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青虾对河蟹养殖水体中浮游动物及水环境因子的影响

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摘要：为探讨青虾对河蟹养殖水体中浮游动物群落结构及其对水环境因子的影响，于 2021 年 3 月至 6 月采集了试验区河蟹养殖池塘和套养青虾的河蟹池塘水体样本，分析了水环境因子、浮游动物的种类构成、生物密度、生物多样性。结果表明: 养殖水体中共鉴定出 25 种浮游动物，其中 12 种为轮虫类，7 种为枝角类，6 种为桡足类，群落结构以轮虫为主，青虾对蟹池塘内轮虫平均密度无显著影响(P＞0. 05)，青虾对枝角类浮游动物和桡足类浮游动物的平均密度有显著影响(P＜0. 05)。

关键词：河蟹; 青虾; 浮游动物; 水环境因子; 冗余分析

Effects of prawn on zooplankton and water environmental factors in crab culture water

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Abstract： In order to study the effects of prawn on zooplankton community structure and water environmental factor in crab culture water，the water samples of the crab pond and prawn-crab mixed culture pond were collected from March to June 2021． The water environmental factors，zooplankton species composition，biological density and biodiversity were analyzed． A total of 25 species of zooplankton were identified，including 12 species of rotifers，seven species of cladocera，and six species of copepods． The community structure was dominated by rotifers，there was no significant difference in the effects of shrimp on the average density of rotifers in crab pond (P＞0. 05)，but there was a significant difference in the effects of shrimp on the average density of cladocera and copepods (P＜ 0. 05)．

Key words:：Eriocheir sinensis; Macrobranchium nipponense; zooplankton; water environmental factor; redundancy analysis

混养青虾对罗氏沼虾养殖池塘水质及浮游植物群落的影响

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摘要：饲料的过量投喂导致罗氏沼虾养殖池塘富营养化和蓝藻爆发。青虾（日本沼虾）是一种杂食性底栖动物，以植物和有机碎屑为食。在本研究中，对照组(CG)为罗氏沼虾单养模式，实验组(EG)为罗氏沼虾与青虾混养。通过 5 次采集水样检测，比较了 CG 和 EG 的水环境因子和浮游植物群落的变化。养殖结束时，CG 中的磷酸盐、亚硝酸盐、硫化物和氨氮显著高于 EG ($P < 0.05$)。在培养中期，EG 的 Margalef 指数、Pielou 指数和 Shannon-wiener 指数显著高于 CG ($P < 0.05$)。EG 的浮游植物生物量和密度低于 CG，蓝藻爆发的时间较晚。结果表明，混养模式下青虾通过消耗残留饵料，有效地转化和储存了部分能量，降低了水体富营养化程度和蓝藻繁殖速度。

关键词：罗氏沼虾；青虾；浮游植物；水环境因子

Effects of Macrobrachium nipponense on phytoplankton communities and water environmental factors in Macrobrachium rosenbergii culture

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Abstract： Excessive feed input led to eutrophication and Cyanobacterial blooms in the culture of giant freshwater prawn (GFP, Macrobrachium rosenbergii). Oriental river prawn (ORP, Macrobrachium nipponense) is omnivorous benthic animals that feed on plant and organic debris. In this study, the control group (CG) only cultured GFPs, while the experimental group (EG) cultured GFPs and ORPs. Water samples were collected from the ponds for 5 times to compared the changes of water environmental factors and phytoplankton communities in CG and EG. Phosphate, nitrite, sulphide and ammonia nitrogen in CG were significantly higher than those in EG at the end of culture ($P < 0.05$). In the middle stage of culture, Margalef index, Pielou index and Shannon-wiener index of EG were significantly higher than those of CG ($P < 0.05$). The biomass and density of phytoplankton in EG were lower than those in CG, and the occurrence of Cyanobacterial blooms in EG was later. The results indicated that ORPs in the mixed culture model effectively transformed and stored part of the energy by consuming the residual bait, which reduced the degree of eutrophication and Cyanobacterial blooms.

Key words:： Macrobrachium rosenbergii, Macrobrachium nipponense, phytoplankton, water environmental factor

一种新型复合微生物制剂对大口黑鲈养殖水体和肠道微生物群落的影响

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摘要：本研究旨在探究微生物制剂对大口黑鲈养殖水体和肠道菌群的影响。结果表明，添加复合微生物制剂（ CMA ：由酵母菌、芽孢杆菌和乳酸菌组成）可升高水体溶解氧水平，降低水体总氮、总磷、氨氮和亚硝态氮含量。CMA 组大口黑鲈具有更高的存活率、末体长、末体重，体重相对增长率、内脏指数、肝脏指数和肥满度。16S rRNA 测序结果表明，添加 CMA 可以有效提高大口黑鲈肠道菌群的丰富度和多样性，抑制肠道中有害菌的增殖，并提高了血清和肝脏中抗氧化酶的活力，同时降低了 MDA 水平。本研究结果可为微生物制剂在大口黑鲈循环水养殖中的应用提供参考，为改善养殖水环境提供了新方法。

关键词：大口黑鲈；微生物制剂；水质；肠道微生物

Effectiveness of a novel compound microbial agent for water quality and the gut microbiota of Micropterus salmoides

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Abstract： The cultivation of largemouth bass (Micropterus salmoides), a species of signifificant economic value in aquaculture, has experienced notable growth recently. However, the deterioration of water quality seriously affects the metabolic responses of M. salmoides. While compound microbial agent (CMA) is widely utilized for ecological rehabilitation and water fifiltration, its application in M. salmoides has not been reported. Here, based on physio-biochemical tests and 16S rRNA sequencing, we investigated the effects of CMA (yeast, Bacillus subtilis, and lactic acid bacteria) on the water quality within the recirculating aquaculture system, along with physiological indices and gut microbiota of M. salmoides. Compared to the control and single microbial agent (yeast), CMA treatment improved the water quality by improving the dissolved oxygen and delaying the increase of pH, total nitrogen, total phosphorus, ammonia nitrogen, and nitrite. The 16s rRNA gene sequencing revealed that the water treated with CMA exhibited elevated levels of chao1, Shannon, Pd, and a larger population of dominant bacterial. Besides, higher values of ACE, chao1, Shannon, and OTU level, and lower Simpson index were found in CMA treated M. salmoides samples, suggesting that CMA treatment enhanced the species richness and diversity of gut microbiota of M. salmoides. Furthermore, CMA treatment hindered the generation and proliferation of harmful bacteria, such as the Mycoplasma mobile 163K species and the Erysipelotrichaceae family, which was associated with enhanced antioxidant enzymatic activity and decreased MDA level in both the serum and liver. These findings shed light on the essential roles of CMA in M. salmoides culturing and introduce an innovative approach to enhance the aquatic environment.

Key words:： Micropterus salmoides, microbial agents, water quality, gut microbiota

投入碳氮比对凡纳对虾零换水养殖系统中生物絮团和虾肠道细菌群落的影响

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摘要：本文在凡纳对虾(Penaeus vannamei)零换水养殖系统中，研究了 3 种投入 C/N 比（8:1、12:1 和 16:1）对水体生物絮团和对虾肠道细菌群落的影响。每种 C/N 比随机设置 3 个试验池（30 m3），每池均以 300 尾/m3 的密度投放幼虾（2.68 ± 0.44 g），进行为期 8 周的养殖试验。在试验的起始（0 d）、中期（28 d）和末期（56 d），采用 16S rRNA 基因测序分析，发现生物絮团细菌群落的 alpha 多样性、组成和相对丰度都发生显著变化；同期的生物絮团和虾肠道细菌群落在 3 组间均存在差异，且生物絮团与虾肠道细菌群落组成具有高度相似性。此外，养殖水体中各形态氮（总氨氮、亚硝酸盐氮、硝酸盐氮、总氮）的动态变化在 3 组间也存在差异，但对虾的生产性能（收获虾重、增重率、存活率、单位产量、饲料转化率）在 3 组间无显著差异。

关键词：凡纳对虾；碳氮比；生物絮团；虾肠道；细菌群落

Effect of Input C/N Ratio on Bacterial Community of Water Biofloc and Shrimp Gut in a Zero-Exchange System with Intensive Production of Penaeus vannamei

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Abstract： An 8-week trial was conducted to investigate the effects of three input C/N ratios (8:1, 12:1 and 16:1) on the bacterial community of water biofloc and shrimp gut in a commercial BFT tank system with intensive aquaculture of P. vannamei. Each C/N ratio group had three randomly assigned replicate tanks (culture water volume of 30 m3), and each tank was stocked with juvenile shrimp at a density of 300 shrimp m−3. Significant changes were found in the alpha diversity, composition and relative abundance of bacterial communities across the stages of the trial, and they showed differences in water biofloc and shrimp gut among the three C/N ratio groups. Meanwhile, high similarity could be found in the composition of the bacterial community between water biofloc and shrimp gut. Additionally, nitrogen dynamics in culture water showed some differences while shrimp performance showed no significant difference among the three C/N ratio groups.

Key words:： biofloc system; Penaeus vannamei; C/N ratio; bacterial community; gut microbiota; nitrogen dynamics; production performance

益生菌添加对养殖水体氮循环的影响

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摘要：近年来，益生菌已被广泛用于水体的原位修复。微生物诱导的氮循环是维持水生生态系统平衡的关键过程。本研究通过宏基因组分析益生菌对养殖水体氮循环的影响。结果显示，添加益生菌显著降低水中氨氮、亚硝酸盐和总氮的浓度。群落结构分析揭示，添加益生菌增加了 Verrucomicrobiota 的相对丰度，降低了 Cyanobacteria 的相对丰度。氮循环功能分析表明，添加益生菌显著增加硝化途径反硝化途径基因的相对丰度。研究表明，添加益生菌可以通过改变氮循环相关功能基因和微生物的相对丰度，促进氮元素的转化和迁移，有利于生态环境保护，并在水产养殖系统中去除含氮化合物。

关键词：益生菌，氨氮，亚硝酸盐，氮循环，硝化作用，反硝化作用

Effect of Probiotics on Nitrogen Cycle in the Aquaculture Pond Water

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Abstract： Recently, probiotics have been widely applied for the in remediation of aquatic water. Nitrogen cycling is a crucial process for maintaining the balance of the aquatic ecosystem. To explore the water quality indicators and their correlation with nitrogen cycling-related functional genes, metagenomic analysis of element cycling was performed to identify nitrogen cycling-related functional genes in Coilia nasus aquatic water between the control group and the groups supplemented with probiotics in feed or water. The results showed that adding probiotics to the aquatic water could reduce the concentrations of ammonia nitrogen, nitrite, and total nitrogen. The nitrogen cycle functional analysis showed that adding probiotics to the water could increase the Nitrification pathways and the Denitrification pathways. Our study demonstrated that adding probiotics to the water can promote nitrogen element conversion and migration, and remove nitrogen-containing compounds in aquaculture systems by altering the relative abundance of nitrogen cycling-related functional genes and microorganisms.

Key words:：probiotics; ammonia; nitrite; nitrogen cycling; nitrification; denitrification

水稻-罗氏沼虾复合养殖对稻田土壤细菌群落及其组装过程的影响

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摘要：稻渔综合养殖已成为提高粮食质量的重要策略之一。为评估水稻-罗氏沼虾综合养殖模式对农业生态系统的影响，采用 16SrRNA 测序技术对土壤细菌群落进行了分析。与水稻单一栽培模式（RM）相比，我们发现，水稻-罗氏沼虾共作（IRPF）对土壤细菌群落的多样性没有显著影响。在培养初期，IRPF 组的 candidate division NC10（门水平）和 Candidatus Methylomirabilis（属水平）的相对丰度显著提高，有助于增强细菌群落中氮循环的相关功能。此外，IRPF 组在中期，降低了细菌群落的复杂性和稳定性。虽然随机过程通常主导这些群落的聚集，但 IRPF 组限制了细菌的迁移并减弱了这些随机过程。另外，IRPF 组对水稻土壤的环境因子有显著影响，特别是亚硝酸盐浓度。这些发现为更好地理解稻渔综合养殖对农业生态系统的微生物影响提供理论见解和参考。

关键词：水稻土壤；罗氏沼虾；土壤细菌群落；稻渔综合养殖

Alterations in Soil Bacterial Community and Its Assembly Process within Paddy Field Induced by Integrated Rice–Giant River Prawn (Macrobrachium rosenbergii) Farming

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Abstract： Integrated rice–aquatic animal farming has become a vital strategy for enhancing food security. To assess the effects of integrated rice–giant river prawn (Macrobrachium rosenbergii) farming (IRPF) on agricultural ecosystems, we used 16S rRNA gene sequencing to analyze soil bacterial communities in comparison with traditional rice monoculture (RM). Our study revealed that the IRPF did not significantly affect the diversity of the soil bacterial community. However, during the initial culture stage, IRPF markedly increased the relative abundance of the phylum candidate division NC10 and the genus Candidatus Methylomirabilis, enhancing nitrogen-cycling-related functions within the bacterial community. Additionally, IRPF reduced the complexity and stability of these communities in the early to middle culture stages. While stochastic processes usually dominate the assembly of these communities, IRPF restricted bacterial migration and reduced the influence of these stochastic processes. Furthermore, IRPF had a significant impact on environmental factors within paddy soils, strongly correlating with shifts in bacterial communities, particularly through variations in soil nitrite concentration. In conclusion, the influence of IRPF on the bacterial community in paddy soils was primarily observed during the early and middle culture stages, and the impacts of IRPF on the soil bacterial community were primarily driven by environmental changes, especially soil nitrite concentration. These findings provide theoretical insights and a reference for understanding the microbiological impacts of different integrated rice–fish farming systems on agricultural ecosystems.

Key words:： paddy soil; giant river prawn; Macrobrachium rosenbergii; soil bacterial community; integrated rice–fish farming

罗平县绿色生态水产养殖业的现存挑战及对策

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摘要：罗平县，位于云南省曲靖市，其水产养殖产业被认定为当地农民经济收益和脱贫的重要支柱。该地区凭借其丰富的水资源和优质的自然条件，具备大力发展绿色生态水产养殖的潜力。然而，其在绿色生态水产养殖的发展道路上面临一些挑战。本文对罗平县的水产养殖现状进行了深入研究，揭示了在环保策略实施、技术推广和产品市场销售等方面存在的问题。为应对这些问题，本文提出了一系列策略性优化建议，目标是促进罗平县水产养殖业的可持续发展，以实现区域经济与生态环境的平衡共存。

关键词：关键词：云南省曲靖市罗平县；绿色生态；水产养殖；优化对策

The existing challenges and countermeasures of the green and ecological aquaculture industry in Luoping County

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Abstract： Abstract: Luoping County, located in Qujing City, Yunnan Province, its aquaculture industry has been identified as an important pillar of local farmers' economic benefits and poverty alleviation. With its abundant water resources and high-quality natural conditions, this region has the potential to vigorously develop green and ecological aquaculture. However, it faces some challenges in the development path of green and ecological aquaculture. This paper deeply studies the current situation of aquaculture in Luoping County, and reveals the problems existing in the implementation of environmental protection strategy, technology promotion and product marketing. To address these problems, this paper proposes a series of strategic optimization suggestions, and the goal is to promote the sustainable development of aquaculture industry in Luoping County to realize the balanced coexistence of regional economy and ecological environment.

Key words:：Key words: Luoping County, Qujing City, Yunnan Province; green ecology; aquaculture; optimization countermeasures

学术出版与水产研究

肇涛澜
约翰威立商务服务有限公司

摘要：肇涛澜，博士，Advanced Science 期刊副主编，Modern Agriculture 期刊执行主编。本科毕业于山东大学生命科学学院。在中国科学院遗传与发育生物学研究所取得博士学位，之后在该研究所从事博士后和助理研究员工作。博士和工作期间的研究内容主要涉及植物表观遗传学和 RNA 分子生物学，曾在 Genome Biology，Genome Research，Plant Cell，PloS Genetics，Protein & Cell 等国际期刊上发表多篇论文。2020 年入选中科院青年创新促进会，并以科学编辑身份加入协会自创期刊 The Innovation，入选 The Innovation 青年编委。2021 年 8 月加入 Wiley，负责 Advanced 系列期刊在农业和食品领域的发展工作和 Modern Agriculture 期刊的整体发展工作。她将介绍水产领域的学术出版趋势。

关键词：Wiley，学术出版，水产

Publishing in Wiley——Aquaculture

Taolan Zhao
Wiley

Abstract：Zhao Taolan obtained her doctor's degree from the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, and later worked as a postdoctoral and assistant researcher in the Institute. She has published papers in international journals such as Genome Biology, Genome Research, Plant Cell, PloS Genetics, Protein&Cell, etc. In 2020, she joined the Youth Innovation Promotion Association, Chinese Academy of Sciences and worked for The Innovation as a scientific editor. In 2021, She joined Wiley as a scientific editor, responsible for the development of Advanced series journals in the fields of agriculture and food, as well as the overall development of Modern Agriculture journals.. She will introduce the publication processes of Wiley journals, especially for those in the field of Aquaculture.

Key words:：Publishing, Wiley, Aquaculture

不同稻田利用模式对稻田土壤理化性质及微生物群落的影响

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摘要：【目的】研究不同稻田种养模式对田块土壤理化性质和微生物群落的影响，进一步探究农业活动对生态环境的作用，为优化稻田综合种养技术提供数据支持。【方法】实验设置了三种稻田利用模式，即稻麦轮作、稻虾轮作（一稻一虾）、稻虾共作（一稻两虾），采集水稻四个种植节点（栽种期、分蘖期、灌浆期、收获期）的稻田土壤样品，检测土壤理化性质及微生物 16S 多样性。【结果】不同稻田利用模式对土壤总有机碳（SOC）、总氮（TN）、速效钾（AK）、含水率（SMC）含量有显著影响，稻麦模式土壤 SOC 及 TN 含量显著高于稻虾种养模式（$P<0.05$）。三种模式土壤的 SOC 含量一直呈升高趋势，但稻麦轮作模式的增量更大（6.58g/kg）。在 TN、TP、AP、AK 等肥力指标上，稻虾轮作模式的土壤营养含量一直低于另外两种模式。

关键词：水稻；克氏原螯虾；微生物；理化性质；温室气体

Effects of different paddy utilization patterns on soil physiochemical properties and microbial communities

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Abstract：[Objective] This study was conducted to explore the effects of different paddy utilization patterns on soil physiochemical properties and microbial communities, and to investigate the roles of agricultural activities on the ecological environment. The results should provide information for the optimization of paddy field comprehensive planting and breeding technology. [Methods] Three paddy utilization patterns were set up, namely rice-wheat rotation, rice-crayfish rotation, and rice-crayfish co-cultivation. Soil samples were collected from rice fields at four stages (planting, tillering, filling, and harvest) to detect soil physicochemical properties and bacterial 16s diversity. [Results] In terms of physiochemical properties, analysis of variance showed that different utilization patterns had significant effects on the contents of total organic carbon (SOC), total nitrogen (TN), available potassium (AK) and soil moisture content (SMC) ($P<0.05$). The contents of SOC and TN in the rice-wheat rotation model were significantly higher than those in the rice-crayfish models. The SOC content in the three cropping patterns showed an increasing trend, with the rice-wheat rotation pattern showing a greater increment (6.58g/kg). In terms of TN, TP, AP, and AK, soil nutrient content in the rice-crayfish rotation model was consistently lower than that of the other two models.

Key words:：Rice, Procambarus clarkii, Microorganism, Physicochemical properties, Greenhouse gas

5 种生境中华绒螯蟹肠道微生物分析

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摘要：本研究旨在探讨不同生境对中华绒螯蟹肠道微生物群落组成的影响。通过高通量测序和宏基因组学方法，分析了来自池塘、稻田、苇田、水库及自然水域的中华绒螯蟹肠道微生物群落。结果显示，尽管生境不同，中华绒螯蟹肠道中的主要细菌门仍然以厚壁菌门为主。不同生境显著影响了肠道微生物的多样性及特有菌属，其中苇田生境的肠道微生物多样性最高，池塘生境最低。此外，肠道微生物功能注释表明，碳水化合物代谢是所有生境中肠道微生物的主要代谢途径。该研究揭示了环境对中华绒螯蟹肠道微生物群落结构与功能的影响，为优化养殖环境及保障中华绒螯蟹健康提供了科学依据。

关键词：中华绒螯蟹；高通量；宏基因组；肠道菌群；生境

Intestinal microbial analysis of Eriocheir sinensis in five habitats

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Abstract： This study aimed to explore the impact of different habitats on the composition of intestinal microbial communities in Eriocheir sinensis. Using high-throughput sequencing and metagenomics, the intestinal microbial communities of E. sinensis from ponds, rice fields, reed fields, reservoirs, and natural water bodies were analyzed. The results showed that despite the habitat differences, the dominant bacterial phylum in the intestines of E. sinensis was Firmicutes. The diversity and specific genera of intestinal microbes were significantly influenced by habitat, with the highest diversity observed in reed field habitats and the lowest in pond habitats. Additionally, functional annotation of the intestinal microbes across different habitats indicated that carbohydrate metabolism was the primary metabolic pathway. This study reveals the influence of the environment on the structure and function of intestinal microbial communities in E. sinensis, providing a scientific basis for optimizing farming environments and ensuring the health of E. sinensis.

Key words:： Eriocheir sinensis; high throughput; macrogene; intestinal flora; habitat

温度对铜鱼幼鱼生长性能、消化酶活性、免疫抗氧化能力及肠道微生物的影响

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摘要：文章研究了不同养殖温度(14、18 、22、26、30 ℃) 对铜鱼(Coreius heterodon) 幼鱼生长性能、消化酶活性、免疫抗氧化能力及肠道微生物变化的影响。结果表明，不同组之间铜鱼体重、特定生长率等指标均表现为高温组（26、30 ℃）>中温组（22 ℃）>低温组（14、18 ℃）。饵料系数在 18.22℃达最大值。摄食率在 28.21℃ 达最大值。各温度组肝脏蛋白酶均无显著性变化，26 ℃肠道蛋白酶显著升高；各温度组脂肪酶无显著变化，肠道均高于肝脏；淀粉酶均在 22℃显著降低。不同温度组丰度最高肠道微生物菌门均为 Bacteroidetes，为 33.4%优势属中丰度最高为 Bacteroides，为 30.52%。丙二醛和溶菌酶各温度组无显著差异，过氧化氢酶在 14 、30 ℃组最高，皮质醇的变化趋势为随温度升高而升高。综合以上结果认为，铜鱼幼鱼生长的适宜温度范围为 26-28.21℃。

关键词：温度；铜鱼；生长性能；消化酶活性；免疫抗氧化能力

Effects of temperature on growth performance, digestive enzyme activity, immune antioxidant capacity and intestinal microbiome of juvenile Coreius heterodon

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Abstract：The effects of different culture temperatures (14, 18, 22, 26, 30 ℃) on growth performance, digestive enzyme activity, immune antioxidant capacity and intestinal microbial changes of juvenile Coreius heterodon were studied. The results showed that the indexes of body weight and specific growth rate of copper fish in different groups were high temperature group (26, 30 ℃) > medium temperature group (22 ℃) > low temperature group (14, 18 ℃). The maximum food coefficient was 18.22℃. The maximum feeding rate was 28.21℃. There was no significant change of liver protease in all temperature groups, and intestinal protease increased significantly at 26 ℃. There was no significant change of lipase in all temperature groups, and the lipase in intestine was higher than that in liver. Amylase decreased significantly at 22℃. The Bacteroidetes with the highest abundance in the different temperature groups are Bacteroidetes (33.4%) and the Bacteroides with the highest abundance (30.52%). There was no significant difference between malondialdehyde and lysozyme in each temperature group, catalase was the highest in 14 ℃ and 30 ℃ groups, and the change trend of cortisol increased with the increase of temperature. Based on the above results, it is concluded that the optimum temperature range for juvenile copper fish growth is 26-28.21℃, in which juvenile copper fish can obtain a larger growth rate.

Key words:：temperature; Coreius heterodon; growth; digestive enzymes; antioxidant capacity; immune indices；Intestinal microbiota

红螯螯虾人工繁育技术研究及在广西的推广示范应用

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摘要：红螯螯虾（Cherax quadricarinatus）原产于澳大利亚，喜欢生活在热带地区的溪流中，俗称“澳洲淡水龙虾”，因其体型大，肉质鲜美，营养价值高，在国内市场备受青睐，近年来年均价格保持在100元/kg以上。红螯螯虾养殖具有食性杂、养殖周期短、养殖利润高等优势。但红螯螯虾自1992年引进我国至今，尚未形成明显规模，主要原因是一直以来红螯螯虾虾苗繁育技术较落后、虾苗产量难以满足本地行业的发展需要、虾苗价格高、养殖成本大、养殖技术不成熟，养殖风险高等问题制约着红螯螯虾产业发展。本文主要介绍中国红螯螯虾人工繁育及养殖概况，广西地区红螯螯虾人工繁育技术研究及推广示范应用，包括红螯螯虾循环水交配、循环水孵化、离体孵化等人工繁育新技术，及“鱼-虾”混养、“渔-光”一体、“大规格虾苗低密度轮捕轮放”等养殖新模式介绍，为相关从业者提供技术参考，以期促进红螯螯虾产业的进一步发展。

关键词：红螯螯虾　广西　人工繁育　养殖模式

Research on artificial breeding technology for Cherax quadricarinatus and its promotion and demonstration applications in Guangxi

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Abstract： Cherax quadricarinatus, commonly referred to as the "Australian freshwater lobster," originates from Australia and flourishes in the tropical streams. Due to its substantial size, delectable meat, and high nutritional value, it is highly valued in the domestic market. Consequently, its average annual price has consistently remained above 100 yuan per kilogram in recent years. Cherax quadricarinatu culture has the advantages of miscellaneous diet, short culture cycle and high profit. Since the introduction of Cherax quadricarinatu to China in 1992, the industry has not yet achieved substantial scale. The primary obstacles include outdated breeding technology for larvae, insufficient production of shrimp seedlings to meet local industry demands, high costs of seedlings, significant breeding expenses, underdeveloped farming techniques, and elevated breeding risks. These challenges collectively impede the growth of the Cherax quadricarinatus industry. This paper provides an overview of artificial breeding and cultivation practices for Cherax quadricarinatu in China. It focuses particularly on the advancements and dissemination of artificial breeding technologies in Guangxi, including innovative techniques such as circulating water mating, circulating water hatching, and in vitro hatching. Additionally, the paper covers new culture models, such as "fish-shrimp" integrated culture, "fish-light" synergy, and "low-density round catching and releasing of large-sized shrimp seedlings." The aim is to offer technical insights to practitioners in the field, fostering the continued growth and development of the red crayfish industry.

Key words:：Cherax quadricarinatus Guangxi artificial breeding culture models

不同种养模式下的稻田浮游生物群落变化研究

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摘要：为了解稻麦轮作（RW）、稻虾轮作（RC1）和稻虾共作（RC2）等种养模式下稻田浮游生物群落结构差异，研究了不同种养模式下稻田浮游生物群落组成、密度及多样性指数。发现不同种养模式水体中浮游生物种类相似，浮游植物优势种以绿藻门和硅藻门为主，浮游动物优势种以轮虫为主。水稻灌浆期，RW 模式下稻田水体中的绿藻门和硅藻门等浮游植物丰度均为最低，平均密度分别为 1203cells/ml、747cells/mL。水稻分蘖期，RC2 模式下浮游植物 Shannon-Wiener 指数和 Pielou 指数均显著高于 RC1 模式（$P<0.05$）；水稻灌浆期，RC2 模式的 Margalef 指数显著高于 RC1 模式（$P<0.05$）。亚硝酸盐（NO2-N）、总磷（TP）是对浮游生物影响最大的环境因子。总体而言，稻虾种养模式下的稻田水体质量更好，浮游生物多样性和丰富度更高。

关键词：克氏原螯虾；稻虾种养；浮游生物；冗余分析

The Variation of Plankton Communities in Different Rice-crayfish Farming Systems

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Abstract： In order to understand the differences of plankton community structure in paddy field under rice-wheat rotation (RW), rice-crayfish rotation (RC1) and rice-crayfish co-cropping (RC2),The composition, density and biodiversity index of plankton in rice field under different cultivation patterns were studied.It was found that the plankton species in the water bodies of different cultivation modes were similar, the dominant species of phytoplankton were chlorophyta and diatom, and the dominant species of zooplankton were rotifers.In the rice filling stage, the abundance of chlorophyta and diatom was the lowest in RW mode, and the average density was 1203cells/ml and 747cells/mL, respectively.At tillering stage, the Shannon-Wiener index and Pielou index were significantly higher in RC2 mode than in RC1 mode ($P < 0.05$);The Margalef index of RC2 mode was significantly higher than that of RC1 mode at filling stage ($P < 0.05$).Nitrite (NO2-N) and total phosphorus (TP) are the most important environmental factors affecting plankton.In general, the water quality of rice paddy under the rice-crayfish cultivation model was better, and the plankton diversity and abundance were higher.

Key words:：Procambarus clarkii; Rice-crayfish co-cultivation; Plankton; Redundancy analysis

黄鳝仔、稚鱼发育及异速生长模式研究

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摘要：为了解黄鳝早期发育阶段的生长特性和异速生长规律，本研究检测了黄鳝仔、稚鱼（1~30 日龄）生长发育特点、全长和体重随日龄的变化、全长与体重的关系、并对身体各功能器官的生长变化与全长进行了回归分析。研究结果表明，黄鳝初孵仔鱼卵黄囊较大，10 日龄完全消失。黄鳝早期发育阶段存在胸鳍，随发育的进行，胸鳍逐渐变小，9 日龄完全消失。黄鳝全长随日龄的生长曲线呈现 S 型，可分为 3 个阶段，且不同阶段的生长率存在显著差异。黄鳝体重随日龄的生长曲线可分为 2 个阶段，不同阶段的生长率也存在显著差异。在仔鱼期和稚鱼期，体重与全长的关系分别为 y = 0.0026x0.6688 和 y = 3E-06x2.599。运用 SPSS 27.0.1 和 Origin 2022 软件将身体各功能器官的生长变化与全长进行回归分析，获得头长、躯干长、尾长、吻长、眼径、头高、体高的异速生长模式，结果表明各功能器官的生长拐点存在一定差异。

关键词：黄鳝；早期发育；仔、稚鱼；异速生长；生长拐点

Allometric growth pattern and development of Monopterus albus at larvae and juvenile stages

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Abstract： The aim of this study was to explore the growth characteristics and allometric growth of Monopterus albus in the early development stages. In this study, the growth and development characteristics, 1 to 30 days post hatching (dph), were described, including total length, body weight, snout length, eye diameter, head height, head length, trunk length, tail length and body height. The results indicated that the yolk sac of the newly hatched larvae of Monopterus albus was large and completely disappeared at 10 dph. A pair of pectoral fins were existed in the early development stage of Monopterus albus, became smaller gradually and disappeared completely at 9 dph. The increase of the total length showed S-Curve, which could be divided into three phases, and the growth rate had significant difference at each phase. The increase of body weight could be divided into two phases, and the growth rate also had significant difference at each phase. The length-weight relationships of larvae and juveniles were: y=0.0026x0.6688, y=3E-06x2.599, respectively. The relationship between various functional organs and the full length was analyzed by SPSS 27.0.1 and Origin 2022 software. The results showed the allometric growth of important functional organs in larvae and juvenile stages of Monopterus albus. The growth inflection points of various functional organs were different, which was coincident with the characteristics of growth, food intake, movement, and so on.

Key words:： Monopterus albus; allometric growth; larvae and juvenile fish; growth inflection point

三种常见双壳类有色外套膜表面微生物群落分析

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摘要：作为经济上重要的物种，双壳类在呼吸和滤食过程中与外部微生物保持密切接触，使它们成为研究微生物群落的首选候选者。尽管对居住在外套膜上的微生物群落进行了大量研究，但居住在有色外套膜的微生物群落的组成和功能仍不清楚。有色区域的色素可能会吸引一些与色素有关的微生物。因此，通过体外培养可快速评估存在于有色外套膜上微生群落的基本特征。我们的研究结果表明，三种双壳贝类(长牡蛎、紫贻贝和栉孔扇贝)的有色外套膜中微生物群落对不同培养基的反应不同，仅在酪氨酸培养基上产生色素沉着。进一步微生物分析显示，在有色外套膜表面产生黑色素的菌株丰度相对较低，这可能与产生黑色素的菌株对特定营养环境的需求有关。然后，我们观察到三种双壳类的着色外套膜中微生物群落的组成存在显著差异（$p<0.05$），不同双壳类动物具有不同的生物标志物。这些微生物通过调节免疫系统和帮助消化、营养吸收和硝化作用来影响宿主。

关键词：微生物多样性； 双壳贝； 颜色 ；外套膜

Analysis of microbial communities on the coloured mantle surface of three common bivalves

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Abstract： As economically significant species, bivalves maintain intimate contact with external microorganisms during respiration and filter feeding, rendering them prime candidates for investigating microbial communities.Although numerous studies have been conducted on the microbial communities inhabiting the mantles, the composition and functions of the microbial community residing within the coloured mantles remain unclear. The pigments in the coloured areas may attract some microorganisms related to pigments. Thus, in vitro culture can be utilized to rapidly assess the fundamental characteristics of the microbial community present in the coloured mantles. Our results indicated that the microbial community in the coloured mantles of three bivalves (Crassostrea gigas, Mytilus edulis, and Chlamys farreri) responded differently to various media, resulting in pigmentation occurring on tyrosine medium. Further analyses by Metabarcoding revealed a relatively low abundance of melanin-producing strains on the surface of coloured mantles, which may be related to the requirement of melanin-producing strains for a specific nutritional environment. Then, we observed that there were significant differences in the composition of the microbial communities in coloured mantles of the three bivalves, with different bivalves possessing distinct biomarkers. These microorganisms affect the host by regulating the immune system and aiding digestion, nutrient absorption, and nitrification. Correlation analysis showed that multiple metabolites of the three bivalves were strongly correlated with bacterial biomarkers and may play an important role in maintaining the dynamic balance of surface microbial communities. In conclusion, this study discussed the multifaceted effects of microorganisms on the dynamic equilibrium of bivalves microbial communities, exploring the intricate connection between the host and the microbe, as well as the composition of microbial communities.

