Using statistical analysis based on the above data with the effort, catch and CPUE for each of the three fishing methods of light lift net, light casting net and jigging during 2017—2019. Through catch gravity analysis, cluster analysis and two-way analysis of variance, the spatial and temporal distribution of the three fishing methods and their differences in the years are studied and analyzed.

Key words: Northern Indian Ocean; *Sthenoteuthis oualaniensis*; fishing methods; fishing ground; spatio-temporal distribution

基于碳氮稳定性同位素探究入侵物种对赤田水库营养级和生态位影响

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摘要： 2019 年 12 月在赤田水库运用稳定同位素方法对主要鱼类进行营养关系和生态位进行研究。结果显示，赤田水库食物网的 δ^{13}C 值为-34.64δ^{13}C/‰～-23.43δ^{13}C/‰,δ^{15}N 值为 7.59δ^{13}N/‰～17.76δ^{13}N/‰。在赤田水库中杂食性鱼类海南似鱎 *Toxabramis houdemeri* 和日本沼虾 *Macrobrachium nipponense* 处于最高营养级，分别为 3.37 和 3.50，可能是杂食性鱼类偏向肉食或摄食其他鱼类的捕食残留物导致营养级偏高。其他鱼类和营养级在 2.28～3.28。对四种入侵鱼类鱼类和海南似鱎进行生态位宽度与重叠比较，淡水石斑鱼生态位宽度最大，鳙生态位宽度最小。莫桑比克罗非鱼与云斑尖塘鳢生态位重叠显著，与淡水石斑鱼生态位重叠达到 0.3 以上.

关键词：生物入侵；稳定同位素；食物网; 生态位

Study on stable isotopes of carbon and nitrogen effects of invasive species on trophic level and niche of Chitian reservoir

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Abstract: In December 2019, the stable isotope method was used to study the nutritional relationship and niche of main fish in Chitian reservoir. The results show that the food web of Chitian reservoir δ^{13}C value is -34.64δ^{13}N/‰～-23.43δ^{13}N/‰, theδ^{15}N value is 7.59δ^{13}N/‰ ～ 17.76δ^{13}N/‰. In Chitian reservoir, the omnivorous fish, toxabramis of Hainan and Macrobrachium nipponense of Japan, are at the highest nutritional level, which are 3.37 and 3.50 respectively. The nutritional level of other fish is 2.28～3.28. Comparing the niche breadth and overlap of four invasive fish species with *Toxabramis houdemeri*. The niche breadth of *Cichlasoma managuensewas* the largest and that *Hypophthalmichthys nobilis* was the smallest. The niche overlap between *Oreochroms mossambicus* and *Oxyeleotris marmorata* is significant, and the niche overlap with *Cichlasoma managuense* is more than 0.3.

Key words: biological invasion, stable isotope, food web, niche

长江安庆段鳜属仔稚鱼时空分布特征及影响因子

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摘要：为了解长江安庆江段鳜属鱼类早期资源现状及其丰度变化与水文环境因子间的关系，于 2018-2020 年 4-8 月份对该江段进行鱼类早期资源调查。结果显示，鳜属仔稚鱼苗汛时间稳定在 4 月底至 5 月初，各年份仔稚鱼丰度高峰期集中出现在 6、7 月份，资源量呈逐年上升的趋势。采样断面鱼苗密度水平分布的差异性检验表明，2018 年左岸密度显著高于中心密度（$P<0.05$），其他则无显著性差异。相关性分析显示，仔稚鱼丰度变化同江水水位、水流量呈显著正相关（$P<0.01$），与透明度呈显著负相关，与温度呈显著正相关（$P<0.05$），结合仔稚鱼丰度变化及其活动规律，初步推测安庆江段鳜属仔稚鱼的适宜温度为 25.6-29.2℃。

关键词： 安庆江段；鳜属仔稚鱼；资源量；丰度

Spatiotemporal distribution characteristics and influencing factors of larvae and juveniles mandarin fish in Anqing section of the lower reaches of the Yangtze River

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Abstract: In order to understand the current situation of the early resources of the mandarin fish in Anqing section of the Yangtze River, and the relationship between abundance changes and the hydrological environmental factors, an Investigation on the early fish resources was carried out from April to August in 2018 to 2020. The results showed that the flood time of larvae and juveniles mandarin fish was stable from late April to early May, the peak of ichthyoplankton abundance was concentrated in June and July, and the resources increased year by year. Examination of differences in the horizontal distribution of fry density in the sampled sections showed that the left bank density was significantly higher than the central density in 2018 ($P<0.05$) and no significant difference in others. Correlation analysis showed that the abundance changes of larval and juvenile fish was significantly positively correlated with river water level and water flow ($P<0.01$), negatively correlated with transparency and positively correlated with temperature ($P<0.05$). Combined with ichthyoplankton abundance changes and their activity rules, it was preliminarily speculated that the appropriate temperature of larvae and juveniles mandarin fish in Anqing section is 25.6-29.2℃.

Key words: Anqing section; larvae and juveniles of mandarin fish; resources; abundance

长江禁捕初期如皋江段鱼类早期资源现状

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摘要：2021 年 5-8 月对长江如皋江段鱼类早期资源展开调查期间，共采集到仔稚鱼 69359 尾，隶属于 6 目 9 科 42 种，仔稚鱼丰度变化范围在 1.50 ind./100m^3-9668.17 ind./100m^3，平均丰度为 502.74 ind./100m^3。Margalef 丰富度指数(*D*)、Shannon-Wiener 多样性指数(*H*)、Pielou 均匀度指数(*J*)和 Simpson 优势度指数(*λ*)分别为 3.68、2.33、0.62 和 0.16。聚类分析将 9 个采样断面在 77.31%的相似水平上归为 2 组，表明各采样断面仔稚鱼群聚特征差异显著(R=0.625，P=0.008)。与课题组前期研究结果相比，结果表明：禁捕初期如皋江段仔稚鱼种类数目、丰度及群落多样性特征较禁捕前有明显改善，受益于已经全面实施近 2 年的禁渔策略，长江如皋江段渔业资源保护逐见成效，恢复效果明显。

关键词：十年禁渔；如皋江段；早期资源；资源恢复；时空分布；群聚特征

Status of early fish resources in Rugao Section of Yangtze River during the early period of fishing ban

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Abstract: During the investigation of early fish resources in Rugao Section of the Yangtze River from May to August in 2021, a total of 69,359 larvae and juveniles were collected, belonging to 42 species, 9 families, 6 orders. The abundance of larvae and juveniles varied from 1.50 ind./100m^3 to 9668.17 ind./100m^3, with an average abundance of 502.74 ind./100m^3. Margalef richness index (*D*), Shannon-Wiener diversity index (*H*), Pielou evenness index (*J*) and Simpson dominance index (*λ*) were 3.68, 2.33, 0.62 and 0.16 respectively. Cluster analysis classified the 9 samples into two groups at the similar level of 77.31%, indicating a significant difference in juvenile and larval fish clustering characteristics among the sampled sections (R=0.625, P=0.008). Compared with the previous research results of the research group, the results showed that the number, abundance and community diversity of larvae and juveniles species in Rugao Section were significantly improved than the ban was implemented. Thanks to the fishing ban strategy in the last two years, the fishery resources protection in Rugao Section of Yangtze River has achieved obvious recovery effect.

Key words: Ten-year fishing ban; Rugao Section; Early resources; Resource recovery; Spatial and temporal distribution; Clustering characteristics

南海北部马面鲀资源利用状况研究

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摘要：根据 2009—2019 年南海北部渔港渔业生产抽样调查数据，统计得出南海北部的马面鲀（Thamnaconus）的产量主要来自单拖，占总产量的 65.50%。剩余产量模型分析结果显示南海北部马面鲀的最大可持续产量在 73913.73～237211.25 t，平均为 111772.83 t。2012 年、2013 年、2016 年的产量超过了平均最大可持续产量，表明当年发生了过度捕捞，该鱼种的总可捕量可设为 8×104 t。

关键词：马面鲀；剩余产量模型；总可捕捞量；南海北部

Stock assessment of Thamnaconus in the northern South China Sea

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Abstract: Based on the data of sampling survey of fishery production at fishing ports along the northern South China Sea from 2009 to 2019, the production of *Thamnaconus* was mainly from otter trawler, accounting for 65.50% of the total catch. The maximum sustainable yield of *Thamnaconus* ranged from 73913.73 to 237211.25 tons, with an average of 111772.83 tons inferred by surplus production models. The catch of 2012, 2013, and 2016 was above the average MSY indicated by models that meant overfishing in the year, and therefore the current total allowable catch could be set to 8×104 t tons.