Key words:：Microbial diversity; Bivalve; Coloration; Mantles

氨氮胁迫对凡纳滨对虾肠道健康稳态的影响

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摘要：氨氮是水产养殖系统中普遍存在的污染物，严重危害对虾机体健康。对虾肠道在机体免疫和代谢中发挥重要作用。本研究将凡纳滨对虾暴露于 2 mg/L 氨氮胁迫 7 天，探索了肠道组织形态、生理状态、微生物群落和代谢功能的变化。研究结果显示，氨氮胁迫导致对虾存活率下降，并损伤对虾肠粘膜形态，导致上皮脱落。氧化应激基因（Nrf2 和 SOD）的 mRNA 相对表达水平升高，而 GPx 水平降低。此外，内质网应激基因（Bip、IRE1 和 XBP1）、炎症细胞因子（NF-κB 和 JNK）和凋亡因子（CytC 和 Casp-3）的相对表达水平升高。氨氮胁迫还导致肠道微生物多样性下降和细菌群落组成的显著变化，干扰了对虾肠道代谢功能，尤其是嘧啶、嘌呤、氨基酸和生物碱的代谢。研究表明，2 mg/L 氨氮胁迫可以通过破坏黏膜完整性、影响生理稳态、诱导微生物群落和代谢紊乱等方式损害对虾肠道健康，进而导致对虾存活率下降有关，在对虾养殖中应引起重视。

关键词：对虾；氨氮；肠道菌群；代谢；生理

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Yafei Duan, Yuxiu Nan, Meng Xiao, Yukai Yang
The adverse impacts of ammonia stress on the homeostasis of intestinal health in Pacific white shrimp (Litopenaeus vannamei)

Abstract： Ammonia is a prevalent pollutant in aquaculture systems that poses a risk to shrimp health. In this study, we exposed Litopenaeus vannamei to 2 mg/L ammonia-N stress for a duration of 7 days, and explored the alterations in intestinal tissue morphology, physiological status, microbial community, and metabolic function. The findings revealed that ammonia stress led to a decrease in shrimp survival rates and inflicted damage to the intestinal mucosa, resulting in epithelial exfoliation. The mRNA relative expression levels of oxidative stress genes (Nrf2 and SOD) were elevated, while the level of GPx was decreased. Additionally, the levels of endoplasmic reticulum stress genes (Bip, IRE1 and XBP1), inflammatory cytokines (NF-κB and JNK), and apoptosis mediators (CytC and Casp-3) were increased. Ammonia stress also caused a decline in intestinal microbial diversity and significant variations in the bacterial community composition. Furthermore, ammonia stress disrupted the intestinal metabolic function, particularly affecting pyrimidine, purine, amino acid, and alkaloid metabolism.

Key words:： Shrimp; Ammonia-N; Intestine microbial; Metabolism; Physiological

密度胁迫显著影响了三倍体虹鳟苗种的生长性能和肠道健康

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摘要：本研究基于 16S rRNA 基因 V3-V4 区的 Miseq 序列，对不同密度下流水养殖的三倍体虹鳟 (Triploid rainbow trout) 的肠道菌群和水体的细菌群落进行了比较。旨在发掘三倍体虹鳟在高原环境下苗种培育的最适宜养殖密度。在肠道菌群中用该序列鉴定出 51 个门。测序数据表明，在不同养殖密度下，肠道菌群微生物区系组成存在统计学显著差异。肠道菌群中优势菌门为变形菌门、厚壁菌门、拟杆菌门、放线菌门、酸杆菌门、绿弯菌门、蓝细菌门；变形菌门、厚壁菌门、拟杆菌门肠道中含量占比较高，可能与鱼体的免疫和消化有关；研究结果显示，LD 组的最终体重和增重率均优于其他两组。不同养殖密度下水样菌群组成、肠道菌群的组成、相对丰度、共发生网络存在差异。综上，在高原环境下更适宜低密度养殖，该研究结果为高原环境下三倍体虹鳟苗种适宜的养殖密度提供基础数据，同时为后期三倍体虹鳟成鱼的生态、高效、健康养殖提供参考依据。

关键词：养殖密度；三倍体虹鳟；肠道菌群；比较分析

Density stress significantly affected the growth performance and intestinal health of triploid rainbow trout seedlings

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Abstract： Based on the Miseq sequence of V3-V4 region of 16s rRNA gene, the intestinal flora and water bacterial community of triploid rainbow trout (Triploid rainbow trout) cultured in different densities were compared. The purpose of this paper is to explore the most suitable breeding density of triploid rainbow trout in plateau environment. 51 phyla were identified by this sequence in the intestinal flora. Sequencing data showed that there were statistically significant differences in the composition of intestinal microflora under different culture densities. The dominant bacteria in intestinal flora were Proteus, Phaeophyta, Bacteroides, actinomycetes, Acinetobacter, Campylobacter, cyanobacteria; the contents of Proteus, Bacteroides and Bacteroides in intestinal tract were relatively high, which may be related to the immunity and digestion of fish. the results showed that the final body weight and weight gain rate of LD group were better than those of the other two groups. There were differences in the composition of water-like flora, the composition of intestinal flora, relative abundance.

Key words:culture density; triploid rainbow trout; intestinal flora; comparative analysis

基于低深度全基因组测序的鲟鱼基因组选择研究

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摘要：鲟鱼具有非常高的经济价值，特别是鲟鱼籽酱号称“黑黄金”，在国际市场供不应求。低深度全基因组测序（LCS）为鲟鱼育种提供了一种具有成本效益的替代方案，特别是在缺乏SNP芯片且全基因组测序费用高昂的情况下。在本研究中，针对643尾已测序的俄罗斯鲟鱼（测序深度约为13.68×），评估了LCS在基因型填充和基因组预测中的效率。结果表明，在测序深度为0.5×且样本量超500的情况下，采用BaseVar+STITCH方法能够实现最高的基因分型准确性。此外，当测序深度降低至0.5×，并通过连锁不平衡修剪将SNP密度减少至50K时，预测准确性仍与高深度全基因组测序的预测准确性相当。进一步，增量特征选择方法具有提高预测准确性的潜力。本研究结果表明，LCS与基因型填充的结合可作为一种具有成本效益的策略，有助于推动水产养殖物种的遗传改良。

关键词：鲟鱼；低深度全基因组测序；基因型填充；基因组预测；连锁不平衡修剪；增量特征选择

Genomic selection in sturgeons based on low-coverage whole-genome sequencing

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Abstract： Sturgeon possesses considerable economic value, particularly for its roe, commonly referred to as “black gold” or caviar, which commands high demand in the international market. Low-coverage whole-genome sequencing (LCS) offers a cost-effective alternative for sturgeon breeding, especially given the lack of SNP chips and the high costs associated with whole-genome sequencing. In this study, the efficiency of LCS for genotype imputation and genomic prediction was assessed in 643 sequenced Russian sturgeons (~13.68×). The results showed that using BaseVar+STITCH at a sequencing depth of 2× with a sample size larger than 300 resulted in the highest genotyping accuracy. In addition, when the sequencing depth reached 0.5× and SNP density was reduced to 50K through linkage disequilibrium pruning, the prediction accuracy was comparable to that of whole sequencing depth. Furthermore, an incremental feature selection method has the potential to improve prediction accuracy. This study suggests that the combination of LCS and imputation can be a cost-effective strategy, contributing to the genetic improvement of economic traits and promoting genetic gains in aquaculture species.

Key words:：Sturgeon; Low-coverage whole-genome sequencing; Imputation; Genomic prediction; Linkage disequilibrium pruning; Incremental feature selection.

投喂人工饲料的鳜鱼（Siniperca chuatsi）肠道微生态及 2 株魏斯氏菌属（Weissella）的潜在益生菌鉴定

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摘要：随着养殖技术的进步，人工饲料在鳜鱼饲养中的应用已日趋成熟并广泛普及，这对缩减产品成本及优化资源利用具有重要意义。然而，食物是肠道微生物的决定性因素，鳜鱼食性由天然饵料向人工饲料的转变对肠道微生物的影响尚未揭示。本研究在鳜鱼养殖中分别投喂活鱼饵料和人工饲料，持续 8 周，研究其对鳜鱼肠道组织学和菌群结构的影响。结果表明，投喂人工饲料显著降低了鳜鱼前肠、中肠的肠绒毛高度和肠肌厚度。此外，微生物组成发生了显著变化，魏斯氏菌属（Weissella）的丰度显著增加。PICRUSt 2 功能预测显示人工饲料组鳜鱼肠道微生物编码的大多数基因与代谢相关。本实验首次从人工饲料喂养的鳜鱼中肠中分离纯化出两种魏斯氏菌：融合魏斯氏菌（Weissella Confusa）和食窦魏斯氏菌（Weissella Cibaria）。抗菌实验表明，这两株菌对多种淡水鱼病原菌具有抗性，作为潜在的益生菌具有广泛的应用前景。

关键词：翘嘴鳜；人工饲料养殖；肠道菌群；魏斯氏菌

The profile of gut microbiota and the identification of two potential probiotics from Weissella in mandarin fish (Siniperca chuatsi) fed on an artificial diet

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Abstract：As culture technology advances, mandarin fish (Siniperca chuatsi) fed by artificial feeds become true and is progressively gaining popularity, which is important for reducing product prices and resource consumption. However, food is the decisive factor of intestinal microbes, and the profound effects of such changes in feeding habits on intestinal microbes of mandarin fish have not been revealed. In this study, live fish bait and artificial diets were used to feed mandarin fish for 8 weeks to study their effects on the gut histology and microbiota structure of mandarin fish. The results indicated that feeding artificial diets resulted in a notable decrease in the intestinal villi height and intestinal muscular thickness in the foregut and midgut of mandarin fish. Additionally, there was a significant shift in microbial composition, and a significantly increase in the abundance of Weissella. The PICRUSt 2 function prediction revealed that the majority of genes encoded by gut microbiota of mandarin fish in the artificial diet group were related to metabolism. Meanwhile, two bacterial species of Weissella, W. confusa and W. cibaria, were isolated and purified at the first time from the midgut of mandarin fish fed artificial diets. The antibacterial experiment showed that these two strains had resistance to a variety of freshwater fish pathogens, and they exhibited a wide range of applications as potential probiotics.

Key words:：Siniperca chuatsi; artificial feed culture; gut microbiota; Weissella

与大眼鳜相比，鳜骨骼肌的快速生长由增生和肥大调控

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摘要：利用转录组探索鳜和大眼鳜骨骼肌生长速率差异原因。结果显示，鳜骨骼肌生长速率显著快于于大眼鳜；肥大生长(占比 97.9%)是大眼鳜骨骼肌的主要生长方式。转录组结果显示，二者骨骼肌生长差异基因在卫星细胞增殖、蛋白质合成和降解过程中富集。对转录组结果的进一步分析显示，鳜肌纤维单位面积的 Pax7 阳性细胞数是大眼鳜的 2.3 倍。鳜 myod、pax3、pax7 和 myf5 mRNA 表达量显著高于大眼鳜。在肌纤维融合过程中，鳜以 5 核、6 核融合为主；大眼鳜以 3 核、4 核融合为主，鳜 mef2、myog 和 myomaker mRNA 相对表达量显著高于大眼鳜。蛋白沉积比较中，鳜由蛋白沉淀引起的肌纤维肥大增长率是大眼鳜的 2.85 倍，鳜 polr2a、beclin 和 atg14 mRNA 表达量显著高于大眼鳜，eef2、cast 的表达量显著低于大眼鳜。结果表明，与大眼鳜相比，鳜骨骼肌的快速生长由增生和肥大调控。

关键词：鳜; 大眼鳜; 骨骼肌; 生长速率; 转录组

Both rapid hyperplasia and hypertrophy promoted skeletal muscle growth in mandarin fish Siniperca chuatsi, compared to big-eye mandarin fish Siniperca kneri

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Abstract： [Objective]To investigate the causes of differences in skeletal muscle growth rates between mandarin fish (Siniperca chuatsi) and big-eye mandarin fiish (Siniperca kneri), [Methods] we used 6 mph (month post hatching) mandarin fish and big-eye mandarin fish to compare differences in skeletal muscle growth over a one-month period, and use transcriptomes to explore the reasons for the growth differences. [Results] The results showed that the different value in number of muscle fibers (2.72 times), density (2.56 times), area (1.95 times) and diameter (2.73 times) of mandarin fish are significantly higher than that of big-eye mandarin fish ($P < 0.05$). Hypertrophy (Contribution rate: 97.9%) is the dominant factor in big-eye mandarin fish, and both hypertrophy and hyperplasia (Contribution rate: 2.1%) were significantly different from mandarin fish ($P < 0.05$). Transcriptome results showed that differential genes were enriched in proliferation of satellite cells, protein synthesis and degradation. Further analysis of the transcriptome results showed that the number of Pax7-positive cells per unit area of mandarin fish was 2.3 fold higher that of big-eye mandarin fish ($P<0.05$). Myod, pax3, pax7, and myf5 mRNA expression of mandarin fish were significantly higher than those of big-eye mandarin fish($P<0.05$). In muscle fiber fusion, mef2, myog, and myomaker mRNA expression of mandarin fish were significantly higher than that of big-eye mandarin fish ($P < 0.05$). In protein deposits, the results showed that the muscle fiber area of mandarin fish was 2.85 times larger than that of big-eye mandarin fish by comparing the muscle fiber area with the same number of nuclei. Polr2a, mtorc1, 4e-bp1, s6, e1, murf, foxo3, atg5, beclin, and atg14 mRNA expression of mandarin fish were significantly higher than that of big-eye mandarin fish ($P < 0.05$), while eef2, eif2α, gcn2, eif2b, capn and cast of mandarin fish was significantly lower than that of big-eye mandarin fish ($P < 0.05$). [Conclusion] This work verified that the skeletal muscle growth rate of mandarin fish is faster than that of big-eye mandarin fish. The greater number and higher activity of satellite cells of mandarin fish increased hyperplasia efficiency, and the faster fusion rate and protein precipitation rate increased hypertrophy efficiency. Both hyperplasia and hypertrophy contribute to faster skeletal muscle growth of mandarin fish than that of big-eye mandarin fish.

Key words:：Mandarin fish; Big-eye mandarin fish; Skeletal muscle; Growth rate; Transcriptome

饲料适应对鳜鱼肠道功能及转录组测序分析的影响

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摘要：本研究旨在阐明人工饲料对鳜鱼（Siniperca chuatsi）肠道生长和基因表达的影响。给鳜鱼饲喂合成饲料 90 天。研究结果表明，人工饲料显著降低了肠道、肝脏和胃中的总蛋白质含量，同时也抑制了胰蛋白酶活性。关于脂质代谢参数，肝脏甘油三酯含量明显降低。关于抗氧化参数，肠道、肝脏和胃中的谷胱甘肽过氧化物酶和超氧化物歧化酶活性升高。组织学检查表明，人工饲料显著降低了前肠和中肠的肌层、绒毛长度和绒毛宽度。前肠的肠宽减小，而中肠的肠宽增加。选择了三种鳜鱼进行转录组测序：CG、EA 和 FP。差异分析发现至少 707 个已知的差异基因。转录组分析结果显示，EA 组和 FP 组基因均显著富集在磷酸戊糖途径中。与 FP 组相比，EA 组的差异基因显著富集在糖酵解/糖异生、PPAR 信号通路、蛋白酶体和铁死亡信号通路中。

关键词：人工饲料；鳜鱼；肠道；转录组

Effects of dietary acclimation on intestinal performance and transcriptome sequencing analysis in mandarin fish (Siniperca chuatsi)

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Abstract：This study aimed to elucidate the effects of artificial feed on intestinal growth and gene expression in mandarin fish (Siniperca chuatsi). A synthetic feed was administered to the fish for a duration of 90 days. The findings revealed that artificial feed significantly diminished the total protein content in the intestine, liver, and stomach, while also inhibiting trypsin activity. Concerning lipid metabolism parameters, hepatic triglyceride content was notably reduced. Regarding antioxidant parameters, activities of glutathione peroxidase and superoxide dismutase were elevated in the intestine, liver, and stomach. Histological examination indicated that the artificial diet markedly decreased the muscularis, villus length, and villus width of the foregut and midgut. The intestinal width of the foregut decreased, whereas the intestinal width of the midgut increased.Three types of mandarin fish were selected for transcriptome sequencing: CG, EA, and FP. Differential analysis revealed at least 707 known differential genes. Transcriptome results indicated that genes in both the EA and FP groups were significantly enriched in the pentose phosphate pathway. Compared to the FP group, the differential genes in the EA group were significantly enriched in glycolysis/gluconeogenesis, PPAR signaling pathway, proteasome, and ferroptosis signaling pathways.

Key words:：Artificial feed; Siniperca chuatsi; Intestine; Transcriptome

无鱼粉日粮条件下饲料效率极高与极低大黄鱼肝脏转录组及代谢组差异

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摘要：大黄鱼是我国养殖量最大的海水鱼，也是鱼粉消耗“大户”，选育出对无鱼粉饲料适应性好、饲料效率高的品系对大黄鱼养殖业的持续发展具有重要意义，目前对投喂无鱼粉饲料的大黄鱼个体饲料效率差异的内在机制还研究甚少。本实验利用无鱼粉饲料饲喂均重 190.53g 的大黄鱼 25 天，利用视频记录观测统计每尾鱼的摄食量，根据体质量变化计算出每尾鱼的饲料效率（FE），然后挑选摄食量相近、但饲料效率排位前 10%和后 10%（极端高与极端低）的个体进行肝脏的转录组学和非靶向代谢组学分析和比较。KEGG 分析的结果显示，两组个体的差异表达基因和代谢物主要富集于氨基酸代谢、脂肪酸代谢、核苷酸代谢以及谷胱甘肽代谢等重要代谢通路，表明机体可能通过调节营养吸收代谢功能以及维持机体氧化还原稳态来影响饲料效率性状。本研究为揭示大黄鱼对无鱼粉饲料的适应性及饲料效率差异的机制提供了基础资料。

关键词：大黄鱼、无鱼粉饲料、饲料效率（FE）、转录组、非靶向代谢组、消化代谢

Transcriptomic and Metabolomic Differences in the Liver of Large Yellow Croaker with Extremely High and Low Feed Efficiency under Fishmeal-free Diet

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Abstract：The large yellow croaker (Larimichthys crocea) is the most extensively farmed marine fish in China and a major consumer of fishmeal. Breeding strains that adapt well to fishmeal-free diets and exhibit high feed efficiency is crucial for the sustainable development of the large yellow croaker aquaculture industry. However, the intrinsic mechanisms behind individual variations in feed efficiency when fed fishmeal-free diets are still poorly understood. In this study, large yellow croakers with an average weight of 190.53g were fed a fishmeal-free diet for 25 days. Each fish's feed intake was observed and recorded through video, and feed efficiency (FE) was calculated based on body weight changes. Individuals with similar feed intake but ranked in the top and bottom 10% of feed efficiency (extremely high and low) were subsequently selected for transcriptomic and untargeted metabolomic analyses and comparisons of liver. KEGG analysis revealed that differentially expressed genes and metabolites between the two groups were mainly enriched in crucial metabolic pathways such as amino acid metabolism, fatty acid metabolism, nucleotide metabolism, and glutathione metabolism. This indicates that the organism might influence feed efficiency traits by regulating nutrient absorption and metabolic functions and maintaining redox homeostasis. This study provides fundamental data to elucidate the mechanisms underlying large yellow croaker's adaptation to fishmeal-free diets and variations in feed efficiency.

Key words:：large yellow croaker; fishmeal-free diet; feed efficiency (FE); transcriptome; untargeted metabolome; digestive metabolism

大黄鱼 amy 和 slc5a1
基因耐高糖功能研究

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摘要：大黄鱼在我国海水养殖中占有重要的经济地位，为探究大黄鱼生长性状相关基因的功能以及耐高糖的能力，本研究将以斑马鱼为受体鱼通过转基因及基因编辑技术来探究大黄鱼 amy 和 slc5a1 基因耐高糖能力。通过生物信息学的方法对大黄鱼及其他物种的 slc5a1 氨基酸进行多重序列对比和系统进化树分析，并根据本实验室 ATAC-seq 数据库预测大黄鱼 slc5a1 基因启动子区域调控元件开放结合区域，采用双萤光素酶报告系统检测。双萤光素酶报告基因系统结果推测−2073～−1723 bp 为核心启动子，−1723～−1404 bp 区域为显著开放区域。研究结果为进一步研究大黄鱼 slc5a1 基因的转录调控机制奠定基础。同时，对大黄鱼 amy 基因和 slc5a1 在斑马鱼上进行基因敲除，得到 F2 代后使用高糖饲料投喂，观察生长情况。为今后大黄鱼转基因优良品种的选育、功能基因以及对饲料中糖类物质的添加量提供重要的参考资料。

关键词：slc5a1 基因；amy 基因；耐高糖；基因编辑

Functional studies on the amy and slc5a1 genes for high glucose tolerance in the yellow croaker

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Abstract： Large yellow croaker occupies an important economic position in China's marine aquaculture, in order to investigate the function of the genes related to growth traits and the ability of high glucose tolerance in Large yellow croaker, this study will investigate the ability of amy and slc5a1 genes of Large yellow croaker to tolerate high glucose by using zebrafish as the recipient fish through transgenic and gene editing techniques. Multiple sequence comparisons and phylogenetic tree analyses of slc5a1 amino acids from Large yellow croaker and other species were performed by bioinformatics methods, and the open binding regions of regulatory elements in the promoter region of the slc5a1 gene were predicted based on the ATAC-seq database of our laboratory, which was detected by the dual fluorokinase reporter system. The results of the dual fluorokinase reporter gene system speculated that -2073 ~ -1723 bp was the core promoter and the -1723 ~ -1404 bp region was the significant open region. The results of the study laid the foundation for further research on the transcriptional regulation mechanism of Large yellow croaker slc5a1 gene. At the same time, amy gene and slc5a1 were knocked out in zebrafish, and the F2 generation was obtained and fed with high sugar feed to observe the growth. This will provide important references for the future selection and breeding of good transgenic varieties of Large yellow croaker, functional genes and the addition of sugars to the feed.

Key words:：slc5a1 gene; amy gene; high glucose tolerance; gene editing

脂多糖刺激下栉孔扇贝外泌体对先天免疫的调控作用

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摘要：外泌体作为细胞内部和细胞间的一种额外的通信媒介，以其运载的生物活性物质作为效应物参与生物体内的生命活动。贝类在响应外界刺激时，外泌体可能通过与免疫调控元件间的交互通信调节机体重要的免疫应答，其潜在的分子基础也有待发掘。为了全面地了解海洋生物先天免疫调控的分子机制，我们对栉孔扇贝在不同来源外泌体刺激后的血淋巴细胞进行了多组学分析，即 LPS 来源、PBS 来源和无处理外泌体刺激组。通过 RNA-seq、miRNA-seq 和质谱法探索栉孔扇贝的全局表达变化，分析基因表达模式并在转录、转录后和蛋白质水平上初步筛查了 LPS 来源外泌体刺激后介导先天免疫调控的关键元件，包括许多免疫相关基因/蛋白及发挥调控作用的 miRNAs，还参与细胞过程、免疫应答、代谢和应激等关键途径。PPI 结果进一步表明外泌体介导并利用互作参与栉孔扇贝的先天免疫调节。本研究表明外泌体在海洋无脊椎动物的先天免疫防御机制中发挥核心调控作用。

关键词：外泌体 栉孔扇贝 转录组学 miRNA 组学 蛋白质组学 先天免疫

The regulatory effect of exosomes of Chlamys farreri on innate immunity stimulated by lipopolysaccharide

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Abstract： Exosomes, as an additional communication medium within and between cells, participate in life activities in organisms with their carrying bioactive substances as effectors. In response to external stimuli, the exosomes of shellfish may regulate the body 's important immune response through interactive communication with immune regulatory elements, but its potential molecular basis needs to be explored. In order to gain a comprehensive understanding of the molecular mechanisms of innate immune regulation in marine organisms, we performed a multi-omics analysis of haemolymphocytes stimulated by different sources of exosomes from Chlamys farreri（C.farreri）, namely LPS-sourced exosome stimulation, PBS-sourced exosome stimulation and no-treatment exosome stimulation groups. The global expression changes of C.farreri were explored by RNA-seq, miRNA-seq and mass spectrometry. The gene expression patterns were analyzed and the key elements of innate immune regulation mediated by LPS-derived exosomes were preliminarily screened at the transcriptional, post-transcriptional and protein levels, including many immune-related genes / proteins and miRNAs involved in exerting regulatory roles. Furthermore, a number of different key pathways are implicated, including those pertaining to cellular processes, immune responses, metabolism and stress responses. And the PPI (protein–protein interaction) results further indicate that exosomes mediate and use interactions to participate in the innate immune regulation of C.farreri. This study shows that exosomes play a core regulatory role in the innate immune defense mechanism of marine invertebrates. At the same time, the relevant results can also provide new ideas for disease prevention and control of cultured shellfish and even disease resistance breeding.

Key words:： Exosomes Chlamys farreri transcriptomics miRNAomics proteomics innate immunity

大黄鱼肌肉 HUFA 含量相关候选基因 rnf5 等功能研究

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摘要：为改良大黄鱼品质，培育 Eicosapentaenoic acid（EPA）、Docosahexaenoic acid（DHA）合成能力强、含量高的优质大黄鱼。本研究将以斑马鱼为受体鱼通过转基因及基因敲除技术来探究大黄鱼肌肉 HUFA 含量相关候选基因 rnf5 的功能，现已成功得到 rnf5 基因敲除 F2 代及 rnf5 转基因 F0 代。后续将对 F2 代阳性鱼与对照组做脂肪酸含量差异分析和转录组分析。

关键词：大黄鱼；HUFA；转基因；基因敲除

Functional study on the candidate gene rnf5 associated with the muscle HUFA content in large yellow croaker

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Abstract：To enhance the quality of large yellow croaker, high-quality specimens with strong synthesis ability and high contents of Eicosapentaenoic acid (EPA) and Docosahexaenoic acid (DHA) were cultivated. In this study, zebrafish were employed as the recipient fish to investigate the function of the candidate gene rnf5 related to the HUFA content in the muscle of large yellow croaker via transgenic and gene knockout technologies. The rnf5 gene knockout F2 generation and rnf5 transgenic F0 generation were successfully obtained. Subsequently, the differences in fatty acid content and transcriptome analysis between the F2 positive fish and the control group will be conducted.

Key words:：Large yellow croaker; HUFA; Transgenic; Gene knockout

大西洋鲑多组织基因调控变异研究

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摘要：大西洋鲑鱼是外来养殖中最大的群体，并且在鱼种中的数据也比较大，拥有大量的 DNA 数据、RNA 数据等遗传数据。然而，目前还没有比较完善的整理和荟萃分析，而 eQTL 技术在人类疾病、动物抗病生长等重要性状上有重要应用通过 eQTL 分析，研究人员可以确定哪些基因型变异(通常是单核苷酸多态性，SNPS)与基因表达水平的变化相关。本次实验构建大西洋鲑鱼 molQTL 图谱，探索其调控变异的保守性，将为大西洋鲑鱼经济性状主要基因的挖掘和鉴定提供依据。之后我们探索了 eGene 中 SNPS 在不同组织中与转录起始位点的距离分布。结果表明，越靠近转录起始位点，eGene 的比例越高，且在 12 个组织中均有相同的趋势。此外，Cis-eQTL、Cis-sQTL 和 Cis-3′aQTL 的结果因变异注释类型的不同而丰富。我们发现 Cis-eQTL 主要富集于基因内、起始密码子缺失、终止子缺失和终止密码子保留等变异区域等。

关键词：大西洋鲑，eQTL，SNP，eGene

Gene regulatory variation in Atlantic salmon in multiple tissues

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Abstract：Atlantic salmon is the largest group in foreign culture, and the data of Atlantic salmon in fish species is also relatively large, with a lot of DNA data, RNA data and other genetic data. However, there is no comprehensive collation and meta-analysis, and eQTL technology has important applications in human disease, animal disease resistance growth and other important traits. Through eQTL analysis, researchers can determine which genotypic variants (usually single nucleotide polymorphisms, SNPS) are associated with changes in gene expression levels. In this study, the molQTL map of Atlantic salmon was constructed to explore the conservativeness of its regulatory variation, which will provide a basis for the mining and identification of major genes of economic traits of Atlantic salmon. We explored the distance distribution of SNPS in eGene from transcription start sites in different tissues. The results showed that the closer the transcription start site was, the higher the proportion of eGene was, and the same trend was observed in all the 12 tissues. In addition, the results of Cis-eQTL, Cis-sQTL, and Cis-3 'aQTL were enriched by different types of variant annotations. We found that Cis-eQTL was mainly enriched in variation regions such as intra gene, start codon deletion, terminator deletion and stop codon retention.

Key words:：Atlantic salmon，eQTL，SNP，eGene

基于公共数据库转录组数据对河蟹（Eriocheir sinensis）的遗传变异挖掘

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摘要：公共数据库存储了大量的转录组数据，有效利用这些数据是科学界的共同兴趣。本研究介绍了一种新策略，利用从转录组数据中鉴定的 SNPs 和 InDels，并结合数据库中的样本记录信息，有效筛选与性状相关的分子标记。我们利用 NCBI 数据库中的 228 个河蟹转录组数据集，鉴定了 96,388 个 SNPs 和 20,645 个 InDels。结合性别记录，通过 GWAS 分析，鉴定了性别偏向的 3456 个 SNPs 和 639 个 InDels。KOG 和 KEGG 注释显示，这些变异相关基因主要参与了河蟹的代谢过程。结合 SnpEff 注释和 PCR 实验验证，我们发现位于基因 Klhdc4 中的一个高度性别偏向的 SNP，CHR67-6415071，改变了 Klhdc4 的剪接位点，产生了两种剪接变体即 Klhdc4_a 和 Klhdc4_b。本研究挖掘了可用于河蟹单性养殖的分子标记，且为公共数据库中转录组数据的合理开发和利用提供了新方向。

关键词：河蟹；性别偏向；SNPs；InDels；Klhdc4；可变剪接

Genetic variation mining of the Chinese mitten crab (Eriocheir sinensis) based on transcriptome data from public databases

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Abstract： At present, public databases house an extensive repository of transcriptome data, with the volume continuing to grow at an accelerated pace. Utilizing these data effectively is a shared interest within the scientific community. In this study, we introduced a novel strategy that harnesses SNPs and InDels identified from transcriptome data, combined with sample metadata from databases, to effectively screen for molecular markers correlated with traits. We utilized 228 transcriptome datasets of Eriocheir sinensis from the NCBI database and employed the Genome Analysis Toolkit software to identify 96 388 SNPs and 20 645 InDels. Employing the genome-wide association study analysis, in conjunction with the gender information from databases, we identified 3456 sex-biased SNPs and 639 sex-biased InDels. The KOG and KEGG annotations of the sex-biased SNPs and InDels revealed that these genes were primarily involved in the metabolic processes of E. sinensis. Combined with SnpEff annotation and PCR experimental validation, a highly sex-biased SNP located in the Kelch domain containing 4 (Klhdc4) gene, CHR67-6415071, was found to alter the splicing sites of Klhdc4, generating two splice variants, Klhdc4_a and Klhdc4_b. Additionally, Klhdc4 exhibited robust expression across the ovaries, testes, and accessory glands. The sex-biased SNPs and InDels identified in this study are conducive to the development of unisexual cultivation methods for E. sinensis, and the alternative splicing event caused by the sex-biased SNP in Klhdc4 may serve as a potential mechanism for sex regulation in E. sinensis. The analysis strategy employed in this study represents a new direction for the rational exploitation and utilization of transcriptome data in public databases.

Key words:： Eriocheir sinensis; sex-biased; SNPs; InDels; Klhdc4; alternative splicing

表观基因组编辑：一种水产育种新方法

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摘要：表观遗传是不改变基因组序列情况下，调控基因表达的遗传机制，包括 DNA 甲基化、组蛋白修饰等。利用位点特异性表观遗传编辑技术对重要经济性状关键基因的转录表达进行精准调控，将有望克服转基因和基因组编辑育种面临的生物安全、生态安全“卡脖子”问题。华南师范大学水产动物遗传育种团队通过将表观遗传学与水产育种学交叉融合，在鱼类中建立了 DNA 甲基化编辑关键技术(Epigenetics, 2023)，提出“表观基因组编辑育种”新思路(Reviews in Aquaculture,2024)，并针对重要经济性状开展一系列种质创制和新品种培育工作。表观基因组编辑育种利用表观遗传编辑技术，通过特异性改变表观修饰调控相关基因表达，以实现改变个体表型、强化某些优良性状的目的。新的育种方法既不改变基因序列，也不会在个体和种群中引入外来基因，因此不会对物种基因库带来威胁，具有其独特优势。

关键词：表观遗传，DNA 甲基化，遗传育种，组蛋白修饰，表观遗传编辑

Epigenome editing: A New Approach to Aquaculture Breeding

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Abstract：Epigenetic modifications are the changes in inheritable materials other than DNA sequence. The major types of epigenetic modifications include DNA methylation, histone modifications, non-coding and small RNAs, and RNA modifications. The CRISPR/dCas9 system can be used for epigenome editing by fusing effector domains from different enzymes. In previous study, we have established a DNA methylation editing method in the zebrafish model. The aquaculture breeding programs aim to enhance the desirable phenotypes or/and eliminate the undesirable phenotypes, and finally bring a better commercially valuable trait. Therefore, a breeding technology, which possesses the genome-editing technology’s capacity to alter gene expression without its controversy, is urgently necessary for sustainable aquaculture development. Herein, we propose that epigenome editing technology can serve as a promising tool in the genetic improvement of farmed species in aquaculture. Epigenome editing technology or epigenetic breeding does not change the genomic DNA sequence, which will not be involved in the controversy faced by transgenic or genome-edited strains and may be more convenient for commercial use.