Key words: *Thamnaconus*, surplus production model, total allowable catch, *the northern South China Sea*

太湖两种滤食性鱼类肠道和水体中的微生物比较

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摘要：肠道微生物在鱼类的健康和发展中发挥着重要作用。本研究对从太湖东部草型湖区和北部藻型湖区采集的 94 份鲢、鳙肠道内容物和 18 份水样进行了 16S rRNA 测序，阐述了太湖两种经济型滤食性鱼类的肠道和周围水体中的微生物组成、多样性、群落结构和预测功能。本研究不仅提高了我们对这两种滤食性鱼类的肠道微生物的认识，阐明了它们与栖息地和宿主物种的关系，也为鱼类的健康养殖提供了科学的理论基础。

关键词：肠道微生物；栖息地；宿主物种；太湖

Microbial comparison in guts of *Hypophthalmichthys moritrix*, *Hypophthalmichthys nobilis* and water in different habitats of Taihu Lake

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Abstract: Intestinal microbes play important roles in the health and development of fish. Hence, this study investigated the microbial composition, diversity, community structure, and predictive function in guts of two economical filter-feeding fish species and surrounding water in an unfed aquaculture system. Ninety-four fish guts and eighteen water samples were collected from the hydrophyte-dominated and the algae-dominated regions in Taihu Lake (China) were subjected to 16S sequencing. Our findings improve our understanding of gut microbes of these two filter-feeding fish and clarify their associations with habitats and host species, providing a scientific theoretical basis for the healthful aquaculture of fish.

Key words: gut microbes; habitats; host species; Taihu Lake

梅梁湖食物网结构对鲢鳙增殖的生态响应

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摘要：为了探究鲢鳙的放养会对自然湖泊食物网结构带来怎样的改变，从而对鲢鳙增殖放流工作提供参考，本研究运用稳定性同位素技术比较了梅梁湖鲢鳙放流区（网围内）与自然湖区（网围外）各基础食物源同位素 δ^{13}C 和 δ^{15}N 性质差别，各消费者营养级的变化，以及食物网结构之间的差异，并探讨了造成这些差别的主要原因。

关键词：梅梁湖；鲢鳙放养；稳定性同位素技术；营养级；食物网结构

Ecological response of the food web structure in the Lake Meiliang to the enhancement of bighead carp and sliver carp

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Abstract: This paper reports on the changes in stable carbon and nitrogen isotope ratios of seston and muscle tissue of consumers between the enhancement water area of sliver carp and bighead carp in the fish pen and other lake area in the Lake Meiliang, the results suggest that the higher average trophic levels within the fish pen, which imply a higher community stability.

Key words: Meiliang Lake, Sliver Carp and Bighead Carp Stocking, Stable Isotopes Technology, Trophic Level, Food Web Structure

长江鱼类新种—三峡金线鲃

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摘要：2019 年 2 月，在长江三峡库区湖北省秭归县江段采集到一尾中国特有金线鲃属鱼类的全盲个体, 从形态上这一个体极易与当前已知的其他金线鲃属鱼类区分开来，经分类学研究确认是一鱼类新种并命名为三峡金线鲃（Sinocyclocheilus sanxiaensis Jiang, Li, Yang & Chang, 2019），发表于《Zoological Research》2019 年第 6 期.这一物种的发现将我国洞穴鱼类代表类群——金线鲃属鱼类已知的分布范围从北纬 25°左右区域扩展到 30°以北，也成为我国丰富的金线鲃属鱼类多样性中的第 75 个物种。鉴于长江三峡区域实际上蕴含着大量的喀斯特地形和发达的地下水网系统，而这一物种又属于典型洞穴鱼类，我们推测其可能由通向长江的某一条地下暗河而来。该鱼类新种的发现丰富了长江鱼类资源基因库，具有极高的科研保护和开发利用价值。

关键词：鲤科；金线鲃属；洞穴鱼类；三峡；长江

A new species of fish from the Yangtze River : Sinocyclocheilus sanxiaensis

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Abstract: A blind fish from the genus Sinocyclocheilus (*Cypriniformes: Cyprinidae*) was caught in open water in the Three Gorges (Sanxia) reservoir in the mainstream of Yangtze River in Zigui County, Hubei Province, China. Which is named Sinocyclocheilus sanxiaensis (Jiang, Li, Yang & Chang, 2019), which is published in Zoological Research. The blind fish can be easily distinguished from all other congeners. The discovery of this species has expanded the distribution of Sinocyclocheilus cavefish from around 25° N (latitude) to above 30° N and increased the diversity of Sinocyclocheilus to 75 valid species. Given the Three Gorges area encompasses a vast karst landscape with abundant underground water systems, this species potentially entered the area via a subterranean river draining into the Yangtze River. The discovery of the new fish species enriches the gene bank of fish resources in the Yangtze River and has high scientific research, protection, development and utilization value.

Key words: *Cyprinidae*, Sinocyclocheilus, cavefish, Three Gorges, Yangtze River

基于图像识别的 5 个不同产地克氏原螯虾(*Procambarus clarkii*)形态差异分析

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摘要：为了解江苏、江西、湖北、上海、河南 5 个地区克氏原螯虾(*Procambarus clarkii*)的形态差异和获取快速、有效的形态鉴别方法，本研究采用传统形态测量法和地标点法来分析各产地形态差异。两种方法均表明其形态差异主要体现在头胸甲及腹部部位,不同产地间克氏原螯虾具有一定的形态差异，且地标点法区分不同产地克氏原螯虾群体差异性效果显著，这将有利于克氏原螯虾生产和选育过程中群体的鉴别及外形特征的快速获取。

关键词：克氏原螯虾；地标点法；传统形态测量法；形态差异性; 产地；

Image-based morphometric discrimination of crawfish (*Procambarus clarkii*) from 5 habitats

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Abstract: To understand the morphological differences of *Procambarus clarkii* in 5 habitats or populations of Jiangsu, Jiangxi, Hubei, Shanghai, and Henan in China, and to obtain rapid and effective morphological identification methods, traditional morphological measurement methods and landmark method were used to analyze the morphological differences among the five habitats. Both methods showed that the morphological differences are mainly reflected in the carapace and abdomen, and there were some morphological differences among different producing areas, and there were significant differences in distinguishing populations of *Procambarus clarkii* from different producing areas by landmark method, this will be beneficial to the population identification and rapid acquisition of appearance characteristics in the process of production and breeding of *Procambarus clarkii*.

Key words: *Procambarus clarkii*, landmark method, traditional morphometry, morphological difference, geographical origin

韩国水产教育发展历程、现状以及对我国水产教育发展的启示

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摘要：韩国水产教育摸索出了适合韩国水产业发展的一些道路，但仍存在着培养体系落后、缺乏多学科融合等一些问题。本文对韩国水产概况、韩国水产教育的起源、发展和问题进行概述，并对新时代下正在推进的中国水产高等教育的改革和实践从中得到的一些启示进行了初步探讨。

关键词：水产教育；韩国水产；多学科融合；可持续发展

The development course and present situation of South Korea's aquatic education and its enlightenment to China's aquatic education

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Abstract: The aquaculture education in South Korea has found some roads suitable for the development of the aquaculture industry in South Korea, but there are still some problems such as backward training system and lack of multi-disciplinary integration. This paper summarizes the general situation of Fishery in South Korea, the origin, development and problems of fishery education in South Korea, and makes a preliminary discussion on the reform and practice of fishery higher education in China in the new era.