Key words:：Epigenetics，DNA methylation，Breeding，Histone modification，Epigenome editing

基于多组学分析的罗氏沼虾幼虾急性低盐胁迫的调控及响应机制

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摘要：罗氏沼虾是中国淡水经济水产养殖的重要物种，但在幼虾阶段，其对盐度的需求较高，这会导致水中的盐度压力。为了阐明罗氏沼虾对急性低盐暴露反应的调控机制，我们对罗氏沼虾在不同盐度（0‰、6‰和 12‰）下暴露 120 小时的反应进行了全面研究。研究了过氧化氢酶、超氧化物歧化酶等酶的活性，暴露在低盐度环境中后，肝胰腺和肌肉中的超氧化物歧化酶和谷胱甘肽过氧化物酶活性显著受抑，导致罗氏沼虾发生氧化损伤和免疫缺陷。转录组中的基因差异表达表明，低盐度胁迫导致罗氏沼虾代谢差异、免疫和炎症反应功能障碍。蜕皮抑制激素、保幼激素酯酶和蜕皮激素受体基因的差异表达表明，罗氏沼虾的生长、发育和蜕皮能力受到抑制。在蛋白质组学水平上，低盐度引起了代谢差异，影响了生物和细胞调节，以及免疫反应。通过代谢组学筛选出了酪胺、反式-1,2-环己二醇、山梨糖醇、乙酰胆碱氯化物和氯喹作为差异代谢标志物。

关键词： 低盐度胁迫；组学；罗氏沼虾；环境；急性胁迫

Regulation and Response Mechanism of Acute Low-Salinity Stress during Larval Stages in Macrobrachium rosenbergii Based on Multi-Omics Analysis

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Abstract: Macrobrachium rosenbergii is an essential species for freshwater economic aquaculture in China, but in the larval process, their salinity requirement is high, which leads to salinity stress in the water. In order to elucidate the mechanisms regulating the response of M. rosenbergii to acute low-salinity exposure, we conducted a comprehensive study of the response of M. rosenbergii exposed to different salinities' (0‰, 6‰, and 12‰) data for 120 h. The activities of catalase, superoxide dismutase, and glutathione peroxidase were found to be significantly inhibited in the hepatopancreas and muscle following low-salinity exposure, resulting in oxidative damage and immune deficits in M.rosenbergii. Differential gene enrichment in transcriptomics indicated that low-salinity stress induced metabolic differences and immune and inflammatory dysfunction in M. rosenbergii. The differential expressions of MIH, JHEH, and EcR genes indicated the inhibition of growth, development, and molting ability of M. rosenbergii. At the proteomic level, low salinity induced metabolic differences and affected biological and cellular regulation, as well as the immune response. Tyramine, trans-1,2-Cyclohexanediol, sorbitol, acetylcholine chloride, and chloroquine were screened by metabolomics as differential metabolic markers.

Key words:： low-salinity stress; omics; Macrobrachium rosenbergii; environment; acute stress

福建牡蛎获得性耐热性状特性与遗传参数研究

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摘要：获得性耐热能力在贝类应对重复胁迫中扮演重要角色，然而这种能力尚未在其耐热性能提升中得到重视，一个重要原因是这种能力的特性和能否遗传均不清楚。本研究以福建牡蛎作为研究对象，通过设置单因素变量，发现预启温度不能低于 34℃，当预启温度在 36℃至 40℃范围时，诱导出的耐热能力会随着预启温度的升高而增强。恢复阶段不可或缺的，且较高的恢复温度（> 24℃）会降低后期获得的耐热能力。并且，福建牡蛎获得的耐热能力的最长可维持 40 天。随着维持时间增加，4 个 HSP 基因的表达以不同的速度和程度下降，其中 HSP10 的下降速度最慢，且其表达量始终高于对照组。同时，通过在 2021 年和 2023 年分别构建 19 和 35 个福建牡蛎全同胞家系，评估得出获得性耐热性状具有低遗传力且与基础性耐热性状的具有低表型和遗传相关，适合分别独立选育。研究结果为福建牡蛎获得性耐热能力的进一步研究利用提供了参考。

关键词：福建牡蛎、获得性耐热、特性、遗传参数

Characteristic and genetic parameters of acquired thermotolerance traits in Fujian oyster (Crassostrea angulata)

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Abstract： Acquired thermotolerance is important for shellfish, but this ability is not yet a focus in heat tolerance enhancement. This is because we don't know much about it, including whether it can be inherited. This study used the Fujian oyster. It found that the pre-starting temperature could not be lower than 34°C. When the pre-starting temperature was between 36°C and 40°C, the induced heat tolerance capacity was enhanced. The recovery stage is important. Higher recovery temperatures would reduce the heat tolerance obtained at later stages. The Fujian oyster can maintained acquired thermotolerance for up to 40 days. The four HSP genes declined at different rates as the maintenance time increased. HSP10 showed the slowest decline and always had higher expression than the control. Meanwhile, 19 and 35 full sibling lines of Fujian oyster were constructed in 2021 and 2023, respectively. The acquired thermotolerance trait had low heritability and low phenotypic and genetic correlation with the basal thermotolerance trait. This is suitable for independent breeding. The results of this study provide a reference for further research and utilisation of acquired heat tolerance in the Fujian oyster.

Key words:：Crassostrea angulata; acquired thermotolerance; characteristic; genetic parameters

辽东湾雄性和雌性斑海豹的比较基因组学研究

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摘要：人类活动和环境变化对海洋哺乳动物的生物多样性产生了重大影响。斑海豹(Phoca largha)是中国唯一的鳍状动物，已被列为国家一级保护物种。然而，目前对该濒危物种的保护基因组学信息报道有限。本研究利用全基因组测序数据，对辽东湾地区的雄性和雌性大叶藻进行了基因组比较。结果表明，雄性大叶藻的基因组大小为 2.39 Gb，雌性大叶藻的基因组大小为 2.49 Gb。PSMC 分析显示，辽东湾斑海豹的数量最近有所下降。本研究报告的基因组资源和分子标记将为进一步开展斑海豹的保护遗传学和进化生物学研究提供参考。

关键词：斑海豹；保护基因组学；性别差异；分子标记

Comparative genomics of male and female spotted seals in the Liaodong Gulf, China

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Abstract： Human activities and environmental changes have substantial effects on biodiversity11 of marine mammals. The spotted seal (Phoca largha) is the only pinniped breeding in12 China, and it has been listed as the Grade 1 State Protection Species in China. Yet13 limited conservation genomics information of this endangered species were reported14 till now. In this study, whole genome sequencing data were used to implement15 genomic comparison of male and female P. largha collected from the Liaodong Gulf.

Key words:： Phoca largha；conservation genomics；sex difference；molecular marker；demographic analysis.

翘嘴鳜 scd1 基因克隆及不同饲喂条件下的表达分析

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摘要：硬脂酰辅酶 A 去饱和酶作为脂肪酸去饱和酶家族的成员，在哺乳动物的脂肪酸代谢、抗氧化和免疫调节等方面起着至关重要的作用。目前为止，关于 scd1 在翘嘴鳜中的作用机制的研究较少。本研究从翘嘴鳜中克隆并鉴定了 scd1，确定了其在不同饲喂条件下的转录模式。scd1 基因的编码序列长度为 1081bp，编码一个含有 333 个氨基酸残基的蛋白质。推定 ScSCD1 无信号肽，1 个 N-连接糖基化位点，24 个磷酸化位点，4 个跨膜结构和 3 个保守的组氨酸元件。多重比对表明 ScSCD1 与硬骨鱼类的同源物具有较高的同一性。系统发育、共线性和基因结构分析进一步表明 scd 基因在脊椎动物中高度保守。Scscd1 在所有受检组织中都有表达，且在雌雄个体间和不同饲喂条件下存在组织表达差异。本研究有助于进一步探明 scd1 的基因的表达模式，为翘嘴鳜的饲料驯化和养殖提供可参考的资料。

关键词：翘嘴鳜（Siniperca chuatsi）；scd1；基因表达

Molecular cloning of scd1 and its expression in response to feeding with different diets in mandarin fish (Siniperca chuatsi)

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Abstract： Stearoyl-coenzyme A desatu-rase(SCD), a member of the fatty acid desaturase family, plays crucial roles in fatty acid metabolism, antioxidant and immune regulation in mammals.Thus far, its roles in Siniperca chuatsi are still rarely known. In the present study, the scd1 gene was identified and characterized from mandarin fish (Siniperca chuatsi), and then its transcription pattern in response to feeding with different diets was determined. The coding sequence of scd1 gene is 1081 bp in length, encoding a protein with 333 amino acids. The putative Sc-Scd1 have no signal peptide, and contains a N-linked glycosylation site, 24 phosphorylation sites, 4 transmembrane structures, and 3 conserved histidine elements. Multiple alignments revealed that Sc-Scd1 shares high identity with its homologs in teleosts. Phylogenetic, syntenic, and gene structure analysis further demonstrated that scd1 genes are highly conserved among verte-brates. Meanwhile, Sc-scd1 was detectable in all tested tissues, there were differences in tissue expression between male and female individuals and under different feeding conditions.Taken together, our findings may play important roles in exploring the expression pattern of scd1 gene, and provide reference data for feed domestication and breeding of mandarin fish (Siniperca chuatsi).

Key words:： scd1, Siniperca chuatsi, Tissue expression

超雄大口黑鲈创制及全雄苗种规模化繁育

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摘要：培育单性化良种对大口黑鲈产业发展具有重要的经济价值，采用不同浓度的 DES 外源激素饲料对大口黑鲈鱼苗进行投喂，通过性别分子标记和性腺组织学鉴定伪雌鱼，研究发现 300ppm DES 可将 XY 大口黑鲈逆转为生理型雌性，性逆转率达到 90%以上。通过对关键基因表达—性激素水平—性腺发育调控网络进行分析，推测类固醇激素合成通路是其性反转的主要信号通路。随后，利用 XY 伪雌鱼和 XY 正常雄鱼配组，通过性别标记筛选获得了 249 尾 YY 超雄大口黑鲈。2024 年繁殖季节，利用 YY 超雄鱼与正常 XX 雌鱼配组，繁育了全雄大口黑鲈苗种 130 万尾，经检测后代 XY 基因型为 100%。本研究建立了超雄大口黑鲈培育及全雄大口黑鲈规模化繁育技术体系，为大口黑鲈良种选育提供了技术保障。

关键词：大口黑鲈；性逆转；YY 超雄鱼；全雄鱼

Creation of YY largemouth bass (Micropterus salmoides) and large-scale breeding of male seedings

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Abstract： In a previous experiment, largemouth bass fry were fed with different concentrations of DES diet, and pseudo-fish were identified by sex molecular markers and gonadal histology. The results showed that 300ppm DES could reverse XY largemouth bass into physiological female, and the sexual reversal rate reached more than 90%. Through the analysis of the regulatory network of key gene expression, sex hormone level and gonad development, it is speculated that steroid hormone synthesis pathway is the main signaling pathway of sexual reversal. Subsequently, 249 YY fish were obtained by sex marker screening using XY pseudo-female and XY normal male. In 2024, 1.3 million full-male fish were bred using YY fish and normal XX female fish, and the tested offspring of XY genotype were 100%. In this study, the technical system of breeding of YY largemouth bass and large-scale breeding of whole male fish was established, which provided technical guarantee for the breeding of largemouth bass.

Key words:： Largemouth bass (Micropterus salmoides); Sex reversal; YYfish; whole male fish

大黄鱼对无鱼粉饲料转化率显著差异个体的蛋白质组学分析

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摘要：大黄鱼是我国重要的海水养殖鱼类，也是鱼粉消耗“大户”，培育对无鱼粉饲料转化率低（饲料效率高）的品系有助于减少对鱼粉的依赖并降低饲料成本。为此，本研究对均重190.53g的266尾大黄鱼投喂无鱼粉饲料25天，拍摄每尾鱼的摄食情况并计算饲料效率。采集饲料效率前后各5%（各抽选5尾）个体的肝脏和前后肠进行蛋白质组学测序。结果显示：饲料效率高组肝脏和前后肠中参与脂质消化和运输的相关蛋白表达量显著上调，细胞凋亡和炎症发生相关蛋白显著下调。并且，APOB和APOA1在肝脏和前肠中均显著上调，APOB和APOA4在肝脏和后肠中均显著上调。研究表明，APOA1和APOA4具有运输脂质和抗炎作用，这些蛋白的高表达使大黄鱼拥有较强抗炎能力，保证了对饲料中营养物质的消化吸收，从而拥有高饲料效率。本研究为理解大黄鱼对无鱼粉饲料的饲料效率差异机制提供了重要资料，也为选育适应无鱼粉饲料的大黄鱼优良品系提供了重要启示。

关键词：大黄鱼；无鱼粉；饲料效率；蛋白质组学；脂质代谢；炎症

Proteomic Analysis of Large Yellow Croaker (Larimichthys crocea) with Significant Differences in Feed Efficiency on Fishmeal-Free Diets

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Abstract: The large yellow croaker (Larimichthys crocea) is an important marine aquaculture species in China and a major consumer of fish meal. Developing strains with low conversion rates (high feed efficiency) for fishmeal-free diets can help reduce the reliance on fishmeal in its aquaculture, lower feed costs, and promote industry efficiency and sustainable development. Therefore, in this study, 266 large yellow croakers with an average weight of 190.53g were fed a fishmeal-free diet for 25 days. Real-time video recording was used to monitor the feeding behavior of each fish, and the feed efficiency of each fish was calculated. Liver and anterior and posterior intestines of individuals in the top 5% and bottom 5% of feed efficiency (five individuals each from high and low efficiency groups) were collected for proteomic sequencing.The results showed that in the liver of the high feed efficiency group, proteins involved in lipid transport and oxidative energy production were significantly upregulated, while proteins related to cell apoptosis and inflammation were downregulated. Additionally, APOB-100, APOA1, and APOA4 were significantly upregulated in the liver, APOB-100 and APOA1 were significantly upregulated in the anterior intestine, and APOB-100 and APOA4 were significantly upregulated in the posterior intestine. Previous studies have shown that APOA1 and APOA4 have roles in lipid transport and anti-inflammatory functions, and their high expression provides the large yellow croaker with strong anti-inflammatory capabilities, ensuring the digestion and absorption of nutrients from the feed and resulting in high feed efficiency.This study provides important data for understanding the mechanisms behind the differences in feed efficiency of large yellow croaker when fed a fishmeal-free diet and offers valuable insights for breeding superior strains of large yellow croaker that are adapted to fishmeal-free diets.

Key words:： Larimichthys crocea; Fishmeal-free diets; Feed efficiency; Proteomic; Lipid metabolism; Inflammation

鲤和罗非鱼的不育品系创制及育性控制技术研究

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摘要：我们选取鲤和罗非鱼为研究对象，利用繁殖障碍、性征背离和染色体组操纵三种方法，力图在解析类固醇激素调节性腺和次级性征发育的分子机制的同时，开发调控配子发生和次级性征发育的育性控制技术。本年度，我们发现生殖内分泌调控轴的垂体 LH、性腺 Star/Cyp17a2 突变体斑马鱼、鲤或罗非鱼的雌性繁殖障碍（100%不育）。进一步研究，发现孕激素信号通过核受体调节金属蛋白酶的表达，进而控制卵母细胞成熟和排卵。基于此卵母细胞成熟和排卵雌性生殖开关技术，于本年度成功规模化构建了全雌不育鲤群体（种源可控、单性）的创制技术。我们期望通过阻断基因编辑位点在自然环境中发生基因编辑位点渐渗，实现野生群体与遗传改良群体的独立共存，保护天然水体的生态安全，适时推动基因编辑等精准育种技术在我国水产种业领域的创新应用。

关键词：性别二态性；繁殖；性类固醇激素；育性控制；单性

Creation of sterile lines and the fertility control techniques in Common carp and tilapia

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Abstract：We chose common carp and tilapia as the models and used three methods of reproductive disruption, sexual deviation, and genome manipulation, to analyze the molecular mechanism of steroid hormone regulation of gonadal and secondary sexual development and to develop fertility control techniques. Deficiency of pituitary LH, gonad Star and cyp17a2, which are involved in the reproductive endocrine axis, resulted in sterility of the mutant fish. Mechanistically, it was found that progestin signaling regulates oocyte maturation and ovulation via its nuclear receptor. Using this effective "on-off" switch for fertility control, we established the sterilized all-female population. We hope that by blocking the infiltration of gene editing sites in the natural environment, we can achieve the independent coexistence of the wild population and the genetically improved population, protect the ecological safety of natural water bodies, and promote the innovative application of precision breeding technology such as gene editing in the field of genetic breeding in aquaculture of China.

Key words:：Sexual dimorphic; Reproduction; Sex steroids; fertility control; Uni-sex

基于转录组和翻译组研究虹鳟急性热应激的转录翻译调控

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摘要：虹鳟是一种重要的冷水性鱼，易受高温胁迫影响。迄今为止，关于虹鳟热应激转录组研究广泛，而在翻译水平上的研究甚少。为了揭示热应激对虹鳟肝脏的翻译调控作用，本研究对正常和热应激条件下虹鳟肝脏进行了核糖体分析。转录组数据与核糖体谱分析数据的对比分析表明，转录水平上基因表达的折叠变化与翻译水平上的基因表达变化适度相关。总共有 1213 个基因在翻译水平上发生了显著改变。然而，只有 32.8%的基因在两个水平之间是共同的，这表明热应激在转录和翻译水平上是协调的。此外，809 个基因的翻译效率存在显著差异，这些基因的翻译效率受到 GC 含量、编码序列长度和上游开放阅读框存在等因素的显著影响。此外，在 2676 个基因中鉴定出 3468 个潜在的 uorf，这些 uorf 可能会影响主要开放阅读框的翻译效率。这些发现有望为鱼类热应激反应的国际文献提供新的数据和理论见解。

关键词：虹鳟；热应激；翻译组；翻译效率；上游开放阅读框

Ribosome Profiling and RNA Sequencing Reveal Translation and Transcription Regulation under Acute Heat Stress in Rainbow Trout (Oncorhynchus mykiss,Walbaum, 1792) Liver

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Abstract： Rainbow trout (Oncorhynchus mykiss, Walbaum, 1792) is an important economic coldwater fish that is susceptible to heat stress. To date, the heat stress response in rainbow trout is more widely understood at the transcriptional level, while little research has been conducted at the translational level. To reveal the translational regulation of heat stress in rainbow trout, in this study, we performed a ribosome profiling assay of rainbow trout liver under normal and heat stress conditions. Comparative analysis of the RNA-seq data with the ribosome profiling data showed that the folding changes in gene expression at the transcriptional level are moderately correlated with those at the translational level. In total, 1213 genes were significantly altered at the translational level. However, only 32.8% of the genes were common between both levels, demonstrating that heat stress is coordinated across both transcriptional and translational levels. Moreover, 809 genes exhibited significant differences in translational efficiency (TE), with the TE of these genes being considerably affected by factors such as the GC content, coding sequence length, and upstream open reading frame (uORF) presence. In addition, 3468 potential uORFs in 2676 genes were identified, which can potentially affect the TE of the main open reading frames. In this study, Ribo-seq and RNA-seq were used for the first time to elucidate the coordinated regulation of transcription and translation in rainbow trout under heat stress. These findings are expected to contribute novel data and theoretical insights to the international literature on the thermal stress response in fish.

Key words:： cold-water fish; high-temperature stress; Ribo-seq; translational efficiency; upstream open reading frames

大黄鱼脂肪酸性状相关基因的挖掘

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摘要：将 672 尾大黄鱼的背部肌肉组织的粗脂肪中 37 种脂肪酸含量作为表型，使用 GEMMA 进行全基因组关联分析（GWAS），参考基因组由本实验室组装，将性别、体重和采样批次纳入协变量并引入亲缘关系矩阵。使用 COLOC 和皮尔逊系数相结合的方法，联合同一亚群的多组织 cis-eQTL 数据进行共定位分析，挖掘大黄鱼脂肪酸相关基因。结果显示，在多个单种脂肪酸如棕榈酸（C16:0）、肉豆蔻酸（C17:0）、花生四烯酸（C20:4n6）等有显著的 GWAS 信号，并在多个组织发现有共定位信号的基因，如脑组织的辛酸（C8:0）、芥酸（C22:1n9）等。本研究为大黄鱼脂肪酸性状相关基因的探索提供了参考，给后续的基因功能验证提供了可信度较高的候选基因。

关键词：大黄鱼； 脂肪酸； GWAS； eQTL； 共定位

Exploration of Fatty Acid-Related Genes in Large Yellow Croaker

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Abstract： The content of 37 fatty acids in the crude fat of dorsal muscle tissue from 672 large yellow croakers was used as the phenotype for a genome-wide association study (GWAS) conducted using GEMMA. The reference genome was assembled by our laboratory, and covariates including sex, body weight, and sampling batch were incorporated along with a kinship matrix. By integrating multi-tissue cis-eQTL data from the same sub-group using a combined approach of COLOC and Pearson correlation coefficients, genes related to fatty acid in large yellow croaker were explored through colocalization analysis. Results indicated significant GWAS signals for several individual fatty acids such as palmitic acid (C16:0), margaric acid (C17:0), and arachidonic acid (C20:4n6). Genes with colocalization signals were identified in multiple tissues, including genes associated with caprylic acid (C8:0) in brain tissue and erucic acid (C22:1n9). This study provides insights into the genetic determinants of fatty acid traits in large yellow croaker, offering credible candidate genes for subsequent functional validation.

Key words:： Large Yellow Croaker; Fatty Acids; GWAS; eQTL; Colocalization

黑鲷“苏海 1 号”新品种简介

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摘要：黑鲷“苏海 1 号”，该品种是以 2001 年从山东莱州湾海区收集的黑鲷野生群体优选繁育后代为选育基础群体。于 2004 年起，选择体重大的个体作为育种亲本，以生长速度为选育目标性状，采用群体选育方法，经连续 4 代选育而成。 在相同的养殖条件下，与未经选育的黑鲷相比，养殖 18～19 个月，黑鲷“苏海 1 号”生长速度提高了 24.37%以上。该品种适宜在我国山东、江苏、浙江、福建和广东等沿海 18～32 ℃非开放海水环境中养殖。

关键词：黑鲷；新品种

Brief Introduction on New Strain of Black Porgy " Suhai No.1"

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Abstract：The new strain of black porgy "Suhai No.1" is a breeding population based on the selected offsprings of a wild population of black porgy collected from the Laizhou Bay sea area in Shandong Province in 2001. Since 2004, individuals with heavy body weight have been selected as breeding parents, with growth rate as the target trait for selection. The population selection method has been used for four consecutive generations of breeding. Under the same breeding conditions, compared with non selected black seabream, the growth rate of black seabream "Suhai 1" increased by more than 24.37% after 18-19 months of breeding. This variety is suitable for aquaculture in non open seawater environments with temperatures ranging from 18 to 32 ℃ along the coasts of Shandong, Jiangsu, Zhejiang, Fujian, and Guangdong provinces in China.

Key words:：Black porgy ; New strain

香港牡蛎渗透压调节分子机制初探

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摘要：香港牡蛎（Crassostrea hongkongensis）是我国华南沿海重要的海产经济贝类，基于产业对耐高盐香港牡蛎新品种的迫切需求，研究者自渗透调节角度开展盐度胁迫应答机理研究，以期为耐盐新品种培育提供参考和理论依据。通过分析不同盐度条件下香港牡蛎体内 25 种游离氨基酸的含量差异及变化规律，发现参与其渗透调节的主效游离氨基酸为牛磺酸，丙氨酸和甘氨酸；对其鳃组织进行全转录组测序，结果显示，大量差异基因在牛磺酸、甘氨酸等氨基酸代谢通路富集，同时鉴定出许多具有调控潜能的非编码 RNA；进一步研究表明甘氨酸代谢通路中的基因可能通过调节游离态甘氨酸含量的方式参与盐度胁迫下的渗透调节，而其中的关键基因及其作用机制有待进一步探究。此外，利用透射电镜可观察香港牡蛎鳃组织存在两种离子细胞，二者可能具有不同的离子转运功能，而如何实现不同渗透条件下的离子跨膜运输是亟待进一步研究的科学问题。

关键词：香港牡蛎，盐度胁迫，渗透压调节，游离氨基酸，离子转运

The primary investigation of osmotic regulation mechanism in Crassostrea hongkongensis

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Abstract：Crassostrea hongkongensis is an important marine economic shellfish along the southern coast of China. Due to the industry's urgent need for a salt-tolerant variety of Hong Kong oysters, we are investigating the salinity stress response mechanisms from the perspective of osmotic regulation. By analyzing the differences and trends in the content of 25 free amino acids under varying salinity conditions, it was found that the main free amino acids involved in osmotic regulation are taurine, alanine, and glycine. Transcriptome sequencing of the gill tissue revealed that many differentially expressed genes are enriched in amino acid metabolism pathways such as taurine and glycine, and several regulatory non-coding RNAs were identified. Further research indicates that genes in the glycine metabolism pathway might be involved in osmotic regulation under salinity stress by modulating free glycine levels, with key genes and their mechanisms still needing exploration. Additionally, transmission electron microscopy observations revealed two types of ionocytes in the gill tissue of Hong Kong oysters, which may have different ion transport functions. Understanding how ion transport across membranes occurs under different osmotic conditions remains an urgent scientific question.

Key words:：Crassostrea hongkongensis , salinity stress, osmotic regulation, FAA, ion transport

大西洋鲑（Salmo sa lar）的
伪雄鱼诱导及性腺发育的比较研究

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摘要：大西洋鲑在国际市场的产量名列前茅，但我国的养殖规模却极为有限，其产业尤为突出的发展瓶颈是雄性鱼卵的进口限制，这一卡脖子问题阻碍了我国在大西洋鲑繁育技术体系构建和种质改良方面的科学研究进展。本研究以大西洋鲑发眼卵为材料，通过人工性腺发育调控，成功诱导 15000 尾大西洋鲑伪雄鱼，诱导率 100%。育苗首年，我们完整追踪了性腺发育的组织学特征：孵化后 30 天，原始性腺形成，可观察到明显的原始生殖细胞，精卵巢无明显差异；30-60 天性腺无明显变化；60 天时卵巢出现卵原细胞；80 天时精卵巢出现明显的结构分化；卵母细胞和精原细胞分别在 130 和 160 天出现；至 310 天精巢发育出精小囊，卵巢发育至Ⅱ期。同期我们还开展了比较转录组分析，鉴定了调控伪雄鱼精巢和雌鱼卵巢分化发育的关键基因、生物学过程和通路。研究的开展突破了国外的种质封锁，为大西洋鲑的人工繁育提供了雄性种质资源，同时为其遗传改良和种质创制创造了条件。

关键词：大西洋鲑，伪雄鱼，性腺发育，转录组

Induction of Salmo salar pseudomale and comparative study on gonadal development

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Abstract：Salmo salar ranks among the top in global aquaculture production, however, the scale of its cultivation in China remains extremely limited. A significant bottleneck in its industry is the restriction on importing male fish eggs, which has impeded scientific advancements in developing breeding technologies and genetic improvement systems for S. salar in China. In this study, eyed eggs of Atlantic salmon were used as materials, and through the artificial regulation of gonadal development, 15,000 pseudomale S. salar were successfully induced, with a 100% induction rate. During the first year of breeding, we comprehensively tracked the histological characteristics of gonadal development: at 30 days post-hatching (dph), primordial gonads were formed, with distinct primordial germ cells visible, but no noticeable differences between testes and ovaries; from 30 to 60 dph, the gonads remained unchanged; at 60 dph, oogonia appeared in the ovaries; at 80 dph, structural differentiation between the testes and ovaries became apparent; oocytes and spermatogonia appeared at 130 and 160 dph, respectively; and by 310 dph, seminal vesicle had developed in the testes, while the ovaries progressed to stage II. Simultaneously, we performed a comparative transcriptomic analysis, identifying key genes, biological processes and pathways regulating the differentiation and development of pseudomale testes and female ovaries. This research has successfully circumvented foreign germplasm restrictions, providing a male genetic resource for the artificial breeding of S. salar, and has created favorable conditions for its genetic improvement and germplasm innovation.

Key words:：Salmo salar, pseudomale, gonadal development, transcriptome

瓦氏雅罗鱼肠道耐盐碱核心菌群的筛选与应用

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摘要：位于内蒙古东北部的达里湖，由于其极高的碳酸盐碱度(53.57mmol/L，pH 9.6)，湖中仅有瓦氏雅罗鱼(Leuciscus waleckii)和鲫鱼(Carassius auratus)两种鲤科鱼类存活并形成优势种群。为了筛选和鉴定鱼类肠道耐碱核心菌群，利用 16S rRNA 高通量测序技术，首先从达里湖瓦氏雅罗鱼和鲫鱼野生群体肠道内筛选出 5 个相对丰度超过 1%的共有菌属；然后进一步对比分析，从达里湖瓦氏雅罗鱼野生群体及其淡水驯养 F2 肠道鉴定了一个与盐碱适应相关的环境敏感型核心菌群— 嗜冷菌属(Psychrobacter)。鉴于 Psychrobacter 在生成脂肪酶和分解含氮物质的特殊功能，推测其可能在极碱环境下瓦氏雅罗鱼能量供给和氨解毒方面发挥重要作用。本研究为瓦氏雅罗鱼碱适应机制解析及鱼类碱化饲料益生菌开发奠定了工作基础。

关键词：瓦氏雅罗鱼；耐盐碱；嗜冷菌属

Identification of core gut microbiota of Amur ide (Leuciscus waleckii) in extremely high-alkali environment

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Abstract：Amur ide (Leuciscus waleckii), which inhabits Lake Dali, a typical soda lake in Northeast China with extremely high titratable alkalinity (~53.57mmol/L) and pH value (~9.6), is considered to be an ideal model for elucidating alkaline adaption mechanisms. Gut microbiota has been shown to promote host adaption to the environments, to ensure their roles in Amur ide, we used 16S rRNA high-throughput sequencing technology to identify the specific gut bacteria related to alkaline adaption and explore their roles in Amur ide’s adaption to extreme alkaline environments. First, we compared and analyzed the shared gut microbiota of Amur ide and goldfish (Carassius auratus) both living in Lake Dali at the genus level, five genera were confirmed at the threshold over 1% relative abundance including Acinetobacter, Bacteroides, Psychrobacter, Enhydrobacter, and Escherichia-Shigella; Second, we compared and analyzed the shared and differential microbiota of Amur ide in Lake Dali and its freshwater domesticated F2 offspring. The results indicated Acinetobacter and Bacteroides existed in both types of Amur ide, with a relative abundance of over 1%. However, the relative abundance of Psychrobacter, Enhydrobacter, and Escherichia-Shigella in alkali-form Amur ide decreased to less than 1% after freshwater domesticated, which were considered environmentally sensitive genera. Among these three genera, the genus Psychrobacter was found to be a differential bacterium with significantly higher relative abundance in alkali-form compared to freshwater type Amur ide. Overall, Psychrobacter was confirmed as an environmentally sensitive core microbiota associated with alkaline adaption of Amur ide. KEGG pathway analysis highlighted that amino acid metabolism (arginine and proline metabolism) and lipid metabolism (fatty acid biosynthesis, glycerolipid and sphingolipid metabolism) were significantly more highly expressed in alkali-form Amur ide than in its freshwater domesticated offspring.

Key words:：Gut microbiota; Leuciscus waleckii; Alkaline adaption; Psychrobacter

脊尾白虾 Duox 基因鉴定及其免疫功能的初步研究

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摘要：为了探究 Duox 基因在脊尾白虾中的免疫功能，本研究从脊尾白虾中成功克隆获得 Duox 基因 cDNA 序列，并对其编码的氨基酸序列进行了分析。在此基础上采用实时荧光定量 PCR 技术，分析该基因的组织表达特征及其在副溶血弧菌(Vp）感染后表达变化情况。最后基于 RNA 干扰技术分析了脊尾白虾 Duox 基因敲降后感染 Vp 的死亡率。研究结果显示，脊尾白虾 Duox 基因编码区序列长度为 4518 bp，编码 1505 个氨基酸，具有双氧化物酶家族典型结构特征。Duox 基因在脊尾白虾不同组织中均有表达，且在鳃组织中表达最高。感染 Vp 后，Duox 基因在鳃组织中的表达量著上升（$P<0.05$）。注射 siRNA 试剂后用 Vp 感染，与对照组相比，干扰组脊尾白虾的存活率显著降低（$P<0.05$）。以上研究表明，Duox 基因在脊尾白虾抵御病原菌感染的免疫反应中发挥作用，为进一步探究 Duox 在脊尾白虾中的免疫功能和作用机制奠定了理论基础。

关键词：脊尾白虾；Duox 基因；免疫功能；RNAi；

Identification and preliminary study of immune function of the Duox gene in Exopalaemon carinicauda

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Abstract：In order to explore the immune function of the Duox gene in Exopalaemon carinicauda, the cDNA sequence of the Duox gene was successfully cloned from E.carinicauda in this study, and the amino acid sequence it encoded was analyzed. On this basis, real-time fluorescence quantitative PCR technology (RT-qPCR) was used to analyze the tissue expression characteristics of the gene and its expression changes after Vibrio parahaemolyticus infection. Finally, the mortality rate of E.carinicauda infected with V. parahaemolyticus after the knockdown of Duox gene was analyzed based on the RNA interference technique. The results showed that the coding region sequence length of the Duox gene in the E.carinicauda is 4518 bp, encoding 1505 amino acids, which reflects the typical structural characteristics of the dual oxidase family. Duox gene was expressed in all tested tissues of the E.carinicauda, with the highest expression level in gill tissues. After V. parahaemolyticus infection, the expression level of Duox gene in gill increased significantly ($P<0.05$). Infection with V. parahaemolyticus after injection of siRNA reagent significantly reduced the survival rate of E.carinicauda in the RNA interference group compared with the control group ($P<0.05$). The above studies show that the Duox gene plays a role in the immune response of E.carinicauda against pathogenic infection, which is essential for further exploration the immune function and mechanism of Duox in E.carinicauda.

Key words:：Exopalaemon carinicauda; Duox gene; immune function; RNAi

福建平潭海域不同年龄仿刺参
骨片种类和形态学研究

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摘要：海参真皮的表层包含有称之为骨片的内骨骼，是海参纲最重要的特征。利用不同类型的海参骨片及其相对比例能够对不同种类的海参予以快速鉴定。本文采用 NaClO 法、蛋白酶 K 法，对福建平潭 1、2、3 龄仿刺参（Apostichopus japonicus）的各组织（棘刺、体壁、触手、管足、纵肌、呼吸树、肠道）进行采集与处理，得到不同年龄仿刺参不同组织骨片类型，并分别比较采用 NaClO 法、蛋白酶 K 法制备的仿刺参骨片的显微图像，利用 SPSS 软件统计不同仿刺参骨片类型的相对比例。在显微镜和扫描电子显微镜镜下能观察到 7 种仿刺参骨片类型，包括 5 种主要类型（桌形体、扣形体、杆状体、长孔状体、花纹状体）和 2 种特殊类型（复合盘状骨片和 C 形体），且不同组织内的仿刺参骨片类型存在显著性差异（P<0.05）。本研究为仿刺参生物学鉴定提供基础资料，为其年龄鉴别提供借鉴。

关键词：平潭海域；仿刺参；骨片；NaClO 法；蛋白酶 K 法；形态学；鉴定

tudy on morphology and species of ossicles of different ages sea cucumber (Apostichopus japonicus) collected from Pingtan sea area, Fujian Province

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Abstract： The dermis surface layer of sea cucumbers contains ossicles, which constitute the distinguishing feature of this class. The types and relative proportions of these ossicles can facilitate rapid identification of different sea cucumber species. In this study, NaClO and protease K methods were employed to extract and process tissues of sea cucumbers (Apostichopus japonicus) aged 1 to 3 years from the Pingtan Sea area (Fujian, China). Tissue samples included spines, body walls, tentacles, tube feet, longitudinal muscles, respiratory trees, and intestines. Bone tablet images obtained through these methods were compared, and the relative proportions of each type of ossicle were analyzed using SPSS software.The results revealed seven types of ossicles: table-shaped, button-shaped, rod-shaped, rosette-shaped, long hole-like body ossicles, composite discoid ossicles, and C-shaped ossicles, observable under both light and electron microscopes, with significant differences (P<0.05).This study provides the basic data for the biological identification of the A. japonicus and the reference for the age identification.

Key words:： Pingtan sea area; sea cucumber (Apostichopus japonicus); bone tablet; morphology; identification

三角鲂受精卵孵化不同发育时期代谢组分析

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摘要：为了探究三角鲂受精卵孵化过程中代谢物的种类和差异，本研究首次采用 LC-MS 非靶向代谢组学方法对三角鲂原肠胚期(17 h)、神经胚期(25 h)、肌节和眼基形成期(32 h)、尾芽期(41 h)、肌肉效应期(50 h)和心跳期(58 h)的受精卵样品进行研究分析。结果表明，在 HMDB 数据库共注释到 884 个代谢物，主要涉及脂质和类脂分子代谢物（35.97 %）、有机酸及其衍生物（20.14 %）和有机杂环化合物（11.54 %）等。KEGG 富集分析结果表明，这些差异代谢物被显著富集到 ABC 转运蛋白、类固醇激素生物合成、氨酰 tRNA 生物合成、甘油磷脂代谢、花生四烯酸代谢等通路。三角鲂受精卵不同发育时期的代谢物呈现差异化表达，推测主要通过甘油磷脂代谢、嘧啶代谢、花生四烯酸代谢、嘌呤代谢、ABC 转运蛋白、视黄醇代谢等通路来影响胚胎发育，本研究可为三角鲂高效孵化技术设施及体系优化提供理论支持。

关键词：三角鲂； 胚胎发育； 代谢组学； 代谢通路；高效孵化

Metabolome analysis of fertilized eggs hatching at different developmental stages of triangular bream

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Abstract： In order to explore the types and differences of metabolites during the incubation of fertilized eggs of triangular bream, LC-MS non-targeted metabolomics was used for the first time to study and analyze the fertilized egg samples of triangular bream at gastrulation stage (17 h), neuroembryonic stage (25 h), sarcomere and ocular base formation stage (32 h), caudal bud stage (41 h), muscle effector stage (50 h) and heartbeat stage (58 h). The results showed that a total of 884 metabolites were annotated in the HMDB database, mainly involving lipid and lipid-like molecules (35.97%), organic acids and derivatives (20.14%), and organoheterocyclic compounds (11.54%). The results of KEGG enrichment analysis showed that these differential metabolites were significantly enriched to ABC transporters, steroid hormone biosynthesis, aminoacyl tRNA biosynthesis, glycerol phospholipid metabolism, arachidonic acid metabolism and other pathways. It is speculated that the metabolites of fertilized eggs of triangular bream at different developmental stages are differently expressed, and it is speculated that the embryonic development is mainly affected by glycerophospholipid metabolism, pyrimidine metabolism, arachidonic acid metabolism, purine metabolism, ABC transporters, retinol metabolism and other pathways Theoretical support is provided for facility and system optimization.

Key words:：triangular bream; Embryonic development; metabolomics; metabolic pathways; Efficient incubation

刀鲚肌肉响应急性低温胁迫的蛋白质组学与代谢组学研究

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摘要：为探讨刀鲚对低温胁迫的响应机制，本研究以体重为 (9.32±2.00) g 的刀鲚幼鱼为试验材料，对其进行急性低温胁迫处理，取肌肉组织进行转录组学和代谢组学测序。结果显示：共鉴定到 284 个差异表达基因。其中，232 个差异基因表达上调及 152 个基因表达下调。差异基因主要参与细胞过程和结合过程。代谢组共发现了 69 个差异代谢物。其中，急性低温胁迫后表达上调的有 39 个，表达下调的有 30 个。KEGG 富集分析表明，差异表达的基因和代谢物都富集脂质和氨基酸代谢途径。转录组学与代谢组学关联分析结果显示，共同富集的通路有 10 条，其中色氨酸代谢和产热两条通路差异显著。富集到最多的差异基因和差异代谢物的共有通路是代谢途径通路，包括 IL4I1,GCDH, gcdH 等差异基因和 2-氧代己二酸、5-羟基色氨酸、L-肉毒碱等差异代谢物。本研究结果为解析刀鲚低温胁迫响应分子机制和耐低温刀鲚新品系选育与改良奠定理论基础。

关键词：刀鲚、低温胁迫、分子机制、转录组、代谢组

Transcriptomics and metabolomics analysis of Coilia nasus muscle responses to low temperature stress

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Abstract： To explore the response mechanism of the Coilia nasus to low temperature stress, this study used juvenile C.nasus weighing (9.32 ± 2.00) g as the experimental material and subjected them to acute (rapidly reducing the water temperature from 22 ℃ to 7 ℃ at a rate of 2.5 ℃/h) low temperature stress treatment. Muscle tissue was taken for transcriptome and metabolomics sequencing. The results showed that a total of 284 differentially expressed genes were identified, among which 232 differentially expressed genes were upregulated and 152 genes were downregulated. The differentially expressed genes are mainly involved in cellular processes and binding processes. A total of 69 differential metabolites were identified in the metabolome. Among them, 39 were upregulated and 30 were downregulated after acute hypothermia stress. KEGG enrichment analysis showed that differentially expressed genes and metabolites are enriched in lipid and amino acid metabolic pathways. The correlation analysis between transcriptomics and metabolomics showed that there were 10 enriched pathways, among which the tryptophan metabolism and thermogenesis pathways showed significant differences. The common pathway that accumulates the most differentially expressed genes and metabolites is the metabolic pathway pathway pathway, including differentially expressed genes such asIL4I1,GCDH, gcdH and differentially expressed metabolites such as Oxoadipic acid, 5-Hydroxy-L-tryptophan, and L-carnitine. The results of this study lay a theoretical foundation for analyzing the molecular mechanisms of low-temperature stress response in the C.nasus, as well as for genetic breeding and improvement of new strains of low-temperature tolerant C.nasus.

Key words:：Coilia nasus, low temperature stress, molecular mechanism, transcriptome, metabolome

大口黑鲈耐高温性能优异种质资源的筛选及杂交育种研究

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摘要：在其原产地，大口黑鲈包括两个亚种：北方亚种，具有耐低温和生长快等优点；和佛罗里达亚种，更耐高温、抗病力更强。本研究首先比较了 3 个大口黑鲈北方亚种群体和 1 个佛罗里达亚种群体的耐高温性能差异。结果表明：34℃养殖 60 天后，佛罗里达亚种的体质量、特定增重率和成活率等均显著高于北方亚种，表明佛罗里达亚种的耐高温性能优于北方亚种。绝对增重率、成活率和饵料系数等结果表明，“优鲈 3 号”的耐高温性能优于台湾群体和北方亚种引进群体。在此基础上，开展了佛罗里达亚种和“优鲈 3 号”的杂交育种。急性高温胁迫下，佛罗里达亚种和杂交子代的成活率显著高于“优鲈 3 号”；慢性高温养殖下，杂交子代的生长性能、成活率等显著高于佛罗里达亚种和优鲈 3 号。这些结果表明杂交子代的耐高温性能优于“优鲈 3 号”。此外，开发出可用于鉴定“优鲈 3 号”、佛罗里达亚种及不同类型杂交子代的分子标记。本研究可为大口黑鲈耐高温新品种培育提供数据支撑。

关键词：大口黑鲈，耐高温，杂交育种，种质鉴定

Comparison of thermal tolerance abilities among different populations and hybridization between two subspecies of Largemouth bass

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Abstract：Largemouth bass (Micropterus salmoides, LMB) is classified into two distinct subspecies: the Northern LMB (M. salmoides, NLMB), which exhibits rapid growth and greater tolerance to low temperatures, and the Florida LMB (M. floridanus, FLMB), known for its resistance to high temperatures and enhanced disease resistance. In this study, we selected three Northern LMB populations: “YouLu No.3” LMB (YL3), a re-imported Northern wild population (NLMB), and a Taiwan LMB (TW) population, along with one Florida LMB population (M. floridanus, FLMB), to assess their responses to chronic thermal stress. After being exposed to 34℃ for 60 days, the FLMB group exhibited the highest final mean body weight (FBW), survival rate (SR), and specific growth rate (SGR) compared to the three Northern LMB groups, indicating that the FLMB population possesses superior thermal tolerance. Based on the data for SGR, SR, and FCR, it is suggested that the YL3 population has better thermal tolerance than the TW and NLMB populations. Furthermore, hybridization was conducted between the YL3 and FLMB populations. Under acute thermal stress, it was observed that both FLMB and hybrid offspring had higher SR than the YL3 population. After exposure to 34°C for 30 days, the FBW and SR of the hybrid offspring were significantly higher than those of the YL3 and FLMB populations. These results indicate that the FLMB and hybrid offspring possess superior thermal tolerance compared to the YL3 population. Additionally, we developed several molecular markers to differentiate the YL3, FLMB, and the two distinct hybrid offspring. Our study provides valuable insights for the selective breeding of LMB varieties with enhanced thermal tolerance in the future.

Key words:：Largemouth bass, thermal tolerance, hybridization, germplasm identification

基于机器学习的全基因组选择技术优化及在大黄鱼育种中的应用

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摘要：基因组选择(Genomic selection,GS)其本质上是一种标记辅助的选择方法，主要利用全基因组标记信息对要测定的性状进行遗传改良的方法。基因组选择技术与传统的基于家系的育种方法相比，具有更高的预测精度。然而，关于水生动物基因组选择模型比较的报道有限。本研究对 546 尾大黄鱼个体的体重和 800 尾大黄鱼的抗流性状进行记录。基因分型数据有两种，芯片杂交的 SNP 数据；靶向测序和分型的 mSNP 扩展数据。对性状分组进行群体结构分析以及全基因组关联分析，估算大黄鱼各性状的遗传力值，大黄鱼体重的遗传力范围在 0.56~0.68，抗流性状的遗传力在 0.51~0.57 之间。并使用 GBLUP、贝叶斯以及机器学习等 12 种模型 进行了基因组预测，得出在 MLP 模型中各性状的准确性值最高。且机器学习模型更适用于分类数据，GBLUP 和 Bayes 模型更适用于连续数据的预测。

关键词：全基因组选择，大黄鱼，GBLUP，Bayes，机器学习

Optimization of Whole Genome Selection Technology Based on Machine Learning and Its Application in Breeding of Large Yellow Croaker

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Abstract： Genomic selection (GS) is essentially a marker-assisted selection method, which mainly uses whole-genome marker information to genetically improve the traits to be measured. Compared with traditional pedigree based breeding methods, genome selection has higher prediction accuracy. However, there are limited reports on the comparison of genomic selection models in aquatic animals. The body weight of 546 large yellow croaker individuals and the anti-current characteristics of 800 large yellow croaker individuals were recorded in this study. There are two kinds of genotyping data, SNP data from chip hybridization; Extended mSNP data for targeted sequencing and typing. Population structure analysis and genome-wide association analysis were carried out to estimate the heritability of various characters. The heritability of body weight was 0.56~0.68, and the heritability of stream-resistance traits was 0.51~0.57. And 12 kinds of models such as GBLUP, Bayes and machine learning were used to predict the genome, and the accuracy value of each trait was the highest in the MLP model. Machine learning models are more suitable for classifying data, while GBLUP and Bayes models are more suitable for continuous data prediction.

Key words:： whole genome selection, Large yellow croaker, GBLUP, Bayes, machine learning

罗氏沼虾糖稳态调节机制研究

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摘要：血糖是机体能量的核心来源，其平衡对维持内环境稳态至关重要。水产动物被称为“先天性糖尿病患者”，因为它们对糖的利用能力较低。为探究甲壳动物的葡萄糖耐受性及糖稳态调控机制，本课题组开展了系列研究。通过葡萄糖耐量实验，发现罗氏沼虾能迅速将外源葡萄糖转化为海藻糖、糖原和甘油三酯，其降血糖速度快于肉食性鱼类。在短期饥饿（2 周）期间，罗氏沼虾通过分解海藻糖、糖原、甘油三酯和蛋白质，维持血淋巴中约 2 mmol/L 的葡萄糖浓度。在摄入含糖量 30%的饲料后，血淋巴葡萄糖浓度在 3 小时内达到峰值，10 小时内恢复正常，主要通过促进糖酵解和糖原合成、抑制糖异生和糖原分解来维持糖稳态。为进一步探究罗氏沼虾糖稳态调节激素，本课题组鉴定获得与胰岛素同源的类胰岛素基因，通过 RNAi 证实了该基因参与糖原合成调控，通过抑制 PI3K 通路，明确了类胰岛素介导 PI3K 通路调控罗氏沼虾糖稳态。

关键词：罗氏沼虾，糖代谢，类胰岛素，PI3K 通路

Study on the Regulation Mechanism of Glucose Homeostasis in Macrobrachium rosenbergii

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Abstract： Blood glucose is a crucial energy source for organisms, and its balanced regulation is essential for maintaining homeostasis. Aquatic animals have a low ability to utilize glucose, often referred to as "natural diabetics." To investigate glucose tolerance and its homeostatic regulation in crustaceans, we conducted a series of studies. In glucose tolerance tests, Macrobrachium rosenbergii rapidly converted exogenous glucose into trehalose, glycogen, and triglycerides, with a faster glucose clearance rate compared to carnivorous fish. During short-term starvation (2 weeks), M. rosenbergii maintained a glucose level of approximately 2 mmol/L in its hemolymph by sequentially utilizing trehalose, glycogen, triglycerides, and proteins. After consuming a diet with 30% glucose, hemolymph glucose levels peaked within 3 hours and returned to normal within 10 hours, primarily through enhanced glycolysis and glycogen synthesis, while inhibiting gluconeogenesis and glycogen breakdown. To further explore hormonal regulation, we identified an insulin-like gene in M. rosenbergii, confirmed its role in glycogen synthesis via RNA interference (RNAi), and demonstrated its regulation of glucose homeostasis through the PI3K pathway.

Key words:： Macrobrachium rosenbergii, glucose matabolism, insulin like peptide, PI3K pathway

基于低深度重测序的长牡蛎高通量低成本基因分型技术体系建立及应用

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摘要：高通量测序技术的进步使得全基因组范围内的 SNP 分型成为可能，推动了遗传学进展和育种应用。然而，较高的测序成本限制了其在非模式物种中的广泛应用。为实现大规模基因分型，我们以长牡蛎为模型，开发了一种适用于水产物种的低深度全基因组重测序技术，能够实现低成本、高效的测序文库构建。此外，我们还进一步开发了低深度重测序基因分型技术，并建立了无参考数据集的基因型填充方法，评估了影响准确性的关键因素。研究表明，STITCH 算法能够在无参考数据的情况下高效填充基因型，高 SNP 密度和连锁不平衡有助于提高填充准确性。利用填充的基因型构建的基因组关系矩阵，评估了其在基因组选择育种中的应用潜力。这项研究为水产物种提供了一种低成本、高通量基因型获取的有效方法，有望广泛应用于水产育种中，加速遗传解析和分子育种进程。

关键词：基因分型；低深度重测序；基因型填充；遗传育种

Development of high-throughput genotyping method by low-coverage whole genome sequencing with genotype imputation in Pacific oyster, Crassostrea gigas.

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Abstract： The advancements in high-throughput sequencing technology have made genome-wide SNP genotyping possible, driving progress in genetics and breeding applications. However, the high cost of sequencing has limited its widespread application in non-model species. To achieve large-scale genotyping, we used the Pacific oyster as a model to develop a low-coverage whole genome sequencing technology suitable for aquatic species, enabling low-cost and efficient sequencing library construction. Additionally, we further developed low-coverage whole genome genotyping technology and established a genotype imputation method without reference datasets, evaluating the key factors affecting accuracy. The study showed that the STITCH algorithm can efficiently impute genotypes in the absence of reference panel, with high SNP density and linkage disequilibrium contributing to improved imputation accuracy. The genomic relationship matrix constructed from the imputed genotypes was assessed for its potential application in genomic selection breeding. This study provides an effective method for obtaining low-cost, high-throughput genotypes in aquatic species, which is expected to be widely applied in aquaculture breeding, accelerating genetic analysis and molecular breeding processes.

Key words:：Genotyping; lcWGS; genotype imputation; genetic breeding

菲律宾蛤仔（Ruditapes philippinarum）长期暴露于17β-雌二醇：性别比例变化和基因表达变化

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摘要：为研究菲律宾蛤仔（Ruditapesphilippinarum）在雌二醇处理条件下对性别分化的影响。使用雌二醇处理菲律宾蛤仔两个月后，通过组织切片的方法对雌二醇处理的菲律宾蛤仔进行切片显微观察并统计各组的雌雄比，在实验组中出现3个雌雄同体蛤仔，比例为2%，高于自然环境中的雌雄同体比例（约千分之一），表明雌二醇对蛤仔性别分化产生影响，存在诱导部分蛤仔性别分化为雌性的现象。此外，对空白组及实验组中性腺成熟的雌、雄蛤仔进行转录组分析发现，DEG在泛素化途径、核糖体、吞噬体和细胞色素P450代谢途径中富集。在差异基因中筛选出如SOX-30、TSK-1、FOSXN5等性别相关基因。同时也发现一些基因如Cullin-4B、BIRC7等基因参与泛素化通路过程，影响甚至直接参与菲律宾蛤仔性别相关基因的表达。

关键词：菲律宾蛤仔；雌激素；雌雄同体；性别分化；差异表达基因

Long-term exposureto17β-estradiol of the Manila clam (Ruditapes philippinarum): shifts of gender ratio and changes of gene expression

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Abstract：Estrogen is widely distributed in the aquatic environment, causing feminization, changes of gender ratio and reduced fecundity in aquatic organisms. 17β-estradiol is a kind of estrogen which is of high estrogenic activity and pseudo-persistence, posing threats to global aquatic ecology. In this study, effects of long-term exposure to 17β-estradiol in the Manila clam (Ruditapes philippinarum) were investigated. The clams were treated with 17β-estradiol for 2 months and then subject to dissection. Gonad tissues were taken and then fixed, sectioned, stained and observed under a microscope to calculate the gender ratiogender ratio. The results showed that the female male ratio of clams in the control group was 0.93:1, which was close to 1:1. Nevertheless, the female male ratio of the 17β-estradiol-treated clams was 1.39:1, which was nearly 50% higher than that in the control group. Furthermore, for clams in the control group, no hermaphrodite was observed. However,forclams treated with 17β-estradiol, 2% of them were hermaphroditic,which was higher than that in natural environment (approximately one thousandth).It implies that long-term exposure to 17β-estradiol might affect sexual differentiation as well as sexual reversal in R. philippinarum, promoting male individuals to reverse into female individuals.Comparative transcriptomics was conducted to identify genes related to sex differentiation in R. philippinarum. Gene expression profiles of the estrogen-treated females were compared with those of the estrogen-treated males and identified 3751 differentially expressed genes (DEGs), among which 1,512 were up-regulated in females, whereas 2239 were up-regulated in males.In parallel, transcripts profiles of the females were compared with those of the males in the control group as well and identified 1718 DEGs, among which 601 were up-regulated in females and 1117 were up-regulated in males. GO (Gene Ontology) and KEGG (Kyoto Encyclopedia of Genes and Genomes) analyses showed that the above mentioned DEGs enriched in the ubiquitination pathway, ribosome, phagosome, and cytochrome P450 metabolic pathways. Additionally, some of the gender related DEGs dentified in the comparison combination of DF vs DM were enriched in ubiquitination, as well. To sum up, the results indicate that exogenous estradiol treatment influenced sex differentiation in R. philippinarum, enriching the knowledge on molecular mechanisms underlying sex differentiation in mollusks.

Key words:：Ruditapes philippinarum; exogenous estradiol; hermaphrodite; gender regulation; Differentially expressed genes

香螺形态性状与质量性状的相关性及通径分析

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摘要：为明确中国黄海北部地区香螺（Neptunea cumingii）自然群体的形态性状对质量性状的影响，测量了香螺的壳高、壳宽、壳口高、壳口宽、体螺层高、体螺层宽 6 个形态性状和体质量、软体部质量 2 个质量性状，采用相关性分析、通径分析和多元回归分析等方法研究了香螺形态性状对其质量性状的影响。研究表明：香螺各性状间均呈极显著相关（P < 0.01），体螺层宽与体质量和软体部质量的相关性均最大；体螺层宽对体质量和软体部质量的直接作用均最大，分别为 0.649 和 0.559；壳宽对体质量的间接作用最大（0.626），壳口宽对软体部质量的间接作用最大（0.606）。研究结果表明，以质量性状为选育香螺目标性状时，应将体螺层宽作为首要形态性状进行选择；以体质量为目标性状时应协同选择壳宽性状，以软体部质量作为目标性状时应协同选择壳口宽性状。本研究可为香螺的生长、人工繁育和遗传育种等提供理论依据。

关键词：香螺；形态性状；质量性状；通径分析

Correlation and path analysis on relationship between morphological traits and qualitative traits in the whelk Neptunea cumingii

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Abstract： In order to determine the influence of morphological traits on the quality traits of natural population of the whelk Neptunea cumingii in the northern Yellow Sea (China), six morphological traits (shell height, shell width, shell aperture height, shell aperture width, body whorl height, body whorl width) and two quality traits (body mass and soft tissue mass) of N. cumingii were measured. Correlation analysis, path analysis and multiple regression analysis were used to study the influence of morphological traits on the quality traits. The results showed that there were significant correlations among all the traits (P < 0.01), the body whorl width had the maximum correlation with body mass and soft tissue mass. The body whorl width had the maximal direct effect on both body mass and soft tissue mass, and the direct effects of body whorl width on body mass and soft tissue mass were 0.649 and 0.559, respectively. Shell width had the maximal indirect effect on body mass (0.626), and shell aperture width had the maximal indirect effect on soft tissue mass (0.606). The results showed that when mass traits were selected as the target traits, the body whorl width should be selected as the primary morphological traits. Shell width should be selected cooperatively when body mass is the target trait, and shell aperture width should be selected cooperatively when soft tissue mass is the target trait. In conclusion, this study can provide scientific reference for the growth, artificial culture and genetic breeding of N. cumingii.

Key words:： Neptunea cumingii; morphological trait; qualitative trait; path analysis

青鱼生长 QTL-qBWE17 区间的精细定位及候选基因的克隆和单倍型功能分析

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摘要：青鱼作为中国最重要的传统养殖淡水鱼类之一，其因生长速度快、存活率高而出名。本实验为了研究青鱼生长性状相关的遗传变异，进一步缩小了青鱼 17 号连锁群上与体重关联的 qBWE17 QTL 区间，在 snp8107 和 snp9562 的特定区间内定位到了 sar1b 和 slc22a5 两个基因。然后，我们对候选基因进行了克隆验证，获得对应的 cDNA 序列，发现 sar1b 和 slc22a5 分别编码 198 和 554 个氨基酸，且通过结构预测和同源性比较，发现均与草鱼的相同基因间存有较高相似性。定量表达分析表明，两基因在快速生长组肌肉和肝脏中的表达水平均大幅下降，猜测可能为生长抑制因子。此外，基于重测序数据库中 480 个样本，对候选基因进行了序列变异检测和生长性状关联分析，经过质控筛选，最终确定了 6 个与体重相关的 SNPs 和 5 个与体长相关的 SNP，为未来青鱼遗传改良和分子标记辅助育种策略提供科学依据。

关键词：青鱼、基因克隆、精细图谱、生长性状、关联分析

Fine mapping of weight-QTL qBWE17 and cloning of candidate genes with functional analysis of growth-related haplotypes in black carp

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Abstract： The black carp, Mylopharyngodon piceus, is one of China's most significant traditional freshwater fish species and is recognized for its rapid growth and high survival rate. To investigate the genetic variation associated with the growth traits of black carp, this study further narrowed down the quantitative trait locus (QTL) qBWE17, associated with body weight, in the linkage group (LG) 17. It localized sar1b and slc22a5 genes within the specific intervals of snp8107 (the SNP with the highest LOD score) and the adjacent SNP snp9562. The two candidate genes were cloned, and variant detection was conducted to identify much more SNPs associated with growth traits. The cDNA and genomic sequences of sar1b and slc22a5 were obtained, encoding 198 and 554 amino acids, respectively. Structural predictions and homology comparisons of sar1b and slc22a5 genes revealed a significant similarity between sar1b and slc22a5 genes of grass carp (Ctenopharyngodon idella) and black carp. Quantitative expression analysis showed a substantial decrease in the mRNA expression levels in the muscle and liver of the fast-growth group, suggesting that these two genes may function as inhibitors of growth. After analyzing the sequencing data from 480 samples in the black carp resequencing database, we screened SNPs in sar1b and slc22a5 and then identified six SNPs associated with body weight and five SNPs associated with body length. Combined analysis showed significant differences among SNP genotypes; males with the CC genotype of snp_15292 and females with the CT genotype of snp_7943 exhibited the highest weight (2043.11±467.93 g) and most extended length (49.13±4.31 cm). Analysis of haplotypes revealed that the D6 haplotype (CCCTCCAAGGTT) displayed notably accelerated growth rates. In conclusion, the candidate genes sar1b and slc22a5 linked to snp8107 and snp9562 were identified and analyzed. The D6 could serve as a potential diplotype for black carp breeding. This study offers valuable information for future enhancement of the genetic traits of black carp.

Key words:：Black carp, Gene cloning, Fine mapping, Growth trait, Association analysis

菲律宾蛤仔 RpMR1 抗鳗弧菌感染的分子机制研究

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摘要：本研究在菲律宾蛤仔基因组中鉴定出 13 个 MR 基因（RpMR1-13）。转录组中具有显著差异变化的 RpMR1-6 基因，蛤仔在鳗弧菌胁迫后 RpMR1、RpMR2、RpMR3 和 RpMR4 的表达在 72 小时达到峰值。对抗性组显著差异的 RpMR1 进行原核表达，获得了 RpMR1 重组蛋白，发现 RpMR1 蛋白对三种革兰氏阴性菌（V.splendius、V.algnolytiacu 和 V.anguillarum）有抑制作用。RpMR1 重组蛋白体内注射实验，发现可以降低蛤仔在鳗弧菌感染后的死亡率。dsRNA-RpMR1 注射到蛤仔中 RpMR1 被沉默。采用 qPCR 检测 TLR 信号通路中的基因表达，在鳗弧菌胁迫后，干扰 MR 基因可以显著抑制 TLR4 基因表达（P<0.05），表明 RpMR1 和 TLR4 在免疫反应中的相互作用。本研究首次揭示了甘露糖受体 1 在贝类中的免疫功能，为进一步了解菲律宾蛤仔抗鳗弧菌感染的分子机制提供了基础。

关键词：菲律宾蛤仔；甘露糖受体；基因表达；免疫功能

Mannose receptor RpMR1 of Manila clam (Ruditapes philippinarum) defense against Vibrio anguillarum infection

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Abstract： Mannose receptor (MR) is a member of the mannose receptor family of C-type lectin superfamily and belongs to type I transmembrane protein. As a pattern recognition receptor (PRRs), MR balance the immune response to foreign substances. In this study, 13 MR genes (RpMR1-13) were identified in the genome of Ruditapes philippinarum. The differential expression of RpMR genes of R. philippinarum was detected after Vibrio anguillarum challenge. The results showed that the expression of RpMR1, RpMR2, RpMR3, and RpMR4 reached the peak at 72 h. In addition, we obtained the purified recombinant RpMR1 protein, and found that RpMR1 protein had inhibitory effect on three gram-negative bacteria (V. splendidus, V. algnolytiacu and V. anguillarum), but have no inhibitory effect on gram-positive bacteria. The obtained RpMR1 recombinant protein was subjected to in vivo injection experiments and found that it could reduce the mortality rate of R. philippinarum after V. anguillarum challenge. Furthermore, dsRNA-RpMR1 was injected into the R. philippinarum and RpMR1 was successfully silenced. Using qRT-PCR to detect gene expression in the TLR signaling pathway interacting with MR, the results showed that after V. anguillarum stress, interference with MR genes could significantly inhibit TLR4 gene expression (P<0.05). This Verified the interaction between RpMR1 and transcription factors TLR4 during the immune response. Thus, all data in this study reveals the immune function of mannose receptor1 in molluscs for the first time, which provides a basis for further understanding on the molecular mechanism of R. philippinarum against V. anguillarum infection.

Key words:：Ruditapes philippinarum; Mannose receptor; Gene expression; Immune function

鱼类信号通路的模块化设计与改造——以白介素 17 通路为例

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摘要：合成生物学和 CAR-T 技术是改造生物通路的典型案例，改变蛋白表达谱和活性属于微调功能，增减基因则可大幅改变或获得新功能。但研究发现自然界中改变和获得新功能的最普遍和有效的方式是蛋白结构域重排。本研究重点分析结构域重排如何重塑 IL-17 通路的功能模式。IL-17 通路在黏膜修复和黏膜免疫中起关键作用，被誉为“免疫总指挥”，是重要的疾病治疗靶点，但在水产动物中研究较少。我们发现，IL-17 通路是由神经营养因子通路和 TLR/IL-1R 通路的结构域重排形成的嵌合通路，并且不同物种的 IL-17 通路功能模式差异巨大。例如，在虾蟹中，IL-17 作为神经递质参与性别分化；在鱼类中，由于丢失死亡结构域，IL-17 的激活能力下降到不足原来百分之一，但恢复死亡结构域可恢复其激活能力并提高仔鱼抗病能力。此研究为鱼类 IL-17 通路的改造提供了理论基础（参考文献 DOI:10.1073/pnas.2400903121）。

关键词：生物通路改造；蛋白结构域重排；IL-17；TLR；IL-1R；神经营养因子；免疫；发育； 内分泌

Modular Design and Engineering of Fish Signaling Pathways: A Case Study of the Interleukin-17 Pathway

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Abstract：Synthetic biology and CAR-T technology represent typical examples of biological pathway engineering. While adjusting protein expression profiles and activity can fine-tune pathway functions, adding or deleting genes can substantially alter or introduce new functions. However, research has shown that the most common and effective way for nature to achieve new functionality is through protein domain rearrangement. This study focuses on how domain rearrangement reshapes the functional pattern of the IL-17 pathway. The IL-17 pathway plays a critical role in mucosal repair and immunity, earning it the title of "immune commander" and making it an important therapeutic target in disease treatment, though it has been less studied in aquatic animals. Our findings reveal that the IL-17 pathway is a chimeric pathway formed by domain rearrangements between the neurotrophin and TLR/IL-1R pathways. Moreover, the functional patterns of the IL-17 pathway vary significantly across species. For example, in crustaceans, IL-17 acts as a neurotransmitter involved in sex differentiation, while in fish, the loss of a death domain reduces IL-17 activation capacity to less than 1% of its original level. However, restoring the death domain recovers its activation capacity and enhances resistence to pathogentic bacteria in fish larvae. This study provides a theoretical foundation for the engineering of the IL-17 pathway in fish (Reference DOI:10.1073/pnas.2400903121).

Key words:：biological pathway engineering, protein domain rearrangement, IL-17, TLR, IL-1R, neurotrophins, immunity, development, endocrine

原油水溶性成分对菲律宾蛤仔肝胰腺转录组及抗氧化防御系统影响的研究

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摘要：为研究原油污染对菲律宾蛤仔（Ruditapes philippinarum）的影响，我们通过组织学观察、氧化应激检测和转录组分析等生物学指标，探究蛤仔不同浓度（0.5、1.0 和 3.0 mg/L）原油水溶性组分（WAF）暴露的影响，并对 3 mg/L 暴露的蛤仔肝胰腺进行转录组分析。结果发现随着暴露时间的持续，体内的抗氧化酶系统，包括 SOD、CAT 和 GPx 的活性显著提升，反映氧化应激程度的脂质过氧化产物 MDA 的含量也显著增加。转录组分析发现与对照组比，蛤仔在 7、15 和 22 天（15 天暴露后在清洁海水中恢复 7 天）的实验暴露后，分别有 129、123 和 2113 个差异表达基因（DEGs）。这些 DEGs 主要涉及解毒代谢、氧化应激、免疫应答和能量代谢等生物学过程。特别是 15 天时，磺基转移酶家族 2A 成员 1(SULT2A1)、细胞色素 P450 家族 2 亚家族 J 成员 2(CYP2J2)等基因显著上调，显示持续的生理压力。

关键词：菲律宾蛤仔、原油污染、转录组分析、生态恢复

Effects of water-soluble components of crude oil on hepatopancreas transcriptome and antioxidant defense system of Ruditapes philippinarum

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Abstract：To study the effects of crude oil pollution on Ruditapes philippinarum, we investigated the effects of exposure to Water-Accommodated Fractions (WAF) of R. philippinarum at different concentrations (0.5, 1.0 and 3.0 mg/L) by histological observation, oxidative stress detection and transcriptomic analysis.Transcriptome analysis was performed on 3 mg/L exposed clam hepatopancreas.The results showed that with the duration of exposure, the activities of antioxidant enzyme systems, including superoxide dismutase (SOD), catalase (CAT) and glutathione peroxidase (GPx), and the content of malondialdehyde (MDA), the product of lipid peroxidation reflecting the degree of oxidative stress, also increased significantly.Transcriptome analysis revealed 129, 123, and 2113 differentially expressed genes (DEGs), respectively, after experimental exposure at 7, 15, and 22 days (7 days of recovery in clean seawater after 15 days of exposure) compared to the control group. These DEGs are mainly involved in biological processes such as detoxification metabolism, oxidative stress, immune response and energy metabolism.In particular, after 15 days, genes such as 2A member 1 of the sulfotransferase family (SULT2A1) and J member 2 of cytochrome P450 family 2 subfamily (CYP2J2) were significantly upregulated, indicating sustained physiological stress. This study provides insights into the molecular adaptation of bivalves to crude oil pollution, and also provides an important scientific basis for the use of biomarkers to assess Marine pollution.