Key words: Aquatic education, South Korea aquatic, South Korea aquatic, Sustainable development

钱塘江渔民对禁渔政策参与意愿的研究

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摘 要：为定量评估钱塘江渔民对禁渔政策的参与意愿，根据渔民的自身意愿，2021年在钱塘江的兰溪、建德和桐庐三个地区发放渔民调查问卷150 份，有效问卷 144份，有效率 96%，符合抽样调查基本要求。调查结果显示，调查对象中年龄主要以 51-60 岁的年龄层为主，大部分渔民家庭人口数为1-6 人，渔民的受教育程度整体偏低，从事捕鱼工作多集中在 10年以上，渔民年收入在 5万元以下。通过 Logistic 回归分析，钱塘江84%的渔民愿意参与禁渔政策的实施，渔民年龄和对补偿政策满意度对于参与禁渔政策实施的意愿具有正向影响；家庭人口数量越多、捕捞收入越高和从事捕鱼工作年份对于其参与禁渔政策实施的意愿具有负向影响；渔民捕捞收入对于其参与禁渔政策实施的意愿无显著影响。

关键词：钱塘江；禁渔；渔民；参与意愿；Logistic 模型

A study on the willingness of Qiantang River fishermen to participate in the fishing ban policy

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Abstract: In order to quantitatively assess the willingness of Qiantang River fishermen to participate in the fishing ban policy, according to their own wishes, the 2021 distributed 150 questionnaires to fishermen in the Lanxi, Kentoku and Tonglu regions of Qiantang River, with an efficiency of 96% (144 valid questionnaires) , meet the basic requirements of sampling survey. The results of the survey show that the majority of the respondents are aged between 51 and 60, most of them have a family population of 1 to 6, the overall education level of the fishermen is low, and most of them have been engaged in fishing for more than 10 years, fishermen earn less than 50,000 yuan a year. By Logistic regression analysis, 84% of the fishermen in Qiantang River were willing to participate in the implementation of the fishing ban policy, and their age and satisfaction with the compensation policy had a positive effect on their willingness to participate in the implementation of the fishing ban policy The larger the family size, the higher the fishing income and the years of fishing work had a negative effect on the willingness to participate in the implementation of the policy.

Keywords: Qiantang River, fishing ban, fishermen, willingness to participate, Logistic model

第六专题：水产品加工与综合利用

香蜂草精油在海鲈鱼保活运输中应激安抚效果的探究

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摘要：为了探究香蜂草精油在海鲈鱼长途保活运输中镇定和安抚效果，减缓运输胁迫引起的应激反应，本实验设置了不同处理组，分别在运输水体中添加不同浓度的香蜂草精油将海鲈鱼运输至 72 h，在运输期间每隔 12 h 测定其免疫功能、组织损伤和生理生化指标,评估整个运输过程中海鲈鱼机体的应激反应程度和生理调控机制，为海水鱼保活运输中的应激镇定安抚提供参考。

关键词：海鲈鱼；保活运输；香蜂草；氧化应激; 镇定剂；麻醉剂

The identification on the stress sedation effect of Lemon Balm essential oil in sea bass (*Lateolabrax maculatus*) alive transportation

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Abstract: In order to alleviate the stress response , investigating the sedative and soothing effects of Lemon Balm essential oil for sea bass during long distance live fish transportation. Different treatment groups were set up in this experiment, added different concentrations of Lemon Balm essential oil into the transportation water for sea bass ,and transported them with 72 h, measured its immune function every 12 h during transportation. Evaluating the stress response degree and physiological regulation mechanism of sea bass during the whole transportation process, as well as to provide reference for stress stabilization and comfort of sea bass during the alive transportation.

Key words: *Lateolabrax maculatus*, alive transportation, Lemon Balm, oxidative stress, sedative, anesthetic

鱼皮明胶稳定鱼油乳液的基础研究

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摘要：哺乳动物明胶占据明胶市场的主要份额，但其存在宗教因素和人兽共患病潜在风险，此外，水产加工行业期望提升副产物高值化利用水平，因此，鱼皮明胶的开发与利用已经引起明胶行业和水产品加工行业的日益重视。本报告将主要汇报课题组在近三年来在鱼皮明胶稳定鱼油乳液的基础研究进展，包括有多尺度制备包裹鱼体系研究、胶原蛋白纳米结构研究、明胶分子修饰技术研究、和明胶来源及工艺研究。

关键词：鱼皮明胶；鱼油乳液；分子修饰；界面层结构

Fish skin gelatins for the stabilization of fish oil-loaded emulsions

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Abstract: Currently, mammalian gelatins occupy the main share of gelatin Market. However, religious factors and potential risks of zoonosis limit the application of mammalian gelatins. Further, the aquatic processing industry shows great interest on the high-value utilization of by-products. Therefore, the development and utilization of fish skin gelatin for the stabilization of fish oil-loaded emulsions have attracted increasing attention in the gelatin industry and aquatic products processing industry. This report will mainly report on the development of fish skin gelatins for the stabilization of fish oil-loaded emulsions in our group in the past three years, including multi-scale preparation techniques of fish oil encapsulations, nanostructure analysis of collagen, gelatin molecular modification technology, and gelatin extraction research.

Key words: Fish skin gelatin; fish oil-loaded emulsion; molecular modification; interfacial layer structure

水产品保鲜技术发展现状及展望

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摘要：水产品凭借丰富的口感以及较高的营养价值在近几十年以来一直受到消费者们的青睐，近三年维持在 6000 万吨的产值并且呈现出稳步上升的趋势。水产食品营养物质含量丰富，在生产、加工、运输、储藏等过程中均会存在腐败变质的风险，所以保鲜技术是水产品产业关注的焦点。本文根据物理保鲜、化学保鲜、生物保鲜，三种保鲜方法，对不同水产品中的指标进行了论述，探究三大保鲜方式的优缺点。目前，生物保鲜方式对于产品以及消费者而言均是最安全的选择，物理、化学保鲜方式优点在于成本低，但保鲜效果不及前者。生物保鲜中的可食用保鲜涂膜是水产品保鲜的发展的核心，通过物理、化学等保鲜方式作为前处理的复合保鲜方式能够使水产品获得较好的保鲜效果。

关键词：腐败变质；保鲜技术；复合保鲜

Fish preservation technology development status and outlook

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Abstract: With rich taste and high nutritional value, aquatic products have been favored by consumers in recent decades, maintaining an output value of 60 million tons in the past three years and showing a steady upward trend. Aquatic foods are rich in nutrients and are at risk of spoilage during production, processing, transportation and storage, so preservation technology is the focus of attention in the aquatic industry. This paper discusses the indicators in different aquatic products based on physical preservation, chemical preservation, and biological preservation, three preservation methods, and explores the advantages and disadvantages of the three major preservation methods. At present, the biological preservation method is the safest choice for both the product and the consumer. The edible freshness coating in biological preservation is the core of the development of aquatic products preservation, and the composite preservation method of physical and chemical preservation methods as pre-treatment can make aquatic products obtain better preservation effect.

Keywords: spoilage; preservation technology; composite preservation

食品热杀菌技术在食品工业中的应用研究与展望

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摘要：食品工业发展至今，杀菌技术仍是工艺流程中至关重要的环节，本文将传统热杀菌技术进行了分类简述，包括：干热灭菌、巴氏灭菌、高压蒸气灭菌、超高温瞬时灭菌、欧姆杀菌、微波杀菌等。对某些常用的灭菌方式在食品中的应用实例进行简述，并对巴氏杀菌乳与超高温瞬时灭菌乳的灭菌条件、物质留存等方面进行了比较；简述了橄榄叶提取物（ole）延长巴氏杀菌乳的研究现状以及传统热杀菌技术的局限性与发展前景。结论：传统热杀菌技术虽具有局限性，但发展时间长，技术成熟度较高，在未来很长的一段时间内依旧是食品加工工艺中的主流杀菌方式。

关键词：热杀菌；食品加工工艺；灭菌方式

Food thermal sterilization technology in the food industry Research and prospects for the application of thermal sterilization technology in the food industry

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Abstract: The food industry has evolved to the point where sterilization technology is still a critical part of the process. In this paper, traditional heat sterilization technologies are briefly categorized, including: dry heat sterilization, pasteurization, autoclaving, ultra-high temperature instant sterilization, oleo-sterilization, and microwave sterilization. Examples of some commonly used sterilization methods in food products are briefly described, and the sterilization conditions and material retention of pasteurized milk and ultra-high temperature instantaneous sterilized milk are compared; the current research status of olive leaf extract (ole) extension of pasteurized milk and the limitations and development prospects of traditional heat sterilization techniques are briefly described. Conclusion: Although traditional heat sterilization technology has limitations, it has been developed for a long time and has a high degree of technical maturity, and will remain the mainstream sterilization method in the food processing process for a long time to come.