Key words:：Ruditapes philippinarum; Crude oil pollution; transcriptome analysis; ecological restoration

虹鳟非编码 RNA 抗病毒天然免疫应答机制研究

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摘要：虹鳟是全世界广泛养殖的冷水性鱼类，而传染性造血器官坏死病毒（IHNV）病的频发严重危害了鲑鳟鱼养殖业的健康发展。因此，探究 IHNV 感染过程中虹鳟的免疫响应及调控机制是非常必要的。本研究通过对 IHNV 感染和对照组的虹鳟脾脏、头肾、肝脏、肠道、皮肤和鳃进行转录组测序及分析，鉴定了大量免疫相关的差异基因和差异非编码 RNA（DEncRNAs）；GO 富集分析显示 DEncRNAs 靶基因主要被注释在免疫系统过程、先天性免疫反应、炎症反应等条目；KEGG 分析发现 DEncRNAs 靶基因在 Toll 样受体、RIG-I 样受体、NOD 样受体和 Jak-STAT 等信号通路显著富集。进而在体内外水平上分别采用过表达和抑制表达等方法对关键 ncRNA 和靶基因的功能及调控机制进行了系统的分析。本研究加深了我们对 ncRNA 参与虹鳟抗病毒天然免疫机制的理解，可为深入探究虹鳟抗病分子育种和靶向药物治疗提供基础资料。

关键词：虹鳟；IHNV；天然免疫；基因；ncRNA

Study on the antiviral innate immune mechanism of non-coding RNA in rainbow trout (Oncorhynchus mykiss)

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Abstract：Rainbow trout (Oncorhynchus mykiss) is a cold-water fish widely farmed around the world, and the outbreak of infectious hematopoietic necrosis virus (IHNV) has seriously harmed the healthy development of the salmon and trout aquaculture industry. Therefore, it is essential to explore the immune response and regulatory mechanisms of rainbow trout during IHNV infection. In this study, a large number of differential genes (DEGs) and differential ncRNAs (DEncRNAs) were identified by mRNA and non-coding RNA (ncRNA) sequencing and co-analysis of rainbow trout spleen, head-kidney, liver, intestine, skin, and gill in IHNV-infected and control group. The immune-associated target genes of DEncRNAs included RIG-I, LGP2, RNF135, TRIM25, TLR3, IRF3, IRF7, TRAF3, RIPK2, and SOCS3. GO functional analysis showed that DEncRNAs target genes were mainly annotated in immune system processes, innate immune response, and inflammatory response items. KEGG enrichment analysis found that DEncRNAs target genes were significantly enriched in Toll-like receptor signaling pathway, RIG-I-like receptor signaling pathway, NOD-like receptor signaling pathway, Jak-STAT signaling pathway and apoptosis. In addition, we systematically analyzed the functions and regulatory mechanisms of key ncRNAs and target genes by overexpression and inhibition assays in rainbow trout in vitro and in vivo. This study deepens our understanding of ncRNA involved in the antiviral innate immune mechanism, and provides basic information for in-depth exploration of disease-resistant molecular breeding and targeted drug treatment in rainbow trout.

Key words:：Rainbow trout; IHNV; Innate immune; Genes; ncRNAs

马氏珠母贝中 MicroRN A novel-13 和 novel-44 对副溶血弧菌感染的响应机制研究

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摘要：马氏珠母贝(Pinctada fucata martensii)是我国人工海水育珠的主要珍珠贝之一，在以近海岸集约化方式养殖过程中，极易受到病原微生物的感染。MicroRNA（miRNA）作为一种新型有效的免疫调控手段来参与马氏珠母贝对外界刺激的免疫应答过程，受到了越来越多学者的关注. 本研究基于实验室前期构建的马氏珠母贝血细胞在副溶血弧菌感染前后的全转录组文库，挑选出两种新型 miRNA novel-13 和 novel-44 进行进一步研究。通过合成 miRNA（novel-13 和 novel-44）相应的模拟物和抑制剂在马氏珠母贝中过表达，发现模拟物组抗氧化相关酶活性显著下降，抑制剂组酶活力显著升高。在攻毒实验中，注射 miRNA 抑制剂组与对照组相比，能提高马氏珠母贝大约 10%的免疫保护率。双荧光素酶结果说明 novel-13 和 PmLAAO 以及 novel-44 和 PmILK 之间存在负向调控关系。

关键词：马氏珠母贝，miRNA，靶向基因，副溶血弧菌

Study on the response mechanism of MicroRNA novel-13 and novel-44 to Vibrio parahaemolyticus infection in Pinctada fucata martensii

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Abstract：Pinctada fucata martensii is one of the main pearl oysters cultured in artificial seawater in China. In the course of intensive cultivation near the coast, it is highly susceptible to pathogen infection. MicroRNA (miRNA), as an innovative and potent regulator of immune function, plays a pivotal role in the immune response of pearl oysters to external stimuli, attracting increasing attention from scholars.This study is based on the full transcriptome library of Pinctada fucata martensii blood cells before and after infection with Vibrio parahaemolyticus, and two novel miRNAs, novel-13 and novel-44, were selected for further investigation. Through the overexpression of synthetic miRNA (novel-13 and novel-44) mimics and inhibitors, it was found that the activity of antioxidant-related enzymes decreased significantly in the mimics group and increased significantly in the inhibitor group. In the challenge experiment, miRNA inhibitor injection group increased the relative percentage survivals by about 10% compared with the control group. The results of dual luciferase indicated that novel-13 and PmLAAO and novel-44 and PmILK were negatively regulated.

Key words:：Pinctada fucata martensii, miRNA, target gene, Vibrio parahaemolyticus

WGBS 结合 RNA-seq 分析揭示菲律宾蛤仔(Ruditapes philippinarum)对鳗弧菌抗性的潜在机制

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摘要：本实验采用浓度为 107 CFU/mL 鳗弧菌(Vibrio anguillarum)悬液胁迫菲律宾蛤仔(Ruditapes philippinarum)，将第 7 天存活和濒死的蛤仔分为抗性组(VaR)和易感组(VaS)。取肝胰腺组织进行全基因组亚硫酸氢盐测序(WGBS)，发现差甲基化区域在 Wnt、Notch、mTOR、FoxO 信号通路显著富集，VaR 甲基化水平显著高于 VaS 和对照组(Con)。WGBS 结合 RNA-seq 分析，筛出 10 个启动子高甲基化低表达和低甲基化高表达差异免疫基因，包括 HCK-like、STING1、MRC1、CASP6 等。通过 qRT-PCR 和线性回分析，启动子区域中基因表达与 RNA-seq 结果一致，与甲基化水平呈负相关关系。高甲基化抑制基因表达，低甲基化促进基因表达。因此，DNA 甲基化通过调控免疫基因表达来参与蛤仔抗鳗弧菌反应。

关键词：菲律宾蛤仔；DNA 甲基化；鳗弧菌；全基因组亚硫酸氢盐测序；RNA 测序

WGBS combined with RNA-seq analysis revealed the underlying mechanism of resistance to Vibrio anguillarum in Ruditapes philippinarum

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Abstract： The experiment lasted for 16 days. Ruditapes philippinarum was stressed with 107 CFU/mL of Vibrio anguillarum suspension. The death rate reached its peak on the 7th day. The surviving and dying clams were divided into resistant group (VaR) and susceptible group (VaS), and the control group (Con) were healthy clams. Whole genome bisulfite sequencing (WGBS) was performed on hepatopancreas. 5355 differential methylation regions (DMRs) were selected, which were significantly enriched in Wnt, Notch, mTOR and FoxO signaling pathways, and the methylation level of VaR was significantly higher than that of VaS and Con. Compared with Con, 4423 differentially expressed genes (DEGs) were identified by VaR, more than 3776 DEGs identified by VaS. WGBS combined with RNA-seq analysis screened out 10 promoter genes with Hypermethylated expression of down genes (Hyper-Down) and hypomethylated expression of up genes (Hypo-Up), including Tyrosine-protein kinase HCK-like (HCK-like), Stimulator of interferon genes protein (STING1), Macrophage mannose receptor 1 (MRC1), Caspase 6 (CASP6) and other differential immune genes. QRT-PCR and linear regression analysis were performed for these genes. The HCK-like expression level of VaR was higher than that of VaS, while the methylation level was lower. STING1 was a Hyper-Down gene in both VaR and VaS, CASP6 was a Hyper-Down gene in VaR, and MRC1 was a Hypo-Up gene.Gene expression in the promoter region was consistent with the results of RNA-seq and negatively correlated with the methylation level. Hypermethylation inhibited gene expression (e.g. CASP6, STING1), and hypomethylation promoted gene expression (e.g. MRC1). Therefore, DNA methylation is involved in the anti-V. anguillarum response of R. philippinarum by regulating the expression of immune genes.

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

比较基因组学探究硬骨鱼类盐度适应性的平行进化

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摘要：盐度是水生生物最为重要的环境因子之一。经过漫长的进化，不同谱系硬骨鱼类的盐度适应性有所差异，可分为淡水鱼类、海水鱼类和广盐性鱼类。然而，其基因组水平盐度适应的平行进化模式尚不清楚。本研究选取 8 种淡水鱼类、8 种海水鱼类和 10 种广盐性鱼类开展比较基因组学研究。结果表明，淡水适应性（淡水鱼类、广盐性鱼类）和海水适应（海水鱼类、广盐性鱼类）个体的基因拷贝数呈现明显差异的分布模式。通过基因共线性分析和转座子的鉴定，发现淡水和海水适应相关基因拷贝数的变化可能是由其上下游 LTR 和 LINE 转座元件所介导。在 BUSTED-PH 和 Relaxed 的强化选择研究中，确定了 84 淡水，70 个海水和 92 个广盐性适应的基因。研究揭示了广盐性鱼类对淡水和海水的选择适应策略，基因拷贝数的变化和氨基酸的替换是广盐性鱼类适应盐度波动环境的重要方式，为硬骨鱼类广盐性适应平行进化提供新的见解。

关键词：硬骨鱼，广盐性，平行进化，比较基因组，拷贝数，选择压力

Comparative genomics explores parallel evolution of salinity adaptation in bony fishes

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Abstract：Salinity is one of the most important environmental factors for aquatic organisms. Over the course of long-term evolution, bony fish from different lineages have developed varying salinity adaptations, classifying them into freshwater species, marine species, and euryhaline species. However, the parallel evolutionary patterns of salinity adaptation at the genomic level remain unclear. In this study, we conducted a comparative genomic analysis on 8 freshwater species, 8 marine species, and 10 euryhaline species. The results revealed distinct distribution patterns of gene copy numbers between freshwater-adapted (freshwater and euryhaline species) and marine-adapted (marine and euryhaline species) individuals. Through synteny analysis and transposon identification, it was found that the changes in gene copy numbers related to freshwater and marine adaptation may be mediated by upstream and downstream LTR and LINE transposable elements. In the BUSTED-PH and RELAX selection analyses, 84 genes were identified for freshwater adaptation, 70 genes for marine adaptation, and 92 genes for euryhaline adaptation. The study reveals the adaptive strategies of euryhaline species to both freshwater and marine environments, where changes in gene copy numbers and amino acid substitutions play significant roles in their adaptation to fluctuating salinity conditions. These findings provide new insights into the parallel evolution of salinity adaptation in bony fish.

Key words:：Bony fish, euryhaline, parallel evolution, comparative genome, copy number, selection pressure

斑马鱼肝脏中 Hdac11 对 creld2 的表观调控研究

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摘要：HDAC11 能够催化组蛋白和非组蛋白赖氨酸残基去乙酰化，是关键的表观调控酶。CRELD2 是内质网应激诱导的分泌蛋白，在多种疾病中有重要作用。研究发现斑马鱼 Hdac11 敲除后肝脏 creld2 表达量上调，本文通过 RT-qPCR、ChIP-qPCR 和 3C-qPCR 研究 Hdac11 在 WT 和 hdac11-/-斑马鱼肝脏中对 creld2 的表观遗传调控机制。结果表明，在 hdac11-/-斑马鱼肝脏中，creld2 的表达量显著升高； creld2 +230kb 区域的 H3K27ac 结合水平上调；creld2 +230kb 区域与 creld2 启动子之间存在空间互作，且该互作频率上调。综上，creld2 +230kb 区域存在 creld2 的增强子。斑马鱼肝脏中 Hdac11 可能通过去乙酰化降低了 creld2 +230kb 增强子与 creld2 启动子互作的频率，抑制了 creld2 的表达。

关键词：关键词：斑马鱼；Hdac11；creld2；增强子

Study on epigenetic regulation of creld2 by Hdac11 in zebrafish liver

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Abstract： [Objective] Histone deacetylases 11 (HDAC11) is the sole member of Class IV HDACs, which can catalyze the deacetylation of lysine residues on histones and non-histones, and is an important epigenetic regulatory enzyme. CRELD2 (cysteine-rich with EGF-like domains 2) is an endoplasmic reticulum stress-induced secreted protein that plays an important role in cardiovascular diseases, cancer, and inflammatory bowel disease. Previous studies have showed that creld2 expression in zebrafish liver is upregulated after Hdac11 knockout. This study investigates the epigenetic regulation mechanism of creld2 by Hdac11 in zebrafish liver. [Methods] The relative mRNA expression levels of creld2 in WT and hdac11-/- zebrafish liver were detected by RT-qPCR. The enrichment levels of Hdac11 and H3K27ac in the +230kb region of creld2 were verified by ChIP-qPCR. The interaction between the +230kb region of creld2 and creld2 promoter was examined by 3C-qPCR. [Results] Compared with WT, the mRNA level of creld2 in hdac11-/- zebrafish liver was significantly increased. Hdac11 knockout enhanced the enrichment level of H3K27ac in the +230kb region of creld2. There is a spatial interaction between the +230kb region of creld2 and its promoter, and the interaction frequency is upregulated in hdac11-/- zebrafish liver. [Conclusion] There is an enhancer located at +230kb region of creld2. Deacetylation of Hdac11 in zebrafish liver reduces the frequency of interaction between creld2 +230kb enhancer and creld2 promoter, thereby inhibiting creld2 expression.

Key words:：Keywords: zebrafish; Hdac11; creld2; enhancer

转录组分析揭示薄片镜蛤（Dosinia corrugata）响应高温胁迫的分子适应机制

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摘要：本研究旨在探索薄片镜蛤（Dosinia corrugata）在极端高温条件下的分子调控机制，以促进薄片镜蛤养殖业的可持续发展。为鉴定与高温相关的基因并阐明其适应机制，我们对薄片镜蛤鳃组织在急性热应激 12h 和 24h 时的转录组进行了分析。在急性热应激 12h 和 24h 时，我们分别检测到 6842 个和 1112 个差异表达基因（DEGs）。KEGG 富集分析显示，在两个时间点上共同富集的通路包括多物种凋亡、泛素介导的蛋白水解、TNF 信号通路和 RIG-I 受体信号通路。基于共同富集的通路，我们构建了蛤仔应对高温的潜在调控网络。我们还发现在急性热应激 12h 时，代谢相关通路显著富集。然而在急性热应激 24h 时，免疫相关通路显著富集。本研究为理解薄片镜蛤应对高温的潜在分子调控机制提供了重要的见解。

关键词：薄片镜蛤; 急性热应激; 差异表达基因; 通路

Transcriptomic Analysis Reveals the Molecular Adaptation Mechanisms of Dosinia corrugata in Response to Heat Stress

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Abstract： This study aims to explore the molecular regulatory mechanisms of Dosinia corrugata under extreme heat conditions to promote the sustainable development of its aquaculture. To identify heat-related genes and clarify their adaptive mechanisms, we conducted transcriptome analyses of gill tissues following acute heat stress at 12h and 24h. A total of 6,842 and 1,112 differentially expressed genes (DEGs) were identified at 12h and 24h of acute heat stress, respectively. KEGG enrichment analysis revealed that pathways commonly enriched at both time points included multi-species apoptosis, ubiquitin-mediated proteolysis, TNF signaling, and RIG-I receptor signaling pathways. Based on these commonly enriched pathways, we constructed a potential regulatory network for the heat stress response in D. corrugata. Notably, metabolic pathways were significantly enriched at 12h of heat stress, while immune-related pathways were predominantly enriched at 24h. This study provides valuable insights into the potential molecular regulatory mechanisms underlying the heat stress response in D. corrugata.

Key words:：Dosinia corrugata; acute heat stress; differentially expressed genes; pathways

Kdm4aa 调控斑马鱼早期胚胎发育的机制

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摘要：KDM4A 是一种重要的表观修饰酶，可以催化 H3K9me2/3 的去甲基化过程，其在斑马鱼中有 Kdm4aa 和 Kdm4ab 两个亚型。前期研究发现在斑马鱼中敲除 kdm4aa 导致早期胚胎发育中死亡率显著增加，表明 Kdm4aa 可能在发育中发挥重要作用。为了探究 Kdm4aa 影响胚胎发育的机制，对 WT 和 kdm4aa-/-斑马鱼 5.25 hpf 胚胎进行 RNA-seq 分析与 RT-qPCR 验证，结果显示，与细胞外基质和细胞骨架相关的基因 acta1a、actc1b、tpm4b、sgca、fhl1b 的表达显著降低。CUT&Tag 结果显示，这些基因的 H3K9me3 水平升高，其中 sgca 和 actc1b 的 TSS 区观察到 H3K4me3 水平下降，说明其表达可能受到抑制。综上，斑马鱼胚胎在早期发育过程中，Kdm4aa 的缺失可能导致 H3K9me3 在细胞外基质和细胞骨架相关的基因处富集增加，使细胞迁移、分化受到阻碍，引起胚胎死亡。

关键词：Kdm4aa；斑马鱼；胚胎发育；细胞骨架

The mechanisms of Kdm4aa on regulating early embryonic development in zebrafish

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Abstract：[Objective] Lysine-specific demethylase 4A (KDM4A) is an important epigenetic enzyme, which catalyzes the demethylation of H3K9me2/3. There are two copies of the kdm4a gene in zebrafish, namely kdm4aa and kdm4ab. Previous evidences shows that knockout of kdm4aa in zebrafish results in a significant increase in mortality in zebrafish during early embryo development, suggesting that Kdm4aa may play an important role in development. Therefore, this study aimes to explore the mechanism of Kdm4aa on regulating zebrafish early embryonic development. [Methods] In this study, we performed RNA-seq, RT-qPCR and CUT&Tag on 5.25 hpf embyos of WT and kdm4aa-/- zebrafish. [Results] The RNA-seq results showed that knockout of kdm4aa significantly decreased the expressions of genes related to extracellular matrix(ECM) and cytoskeleton, such as acta1a, actc1b, tpm4b, sgca and fhl1b. The CUT&Tag results showed that H3K9me3 levels significantly increased in these genes, and H3K4me3 levels significantly decreased in the TSS regions of sgca and actc1b. [Conclusion] During the early development of zebrafish embryos, the deletion of Kdm4aa may lead to increased H3K9me3 levels in ECM and cytoskeleton-related genes, regulate the expressions of related genes positively, and inhibit the cell migration and differentiation, thus causing the death of embryos.

Key words:：Kdm4aa; zebrafish; embryonic development; cytoskeleton

17α-甲基睾酮对罗氏沼虾生长、性别分化、性腺发育及肠道微生物的影响

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摘要：17α-甲基睾酮（MT）具有抑制卵巢、诱导精子发生的功能，现已广泛用于鱼类的性逆转。本研究通过在基础饲料中添加不同浓度的 MT，通过性别比例、组织学观察、生殖发育相关基因表达水平检测及肠道微生物多样性分析来评估饲料中添加 MT 对罗氏沼虾幼虾生长与性腺发育的影响。饲喂 60 天后，与其他组相比，1000 mg/kg MT 剂量的罗氏沼虾雄雌性别比例最高，饲喂 150 天后，500 mg/kg MT 剂量的雄雌性别比例转变为最高，而 1500 mg/kg MT 剂量的雄雌比例最低且精巢中的生殖细胞处于发育初期并出现了性腺发育迟缓现象。肠道菌落分析显示：MT 的添加不仅显著提高罗氏沼虾肠道微生物的丰度而且还能诱导肠道微生物群落结构的显著变化。本研究明确了饲料中添加 MT 对罗氏沼虾幼虾的生殖发育及肠道菌落的的影响，为甲壳类性别控制实施提供了的理论依据。

关键词：罗氏沼虾；甲基睾酮；性别分化；肠道微生物

Effects of 17α-methyltestosterone on growth, sex differentiation, gonadal development and intestinal microbiome of Macrobrachium rosenbergii

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Abstract： The function of 17α-methyltestosterone (MT) includes the inhibition of ovaries and induction of spermatogenesis, making it widely used in fish for artificial sex reversal induction. In this study, various concentrations of MT were added to the basal diet to evaluate its effects on the growth and gonadal development of juvenile Macrobrachium rosenbergii through assessments such as sex ratio, histological observation, gene expression related to reproductive development, and analysis of intestinal microbial diversity. After a feeding period of 60 days, the group supplemented with 1000 mg/kg MT exhibited the highest sex ratio compared to other groups. Following a feeding period of 150 days, the group supplemented with 500 mg/kg MT had the highest sex ratio while the group supplemented with 1500 mg/kg MT had the lowest ratio; moreover, testicular germ cells were found to be in an early stage of development and gonad development was delayed. Intestinal colony analysis revealed that MT supplementation significantly increased intestinal microorganism abundance and induced notable changes in intestinal microbial community structure of M. rosenbergii. Related gene detection confirmed that dietary addition of MT can significantly reduce vitellogenin (Vg), vitellogenin receptor (Vgr), and sperm gelatinase (SG) gene expression levels ($p < 0.05$). This study provides insights into how dietary intake of MT affects reproductive development and intestinal microbiota in juvenile M. rosenbergii individuals, thereby offering a theoretical foundation for crustacean sex control implementation.

Key words:：Macrobrachium rosenbergii: 17α-methyltestosterone; Sex differentiation; Intestinal microbiota

侏儒蛤胚胎发育的表观遗传调控与母源合子基因表达转换规律

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摘要：双壳纲软体动物是软体动物门中最大且最具经济价值的类群之一，但其胚胎发育研究较为有限。侏儒蛤是研究双壳类胚胎学的理想模型。本研究首次在侏儒蛤上应用 CUT&Tag 技术，绘制了组蛋白修饰 H3K4me1、H3K4me3、H3K27me3 和 H3K27ac 在多个关键发育阶段的高分辨率图谱。组蛋白修饰的动态变化显示，其早期胚胎发育中染色质状态发生了广泛重塑，结合转录组数据，我们确定侏儒蛤在桑葚期至原肠胚阶段发生母源到合子基因表达的转换（MZT）。通过组蛋白修饰和转录组数据的联合分析，我们识别出多个可能对侏儒蛤胚胎发育至关重要的候选基因。此外，我们推测 EZH2 介导的 H3K27me3 在囊胚阶段的基因组重编程中至关重要。本研究加深了对双壳类胚胎发育表观遗传调控机制的理解，为研究海洋无脊椎动物提供了新方法，并为双壳类基因功能研究尤其是基因表达调控研究提供了丰富的数据资料，为双壳贝类的水产养殖优化奠定基础。

关键词：侏儒蛤，CUT&Tag，组蛋白修饰，表观遗传调控，胚胎发育

Epigenetic Regulation and Maternal-to-Zygotic Transition in Mulinia lateralis: Insights from Chromatin State Profiling and Transcriptomics

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Abstract： Bivalve mollusks constitute one of the largest and most economically significant classes within the Mollusca phylum. However, fundamental biological research, particularly on embryonic development, remains limited for bivalves. Mulinia lateralis has emerged as an ideal model for bivalve embryology due to its short life cycle and high reproductive rate. In this study, we investigated the epigenetic regulations underlying embryogenesis in M. lateralis through chromatin state analysis and transcriptomics, focusing on the critical process of the maternal-to-zygotic transition (MZT). We successfully established the CUT&Tag technique in M. lateralis, obtaining high-resolution profiles of H3K4me1, H3K4me3, H3K27me3, and H3K27ac across key developmental stages. Our results revealed widespread remodeling of histone modifications during early embryonic development, and, in conjunction with transcriptomic data, identified the MZT as occurring between the morula and gastrula stages in M. lateralis. These profiles highlighted dynamic changes in chromatin modifications and identified several candidate genes potentially crucial for embryogenesis, including yap1, ppp2r1b, β-actin, mtor, 14-3-3 zeta, smad4, sec61a, and genes containing the EF-hand domain. Our findings suggest these genes play significant roles in cell proliferation, differentiation, and the development of the nervous and immune systems. Additionally, we hypothesize that EZH2-mediated H3K27me3 is pivotal in genome reprogramming during the blastula stage, supported by the expression of P-body-associated genes involved in maternal mRNA degradation. This research enhances our understanding of epigenetic mechanisms in bivalve development and introduces novel methodologies for studying marine invertebrates. The findings not only offer theoretical support for optimizing bivalve aquaculture but also establish M. lateralis as a valuable model organism. Furthermore, this study lays the groundwork for future experimental validation of these candidate genes and for extending research to other bivalve species to further elucidate embryonic development mechanisms.

Key words:： Mulinia lateralis; CUT&Tag; Histone modifications; Epigenetic regulations; Embryonic development

不同壳色四角蛤蜊响应海洋酸化胁迫的能量代谢及分子机制初探

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摘要：四角蛤蜊(Mactra veneriformis)作为一种重要的海洋经济双壳类动物，由于在快速生长期壳较为脆弱而易受到海洋酸化(OA)的影响，本研究以四角蛤蜊白壳和紫壳自然群体为研究对象，进行酸化胁迫下(pH=7.6)的死亡率、耗氧率、排氨率测定及外套膜组织转录组分析，结果表明:两种壳色四角蛤蜊酸化组死亡率、耗氧率和排氨率均显著高于对照组，除白壳组耗氧率显著高于紫壳组外，死亡率和排氨率两壳色组无显著差异;转录组测序结果显示两个壳色组在酸化胁迫下，在氧化还原、金属离子结合及脂肪酸生物合成过程都具有共同的机制以减级酸化对自身的损伤。而紫壳四角蛤蜊中与酸碱离子平衡和钙转运相关的基因也出现显著变化进一步协助其维持细胞内稳态，本研究为四角蛤蜊应对海洋酸化胁迫提供了重要的基础数据，同时也为今后四角蛤蜊优良品系的选育奠定基础。

关键词：四角蛤蜊；海洋酸化；耗氧率；排氨率；转录组测序

Preliminary Study on Energy Metabolism and Molecular Mechanism of Mactra veneriformis with Different Colors under Ocean Acidification Challenge

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Abstract： Mactra veneriformis is highly susceptible to ocean acidification (OA) due to its low shell hardness during the rapid growth period. in this study, mortalitly, oxygen consumption rate 、 ammonia excretion rate and transcriptome sequencing in mantle tissue were conducted in white and purple color natural populations of M. veneriformis under acidification stress (pH=7.6). The results showed that the mortality rate 、 oxygen consumption rate and ammonia excretion rate increased siqnificantly after acidification in both two shell colors, and the oxygen consumption rate in white shell color was significantly higher than that in purple shell color but no significant difference in mortality rate and ammonia excretion rate.Transcriptomic analyses demonstrate two colored clams shared common mechanisms in oxidation-reduction, metal ion binding and fatty acid biosynthesis to reduce OA damage to seif. However, significant regulation in carbonic anhydrase and calmodulin expression were found in purple shell color but not in white shell color after OA exposure, which are factors associated with acid-base balance and Ca2+ transport. This difference may further contribute to maintenance of intracellular homeostasis in purple shell color. This study provides useful information related to the response of M. veneriformis to OA stress, and also help predict future breeding of excellent strains in M. veneriformis.

Key words:：Mactra veneriformis; Ocean acidification; Oxygen consumption rate; Ammonia excretion rate；Transcriptome;

软体动物生殖系调控通路和精原细胞表面标记的系统筛选和动态分析

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摘要：精原细胞可以自我更新并能够将遗传信息传递给下一代，对于雄性生殖和精子形成至关重要。然而，精原细胞表面标记物的缺失限制了对精原细胞的深入研究，并且表面标记物在不同物种之间并不通用。在本研究中，我们开发了一种用于筛选非模式生物生殖系调控途径和精原细胞表面标志物的策略。该策略结合了加权基因共表达网络分析、基因过表达分析和功能富集分析。利用该策略确定了精原细胞相关模块，并在该模块中富集到了生殖干细胞相关通路。从该通路中发现了一种跨膜蛋白--成纤维细胞生长因子受体（FGFR）。通过免疫小鼠获得 FGFR 抗血清。使用 Western blot、免疫组织化学和免疫细胞化学分析表明，抗血清能特异性检测到虾夷扇贝精原细胞中的 PyFGFR。本研究证明该策略在筛选扇贝精原细胞表面标记物方面的可行性。这种方法将促进非模式生物精原细胞的培养和操作，从而有助于水产养殖业的遗传改良。

关键词：Fgfr；细胞表面标记物；WGCNA；精原细胞；虾夷扇贝

Systematic screening and dynamic profiling of germline regulatory pathways and spermatogonial surface markers in a bivalve mollusc

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Abstract：Spermatogonial cells are capable of transmitting genetic information to the next generation and have the potential for self-renewal. However, research on spermatogonial cells is generally limited by the paucity of cell surface markers, which are not universal among species. In this study, we developed a systematic screening strategy for germline regulatory pathways and spermatogonial surface markers in non-model organisms. This was achieved by combining weighted gene co-expression network analysis (WGCNA), differential expressed gene (DEG) overrepresentation analysis, and functional analysis. The strategy was employed to identify a spermatogonia-related module, which was found to be enriched with stem cell-related pathways in the scallop Patinopecten yessoensis. From this module, a transmembrane protein, fibroblast growth factor receptor (FGFR), was identified. A single copy of Fgfr (PyFgfr) was confirmed in the P. yessoensis genome, which exhibited the canonical functional domains of FGFRs. PyFgfr was universally expressed in multiple tissues, including the testis. The highest expression was observed at the resting stage of the testis, with exclusive localization in spermatogonia. To obtain antibodies that recognize the cell surface region, the extracellular domains of PyFGFR were used as an antigen to prepare antiserum. Western blotting, immunohistochemical, and immunocytochemical analyses demonstrated that the antiserum specifically detected PyFGFR in the spermatogonia. Our study demonstrated the feasibility of the strategy in screening spermatogonial surface markers in the scallop. This approach will facilitate the culture and manipulation of spermatogonia in non-model organisms, which may contribute to genetic improvement in aquaculture.

Key words:：Fgfr; Surface marker; WGCNA; Spermatogonial cells; Patinopecten yessoensis

牡蛎基因编辑技术体系构建与应用

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摘要：CRISPR/Cas9 技术的出现为生命科学领域带来一场技术革命，高效、精准、低成本的 CRISPR 技术已成为探究基因功能、解析生命现象的重要工具。本研究以长牡蛎为主要研究对象，利用显微注射成功构建了牡蛎 CRISPR/Cas9 基因编辑技术体系；阐明了各编辑元件对牡蛎基因编辑效率的影响；建立了高效、便捷的体外 sgRNA 筛选体系；开发了牡蛎基因编辑效率精准评估技术；筛选了牡蛎内源性和外源性启动子，构建了牡蛎外源基因高效表达系统；利用所构建的 CRISPR/Cas9 技术体系对牡蛎 MHC、MLCE、Tyr 等基因进行编辑，在 G0 幼虫中观察到表型变化，证实了这些基因在牡蛎肌生成、壳发生等生物过程中的重要调控作用；探究了电穿孔法在牡蛎基因编辑中的可行性。以上研究结果为双壳贝类基因编辑提供了重要参考信息，也为牡蛎基因编辑育种奠定了基础。

关键词：牡蛎，基因编辑，CRISPR/Cas9，启动子

Establishment and Application of Gene Editing Technology in Oysters

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Abstract： The advent of CRISPR/Cas9 technology has revolutionized life sciences, offering a powerful, efficient, and cost-effective tool for exploring gene function and deciphering biological phenomena. This study focuses on the Pacific oyster (Crassostrea gigas), successfully establishing a CRISPR/Cas9 gene editing system through microinjection. The effects of various editing components on gene editing efficiency in oysters were elucidated. A highly efficient and convenient in vitro sgRNA screening system was developed, alongside a precise method for assessing gene editing efficiency in oysters. Both endogenous and exogenous promoters were screened, leading to the construction of an effective exogenous gene expression system in oysters. Using this CRISPR/Cas9 platform, genes such as MHC, MLCE, and Tyr were edited, resulting in phenotypic changes observed in G0 larvae, confirming the crucial regulatory roles of these genes in biological processes such as muscle development and shell formation in oysters. Additionally, the feasibility of electroporation in oyster gene editing was investigated. These findings provide important reference information for gene editing in bivalves and lay a foundation for oyster breeding via gene editing.

Key words:：oyster, gene editing, CRISPR/Cas9, Promoter

鲤科鱼类卵巢组织细胞冷冻保存及复苏培养技术研究

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摘要：鱼类卵巢组织超低温保存在遗传资源保护、鱼类种质创制管理等方面极具重要价值。本研究以鲫鱼、齐口裂腹鱼和斑马鱼卵巢为材料，建立了一种简便高效的鲤科鱼类卵巢组织冷冻保存及复苏培养技术。用该方法对几种鱼卵巢组织进行冷冻保存，7 天内复苏卵巢细胞（6-20 μm）的活率可达 50%，120 天后活率为 33.81%并不再随着冷冻时间延长而显著下降，且复苏后的卵巢组织细胞可用于体外培养建系。为探究低温对卵巢细胞代谢的影响及进一步优化冻存技术，利用代谢组分析技术，比较了齐口裂腹鱼卵巢组织冷冻前后的代谢组份变化。研究发现，冷冻对维甲酸等代谢物及 TCA 循环等信号通路有显著影响。在此基础上，我们对冷冻保存剂中分别添加了一定量的 A、B、C 组分，经过 7 天冷冻，复苏组织的细胞活率可提高至 60 %。同时，利用细胞免疫荧光检测了培养细胞中 PCNA、Nanog 蛋白的表达，表明优化后的冷冻剂不但可提细胞活率还能保护其增殖能力。

关键词：卵巢组织；冷冻保存；代谢组分析；卵巢细胞培养；鲤科鱼类

Ovarian tissues’ cryopreservation and in vitro culture in the cyprinid fish species

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Abstract： Fish ovaries’ cryopreservation plays crucial roles in preserving the genetic resources, germplasm creation and management. The present study establishes an efficient and simple method to cryopreserve the ovarian tissues in the cyprinid fish species, including crucial carp (Carassius auratus), zebrafish (Danio rerio) and Schizothorax prenanti. The results showed that more than 50% of ovarian cells at 6-20 um could be saved after a 7-day-cryopreservation using the optimized cryomedium though slow-freezing, the viability decreased to 33.81% after 120 days’ cryopreservation and became stable after even longer time freezing and the thawed ovarian tissues could be used for in vitro culture and exhibited the high potency of proliferation. Furthermore, metabonomics was applied to explore the effects of cryopreservation on metabolic regulation in Schizothorax prenanti ovarian tissues and further optmize the cryopreservation protocol. The results showed that, freezing has significant influence on 318 differential metabolites (palmitic acid, retinoic acid, arachidonic acid, etc.) and 25 metabolic pathways (Purine metabolism, TCA cycle, etc.). Based on this, a certain amount of A, B, C metabolites were supplemented in cryomedium, and the cells' viability of thawed Schizothorax prenanti ovarian tissues increased to about 60.04% from 51.8% after cryopreservation of 7 days. Especially, though cell immunofluorescence analysis, the expression of PCNA and NANOG proteins in cultured cells was detected and similar expression level was observed between fresh and thawed ovarian tissues. Thereby, the optimized cryomedium could improve not only the survival rate of ovarian tissues but also the proliferation ability of ovarian cells. In a conclusion, this study established an efficient method for cryopreserving fish ovarian tissues and in vitro culture of thawed ovarian tissues, this may provide a valuable basis for other aquatic species resource preservation.

Key words:：Ovarian tissues; Cryopreservation; Metabonomics; Ovarian cells’ in vitro culture; Cyprinid species

仿刺参南方秋季苗种繁育胚胎发育观察及生长分析

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摘要：仿刺参（Apostichopus japonicus）是我国最具经济价值的海参种类之一，在南方地区的规模化人工繁育仍然薄弱。本研究通过仿刺参性腺低温控制诱导促熟技术，并于 10 月进行催产孵化。结果显示，阴干流水刺激后获得的受精卵为圆形、透明、沉性卵，卵径为(151.5±1.5) μm；在水温 21.5~22.5 ℃、盐度 29‰~30‰、pH 7.8~8.3 的条件下，胚胎及胚后发育正常，耳状幼体孵化率为 75％、樽形发生率为 84.4±4.85％、附着变态率为 82.37±2.83％；由受精卵发育到稚参时间为 16 d，刚开始为透明白色，至 30 d 后开始变深，到 60 d 时变成青色或红棕色，体长达到(30.00±1.37) mm。本研究结果表明，在人工可控条件下，我国南方地区可实现仿刺参的秋季规模化苗种繁育，在 60 d 后较北方培育苗种表现出一定的生长优势，本研究为我国仿刺参的秋季苗种繁育提供研究基础。

关键词：仿刺参；秋季；苗种繁育；胚胎发育；稚参生长

Observation of embryonic development and analysis of larval growth in autumn-bred seedlings of Apostichopus japonicus in Southern China

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Abstract： The sea cucumber Apostichopus japonicus is one of the most economically valuable sea cucumber species in China. However, large-scale artificial breeding of Apostichopus japonicus in southern regions remains underdeveloped. This study utilized low-temperature induction enhancement techniques to induce gonadal maturation . Spawning and hatching were conducted in October.The results showed that the fertilized eggs obtained through dry-flow stimulation were spherical, transparent, and demersal, with an average diameter of (151.5±1.5) μm. Under conditions of water temperature 21.5-22.5℃, salinity 29‰-30‰, and pH 7.8-8.3, normal embryonic and post-embryonic development was observed.. The hatching rate of auricularia larvae was 75%, the occurrence rate of doliolaria was 84.4±4.85%, and the attachment and metamorphosis rate was 82.37±2.83%. It took 16 days for the fertilized eggs to develop into juveniles, which initially appeared transparent white, then darkened after 30 days, and turned green or reddish-brown by 60 days, reaching a body length of (30.00±1.37) mm.The findings of this study indicate that under controlled conditions, large-scale autumn breeding of Apostichopus japonicus seedlings can be achieved in southern China. After 60 days, these juveniles exhibited a growth advantage compared to those bred in northern regions. This research provides a foundational basis for autumn seedling breeding of Apostichopus japonicus in China.

Key words:： Apostichopus japonicus; autumn; seedling breeding; embryonic development; juvenile growth

短神经肽 F 在三疣梭子蟹卵巢发育中的功能探究

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摘要：本研究旨在探究短神经肽 F（sNPF）在三疣梭子蟹卵巢发育中的功能。采用反转录 PCR 克隆了三疣梭子蟹 sNPF（PtsNPF）及其受体（PtsNPFR）的 cDNA 序列，PtsNPF 编码 3 个 sNPF 成熟肽，而 PtsNPFR 则为典型的 GPCR 结构。在人 HEK293T 细胞中成功表达 PtsNPFR，并利用双荧光素酶报告系统验证了 3 种 sNPF 肽对 PtsNPFR 的激活能力。PtsNPF 及其受体的基因表达水平在卵黄发生晚期升至最高，推测其可能参与卵黄发生的调控。基于 sNPF 处理和 sNPFR 干扰的离体实验证实，sNPF3 能够促进肝胰腺中的卵黄蛋白原合成以及卵巢中的 Vg 摄取和卵黄蛋白沉积。分别检测不同处理组中的 cAMP、IP3 等第二信使含量，发现 PtsNPF 系统在肝胰腺和卵巢中可能激活不同种类的 G 蛋白发挥作用。本研究表明 PtsNPF 系统可促进三疣梭子蟹的卵黄发生，对于其性腺人工调控技术的开发具有理论指导。

关键词：短神经肽 F；短神经肽 F 受体；三疣梭子蟹；卵巢发育；RNA 干扰

Molecular characterization of a short neuropeptide F signaling system in the swimming crab, Portunus trituberculatus, and its role in ovarian development

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Abstract： Short neuropeptide F (sNPF) is a neuropeptide that widely distributed among arthropods. This neuropeptide has been proposed to play pleiotropic roles in insects, but its physiological functions in crustaceans are poorly understood. Here, we cloned the cDNA sequences of sNPF and its putative receptor (sNPFR) from the swimming crab, Portunus trituberculatus, and determined their possible roles during ovarian development. PtsNPF encodes three sNPF mature peptides with a conserved C-terminal "RLRFG" motif. All three PtsNPF peptides concentration-dependently activated PtsNPFR expressed in HEK293T cells, with EC50 values in the nanomolar range. PtsNPF and PtsNPFR transcripts showed a broad distribution among neural and non-neural tissues. During the ovarian development, expression of PtsNPF and PtsNPFR in hepatopancreas and ovary both increased to the highest levels at the late-vitellogenic stage, a period for rapid vitellogenesis. The in vitro experiments further showed that, among the three sNPF peptides, sNPF3 treatments can induce the vitellogenin (Vg) gene and protein levels in the hepatopancreas, as well as the Vg receptor (VgR) gene and protein levels and vitellogenin (Vn) deposition in the ovary. Opposing effects were observed for the dsPtsNPFR treatments, suggesting that PtsNPFR plays a role in the PtsNPF-mediated vitellogenesis. Additionally, it was found that the PtsNPF/PtsNPFR system can activate different second messengers species in hepatopancreas and ovary, suggesting it may act via different G proteins.

Key words:： short neuropeptide F, short neuropeptide F receptor, Portunus trituberculatus, ovarian development, RNA interference

卵形鲳鲹促性腺激素β亚基的克隆鉴定及其受雌二醇的调控

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摘要：本文利用分子克隆的方法得到卵形鲳鲹 fshβ ORF 长度为 363 bp，lhβ ORF 长度为 447 bp；fshβ和 lhβ基因在卵形鲳鲹的下丘脑-垂体-性腺轴显著表达，在垂体中的表达水平最高，其次是下丘脑和性腺；10 µmol/L E2 处理 6 h 后，GtH β亚基基因的表达被极显著抑制。使用雌激素受体（ER，estrogen receptor）拮抗剂体外孵育卵形鲳鲹垂体组织后，三种拮抗剂均能够消除 E2 对 GtH β亚基基因表达的抑制作用。GTH 在促进性腺发育和成熟过程中发挥重要作用，E2 负调控卵形鲳鲹 GtH β亚基基因的表达。

关键词：卵形鲳鲹,GTH,雌激素

Cloning and characterization of gonadotropin β subunit genes in pompano (Trachinotus ovatus) and their regulation by estradiol

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Abstract：The length of fshβ ORF is 363 bp, and the length of lhβ ORF is 447 bp;The fshβ and lhβ genes were significantly expressed in the hypothalamus-pituitary-gonadal axis of pompano, with the highest expression level in the pituitary, followed by the hypothalamus and gonads;After treatment with 10 µmol/L E2 for 6 h, the expression of GtH β subunit gene was significantly inhibited;After the pituitary tissue of pompano was incubated with estrogen receptor antagonist in vitro, all three antagonists could eliminate the inhibitory effect of E2 on the expression of GtHβ subunit gene.GTH plays an important role in promoting gonadal development and maturation. E2 negatively regulates the expression of GtHβ subunit gene in pompano.

Key words:：pompano（Trachinotus ovatus）；gonadotropin hormones（GtH）；17β-estradiol（E2）

不同群体中华绒螯蟹肠道核心微生物群的性别偏向性

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摘要：肠道菌群组成差异是由宿主的内外因素协同形成的。核心菌群在维持肠道平衡中发挥着重要作用。本研究通过 16S rRNA 测序分析，探讨了六个群体中华绒螯蟹（雌 105 只；雄 110 只）肠道菌群的稳定性和性别偏向性。优势菌门为变形菌门、软壁菌门、拟杆菌门和厚壁菌门，但其相对丰度有显著差异。共筛选出 27 个核心分类操作单元（OTUs），对应 18 个属。相关分析表明，长江水系四个群体的 OTUs 在维持肠道微生物群的稳定性方面发挥重要作用。此外，核心肠道菌群具有明显性别差异，相对丰度排名前三位的菌属（Acinetobacter、Vibrio 和 Candidatus_Hepatoplasma）在雌蟹中占明显优势。网络结构分析也证实了肠道菌群关联模式的性别差异。雄蟹肠道微生物群的功能富集程度更高。该研究为进一步探讨性别和地理因素对中华绒螯蟹肠道菌群的影响提供了理论依据。

关键词：核心肠道微生物群，肠道菌群稳态，地理位置，性别差异，中华绒螯蟹

Sex-bias of core intestinal microbiota in different stocks of Chinese mitten crabs (Eriocheir sinensis)

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Abstract：The differences in intestinal microbiota composition are synergistically shaped by internal and external factors of the host. The core microbiota plays a vital role in maintaining intestinal homeostasis. In this study, we conducted 16S rRNA sequencing analysis to investigate the stability of intestinal microbiota and sex-bias of six stocks of Chinese mitten crabs (105 females; and 110 males). The dominant phyla in all six stocks were Proteobacteria, Tenericutes, Bacteroidetes and Firmicutes; however, their relative abundance differed significantly. Twenty-seven core operational taxonomic units (OTUs), corresponding to 18 genera, were screened. Correlation analysis revealed that OTUs of four stocks in the Yangtze River system play important roles in maintaining the stability of intestinal microbiota. Additionally, the core intestinal microbiota was significantly sex-biased, and the top three genera in terms of relative abundance (Acinetobacter, Vibrio, and Candidatus_Hepatoplasma) were significantly dominant in female crabs. Network structure analysis also confirmed gender differences in the association pattern of intestinal microbiota. The intestinal microbiota of male crabs has a higher degree of functional enrichment. This study provided a theoretical basis for further investigating exploring the shaping effect of gender and geographical factors on the intestinal microbiota of Chinese mitten crabs.

Key words:：Core intestinal microbiota, Intestinal microbiota stability, Geographic location, Sex differentiation, Chinese mitten crabs

Rln3b 通过 HPG 轴调节
罗非鱼精巢发育和育性

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摘要：松弛素 3 是一种在哺乳动物生殖功能中起着至关重要作用的神经肽。前期研究已证实 rln3a 在罗非鱼雄性生殖中起着重要作用。为了进一步探究其旁系同源基因 rln3b 对雄性育性的作用，我们在尼罗罗非鱼中构建了 rln3b 纯合突变系。研究结果表明 rln3b 突变延迟了精子发生并导致精巢结构异常。敲除 rln3b 基因导致精子数量、精子活力和雄鱼育性降低。TUNEL 检测显示，孵化后 390 天的 rln3b−/−雄鱼精巢中有少量细胞凋亡。RT-qPCR 分析表明，rln3b 基因突变导致类固醇合成相关基因（cyp17a1 和 cyp11b2）、生殖细胞标记基因 Vasa 以及性腺体细胞标记基因（amh 和 amhr2）显著下调。此外，我们发现 rln3b−/−雄鱼中下丘脑-垂体-性腺（HPG）轴相关基因显著下调，而多巴胺合成酶基因显著上调。综上所述，我们的研究表明 Rln3b 通过调节 HPG 轴基因在雄性罗非鱼的育性中发挥了关键作用。

关键词：尼罗罗非鱼；rln3b；雄鱼育性；HPG 轴

Rln3b regulates testis development and fertility through HPG axis in Nile tilapia

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Abstract：Relaxin 3 is a neuropeptide that plays a crucial role in mammalian reproductive function. Previous studies have confirmed that RLN3A plays an important role in male reproduction of tilapia. To further investigate the role of its paralogous gene rln3b in male fertility, we constructed a homozygous mutant line of rln3b in Nile tilapia. The research results indicate that RLN3B mutation delays spermatogenesis and leads to abnormal testicular structure. Knocking out the rln3b gene leads to a decrease in sperm count, sperm motility, and male fish fertility. TUNEL detection showed that there was a small amount of cell apoptosis in the testes of RLN3B −/− male fish 390 days after hatching. RT qPCR analysis showed that mutations in the rln3b gene led to significant downregulation of steroid synthesis related genes (cyp17a1 and cyp11b2), germ cell marker gene Vasa, and sex gland cell marker genes (amh and amhr2). In addition, we found that genes related to the hypothalamic pituitary gonad (HPG) axis were significantly down regulated in rln3b −/− male fish, while dopamine synthase genes were significantly up-regulated. In summary, our research indicates that Rln3b plays a crucial role in male tilapia fertility by regulating the HPG axis gene.

Key words:：Nile tilapia; rln3b; Male fish fertility; HPG axis

主要经济鱼类结构变异检测图谱构建及其关键性状中的潜在作用

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摘要：结构变异（SVs）是基因组多态性的一种形式，涵盖了缺失、插入、倒置和重复等类型。相较于单核苷酸多态性（SNPs），SVs 的规模通常更大（通常定义为>50bp），且通过影响基因功能和表达，更有可能对性状产生显著影响。然而，由于识别和分型这些变异的难度较大，SVs 在遗传学研究中的应用相对较少。近年来，随着技术进步，人们对将 SVs 纳入具有经济重要性和价值的养殖鱼类的遗传学研究的兴趣迅速增长。鱼类如三文鱼、海鲈鱼、大菱鲆等主要经济物种对全球粮食生产具有重要意义，研究它们的基因组结构变异有助于更好地理解它们的遗传基础，进而优化养殖性能和产量。为了应对 SVs 研究中的挑战，我们对这些物种进行了结构变异的检测，进而构建了它们的结构变异图谱。这一成果为未来的鱼类育种和遗传改良提供了重要的基础数据，将促进更高效和可持续的水产养殖发展。

关键词：结构变异；遗传育种；抗病性；三文鱼；海鲈鱼；大菱鲆

The structural variation landscape in major economic fishes and its potential role in some key traits

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Abstract： Structural variations (SVs) are a type of genomic polymorphism that include deletions, insertions, inversions, and duplications. Compared to single nucleotide polymorphisms (SNPs), SVs are typically larger in size, usually defined as greater than 50 base pairs (bp), and have a higher likelihood of affecting traits by altering gene function and expression. Despite their significant potential impact on phenotypes, SVs have been less frequently utilized in genetic studies due to the challenges in accurately identifying and genotyping these variations. However, recent advancements in sequencing technologies and computational tools have sparked growing interest in incorporating SVs into genetic research, particularly for species of economic importance in the aquaculture industry. In aquaculture, key species such as Atlantic salmon, European sea bass, and turbot play vital roles in global food production. Understanding the genetic basis of traits in these species is crucial for improving breeding programs aimed at enhancing growth, disease resistance, and other economically important traits. The integration of SV data into such studies provides an additional layer of genetic information that can complement traditional SNP-based analyses. By identifying SVs that contribute to variation in traits such as growth rate, stress tolerance, and disease resistance, we can gain a more comprehensive understanding of the genetic mechanisms underlying these traits, leading to more targeted and effective breeding strategies.

Key words:： structural variation; genetics breeding; disease resistance; Atlantic salmon; European sea bass; turbot

神经肽 Y 在罗非鱼不同能量水平下的功能研究

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摘要：尼罗罗非鱼（Oreochromis niloticus）是一种世界性的重要淡水养殖鱼类，可以适应高温养殖水环境而无法应对低温，因此进一步提高其耐热和耐寒能力成为扩大罗非鱼养殖范围需要解决的首要问题。神经肽 Y（Neuropeptide Y，NPY）具有强大的促食欲作用，通过多种方式调节机体能量产生与耗散，维持机体能量稳态。关于 NPY 在鱼类处于不同能量水平状态中的功能研究有限，分子机制尚不明确。实验室前期研究证实通过腹腔注射 NPY 可以维持冷应激状态下罗非鱼血清中血糖的稳定，本研究结果表明热应激状态下罗非鱼不同脑区中 NPY 及其受体家族基因表达水平提高，表明 NPY 通过参与调节代谢活动和减少应激反应，维持机体能量分配平衡。探究 NPY 及其关键作用因子在罗非鱼应对急性温度胁迫中的作用机制，可以为提高罗非鱼耐寒性和阐明鱼类适应环境温度中能量分配问题提供理论基础，为筛选具有更强抗寒性的罗非鱼品种选育提供标记。

关键词：神经肽 Y；温度胁迫；罗非鱼；能量稳态

Study on the Functions of Neuropeptide Y in Nile Tilapia Under Different Energy Levels

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Abstract： Nile tilapia (Oreochromis niloticus) is a globally significant freshwater aquaculture fish species that can adapt to high-temperature aquaculture environments but struggles to cope with low temperatures. Consequently, enhancing its heat tolerance and cold resistance has emerged as a primary challenge for expanding the range of tilapia aquaculture. Neuropeptide Y (NPY) possesses potent orexigenic properties, regulating energy production and dissipation through various mechanisms to maintain energy homeostasis in organisms. However, research on the functions of NPY in fish under different energy levels is limited, and the underlying molecular mechanisms remain elusive. Previous laboratory studies have confirmed that intraperitoneal injection of NPY can stabilize blood glucose levels in tilapia under cold stress. The present study reveals that under heat stress, the expression levels of NPY and its receptor family genes increase in different brain regions of tilapia, suggesting that NPY contributes to maintaining energy allocation balance by modulating metabolic activities and mitigating stress responses. Investigating the mechanisms of NPY and its key effectors in tilapia's response to acute temperature stress can provide a theoretical foundation for improving the cold tolerance of tilapia and elucidating energy allocation in fish adapting to ambient temperatures. Furthermore, it offers potential marker genes for the selective breeding of tilapia varieties with enhanced cold resistance.

Key words:：neuropeptide Y; temperature stress; tilapia; energy homeostasis

牡蛎 INPP5K 错义突变通过负向调控 PI3K/AKT 信号通路参与生长过程

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摘要：生长是由多种因素影响的复杂生物性状，受遗传和环境因素共同影响。挖掘和研究生长相关候选基因对深入理解牡蛎的生长调控机制以及提高选择育种的精准性具有重要意义。在本研究中，我们在熊本牡蛎（Crassostrea sikamea）INPP5K 基因中发现了一个物种特异性的错义突变，突变位于蛋白磷酸酶结构域。INPP5K 作为一种关键的磷酸酶，在调节细胞内信号传导和代谢过程中发挥着重要作用。尽管 INPP5K 在脊椎动物中已被证明参与了胰岛素信号通路、细胞骨架动态调节和细胞存活等多种生理过程，其在海洋无脊椎动物中的功能仍然知之甚少。为评估突变对 INPP5K 蛋白功能的影响，我们通过原核表达系统构建了三种不同基因型的 INPP5K 重组蛋白，并检测了它们对底物 PI(4,5)P2 和 PI(3,4,5)P3 的磷酸酶活性。

关键词：熊本牡蛎；体型大小；胰岛素样肽；PI3K/AKT 信号通路

A missense mutation of INPP5K is involved in growth regulation through negative regulation of the PI3K/AKT signaling pathway

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Abstract： Growth is a complex biological trait influenced by environmental and genetic factors. Investigating potential growth-related genes is essential for improving selective breeding and expanding our comprehension of growth regulating mechanisms. In this study, we identified a species-specific missense mutation in Crassostrea sikamea at a conserved protein phosphatase domain of inositol polyphosphate 5-phosphatase K (INPP5K), which has multiple insulin and non-insulin related signal transduction functions in vertebrates. To determine the effect of the species-specific mutation, we constructed three INPP5K recombinant proteins with different genotypes via prokaryotic expression and assessed their phosphatase activity towards its substrates PI(4,5)P2 and PI(3,4,5)P3. The results indicated that a species-specific missense mutation in the INPP5K gene enhances the protein phosphatase activity for its substrate, PI(3,4,5)P3. This heightened activity leads to the inhibition of the PI3K/AKT signaling pathway by suppressing AKT phosphorylation, without impacting the activity of the autophagic lysosomal pathway. Furthermore, INPP5K in oysters displays greater phosphatase activity towards PI(3,4,5)P3 compared to PI(4,5)P2, suggesting that during evolution, INPP5K may have undergone functional divergence. In summary, the species-specific missense mutation in the INPP5K gene of C. sikamea enhances the enzyme's catalytic efficiency towards PI(3,4,5)P3, initiating a molecular cascade that may regulate oyster growth and development, potentially contributing to the slower growth rate observed in C. sikamea.

Key words:：Crassostrea sikamea, Growth, Insulin, PI3K/AKT signaling pathway

KDM4A 调控斑马鱼早期胚胎发育的机制研究

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摘要：KDM4A 在调节染色质活性、发育、代谢方面发挥重要作用。前期研究发现敲除 kdm4ab 会导致斑马鱼胚胎存活率显著降低，表明 kdm4ab 可能在斑马鱼的早期胚胎发育中起着重要作用。本研究选取 kdm4ab-/-斑马鱼的原肠期(5.25 hpf)胚胎作为样本，RNA-seq 结果表明，花生四烯酸代谢通路（ARA）相关基因的表达量显著下调（P＜0.01）。CUT&Tag 结果发现 H3K4me3 在 ARA 代谢相关的 cyp2j20、ptgis 等基因的启动子区域富集水平显著下降；而 cyp2p6、ptgis 基因区域的 H3K9me3 富集水平显著升高，以上结果与转录组数据一致。最后我们对 ARA 相关基因进行 RT-qPCR、CUT&Tag-qPCR 验证，最终的趋势与以上联合分析的结果保持一致。综上所述，在斑马鱼中敲除 kdm4ab 基因后抑制了 ARA 通路相关基因的表达，从而阻碍斑马鱼早期胚胎的发育。

关键词：kdm4ab；花生四烯酸；斑马鱼；胚胎发育

Mechanism of KDM4A Regulating Early Embryonic Development in Zebrafish

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Abstract： KDM4A plays an important role in regulating chromatin activity, development, and metabolism. Previous studies have found that knocking out the kdm4ab significantly reduces the survival rate of zebrafish embryos, indicating that kdm4ab may play an important role in the early embryonic development of zebrafish. This study selected the protointestinal stage (5.25 hpf) embryos of the kdm4ab -/- zebrafish as samples. RNA-seq results suggested that the expression levels of genes related to the arachidonic acid metabolic pathway (ARA) were significantly downregulated ($P<0.01$). Relevant studies have shown that arachidonic acid can generate lipid small molecules with strong biological functions through three metabolic pathways: cyclooxygenase, lipoxygenase, and cytochrome, playing important roles in neurological development, skeletal development, and antioxidant activity. The CUT&Tag results suggested a significant decrease in the enrichment level of H3K4me3 in the promoter regions of genes related to ARA , such as cyp2j20 and ptgis; The enrichment levels of H3K9me3 in the cyp2p6 and ptgis regions were significantly increased, which is consistent with the transcriptome data. Finally, we validated the ARA related genes using RT-qPCR and CUT&Tag-qPCR, and the final trend was consistent with the results of the joint analysis mentioned above. In conclusion, the deletion of kdm4ab in zebrafish inhibits the expression of genes related to ARA, thus hindering the development of zebrafish early embryos, which provides a theoretical basis for further research on the role of kdm4ab in zebrafish growth and development.

Key words:：kdm4ab;arachidonic acid;zebrafish;embryonic development

基于 GWAS 挖掘高渗环境下大口黑鲈生长 SNP 标记及相关候选基因

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摘要：生长性状是鱼类遗传育种和商业养殖的重点关注内容，但鱼类的生长易受环境中盐度的影响。目前，大口黑鲈主要养殖于淡水区域，关于盐度对生长的影响方面资料较少。因此，本研究利用重测序技术对 11‰盐度下养殖 2 个月的 500 尾大口黑鲈体重、体高、体厚、体长 4 个生长性状进行全基因组关联分析。共获得 10 个潜在生长 SNPs，其中体重和体高各自关联到 1 个 SNP、体厚关联到 9 个 SNPs。基于候选 SNPs，在全基因组范围内注释到 23 个候选基因，这些基因主要在代谢通路中显著富集。本研究有助于理解高盐度下大口黑鲈的生长遗传结构。

关键词：大口黑鲈; 盐胁迫; 生长性状; GWAS

GWAS-based search for SNP markers and related candidate genes for largemouth bass growth in hypertonic environments

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Abstract：Growth is a pivotal trait in the breeding of fish and commercial aquaculture. However, this trait can be affected by salinity fluctuations. Currently, largemouth bass (Micropterus salmoides) are mainly cultured in freshwater areas, and there is a lack of sufficient information about the effect of salinity on its growth. Therefore, this study applied whole-genome resequencing techniques to perform genome-wide association analysis on four growth-related factors (Body Weight, Body Height, Body Thickness, and Body Length) in 500 largemouth bass stock at 11‰ salinity levels for two months. A total of 10 potential growth SNPs were identified, comprising 1 SNP each for body weight and height and 9 for body thickness. Based on these SNPs, 23 candidate genes significantly enriched in metabolic pathways were annotated in the genome. This study can help understand the growth genetic structure of Largemouth Bass cultured in high-salinity environments and provide essential information to develop further molecular marker-assisted breeding and genome-wide selection.

Key words:：Micropterus salmoides; salinity stress; growth traits; GWAS

ScRNA-seq 揭示日本囊对虾潜沙行为的内在调控基因

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摘要：日本对虾具有重要的经济价值但单位面积养殖产量不高，主要是因为其潜沙的生活习性限制了养殖密度的提高。为改善这一情况，我们试图探究日本对虾潜沙行为的内在调控机制，设置 3 种养殖条件：沙底环境养殖组（SHA）、无底质环境养殖组（WU）和在转移应激组（YI）；分别抽取他们的血淋巴进行单细胞转录组测序，分析比较三个实验组的基因表达差异，获得以下类型：颗粒细胞、半颗粒细胞、透明细胞及前体细胞；同时，通过 mRNA-FISH 对细胞群的标记基因进行验证；通过组间差异对比，发现 TRP 家族中的相关基因：trpa-1 和 trpm，这两个基因在 WU 中这两个基因都有较高的表达水平。针对他们进行 RNAi 和 mRNA 过表达验证实验，结果表明 trpa-1 在眼柄中显著表达，基因敲低后的夜间 28.5%的虾在观察时间保持仅停留于沙子表面的状态；trpm 在心脏中显著表达，基因敲低后所有虾都始终保持潜沙状态。

关键词：日本对虾; scRNA-seq; 潜沙行为; trpa; trpm

ScRNA-seq reveals intrinsic regulatory genes of shrimp sand diving behavior in Penaeus japonicus

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Abstract：Penaeus japonicus has important economic value but their unit area aquaculture yield is not much,mainly because their sand diving habits limit the increase of aquaculture density.To improve the situation, we set up three kinds of culture conditions:the sand group (SHA);the sand-free group (WU),mobile group (YI).The hemolymph of different groups of Penaeus japonicus were extracted and sequenced by ScRNA-seq to analyze and compare the differences of hemolymph gene expression among the three groups.According to the gene expression characteristics,shrimp hemocytes were classified, and the related cell atlas was obtained:hyalinocytes,semi-granulocytes and precursor cells;we also conducted tissue localization of cell population marker genes through mRNA-FISH validation.We found trend-related genes trpa1 and trpm in transient receptor potential.The expression level of melastatin in WU was significantly higher than that in SHA and YI.We conducted RNAi experiments.The results showed that trpa1 was significantly expressed in XO-SG,and 28.5%of the shrimp in the interference group kept swimming.

Key words:：Penaeus japonicus, scRNA-seq, sand diving habits, trpa, trpm

典型有害甲藻对脊尾白虾生理、免疫及肠道菌群的影响

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摘要：甲藻藻华在近海和养殖池塘的爆发对水环境和养殖动物造成严重影响，甚至导致死亡，引发经济损失。本研究以太平洋亚历山大藻为例，探究了急性（72h）处理后脊尾白虾存活、组织病理结构、抗氧化酶活性、免疫基因，以及和慢性（7 d）处理后肠道菌群结构的变化。结果显示，72 小时急性暴露显著降低白虾存活率（P＜0.05），存活率随浓度增加而减少，还造成鳃、肝胰腺和肠道的病理损伤。抗氧化酶活性变化表明 SOD 和 GPX 活性升高（P＜0.05），CAT 活性降低（P＜0.05）。鳃中 HSP70 表达上调，proPO 和 Serpin 表达下调；肝胰腺中 HSP70、GST、lysozime、proPO 和 Serpin 表达均上调。急性处理 7 天，肠道菌群α多样性降低，变形菌门丰度升高，弧菌科和发光菌属增加，功能预测显示辅酶和维生素代谢等代谢途径受抑制。以上结果说明有害甲藻暴露导致脊尾白虾生理机能受损，肠道菌群多样性下降，结构紊乱。

关键词：太平洋亚历山大藻；脊尾白虾；免疫；肠道菌群

Impact of typical harmful dinophytes on the physiology, immunity and intestinal flora of the Ridgetail White Shrimp (Exopalaemon carinicauda)

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Abstract：Harmful algal blooms (HABs), like Alexandrium pacificum, severely affect aquatic life and aquaculture, leading to economic losses. This study assessed the effects of A. pacificum on Exopalaemon carinicauda after acute (72h) and chronic (7d) exposures, evaluating survival, histopathology, antioxidant enzymes, immune genes, and intestinal flora. Acute exposure reduced E. carinicauda survival ($P<0.05$), with higher mortality at increased concentrations, and induced histopathological damage in gills, hepatopancreas, and intestine. There was an increase in SOD and GPX activities ($P<0.05$) and a decrease in CAT activity ($P<0.05$). HSP70 expression rose in gills, while proPO and Serpin declined; in hepatopancreas, HSP70, GST, lysozime, proPO, and Serpin were upregulated. Chronic exposure decreased gut microbiome diversity, elevated Proteobacteria, Vibrionaceae, and Photobacterium, and suggested metabolic disruptions in coenzyme and vitamin metabolism. HAB exposure thus triggers physiological and microbiome dysbiosis in E. carinicauda.

Key words:：Alexandrium pacificum;Exopalaemon carinicauda;immunity;intestinal flora

肌肉生长抑制素及其突变体在罗氏沼虾生长和蜕皮中的作用

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摘要：Mstn 基因在动物肌肉分化中起重要作用。本研究以罗氏沼虾 Mstn 基因及其启动子区域的 24 个碱基的突变体为研究对象，开展了 Mstn 基因及其突变体在罗氏沼虾中的调控研究。Mstn 基因时空表达显示，该基因在胚胎发育期及体组织中均有表达，尤其是高表达于原肠胚期和肝胰腺中；在三个蜕皮周期中的表达水平从高到低依次为蜕皮后期（A 期）、蜕皮前期（D3 期）及蜕皮期。该基因启动子（正常与缺失两种基因型）敲降结果表明：两种基因型的敲降显著影响了虾的生长速度，并伴随着蜕皮周期的延长；同样，该基因的敲降显著提高了抗变态因子表达水平的上升，然而造成了维甲酸类 X 受体和蜕皮激素受体表达水平的显著下降。F2 代的敲降结果同样证实该基因启动子区域的敲降不仅延长了罗氏沼虾的脱皮周期，而且会导致该虾生长速度迟缓。

关键词：罗氏沼虾；肌肉生长抑制素；RNAi；蜕皮

The Role of Myostatin and Its Mutants in the Growth and Molting of Macrobrachium rosenbergii

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Abstract：The myostatin (MSTN) gene, a pivotal regulator of muscle differentiation in animals, was investigated in the context of Macrobrachium rosenbergii, focusing specifically on the Mstn gene and its mutant harboring a 24-base mutation within the promoter region. This study aimed to elucidate the regulatory mechanisms of the Mstn and its mutant variant in M. rosenbergii. Spatiotemporal expression profiling revealed that the Mstn is expressed throughout embryonic development and across various body tissues, with peak expression observed during the gastrula stage and in the hepatopancreas. Analysis across three molting cycles indicated that gene expression is highest in the post-molting phase (A phase), followed by the pre-molting phase (D3 phase), and is lowest during the molting phase. Knockdown experiments targeting both the wild-type and mutant gene promoters revealed significant impacts on shrimp growth rates, accompanied by prolonged molting cycles. Notably, downregulation of Mstn resulted in a notable upregulation of krüppel-homolog1 (Kr-h1) gene expression, while simultaneously causing a marked decrease in the expression of retinoid X receptor (RXR) gene and ecdysone receptor (ECR) gene. These findings suggest complex regulatory interactions involving Mstn in the hormonal and molecular pathways governing molting and growth. Furthermore, knockdown results in the F2 generation confirmed the persistent effects of Mstn promoter downregulation, extending molting cycles and slowing down the growth rate of M. rosenbergii. This study sheds light on the functional roles of the Mstn gene and its mutants in modulating growth and molting processes in M. rosenbergii, offering novel insights into the underlying mechanisms behind the "iron shrimp" phenomenon observed in this species.