Keywords: thermal sterilization, food processing, sterilization methods

清洗技术对鲜切水果和蔬菜的保存和质量影响的研究进展

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摘要:鲜切水果和蔬菜以其良好的新鲜度、丰富的含水量和营养成分，占据了广泛的消费市场。但在贮藏过程中，由于切口暴露，营养物质流出并覆盖在表皮上，微生物会大量繁殖，果蔬会腐烂，果蔬的保质期会明显下降，清洗鲜切果蔬可以有效提高产品的保质期，本文介绍了物理法、化学法和生物法三种常规清洗技术，总结了每种清洗技术在鲜切果蔬中的研究现状，并预测了未来鲜切果蔬清洗技术的发展方向。

关键词：清洗技术；腐烂；鲜切水果和蔬菜

Research progress on the effect of cleaning technology on preservation and quality of fresh-cut fruits and vegetables

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Abstract: Fresh-cut fruits and vegetables have occupied a wide range of consumer markets because of their good freshness, rich water content and nutrients. However, due to incision exposure and nutrients flowing out and covering the epidermis in the storage process, microorganisms will reproduce massively, fruits and vegetables will rot, and the shelf life of the fruits and vegetables will decrease significantly. Washing fresh cut fruits and vegetables can effectively improve the shelf life of products. This paper introduces three kinds of conventional cleaning techniques: physical method, chemical method and biological method. The research status of each cleaning technology in fresh-cut fruits and vegetables was summarized, and the development direction of cleaning technology in fresh-cut fruits and vegetables in the future was predicted.

Key words: cleaning technology, rot, fresh-cut fruits and vegetables

射频技术在食品工业中的应用研究与展望

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摘要：射频加热是一种新兴的介电加热技术，具有加热速度快，穿透性强，加热较均匀等优点，在低水分农产品的杀菌和杀虫等领域的应用越来越受到人们的关注。本文介绍了射频加热的原理、优缺点以及射频在食品加工中在杀菌、杀虫、干燥、灭酶、蒸煮、解冻领域内的应用。同时，提出关于射频加热技术应用存在的主要问题，如射频目前应用物料的局限性，射频干燥食品的相关干燥品质数据的缺乏，射频干燥过程中，受到的尖角效应无法解决，导致物体边角处容易出现过热现象等，同时提出展望，根据射频技术处理过程中的传热传质特性，可以应用于更多特殊行业。

关键词：射频加热；应用；干燥；杀菌；优缺点

Application research and prospect of radio frequency technology in food industry

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Abstract: Radio frequency heating is a new dielectric heating technology, which has the advantages of fast heating speed, strong penetrability and uniform heating, and its application in the fields of sterilization and disinfestation of low moisture agricultural products has attracted more and more attention. This paper introduces the principle, advantages and disadvantages of radio frequency heating, and the application of radio frequency in the fields of sterilization, insecticidal, drying, enzyme inactivation, cooking and thawing in food processing. At the same time, the main problems existing in the application of radio frequency heating technology are put forward, such as the limitation of materials used by radio frequency at present, the lack of relevant drying quality data of food dried by radio frequency, and the inability to solve the horn effect in the process of radio frequency drying, which leads to overheating at the corners of objects. At the same time, the prospect is put forward, which can be applied to more special industries according to the heat and mass transfer characteristics in the process of radio frequency technology treatment.