Key words:：Macrobrachium rosenbergii; Myostatin; RNAi; Molt

共生微生物在增强紫菜适应潮间带环境中的作用机制

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摘要：本研究使用 Symbiont-Screener 方法获得了坛紫菜（Pyropia haitanensis）染色体级别的无共生体基因组（47.2 Mb），共鉴定出 286 个水平基因转移（HGT）基因，其中 251 个含有转座子插入，这反映了转座子在促进基因向坛紫菜基因组转移中的重要性。同时，BSA 结果显示两个 HGT 基因 sirB 和 msrB 是坛紫菜应答高温胁迫的关键基因。此外，综合基因组过滤数据集、HGT 基因候选供体等结果发现，假单胞菌、放线菌和拟杆菌是坛紫菜共生细菌中的主要分类群。基于此，本研究分离出了一种在坛紫菜耐高温品系藻体特异富集的放线菌（Saccharothrix sp.），其能够通过调控与脯氨酸合成（proC）、氧化还原稳态（ggt）和蛋白质折叠（HSP20）相关的基因，以增强坛紫菜的耐热性。综上所述，本研究为深入理解 HGT 事件和藻际微生物在潮间带海藻适应性进化中的功能提供了新的视野。

关键词：坛紫菜；基因组；共生微生物；水平基因转移

The mechanism of symbiotic microorganisms in enhancing the adaptation of Pyropia/Porphyra to intertidal environments

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Abstract： Intertidal algae may adapt to environmental challenges by acquiring genes from other organisms and relying on symbiotic microorganisms. Here, we obtained a symbiont-free and chromosome-level genome of Pyropia haitanensis (47.2 Mb), a type of intertidal algae, by using multiple symbiont screening methods. We identified 286 horizontal gene transfer (HGT) genes, 251 of which harbored transposable elements (TEs), reflecting the importance of TEs for facilitating the transfer of genes into P. haitanensis. Notably, the bulked segregant analysis revealed that two HGT genes, sirohydrochlorin ferrochelatase and peptide-methionine (R)-S-oxide reductase, play a significant role in the adaptation of P. haitanensis to heat stress. Besides, we found Pseudomonas, Actinobacteria, and Bacteroidetes are the major taxa among the symbiotic bacteria of P. haitanensis (nearly 50% of the HGT gene donors). Among of them, a heat-tolerant actinobacterial strain (Saccharothrix sp.) was isolated and revealed to be associated with the heat tolerance of P. haitanensis through its regulatory effects on the genes involved in proline synthesis (proC), redox homeostasis (ggt), and protein folding (HSP20). These findings contribute to our understanding of the adaptive evolution of intertidal algae, expanding our knowledge of the HGT genes and symbiotic microorganisms to enhance their resilience and survival in challenging intertidal environments.

Key words:：Pyropia haitanensis; genome; symbiotic microorganism; horizontal gene transfer

甲状腺激素对福建牡蛎(Crassostrea angulata)胚胎及幼虫发育的影响

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摘要：本研究通过胚胎和母体甲状腺素 T4 浸泡，以及甲状腺激素抑制剂 TU 处理母体后 T4 浸泡胚胎的方法，研究 T4 对福建牡蛎胚胎和幼虫发育的影响。结果发现，中低浓度 T4 显著（$P < 0.05$）提高了 D 形幼虫孵化率和壳长，母体给药最佳浓度低于直接给药；高浓度 T4 及 TU 处理则表现出显著负面作用（$P < 0.05$），并随时间延长加剧。化学发光免疫法测定 THs 含量表明，T4 直接给药后，各发育时期幼虫体内 THs 含量与 T4 给药浓度呈显著正相关（$P < 0.05$），TU 组与对照组无显著差异（$P > 0.05$）；母体给药后，1.29×10-8 mol/L 的 T4 处理组的胚胎从卵裂期发育至囊胚期时，三碘甲状腺原氨酸 T3 与 T4 比值升高，其它处理组相反。综上，中低浓度 T4 可促进福建牡蛎幼虫孵化与生长，卵裂期至囊胚期幼虫体内 T3/T4 比值变化可能是影响其生长发育的重要调控因素，母体给药是研究 THs 对其胚胎发育影响的更佳给药方式。

关键词：福建牡蛎；甲状腺激素；胚胎发育

The effects of thyroid hormones on the embryonic and larval development of Crassostrea angulata

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Abstract： This study investigated the effects of thyroid hormone T4 on the embryonic and larval development of Crassostrea angulata through T4 immersion embryos and broodstock, as well as T4 immersion after broodstock treatment with the thyroid hormone inhibitor TU. Results showed that low to moderate T4 concentrations significantly increased ($P < 0.05$) D-larvae hatching rates and shell length, with lower optimal concentrations for broodstock. High T4 and TU concentrations had adverse effects ($P < 0.05$), worsening over time. Chemiluminescence immunoassay showed a significantly positive correlation between THs levels and T4 concentration in larvae after direct T4 treatment ($P < 0.05$), with no significant difference between TU and control groups. After broodstock treatment, the T3/T4 ratio increased with 1.29×10^{-8} mol/L T4 from cleavage to blastula stage but decreased in other groups. Low to moderate T4 levels promote larval growth, with T3/T4 ratio changes in cleavage to blastula stage may regulate development. Broodstock treatment is better for studying THs' impact on embryonic development.

Key words:： Crassostrea angulata; thyroid hormones; embryonic development

军曹鱼 Col10a1 基因的克隆及其表达模式研究

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摘要：X 型胶原蛋白(COL10)作为胶原蛋白家族的核心成员，在脊椎动物软骨内骨化的过程中扮演着重要角色。本研究以军曹鱼(Rachycentron canadum)col10a1 基因为研究对象，克隆了其基因全长序列及其 5'侧翼区 2000 bp 片段，并进行了生物信息学分析和启动子活性检测。结果显示：军曹鱼 col10a1 基因全长为 1977 bp，编码 659 个氨基酸。系统进化分析显示其与鮣鱼 col10a1 亲缘关系最近。此外，对该基因 5'侧翼区域分析发现了 Sp1、AP1 及 Oct-1 等多种转录因子结合位点。利用双萤光素酶报告基因检测系统发现，-1500 至-1000 bp 区域的启动子活性最高。最后，采用实时荧光定量 PCR 研究了 col10a1 的表达模式。组织表达谱显示，col10a1 在骨组织中的表达量显著高于其他组织。在军曹鱼早期发育阶段，该基因在胚胎期的表达呈升高趋势，而进入仔稚鱼期后则先升高后降低。

关键词：军曹鱼；col10a1；基因克隆，启动子活性；基因表达

Identification, phylogeny and expression analysis of Col10a1 gene in cobia (Rachycentron canadum)

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Abstract：Collagen X(COL10) is a crucial component of the collagen family and plays a key role in the process of endochondral ossification in vertebrate cartilage.In this study,the col10a1 gene was used as a research object,the full-length sequence of its gene and a 2000 bp fragment of its 5' flanking region was cloned and analyzed for bioinformatics and promoter activity.The results show:the full length was 1977 bp,encoding 659 amino acids.Phylogenetic analysis showed it to be the closest relative to Echeneis naucrates.In addition,analysis of the 5' flanking region of the gene identified multiple transcription factor binding sites such as Sp1,AP1 and Oct-1.The highest promoter activity was found in the region of -1500 to -1000 bp using the Dual-Luciferase Reporter Assay System.Finally,the expression of col10a1 was significantly higher in bone tissue than in other tissues.In the early developmental stage of cobia,the expression of this gene showed an elevated trend in the embryonic stage,while it first increased and then decreased after entering the larval and juvenile fish stage.

Key words:：Rachycentron canadum; col10a1; gene cloning; promoter activity; gene expression

对虾 m6A 甲基化修饰调控因子的演化及功能研究

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摘要：N6 甲基腺苷（m6A）是真核生物中最常见的 RNA 修饰类型，但对虾等十足目甲壳动物的 m6A 甲基化现象仍属于未解之谜。我们发现，十足目甲壳类拥有完整的 m6A 甲基转移酶和 m6A 结合蛋白，但经典的 m6A 去甲基化酶 FTO 和 ALKBH5 普遍缺失，而对虾 LvALKBH1 和 LvALKBH8 表现出去甲基化酶活性。沉默 LvMETTL3、LvWTAP 或 LvYTHDF2 等基因后，对虾蜕皮率显著增加，而卵巢发育则停滞在 0 期或 I 期。卵巢中有 4373-5243 个基因在甲基化和表达水平上同时发生显著变化，这些基因与“卵巢类固醇激素生成”、“细胞周期”和“催乳素信号通路”等多个生殖相关通路密切相关。功能实验表明，METTL3/YTHDF2 途径介导的 m6A 修饰通过 MF/Met/Kr-h1 基因轴调控对虾卵巢发育。本研究为深入阐明 m6A 甲基化修饰在甲壳动物生理活动调节中的功能及作用机制奠定了基础。

关键词：甲壳动物；对虾；RNA 甲基化；m6A；繁殖和发育

Evolution and functional investigation of m6A modification regulators in shrimp

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Abstract： N6-methyladenosine (m6A) is the most abundant RNA modification in eukaryotes. However, patterns of m6A methylation in decapod crustaceans like shrimp remains as a mystery. Our study revealed that decapod crustaceans have a complete set of m6A methyltransferases and m6A binding proteins, but classic m6A demethylases FTO and ALKBH5 are missing, while shrimp LvALKBH1 and LvALKBH8 exhibit significant demethylase activities. The m6A levels showed dynamic changes at different molting stages and ovarian development stages. After silencing of LvMETTL3, LvWTAP or LvYTHDF2, the molting rate of shrimp significantly increased, while ovarian development stagnated at stage 0 or I. In the ovary, 4373-5243 genes showed significant changes in methylation and expression levels simultaneously, and a subset of them are associated with reproduction related pathways such as "ovarian steroid hormone production" and "cell cycle". Functional experiments further demonstrated that the METTL3/YTHDF2 pathway-mediated m6A modification regulates shrimp ovarian development via the MF/MET/Kr-h1 gene pathway.

Key words:：Crustacean; Shrimp; RNA methylation; m6A; Reproduction and development

不同大口黑鲈群体生长性能、肌肉营养成分、肠道形态结构及菌群组成的比较研究

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摘要：本试验旨在比较不同大口黑鲈群体生长性能、肌肉营养成分、肠道形态结构及菌群组成的差异。试验选用 4 个国内主要大口黑鲈养殖群体：“优鲈 3 号”、“优鲈 1 号”、台湾群体与杂交群体各 180 尾，每群 3 个重复，每个重复 60 尾，养殖 120 d。结果表明：杂交群体的生长性能显著高于其他群体，并且后肠绒毛宽度以及肌肉中饱和脂肪酸、单不饱和脂肪酸和多不饱和脂肪酸含量显著高于其他 3 个群体($P<0.05$)。基于 16S rRNA 测序发现，大口黑鲈肠道优势菌门是厚壁菌门、变形菌门、梭杆菌门以及放线菌门，肠道鲸杆菌属显著富集于杂交群体；PICRUSt2 功能预测表明新陈代谢、遗传信息处理以及环境信息处理等功能在杂交群体中的平均丰度更高；通过斯皮尔曼相关性分析发现，肠道菌群功能与后肠的绒毛高度和绒毛宽度呈显著正相关($P<0.05$)。

关键词：大口黑鲈; 不同养殖群体; 生长性能; 肌肉营养成分; 肠道形态结构;肠道菌群

Comparative Study on Growth Performance, Muscle Nutrients, Intestinal Morphology and Structure and Microflora Composition of Different Largemouth Bass (Micropterus salmoides) Populations

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Abstract: The purpose of this experiment was to compare the growth performance, muscle nutrients, intestinal morphology and structure and microflora composition of different largemouth bass populations. Four major domestic largemouth bass breeding populations were selected in the experiment which were “Youlu No.3”,“Youlu No.1”, Taiwan population and hybrid population. The results showed that growth performance, intestinal tissue structure and muscle fatty acid content were significantly higher in the hybrid population than in the other three populations. Based on 16S rRNA sequencing, we found that the dominant intestinal phyla in largemouth bass were Firmicutes, Proteobacteria, Fusobacteriota, and Actinobacteriota; PICRUSt2 function prediction indicated that metabolism, genetic information processing, and environmental information processing were more abundant on average in the hybrid population; and we found that intestinal colony Functions were significantly and positively correlated with villus height and villus width in the hindgut.

Key words:: Micropterus salmoides; different cultivated populations; growth performance; muscle nutrients;intestinal morphology and structure; intestinal microflora

鳗鲡不同游动状态下的特征分析

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摘要：为了探究鳗鲡（Anguilla japonica）在不同游动状态下身体各部位所发挥的作用，实验采用粒子图像测速技术（particle image velocimetry，PIV）对其在前进和后退过程中产生的涡量、涡环推力进行了分析。结果显示：鳗鲡在游动一个周期内，会有一对方向相反的漩涡脱落，尾部产生的涡量、涡环推力最大，发挥主要作用；鳗鲡的体部在一个周期的后退过程中产生的涡环推力是前进状态下的 1.6 倍，头部产生的涡环推力是前进状态下的 10 倍左右。研究表明，头部和体部在鳗鲡式游动鱼类的后退过程中具有重要作用。本研究结果有助于了解鳗鲡式游动鱼类的运动学机理，同时为仿生机器鱼的研究设计提供思路。

关键词：鳗鲡；粒子图像测速技术（PIV）；涡量；推力

Analysis of the characteristics of eel in different swimming states

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Abstract： In order to explore the role of different parts of the body of Anguilla japonica in different swimming states, particle image velocimetry (PIV) was used to analyze the vorticity and vor-tex ring thrust generated in the process of forward and backward. The results show that there will be a pair of vortexes shedding in the opposite direction in a cycle of eel swimming, and the vorticity and vortex ring thrust generated at the tail are the largest and play a major role. The vortex ring thrust generated by the body of the eel during a period of retreat is 1.6 times that in the forward state, and the vortex ring thrust generated by the head is about 10 times that in the forward state. Studies have shown that the head and body play an important role in the retreat of eel-like swimming fish. The results of this study are helpful to understand the kine-matic mechanism of eel-like swimming fish, and provide ideas for the research and design of bionic robotic fish.

Key words:： eel; vorticity; thrust; particle image velocimetry

一种新型厚壳贻贝抗氧化足丝蛋白的表征

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摘要：本研究从海洋重要经济种厚壳贻贝足丝中鉴定出了一种富含半胱氨酸的新型抗氧化足丝蛋白 Mfp-20，本研究对天然 Mfp-20 进行了序列特征分析、表达谱分析及重组表达蛋白的功能分析。结果显示：mfp-20 的表达水平在不同浓度不同价态铁离子和不同附着基质的诱导下发生了显著的变化，而偏酸海水增强了 mfp-20 的表达。重组 Mfp-20 在 DPPH 实验中展现出较强的抗氧化能力，其可能与 Mfp-6 的抗氧化作用机制相似，利用其丰富的半胱氨酸发挥抗氧化活性。本研究揭示了与已有报道的 Mfp-6 序列完全不同的新蛋白的抗氧化功能，为探索贻贝足丝在粘附过程中的氧化还原平衡提供了新的线索。

关键词：厚壳贻贝，抗氧化足丝蛋白，半胱氨酸

Characterization of a novel antioxidant byssal protein from Mytilus coruscus foot

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Abstract：In this study, a novel antioxidant byssal protein Mfp-20 rich in cysteine was identified from the foot of a marine economic species, Mytilus coruscus. Sequence analysis, expression profile and functional analysis of Mfp-20 were carried out. The results showed that the expression level of mfp-20 was significantly changed under the induction of different concentrations of different valences of iron ions and different attachment substrates, and acidic seawater enhanced the expression of mfp-20. Recombinant Mfp-20 showed strong antioxidant ability in DPPH assay, which might be similar to the antioxidant mechanism of Mfp-6, using its abundant cysteine to exert antioxidant activity. The present study reveals the antioxidant function of a novel protein with a completely different sequence from the previously reported Mfp-6, providing new clues to explore the redox balance of mussel byssus during adhesion.

Key words:：Mytilus coruscus, antioxidant protein, cysteine-rich byssal protein

斑点叉尾鮰 period 家族基因的克隆、组织分布及对摄食节律的影响

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摘要：本研究描述了斑点叉尾鮰在进食与不进食情况下周期家族基因的克隆和表征，以及其 mRNA 表达的分析。在斑点叉尾鮰中发现了 4 个成员：Ipperiod1b、Ipperiod 2、Ipperiod 2l 和 Ipperiod 3，它们的全长分别为 4332 bp、4122 bp、3942 bp 和 3837 bp，编码 1443、1373、1313 和 1278 个氨基酸，这些基因与其他鱼类的周期基因高度同源。周期家族成员具有广泛的组织分布，但不同成员的组织表达水平有所差异。在本研究中，我们探讨了食物获取和进餐时间是否影响大脑和肝脏中 period 周期家族基因的表达。结果显示，period 家族基因在大脑和肝脏中的表达模式存在差异。此外，严格的摄食节律与大脑和肝脏中周期家族基因表达模式的变化有关。这项研究首次鉴定了斑点叉尾鮰的周期家族基因，并证明了摄食节律反馈影响生物钟基因的表达。

关键词：period；基因家族；摄食节律；基因克隆

Cloning and characterization of period family genes in channel catfish under both feeding and non-feeding conditions

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Abstract： This study presents the cloning and characterization of period family genes in channel catfish under both feeding and non-feeding conditions, alongside an analysis of their mRNA and protein expression. Four members of this gene family have been identified in channel catfish: Ipperiod1b, Ipperiod2, Ipperiod2l, and Ipperiod3. The full lengths of these genes are 4332 bp, 4122 bp, 3942 bp, and 3837 bp, respectively, encoding proteins of 1443, 1373, 1313, and 1278 amino acids. Notably, these genes exhibit high sequence identity with periodic genes from other fish species. Members of the periodic family are distributed across various tissues, though the expression levels differ among them. Specifically, in channel catfish, Ipperiod1b shows high expression in the intestine and ovary, Ipperiod2 is predominantly expressed in the liver and ovary, Ipperiod2l is highly expressed in the ovary and testis, while Ipperiod3 exhibits high expression in the brain and intestine. This study investigates the impact of food access and meal timing on the expression of period family genes in the brain and liver. The findings indicate distinct expression patterns of these genes in the brain and liver, with strict feeding rhythms correlating with alterations in their expression patterns. This research identifies period family genes in channel catfish for the first time and demonstrates that feedback from feeding rhythms influences the expression of circadian clock genes.

Key words:：period; family genes; feeding rhythm； gene clone

卵形鲳鲹(Trachinotus ovatus)鳃盖畸形的形态学特征及转录组分析

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摘要：卵形鲳鲹是我国最主要的海水经济鱼类之一，近年来出现了较高比例的鳃盖畸形问题。因此本研究采用 Micro-CT 扫描、电感耦合等离子体质谱(ICP-MS)分析、石蜡切片及染色等技术手段，对单侧鳃盖畸形个体的畸形侧和正常侧鳃盖骨系进行了结构、组织学和生化分析。三维重构结果显示畸形侧主鳃盖和下鳃盖骨均发生了向内折叠的现象，导致鳃盖缩短。ICP-MS 结果显示畸形侧主鳃盖骨中的钙、磷和镁含量显著高于正常侧。HE 和 TRAP 染色显示，畸形侧主鳃盖骨表现出更高的破骨细胞活性，同时骨吸收面积增加。转录组测序结果鉴定出 1220 个差异表达基因（DEG），其中 508 个基因表达上调，712 个下调。DEG 中发现了与成骨细胞和破骨细胞分化相关的基因，这揭示了骨代谢在鳃盖畸形形成过程中起着重要作用。GO 和 KEGG 分析显示这些 DEG 在肌肉收缩、离子稳态等功能和途径中显著富集，表明鳃盖畸形可能对鳃的呼吸和渗透调节等造成不良影响。

关键词：卵形鲳鲹；鳃盖畸形；形态学；转录组；基因表达

Morphological characterization and transcriptome analysis of opercular deformity in golden pompano (Trachinotus ovatus)

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Abstract：Skeletal deformity is one of the major threats to aquaculture because of its negative effects in important economic losses. Recently, a high rate of opercular deformities was observed in farmed golden pompano (Trachinotus ovatus), which is a key species for marine cage culture in the South China Sea. In the present study, a structural, histological, and biochemical analysis of the deformed opercular complex in T. ovatus was carried out using micro-CT, Inductively Coupled Plasma Mass Spectrometry (ICP-MS), paraffin section, and staining. A 3D reconstruction of the deformed and normal opercular complex has revealed an inward folding of both opercle and subopercle, and frequently affected branchiostegal rays being coated by the deformed opercle and subopercle. In addition, an increased Ca, P, and Mg content was identified in the deformed opercle. The Hematoxylin-eosin (HE) and tartrate resistant acid phosphatase (TRAP) staining of the deformed opercle have shown a higher osteoclast activity and increased bone resorption area. Further analyses on the difference of gene expression between the deformed and normal opercle have been performed using Illumina sequencing platform. As a result, a total of 1220 DEGs (including 508 up-regulated and 712 down-regulated genes) were identified. DEGs related to osteoblast and osteoclast differentiation revealed an important role of bone metabolism in opercular deformity. Moreover, GO and KEGG analysis of these DEGs showed that they were significantly enriched in functions and pathways related to muscle form, development and contraction. Additionally affected pathways including ion homeostasis suggested that functions of gills such as breathing and osmoregulation might be affected by the deformed opercle.

Key words:：Trachinotus ovatus； Opercular deformity； Morphology； Transcriptome； Gene expression

虹鳟低氧胁迫下 ceRNA 调控网络的鉴定和功能研究

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摘要：为探讨 ncRNA 在虹鳟响应低氧胁迫中的作用，本研究系统分析了虹鳟肝脏、鳃、肌肉、脾脏和头肾在不同低氧胁迫浓度和中度低氧胁迫下不同时间相比于常氧的组织学、生理生化指标和全转录组变化，筛选鉴定低氧相关 lncRNA-miRNA-mRNA 网络并进行体内外功能验证。组织学结果显示，重度低氧胁迫 12h（Ts12L）肝脏的损伤程度比中度低氧胁 12h（Tm12L）严重，中度低氧胁迫 1 month（TmlL）的肝脏与常氧相比无明显病理性变化。Tm12L 和 Ts12L 均提高了机体的无氧代谢、脂质代谢和蛋白质代谢水平，而 TmlL 中抗氧化和免疫水平已恢复至正常水平。通过功能验证证实了 LOC110519952-novel-m0023-5p-glut1a、LOC110520012-miR-206-y-vegfaa 和 LOC110520201-miR-2188-y-sod1 网络存在 ceRNA 调控关系。

关键词：虹鳟；低氧；生理生化指标；lncRNA-miRNA-mRNA 网络

Identification and functional studies of the ceRNA regulatory network in rainbow trout (Oncorhynchus mykiss) under hypoxia stress

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Abstract： Rainbow trout (Oncorhynchus mykiss) is susceptible to hypoxia, which severely restricts the development of its aquaculture industry. To investigate the roles of ncRNA in the response of rainbow trout to hypoxia stress, this study systematically analyzed the histological, biochemical and whole transcriptome changes in the liver, gill, muscle, spleen and headkidney of rainbow trout under different hypoxic concentrations and moderate hypoxia stress for different durations, and screened and identified hypoxia-related lncRNA-miRNA-mRNA networks and verified their interactions in vitro and in vivo. The full-length cDNAs of vegfaa, ho and ppara were 2914 bp, 1977 bp and 2882 bp. Liver injury was more severe in Ts12L than in Tm12L, and there were no obvious pathological changes in the liver of TmlL compared with normoxia. It was found that Tm12L and Ts12L increased the levels of anaerobic, lipid and protein metabolism, whereas antioxidant and immune levels were restored to normal in TmlL. Additionally, there were ceRNA regulatory relationships in the LOC110519952-novel-m0023-5p-glut1a, LOC110520012-miR-206-y-vegfaa and LOC110520201-miR-2188-y-sod1 networks. There results can provide a theoretical basis for molecular breeding for hypoxia-resistant traits in fish.

Key words:： Rainbow trout; Hypoxia stress; Biochemical indicators; LncRNA-miRNA-mRNA network

CRISPR/Cas9 系统介导的崇明鲫 fgf8 基因突变体的建立及功能研究

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摘要： 为了获知成纤维细胞生长因子 8(fibroblast growth factor8，FGF8)在鲫肌间刺及生长发育中的作用，本研究以长江下游地区特色养殖种二倍体崇明鲫为对象，用 CRISPR/Cas9 基因编辑技术敲除了崇明鲫 fgf8 两个同源基因。fgf8a+/-、fgf8b+/-、(fgf8a+/-+fgf8b+/-)的突变率分别为 87.5%、85%、63.6%。形态学观察发现，fgf8b+/-突变体崇明鲫的体长和体重指标都要明显快于野生型对照组。骨骼染色发现 fgf8b+/-与(fgf8a+/-+fgf8b+/-)突变体肌间刺均出现了显著减少。通过 qPCR 分析与肌间刺发育相关基因的表达，发现 fgf8b+/-与(fgf8a+/-+fgf8b+/-)突变体 bmp2、smad5 和 runx2b 等基因的表达都显著下调。本研究为 fgf8 基因在崇明鲫肌间刺及生长发育中起着重要的作用提供了依据。

关键词：CRISPR/Cas9；fgf8；肌间刺；生长

Establishment and functional study of CRISPR/Cas9 system-mediated mutants of fgf8 gene in Chongming crucian carp (Carassius auratus)

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Abstract： In order to gain knowledge of the role of fibroblast growth factor8 (FGF8) in the interosseous spines and growth and development of crucian carp, the present study was carried out with the diploid Chongming crucian carp, a characteristic breeding species in the lower reaches of the Yangtze River, and two homologous genes of fgf8 of Chongming crucian carp were knocked out by CRISPR/Cas9 gene editing technology. fgf8a+/-,fgf8b+/- and (fgf8a+/-+fgf8b+/-) with mutation rates of 87.5%, 85%, and 63.6%, respectively. Morphological observations, bone staining, and qPCR were performed to analyze the expression of genes associated with interosseous bone development. This study provides a basis for the fgf8 gene to play an important role in the intermuscular spines and growth and development of Chongming crucian carp, and also lays the foundation for its role in reproduction.

Key words:：CRISPR/Cas9, fgf8, Intermuscular bone, growth

克氏原螯虾肝胰腺细胞异质性及其与性腺发育的相关性研究

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摘要：肝胰腺是甲壳动物卵巢发育过程中卵黄物质合成的关键位点，但是肝胰腺组织的细胞组成特点及其在克氏原螯虾性腺发育过程中的生物学功能还不清楚。我们对克氏原螯虾卵巢发育过程中的肝胰腺指数（肝胰腺重/体重）进行了系统监测，发现卵巢发育Ⅰ-Ⅳ期个体的肝胰腺指数从6.61%增长到8.14%，到卵巢发育Ⅵ期减小至4.35%。对处于卵巢发育大生长期（Ⅲ期）、成熟期（Ⅴ期）、恢复期（Ⅵ期）的克氏原螯虾肝胰腺组织进行单细胞转录组测序，共获得16626个肝胰腺细胞，根据细胞Marker基因将其分为R细胞、B细胞、F细胞、E细胞以及M细胞5种细胞类型。其中R细胞占比最高（52.86%），其在处于性腺发育Ⅲ期、Ⅴ期以及Ⅵ期个体的肝胰腺组织中的占比分别为65.10%、26.42%以及50.62%；E细胞占比为24.68%，其在处于性腺发育Ⅲ期、Ⅴ期以及Ⅵ期个体的肝胰腺组织中的占比分别为17.99%、30.06%以及30.

关键词：克氏原螯虾；单细胞转录组测序；肝胰腺细胞；性腺发育

Hepatopancreatic cell heterogeneity and its correlation with gonadal development in Procambarus clarkii

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Abstract： The hepatopancreas is a key site for the synthesis of yolk substances during the ovarian development of crustaceans, but the cell composition characteristics of the hepatopancreas and its biological function in the gonadal development of Procambarus clarkii are still unclear. We systematically monitored the hepatopancreas index (hepatopancreas weight/body weight) during the ovarian development of P. clarkii and found that the hepatopancreas index of individuals in stages I-IV of ovarian development increased from 6.61% to 8.14%, and decreased to 4.35% in stage VI of ovarian development. Single-cell transcriptome sequencing was performed on the hepatopancreas tissues of P. clarkii in the large growth period (stage III), mature stage (stage V), and recovery stage (stage VI) of ovarian development, and a total of 16,626 hepatopancreas cells were obtained. According to the cell marker genes, they were divided into five cell types: R-cells, B-cells, F-cells, E-cells, and M-cells. Among them, R-cells accounted for the highest proportion (52.86%), accounting for 65.10%, 26.42%, and 50.62% of the hepatopancreatic tissues of individuals in gonadal development stages III, V, and VI, respectively; E-cells accounted for 24.68%, accounting for 17.99%, 30.06%, and 30.49% of the hepatopancreatic tissues of individuals in gonadal development stages III, V, and VI, respectively.

Key words:： Procambarus clarkii; single-cell RNA sequencing; hepatopancreas cells; gonadal development

刺参 NLR1 介导灿烂弧菌诱导细胞裂解性死亡的分子机制

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摘要：本研究以刺参为模型，探讨了含有死亡结构域的 NLR 家族成员 AjNLR1 在无脊椎动物先天免疫系统中的作用。AjNLR1 是一种新型 NOD 样受体，具有死亡结构域和 NACHT 结构域，但缺少 CARD 和 LRR 结构域。通过 RNA 干扰和过表达实验，发现 AjNLR1 能够促进细胞裂解性死亡，增强细胞对灿烂弧菌的抵抗力。进一步实验揭示 AjNLR1 与含有死亡结构域的 AjDD-Caspase 相互作用，且 AjDD-Caspase 也参与介导细胞裂解性死亡。使用泛 Caspase 抑制剂的回补实验进一步证实了 AjNLR1 通过 AjDD-Caspase 介导细胞裂解。这些发现为理解 NLR 家族的起源和功能提供了新的视角，对无脊椎动物免疫系统的研究具有重要意义。

关键词：刺参，灿烂弧菌，核苷酸结合寡聚化结构域样蛋白受体，裂解性细胞死亡

The Molecular Mechanism of NLR1 in Apostichopus japonicus Mediating Cell Lytic Death Induced by Vibrio splendidus

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Abstract： This study uses Apostichopus japonicus as a model to explore the role of the NLR family member AjNLR1, which contains a death domain, in the innate immune system of invertebrates. AjNLR1 is a novel NOD-like receptor with a death domain and a NACHT domain, but lacks CARD and LRR domains. Through RNA interference and overexpression experiments, it was found that AjNLR1 can promote cell lytic death and enhance the cell's resistance to Vibrio splendidus . Further experiments revealed that AjNLR1 interacts with AjDD-Caspase, which also contains a death domain, and is involved in mediating cell lytic death. The use of pan-Caspase inhibitors in a rescue experiment further confirmed that AjNLR1 mediates cell lysis through AjDD-Caspase. These findings provide new insights into the origin and function of the NLR family and are of significant importance for the study of the immune system in invertebrates

Key words:： Apostichopus japonicus, Vibrio splendidus, Nucleotide-binding oligomerization domain-like receptor (NLR), Lytic cell death.

拟穴青蟹 BHMT1 基因表征及其对盐度、饥饿的调控分析

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摘要：BHMT 以甜菜碱为甲基供体催化了同型半胱氨酸到蛋氨酸的反应。先前，我们发现BHMT 在节肢动物的昆虫分支中缺失，但在拟穴青蟹的大颚器中高度表达。本研究对拟穴青蟹BHMT 的调控进行了初步分析。系统发育分析表明，BHMT 属于 BHMT1 分支，命名为 Sp-BHMT1。Sp-BHMT1 的开放阅读框长度为 1203bp，编码 400 个氨基酸。序列比对结果表明，BHMT1 在不同动物中具有高度保守性，在近缘物种中同源性较高。Sp-BHMT1 在雌雄蟹的MO 中表达量最高，在雄蟹 MO 中的表达量是雌蟹的 1.6 倍。在幼体发育过程中，Sp-BHMT1在大部分时间低表达，但在蚤状幼体 2 期和 3 期的第一天显著升高。Sp-BHMT1 在盐度为 10‰时表达量最高，在盐度为 30‰时表达量最低。随着盐 Sp-BHMT1 的表达在 6 h 时显著升高，8 h 时又有所回升。饥饿处理后，与投喂组相比，Sp-BHMT1 在所有检测时间点的表达均显著上调。

关键词：BHMT;盐度、饥饿胁迫；拟穴青蟹

Characterization and regulation analysis of betaine homocysteine S-methyltransferase gene 1 (BHMT1) in the Mud Crab: A gene respond to salinity and feed behavior

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Abstract： BHMT catalyzed the homocysteine to methionine reaction using betaine as the methyl donor. Previously, we found that BHMT was lost in the insects' clade of the arthropod but highly expressed in the mandibular organ (MO) of the mud crab, Scylla paramamosain. To further explore its significant role, this study made a primary regulation analysis of BHMT in the mud crab. The open reading frame length of Sp-BHMT1 was 1,203 bp, encoding 400 amino acids. Sequences alignment revealed that BHMT1 was highly conserved in different animals, and the identities were higher in the nearer related species. Sp-BHMT1 had the highest expression in the MO of both genders, while its expression in the MO was 1.6 times higher in males than in females; similar things were also found in cerebral ganglion, hepatopancreas, and thoracic ganglia tissues. Sp-BHMT1 had the highest expression in the salinity 10 while lowest in salinity 30. With the decrease of salinity, the expression of Sp-BHMT1 increased significantly at 6 hours then followed back at 8 hours. After starvation treatment, the expression of Sp-BHMT1.

Key words:：BHMT1; salinity; starvation; expression; Scylla paramamosain

不同纬度野生厚壳贻贝群体的遗传结构和足丝附着力差异分析

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摘要：厚壳贻贝是我国重要的海水经济贝类，其可分泌足丝附着于养殖绳上，足丝附着强度减弱引发贻贝掉落造成经济损失，温度可影响足丝附着强度。本研究以舟山、台州和福鼎海域的野生厚壳贻贝为研究对象，利用 10 个高多态性微卫星标记研究了不同纬度地理群体的遗传多样性和遗传结构，同时比较不同群体间生长和足丝附着力差异。三个群体均具有较高的遗传多样性，舟山群体高于另外两个群体。三个群体的大多数位点偏离哈温平衡，且杂合不足，可能由于在长期适应各自环境中导致部分杂合子缺失。分子方差分析表明遗传变异主要发生在样本间；群体间遗传分化较低。邻接树显示，舟山群体聚为一支，而台州和福鼎群体聚为一支。舟山群体的足丝分泌数最多，足丝破断力与黏附力最强，具有较强的足丝附着力。研究结果表明，因环境不同群体间存在遗传分化，且舟山群体具有较高的遗传多样性和优良的足丝表型。为保护厚壳贻贝种质资源和选育具有较强足丝附着力的新品种提供了数据参考。

关键词：厚壳贻贝；微卫星；遗传多样性；遗传结构；足丝表型

Microsatellite-based genetic structure and byssal attachment strength differential analysis of wild populations of Mytilus coruscus at different latitudes

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Abstract：Mytilus coruscus is an important marine economic shellfish in China, capable of secreting byssal threads to attach to ropes. Reduced byssal attachment strength can lead to mussel drop-off and economic losses, with temperature affecting this strength. This study investigated the genetic diversity and structure of wild M. coruscus from the Zhoushan, Taizhou, and Fuding marine areas using 10 highly polymorphic microsatellite markers and compared growth and byssal attachment strength among these populations. All three populations exhibited high genetic diversity, with the population of Zhoushan showing the highest diversity. Most loci deviated from Hardy-Weinberg equilibrium, with a deficiency of heterozygotes, possibly due to long-term adaptation to their respective environments. AMOVA analysis indicated that genetic variation mainly occurs among samples, with low genetic differentiation between populations (Fst < 0.05). The neighbor-joining tree showed that the population of Zhoushan clustered separately from the populations of Taizhou and Fuding. The population of Zhoushan had higher numbers of byssus threads, as well as greater byssus breaking force and adhesive force, indicating stronger byssal attachment. These results suggest genetic differentiation among populations due to environmental differences, with the population of Zhoushan exhibiting higher genetic diversity and better byssal phenotypes. This provides data for the protection of M. coruscus genetic resources and the development of new strains with strong byssal attachment.