Key words: Radio frequency heating; Application; Drying; Sterilization; Advantages and disadvantages

不同产地刺参加工过程中多糖等主要成分的变化

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摘要：海参是一种极为珍贵的海产品，营养丰富，富含多种利于人体健康的活性物质而备受关注，其中，海参多糖是重要的活性成分。 本文以两个产地的刺参为对象，研究加工过程中的多糖等营养功能成分的变化，并提取、分离和纯化多糖，主要研究结果如下：海参加工过程中重量和体积都发生了明显的变化，海参从蒸煮、盐渍到泡发，多糖等营养功能成分随之流失，海参蒸煮过程中体积和重量明显减少，多糖等营养功能成分流失在蒸煮液中，并随着加热时间不断增加；海参发制过程中，海参重量和体积不断增大，多糖等营养功能成分在泡发过程中也会发生少量损失。蒸煮过程中损失的多糖等营养功能成分明显多于泡发过程，不同产地刺参的多糖等营养功能成分损失程度不同，发制后得到的即食海参出成率也不同。

关键词：不同产地；刺参多糖；提取；变化；

Changes of polysaccharides and other main components in *stichopus japonicus* from different origins during processing

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Abstract: Sea cucumber, a kind of extremely precious marine product, is rich in nutrition and contains various active substances beneficial to human health, which attracts much attention. Among them, sea cucumber polysaccharide is an important active ingredient. In this paper, *Stichopus japonicus* from two producing areas were taken as material to study the changes of nutritional functional components such as polysaccharides during processing, and to extract, separate and purify polysaccharides. The main research results were as follows: Significant changes took place in weight and size during the processing of sea cucumbers. Nutritive functional components such as polysaccharides lost along with sea cucumbers from cooking, to soaking. The size and weight of sea cucumbers reduced during the cooking process. Nutritional functional components such as polysaccharides lost in the cooking liquor before and with the increasing heating time. The weight and volume of sea cucumbers increased in the process of making sea cucumbers, and the nutritional functional components such as polysaccharides also suffered a small loss in the soaking process. The loss of polysaccharide and other nutritional functional components in cooking process was significantly higher than that in soaming process. The loss degree of polysaccharide and other nutritional functional components in *Stichopus japonicus* from different producing areas was different, and the yield rate of ready-to-eat S *Stichopus japonicus* after brewing was also different.

Key words: Different producing areas; *Stichopus japonicus* polysaccharide; Extraction; chang

冷冻解冻、热处理和超高压对小龙虾肌原纤维蛋白凝胶特性和体外消化率的影响

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摘要：采用冷冻解冻、热处理和超高压对小龙虾进行辅助脱壳，考察脱壳方式对热凝胶品质、消化性及抗氧化活性的影响。与对照比，高压处理（300 MPa，25℃，3 min）能够较好地保持凝胶强度和色泽，但会在一定程度上降低持水性和不易流动水的含量。扫描电镜观察发现，300 MPa 的高压处理能够得到均匀、有序的，且空隙较小的凝胶微观结构。蛋白电泳分析表明，该压力下的高压处理能够使得更多的肌球蛋白重链参与交联。然而，FTIR 表明凝胶中蛋白质二级结构没有发生明显变化。此外，高压处理显著提高了热凝胶的胃蛋白酶消化率，消化产物具有更强的 ABTS 自由基清除能力。研究结果可为开发基于小龙虾肉的凝胶制品提供理论参考。

关键词：脱壳；小龙虾肉；热凝胶；品质；消化性；抗氧化性

Effect of freeze-thawing, heating, and high pressure processing on the gel properties and *in vitro* digestibility of myofibrillar protein from red swamp crayfish (*Procambarus clarkii*)

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Abstract: Red swamp crayfishes were subjected to three shucking treatments (freeze-thawing, cooking and high pressure processing (HPP)), followed by manual separation of the meat. The heat-induced gels made from the obtained meat were evaluated for texture, color, water holding capacity, water distribution, microstructure, protein secondary structure as well as the pepsin digestibility and antioxidant activity. HPP at 300 MPa resulted in good-quality gels with acceptable mechanical properties and desirable color, although it slightly reduced the water holding capacity and proportion of T_{22} water. SEM analysis showed that the gels treated by HPP of 300 MPa have a more orderly and uniform microstructures with reduced pore size, and more myosin heavy chains may be involved in the crosslinking as revealed by SDS-PAGE. However, FTIR results suggested that no obvious change was observed in the protein secondary structure of gels. Additionally, digestion in vitro indicated that HPP shucking improved the pepsin digestibility and ABTS-radical scavenging activity of the gels. These findings could provide a basis for creating new gel-type products based on crayfish meat paste.

Key words: shucking; crayfish meat; heat-induced gels; quality; digestibility; antioxidant activity