Key words:：Mytilus coruscus; microsatellite; genetic diversity; genetic structure; byssal phenotype

急性盐度胁迫对大口黑鲈死亡率、渗透压调节、抗氧化能力及 NKCC1a 基因表达的影响

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摘要：为探究不同盐度下大口黑鲈（Micropterus salmoides）的耐盐性和生理生化调节机制，分别在 0、6、9、12、15 和 18ppt 盐度组下放入 20.3±1.3g 的大口黑鲈进行 96h 急性盐度胁迫实验。测定各组胁迫 96h 内的死亡率，各组盐度胁迫后的血清生化指标、渗透酶活性等指标。结果显示，0、6、9、12、15 和 18 盐度组死亡率分别为 0%、0%、0%、5%、80%、100%。96h 盐度胁迫下，6、9 和 12ppt 血清渗透压随着时间推移逐渐升高，在同一时间点下，12ppt 要显著高于 9ppt 和 6ppt（$p < 0.05$）。对鳃和肠进行组织学观察，盐度为 6ppt 时大口黑鲈的鳃和肠组织未受到影响；在 9ppt 和 12ppt 时，鳃中鳃小片膨大、泌氯细胞数量增多，肠中杯状细胞数量变多。NKCC1a 基因在鳃和肠的表达水平均呈现先上升后下降的变化趋势。综上所述，盐度升高可显著影响大口黑鲈渗透压调节和抗氧化能力。

关键词：盐度胁迫、大口黑鲈、生理生化

Effects of acute salinity stress on mortality, osmotic regulation, antioxidant capacity and NKCC1a gene expression in largemouth bass

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Abstract： In order to explore the salt tolerance and physiological and biochemical regulation mechanism of largemouth bass (Micropterus salmoides) under different salinity, 20.3±1.3g of largemouth bass were placed in the 0, 6, 9, 12, 15 and 18ppt salinity groups for 96 hours of acute salinity stress. The mortality rate within 96 h of salinity stress in each group, serum biochemical indexes and osmoenzyme activity after salinity stress in each group were measured. The results showed that the mortality rates in the 0, 6, 9, 12, 15 and 18 salinity groups were 0%, 0%, 0%, 5%, 80% and 100%, respectively. Under 96h salinity stress, the osmolality of 6, 9 and 12 ppt increased gradually with the passage of time, and 12 ppt was significantly higher than that of 9 ppt and 6 ppt at the same time point ($P<0.05$). Histological observation of the gills and intestines showed that the gill and intestinal tissues of largemouth bass were not affected at a salinity of 6 ppt. At 9 ppt and 12 ppt, the gills in the gills are enlarged, the number of chlorine-secreting cells increases, and the number of goblet cells in the intestine increases. The expression level of NKCC1a gene in gills and intestine first increased and then decreased. In conclusion, increased salinity can significantly affect osmotic regulation and antioxidant capacity of largemouth bass.

Key words:：Salinity stress, largemouth bass, physiological and biochemical

不同纬度野生厚壳贻贝群体的遗传结构和足丝附着力差异分析

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摘要：厚壳贻贝是我国重要的海水经济贝类，其可分泌足丝附着于养殖绳上，足丝附着强度减弱引发贻贝掉落造成经济损失，温度可影响足丝附着强度。本研究以舟山、台州和福鼎海域的野生厚壳贻贝为研究对象，利用 10 个高多态性微卫星标记研究了不同纬度地理群体的遗传多样性和遗传结构，同时比较不同群体间生长和足丝附着力差异。三个群体均具有较高的遗传多样性，舟山群体高于另外两个群体。三个群体的大多数位点偏离哈温平衡，且杂合不足，可能由于在长期适应各自环境中导致部分杂合子缺失。分子方差分析表明遗传变异主要发生在样本间；群体间遗传分化较低。邻接树显示，舟山群体聚为一支，而台州和福鼎群体聚为一支。舟山群体的足丝分泌数最多，足丝破断力与黏附力最强，具有较强的足丝附着力。研究结果表明，因环境不同群体间存在遗传分化，且舟山群体具有较高的遗传多样性和优良的足丝表型。为保护厚壳贻贝种质资源和选育具有较强足丝附着力的新品种提供了数据参考。

关键词：厚壳贻贝；微卫星；遗传多样性；遗传结构；足丝表型

Microsatellite-based genetic structure and byssal attachment strength differential analysis of wild populations of Mytilus coruscus at different latitudes

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Abstract：Mytilus coruscus is an important marine economic shellfish in China, capable of secreting byssal threads to attach to ropes. Reduced byssal attachment strength can lead to mussel drop-off and economic losses, with temperature affecting this strength. This study investigated the genetic diversity and structure of wild M. coruscus from the Zhoushan, Taizhou, and Fuding marine areas using 10 highly polymorphic microsatellite markers and compared growth and byssal attachment strength among these populations. All three populations exhibited high genetic diversity, with the population of Zhoushan showing the highest diversity. Most loci deviated from Hardy-Weinberg equilibrium, with a deficiency of heterozygotes, possibly due to long-term adaptation to their respective environments. AMOVA analysis indicated that genetic variation mainly occurs among samples, with low genetic differentiation between populations ($Fst < 0.05$). The neighbor-joining tree showed that the population of Zhoushan clustered separately from the populations of Taizhou and Fuding. The population of Zhoushan had higher numbers of byssus threads, as well as greater byssus breaking force and adhesive force, indicating stronger byssal attachment. These results suggest genetic differentiation among populations due to environmental differences, with the population of Zhoushan exhibiting higher genetic diversity and better byssal phenotypes. This provides data for the protection of M. coruscus genetic resources and the development of new strains with strong byssal attachment.

Key words:：Mytilus coruscus; microsatellite; genetic diversity; genetic structure; byssal phenotype

PFOS 及其替代物 F53B 对厚壳贻贝幼体肌肉发育和变态发育的影响研究

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摘要：全氟辛烷磺酸（PFOS）和 6:2 氯代多氟烷醚磺酸（F53B）在水体中普遍存在，已引起广泛关注。PFOS 和 F53B 能在水生动物体内富集，厚壳贻贝（Mytilus coruscus）是我国重要海洋经济贝类，其幼体生长发育需经历 4 个阶段。本研究将厚壳贻贝各发育阶段幼虫在不同浓度 PFOS 和 F53B 中暴露，观察幼虫存活和变态，通过鬼笔环肽对幼虫肌肉染色，观察药物对肌肉发育的影响。结果表明 PFOS 和 F53B 对各阶段幼虫均无显著影响。药物暴露显著抑制幼虫变态，其中 PFOS 对幼虫变态抑制效果为正相关，F53B 对幼虫的变态抑制呈现非浓度依赖。幼虫肌肉染色结果发现正对照组幼虫面盘高度退化，药物暴露后面盘退化不完全，表明 PFOS 和 F53B 抑制幼虫肌肉退化。转录组分析发现 PFOS 及 F53B 暴露影响幼虫神经系统、肌肉发育和解毒等方面。本研究表明 PFOS 和 F53B 是影响贻贝幼体肌肉发育和变态发育的神经内分泌干扰物。

关键词：厚壳贻贝；肌肉发育；幼虫变态；PFOS；F53B

Studies on the impact of PFOS and its substitute F53B on muscle development and metamorphosis in larvae of the Mytilus coruscus

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Abstract：The development of Mytilus coruscus larvae involves four stages. In this study, larvae at different developmental stages were exposed to various concentrations of PFOS and F53B to observe survival and metamorphosis. The effect of these chemicals on muscle development was assessed using phalloidin staining. The results indicated that PFOS and F53B had no significant effect on larval survival across all stages. However, drug exposure significantly inhibited larval metamorphosis, with PFOS showing a positive correlation with metamorphosis inhibition, while F53B's inhibitory effect was not concentration-dependent. Muscle staining revealed that larvae in the positive control group exhibited severe loss of the velum, whereas drug-exposed larvae showed incomplete degeneration of the velum, suggesting that PFOS and F53B inhibit muscle degeneration. Transcriptomic analysis revealed that PFOS and F53B exposure affected the larval nervous system, muscle development, and detoxification processes. This study demonstrates that PFOS and F53B are endocrine-disrupting chemicals impacting muscle development and metamorphosis in mussel larvae.

Key words:：Mytilus coruscus; muscle development; larval metamorphosis; PFOS; F53B

srsf3 基因在中国大鲵组织表达特征分析

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摘要：为探究 srsf3 基因在中国大鲵（Andrias davidianus）性别分化中作用机制，采用 qRT-PCR 技术分析大鲵不同组织，不同发育时期与甲基睾丸酮处理后伪雌性与伪雄性性腺中表达量的变化；荧光原位杂交技术确定 srsf3 基因在大鲵精巢与卵巢中的表达定位。通过前期对大鲵性腺转录组测序结果分析，srsf3 基因全长为 1478bp，开放阅读框 504bp，编码 167 个氨基酸。生物信息学分析显示，蛋白二级结构为α-螺旋占比 12.57%、β-折叠占比 12.57%、无规卷曲占比 74.85%。系统进化分析表明，大鲵 SRSF3 氨基酸序列与两栖纲热带爪蟾（Xenopus tropicalis）亲缘关系密切。实时荧光定量 PCR 结果表明，srsf3 基因在卵巢中表达水平最高，在大鲵垂体组织中次之，肌肉与心脏组织中表达稍低；肝脏、脾脏、肺、胃组织中低表达。

关键词：srsf3 基因；中国大鲵（Andrias davidianus）；性逆转；表达分析；荧光原位杂交

Expression Analysis of SRSF3 Gene in Gonadal Tissues of Andrias davidianus at Different Growth Periods

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Abstract：In order to investigate the role of the srsf3 gene in the sex differentiation of the Chinese giant salamander (Andrias davidianus), quantitative reverse transcription polymerase chain reaction (qRT-PCR) was employed to analyse the changes in expression in pseudo-female and pseudo-male gonads of Andrias. The expression of the srsf3 gene was analysed in different tissues and developmental periods of the Chinese giant salamander (Andrias davidianus) following treatment with methyltestosterone. Fluorescence in situ hybridization (FISH) was employed to determine the localization of the srsf3 gene in the spermathecae and ovaries of the Andrias davidianus. The transcriptome sequencing results of the salamander gonads indicated that the srsf3 gene was 1478 bp in length, with an open reading frame of 504 bp, encoding 167 amino acids. Bioinformatics analysis demonstrated that the secondary structure of the protein was 12.57% α-helix, 12.57% β-folding, and 74.85% random curling. A phylogenetic analysis revealed that the amino acid sequence of the salamander SRSF3 was closely related to that of the amphibian Xenopus tropicalis.The results of real-time fluorescence quantitative PCR demonstrated that the srsf3 gene was expressed at the highest level in the ovary, followed by the salamander pituitary tissue, and exhibited a slightly lower expression in muscle and heart tissues, and a low expression in liver, spleen, lung and stomach tissues.

Key words:：srsf3 Gene, Andrias davidianus, fluorescence in situ hybridization, expression analysis

大口黑鲈肌肉品质提升方法研究

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摘要：为寻求大口黑鲈肌肉品质提升方法，研究了工厂化暂养及植物精油对大口黑鲈肌肉品质的影响，结果显示，（1）肌肉氨基酸总量以及 EPA 和 DHA 均在暂养第 30 天含量最高；通过构建大口黑鲈肌肉中挥发性风味物质的指纹图谱，发现肌肉中 2-庚酮、2-戊酮、2-丁酮、环戊酮、1-辛烯-3-醇、1-己醇等愉悦气味物质含量随着工厂化循环水暂养时间的延长而增加；（2）摄食精油 200mg/kg 饲料组大口黑鲈全鱼粗脂肪含量显著低于对照组，肌肉粗蛋白含量以 150mg/kg 组最低，肌肉粗脂肪含量则以 150mg/kg 组最高；添加精油后大口黑鲈肌肉总氨基酸、必需氨基酸和呈味氨基酸含量均显著高于对照组，以精油添加水平 150mg/kg 组最高；大口黑鲈肌肉 PUFA、EPA+DHA 组成均显著高于对照组，PUFA 以精油添加水平 150mg/kg 组最高，EPA+DHA 以精油添加水平 100mg/kg 组最高。

关键词：大口黑鲈；肌肉品质；工厂化暂养；植物精油

Research on the Methods to Improve the Muscle Quality of Micropterus salmoides

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Abstract： In order to seek methods to improve the muscle quality of Micropterus salmoides, the effects of industrialized temporary rearing and plant essential oils on the muscle quality of Micropterus salmoides were studied. The results showed that: (1) Transferring adult Micropterus salmoides from pond culture to the industrialized recirculating water culture system for temporary rearing for different periods had no significant effect on the crude protein and crude fat content in the muscle of Micropterus salmoides; the total amino acid content, EPA, and DHA in the muscle were the highest on the 30th day of temporary rearing; by constructing the fingerprint map of volatile flavor substances in the muscle of Micropterus salmoides, it was found that the content of pleasant odor substances such as 2-heptanone, 2-pentanone, 2-butanone, cyclopentanone, 1-octen-3-ol, and 1-hexanol in the muscle increased with the extension of the temporary rearing time in the industrialized recirculating water. (2) The crude fat content in the whole fish of the group fed with 200mg/kg essential oil feed was significantly lower than that of the control group, the crude protein content in the muscle was the lowest in the 150mg/kg group, and the crude fat content in the muscle was the highest in the 150mg/kg group; after adding essential oil, the total amino acid, essential amino acid, and flavor amino acid contents in the muscle of Micropterus salmoides were significantly higher than those of the control group, and the highest was in the 150mg/kg essential oil addition group; the PUFA, EPA + DHA compositions in the muscle of Micropterus salmoides were significantly higher than those of the control group, among which the PUFA was the highest in the 150mg/kg essential oil addition group, and the EPA + DHA was the highest in the 100mg/kg essential oil addition group, which was 16.81% higher than that of the control group; after feeding with essential oil-containing feed, the content of high alcohols and aldehydes in the muscle of Micropterus salmoides increased, which promoted the improvement of the muscle flavor of Micropterus salmoides. In conclusion: (1) Transferring adult Micropterus salmoides from pond culture to the industrialized recirculating water system for temporary rearing can improve the nutritional quality and flavor of the muscle of Micropterus salmoides, and it is an effective technical measure to improve the quality of adult Micropterus salmoides. It is recommended to promote and apply this method in the quality improvement of adult Micropterus salmoides from pond culture. (2) Spraying essential oil in the compound feed can significantly improve the essential amino acid, flavor amino acid, PUFA, and EPA + DHA compositions in the muscle of Micropterus salmoides.

Key words:：Micropterus salmoides; Muscle Quality; Industrialized Temporary Rearing; Plant Essential Oil

四种饲料添加剂对花刺参幼参生长及生理特性的影响

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摘要：花刺参（Stichopus monotuberculatus）是一种高营养价值食品，不仅含有丰富的蛋白质和必需氨基酸，还含有多种对人体有益的矿物质和活性成分。尽管花刺参育种技术已成功突破，但在其幼参养殖过程中存在生长缓慢、死亡率较高等问题。本研究通过探索不同饲料添加剂，分析其对花刺参幼参存活率、生长性能、非特异性免疫、抗氧化活性、营养组成以及消化生理的影响。结果显示，在日粮中添加鹧鸪茶粉、大蒜素及益生菌，可有效改善花刺参的生长性能，而蚯蚓发酵液未产生积极影响。所添加的四种饲料添加剂均能对花刺参的消化生理产生积极影响。对于免疫特性，鹧鸪茶粉和大蒜素均提升了所检测的免疫相关酶活性，而益生菌和蚯蚓发酵液的作用则较为复杂。此外，在海参体壁组织的营养组成方面，研究发现，实验所用添加剂会影响营养素的代谢过程。综上所述，我们的结果为热带海参的饲料添加剂研究提供新的选择和数据参考。

关键词：花刺参；饲料添加剂；生长性能；抗氧化免疫；营养组成

Effects of four feed additives on the growth and physiological characteristics in juvenile Stichopus monotuberculatus

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Abstract：Stichopus monotuberculatus is a kind of food with high nutritional value, which is not only rich in protein and essential amino acids, but also contains a variety of minerals and active ingredients that are beneficial to human body. Although the breeding technology of S. monotuberculatus has been successfully broken through, there are problems such as slow growth and high mortality rate in the culture of its juveniles. In this study, we explored different feed additives and analysed their effects on the survival rate, growth performance, non-specific immunity, antioxidant activity, nutrient composition and digestive physiology of juvenile S. monotuberculatus. The results indicated that the addition of partridge tea powder, allicin and probiotics to the diet was effective in improving the growth performance of the juveniles, whereas earthworm fermentation broth did not have a positive influence. All four feed additives were able to positively affect the digestive physiology of S. monotuberculatus. For immune characteristics, both partridge tea powder and allicin enhanced the activities of the detected immune-related enzymes, whereas the roles of probiotics and earthworm fermentation broth were more complex. In addition, with regard to the nutrient composition of sea cucumber body wall tissues, it was found that the additives used in the experiments affected the metabolic processes of the nutrients. Taken together, our results provide new options and data references for the study of feed additives for tropical sea cucumbers.

Key words:：Stichopus monotuberculatus; feed additives; growth performance; antioxidant immunity; nutritional component

低鱼粉饲料中添加解淀粉芽孢杆菌对三倍体虹鳟幼鱼生长、免疫和肠道健康的影响

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摘要：本研究旨在评估低鱼粉饲料中添加解淀粉芽孢杆菌对三倍体虹鳟幼鱼生长、免疫及肠道健康的影响。选取初始体重为（7.68 ± 0.20）g 的三倍体虹鳟为研究对象，分 5 组，每组 3 个平行，每个平行 23 尾鱼，在低鱼粉（10%）饲料中添加 5 种不同水平（0、3.34×107、2.7×108、2.7×109、1.5×1010）CFU/g 解淀粉芽孢杆菌，养殖周期为 8 周。结果表明：相较于未添加芽孢杆菌的对照组，当饲料中添加 2.7×108 CFU/g 芽孢杆菌时，其 WGR、SGR、PER 显著提高，FCR 显著降低，鱼体粗蛋白含量显著提高，肠道蛋白酶及淀粉酶活性显著升高，肝脏和血清抗氧化酶活性显著升高，肠道形态结构显著改善，提高肠道菌群中有益菌的丰度，降低了致病菌的丰度。而高水平芽孢杆菌添加组则造成肠道菌群失衡和肠道屏障损伤。综上，在低鱼粉饲粮中添加适量解淀粉芽孢杆菌对提高三倍体虹鳟生长、免疫、肠道健康方面具有积极作用。

关键词：解淀粉芽孢杆菌；低鱼粉；三倍体虹鳟；生长；免疫；肠道健康

Effects of dietary bacillus amyloliquefaciens on growth performance, immunity and intestinal health of juvenile triploid rainbow trout (Oncorhynchus mykiss) in low fishmeal diets

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Abstract： This study evaluates the effects of dietary Bacillus amyloliquefaciens on growth performance immunity and intestinal health in juvenile triploid rainbow trout (Oncorhynchus mykiss). A total of 345 triploid rainbow trout (7.68±0.20g) were allotted in 5 groups with 3 tanks each and fed with 5 diets including G1 (control diet) , G2(control diet containing 3.34×107 colony-forming unit (CFU)/g B. amyloliquefaciens), G3(control diet containing 2.7×108 CFU/g B. amyloliquefaciens), G4(control diet containing 2.7×109 CFU/g B. amyloliquefaciens) and G5 (control diet containing 1010 CFU/g B. amyloliquefaciens), respectively. After 8 weeks, addition of B. amyloliquefaciens restored growth retardation and intestinal injury induced by soybean meal in rainbow trout. Significant enhancements in growth performance, including improved weight gain rates, protein efficiency rates, specific growth rates and decreased feed conversion ratios in the G3 group, were indicative of enhanced nutrient utilization ($P<0.05$). With the increase of B. amyloliquefaciens supplementation level, there were no significant differences in crude lipid and moisture content ($P>0.05$). the crude protein content of fish significantly increased first and then decreased ($P<0.05$). The contents of superoxide dismutase, catalase and lysozyme in serum and liver of the experimental group significantly increased first and then decreased, the contents of malondialdehyde and trace reduced glutathione in liver significantly decreased first and then increased ($P<0.05$), and the alkaline phosphatase content did not change significantly ($P>0.05$). Compared with the control group, when supplemented with 108-1010 CFU / g B.amyloliquefaciens, the levels of intestinal protease and amylase significantly increased ($P<0.05$), the intestinal lipase levels were no significant change ($P>0.05$). when supplemented with 2.7×108 CFU / g B.amyloliquefaciens, the villi height, villi width and basal layer thickness were significantly improved ($P<0.05$), the expression of intestinal tight junction protein(Cldn-1 、 Ocldn) were significantly increased, and the expression of intestinal inflammatory factors(TNF-α、IL-6、IL-8) were significantly decreased($P<0.05$).

Key words:： Bacillus amyloliquefaciens, Low-Fishmeal diets, Triploid Oncorhynchus mykiss, Growth performance, Immunity, Intestinal health

小球藻生长因子（CGF）对凡纳滨对虾生长、免疫机制的转录组分析

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摘要：本文采用高通量转录组测序和实时定量聚合酶链式反应(quantitative real time polymerase chain reaction,qRT-PCR)技术,在分子水平揭示在饲料中添加一定浓度的小球藻生长因子对凡纳滨对虾的生长、免疫等机制的影响。养殖凡纳滨对虾作为实验材料，基于 Illumina 测序平台，开展投喂添加 1%CGF 的饲料和原始饲料作比较的转录组测序。结果表明：与对照组相比，实验组共获得 37025 个差异表达基因，筛选获得 13 个免疫相关基因。对差异表达基因进行 GO 富集分析发现，葡萄糖代谢过程、己糖代谢过程等与免疫相关的条目被显著富集；差异表达基因经 KEGG 富集分析显示，CGF 添加到凡纳滨对虾的饲料中可诱导脂肪细胞因子信号通路、AMPK 信号通路等多个免疫通路被显著富集。推测上述基因和通路可能在凡纳滨对虾生长、免疫机制中起重要作用。

关键词：凡纳滨对虾；转录组；分子机制；生长免疫

Transcriptome analysis of Chlorella growth factor (CGF) on growth and immune mechanism of Litopenaeus vannamei

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Abstract：In this study, high-throughput transcriptome sequencing and quantitative real time polymerase chain reaction (qRT-PCR) technology were used to reveal the effects of chlorella growth factor added to feed on the growth and immunity of Penaeus vannamei at the molecular level. Based on the Illumina sequencing platform, transcriptome sequencing was carried out to compare the feed with 1% CGF and the original diet. The results showed that compared with the control group, a total of 37025 differentially expressed genes were obtained in the experimental group, and 13 immune-related genes were screened. GO enrichment analysis of differentially expressed genes showed that immune-related items such as glucose metabolism and hexose metabolism were significantly enriched. KEGG enrichment analysis showed that the addition of CGF to the diet of Penaeus vannamei could induce significant enrichment of adipocytokine signaling pathway, AMPK signaling pathway and other immune pathways. It is speculated that the above genes and pathways may play an important role in the growth and immune mechanism of Penaeus vannamei.

Key words:：Penaeus vannamei; transcriptome; molecular mechanisms; Growth immunity

丁酸梭菌和乳酸菌对大口黑鲈生长性能、肝功能的影响

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摘要：为研究饲料中添加丁酸梭菌、乳酸菌对大口黑鲈生长性能、肝功能的影响，将 210 尾试验鱼随机分为 5 组，每组 3 个重复，每个重复 14 尾鱼。对照组鱼饲喂基础饵料，实验组分别投喂基础饲料中添加丁酸梭菌 (1.58× 108 CFU/kg)、乳酸菌 (0.4 × 106 CFU/kg) 、丁酸梭菌+乳酸菌 (1.58×108CFU/kg + 0.4×106CFU/kg) 和半量丁酸梭菌+乳酸菌 (1.58×108CFU/kg + 0.4×106CFU/kg)的试验饲料，试验期 60d。结果显示：与对照组相比，各试验组大口黑鲈总胆固醇（TC）、谷丙转氨酶（ALT）、谷草转氨酶（AST）、超氧化物歧化酶（SOD）、过氧化氢酶（CAT）、丙二醛（MDA）含量显著降低（P<0.05），其中 T3、T4 组效果较好。研究表明，饲料中添加丁酸梭菌、乳酸菌可促进大口黑鲈生长，改善其机体营养成分，维护肝功能。

关键词：丁酸梭菌;乳酸菌;大口黑鲈;生长性能;肝功能

Effects of Clostridium butyricum and lactic acid bacteria on growth performance and liver function of Micropterus salmoides

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Abstract：In order to study the effects of Clostridium butyricum and lactic acid bacteria on the growth performance and liver function of Micropterus salmoides, 210 test fish were randomly divided into 5 groups, with 3 replicates in each group and 14 fish in each replicate. The control group was fed bait, and the experimental group was fed with Clostridium butyricum (1.58×108 CFU/kg), lactic acid bacteria (0.4 × 106 CFU/kg), Clostridium butyricum + lactic acid bacteria (1.58×108CFU/kg + 0.4×106 CFU/kg) and half a dose of Clostridium butyricum + lactic acid bacteria (1.58×108 CFU/kg + 0.4×106 CFU/kg) for 60 days. The results showed that compared with the control group, the contents of total cholesterol (TC), alanine aminotransferase (ALT), aspartate aminotransferase (AST), superoxide dismutase (SOD), catalase (CAT) and malondialdehyde (MDA) in each group were significantly reduced (P<0.05), and the T3 and T4 groups had better effects. Studies have shown that adding Clostridium butyricum and lactic acid bacteria to the feed can promote the growth of Micropterus salmoides, improve its body nutrients, maintain liver function, and improve the structure of intestinal flora.

Key words:：Clostridium butyricum;Lactic acid bacteria; Micropterus salmoides;Growth performance;Liver function

基于脂质组学和转录组学解析不同磷脂对中间球海胆 (Strongylocentrotus intermedius)性腺发育和脂质代谢的影响

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摘要：目的：本试验结合脂质组学和转录组学解析不同磷脂源饲料(鱼油+大豆卵磷脂(FO+SL)、棕榈油+大豆卵磷脂(PO+SL)和棕榈油+磷虾油(PO+KO))对中间球海胆性腺发育、脂质积累和代谢机制的影响。结果：3 种饲料对海胆生长及性腺发育无显著影响。海胆消化道和性腺中主要磷脂类型相同，PO+KO 组 PC、PE、PG 和 PI 的相对含量最高。LC-PUFAs 主要沉积在磷脂的 sn-2 位，LC-PUFAs 含量较低的 FO+SL 组海胆 TG 中 LC-PUFAs 含量却显著高于其他两组；而 PO+KO 组海胆 PC、PE 中 LC-PUFAs 含量显著高于其他两组。海胆磷脂转运、LC-PUFAs 合成和磷脂重塑相关的基因表达量变化与脂质组学结果对应。结论：不同磷脂对中间球海胆性腺发育和脂质代谢有不同作用，KO 提高其极性磷脂中 LC-PUFAs 的合成、转运及重塑，SL 则提高中性磷脂中 LC-PUFAs 的转运和重塑。

关键词：中间球海胆，磷脂，性腺发育，脂质代谢，脂质组学，转录组学

The potential mechanisms for phospholipids on gonadal development and lipid metabolism of sea urchin (Strongylocentrotus intermedius) revealed by lipidomic and transcriptomic

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Abstract：This experiment was conducted to investigate the effects of formulated feeds with different phospholipid sources (fish oil + soybean lecithin (FO+SL), palm oil + soybean lecithin (PO+SL) and palm oil + krill oil (PO+KO)) on the gonad development, lipid accumulation and metabolism mechanism of juvenile Strongylocentrotus intermedius combining with lipidomic and transcriptomic. Three formulated feeds did not significantly affect the growth and gonadal development of sea urchins. The main types of phospholipids in digestive tracts were the same as that in gonads of sea urchins. The relative contents of PC, PE, PG and PI of sea urchins fed PO+KO were highest. The majority of LC-PUFAs in phospholipids was deposited at the sn-2 position. The relative contents of LC-PUFAs in TG were significantly higher of sea urchins fed FO+SL than those fed PO+SL and PO+KO,but the relative contents of LC-PUFAs in PC and PE were significantly higher of sea urchins fed PO+KO than those fed PO+SL and FO+SL. The expression of genes related to phospholipid transport, LC-PUFAs synthesis and phospholipid remodeling showed significantly differentice corresponded to the result of lipidomic. It was observed that different phospholipids have different effects on gonad development and lipid metabolism of S. intermedius. KO enhanced the synthesis, transport and remodeling of LC-PUFAs in polar phospholipids, while SL enhanced the transport and remodeling of LC-PUFAs in neutral phospholipids.

Key words:：Strongylocentrotus intermedius, phospholipid, gonad development, lipid metabolism, lipidomic, transcriptomic

维生素 E 通过抗氧化作用及 TGF-β/Smads 通路调节海参（Apostichopus japonicus）体壁胶原蛋白沉积

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摘要：为探讨维生素 E 对海参体壁胶原含量的影响及调控机制，配制不同水平的维生素 E（0、100、200、400 mg/kg）饲料，投喂初始体重为 13±0.2g 的海参 70 天。结果：（1）200 mg/kg 维生素 E 显著提升了海参羟脯氨酸（Hyp）和 III 型胶原含量以及 SOD 活性，同时促进了 Tenascin、SMAD1 和 TGF-β相关基因的上调。（2）400 mg/kg 维生素 E 则抑制了生长速率，降低了 Hyp 含量，增加了 I 型胶原含量，导致胶原纤维聚集和质地硬化胶原纤维聚集和质地硬化，并引发氧化应激，表现为 SOD、GSH-Px 和 POD 活性下降及 TGF-β/SMAD 信号通路相关基因下调。综上，适量维生素 E（100-200 mg/kg）有助于提升海参抗氧化能力及胶原含量，过量维生素 E（400 mg/kg）会引发氧化应激，损害海参体壁胶原蛋白沉积。

关键词：海参；维生素 E；抗氧化；TGF-β/SMAD；胶原蛋白

Vitamin E Regulates the Collagen Contents in the Body Wall of Sea Cucumber (Apostichopus japonicus) via its antioxidant effects and the TGF-β/Smads Pathway

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Abstract：A 70 d feeding experiment was performed to investigate the effects of dietary vitamin E at different addition levels (0, 100, 200, and 400 mg/kg) on the growth, collagen content, antioxi-dant capacity, and the expression of genes related to the transforming growth factor beta (TGF-β)/Sma- and Mad-related protein (SMAD) signaling pathway in sea cucumbers (Apostichopus japonicus). The results showed that A. japonicus in the group with 200 mg/kg vitamin E exhibited significantly higher growth rate, hydroxyproline (Hyp) and type III collagen contents, higher activity of superoxide dismutase (SOD), as well as the upregulation of genes related to Tenascin, SMAD1, and TGF-β. Additionally, A. japonicus in the group with 100 mg/kg vitamin E exhibited significantly higher body wall index, denser collagen arrangement and improved tex-ture quality, higher activities of glutathione peroxidase (GSH-Px) and peroxidase (POD), as well as the upregulation of genes related to collagen type I alpha 2 chain (COL1A2), collagen type III alpha 1 chain (COL3A1), and Sp-Smad2/3 (SMAD2/3). In contrast, A. japonicus in the group with 400 mg/kg vitamin E showed a decrease in growth rate, reduced Hyp content, increased type I collagen contents, collagen fiber aggregation and harder texture, alog downregulation of genes related to the TGF-β/SMAD signaling pathway. Furthermore, A. japonicus in the group with 400 mg/kg exhibited oxidative stress reflected by lower activities of SOD, GSH-Px, and POD. These results indicated that A. japonicus fed diets added with 100-200 mg/kg vitamin E improved col-lagen retention and texture quality of A. japonicus by increasing activities of antioxidant enzymes and expression of genes in the TGF-β/SMAD signaling pathway. However, excessive addition of vitamin E (400 mg/kg) induced oxidative stress, which could increase the collagen degradation and fibrosis, and pose threat to the growth and texture quality of A. japonicus.

Key words:：Apostichopus japonicus; VE; antioxidant; TGF-β/SMAD; Collagen

艾叶粉添加至高脂日粮对鲤生长性能及脂质代谢的影响

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摘要：本研究旨在探讨艾叶粉（MLP）在高脂日粮中对鲤生长性能及脂代谢的影响。实验设置对照组（CT，5%脂质）和高脂组（HF，10%脂质），并在高脂日粮中分别添加 0.6%（MLP1）、1.2%（MLP2）、1.8%（MLP3）和 2.4%（MLP4）艾叶粉后饲喂鲤八周。MLP1、MLP2 组鲤较 HF 组 FBW 和 SGR 显著升高。添加适量艾叶粉能降低血清和肝脏的脂质水平；MLP 添加组鲤血清 ALT 和 AST 较 HF 组相比均显著降低，MLP1、MLP2 组 MDA 含量显著降低（$P < 0.05$），适量艾叶粉添加会下调肝脏和脂肪中脂生成基因的表达，且艾叶添加组脂肪组织脂分解基因均有上调趋势；艾叶粉添加能减轻肝细胞空泡化程度，减小脂肪细胞面积。此外，MLP2、MLP3 组显著增加了肠绒毛高度，MLP2 组肠 il-10 的表达上调，MLP4 组肠 tnf-α的表达下调。因此，适量艾叶粉添加可以改善鲤生长性能、调节脂质代谢、促进鱼体健康。

关键词：鲤；艾叶粉；生长；脂质代谢

Effects of mugwort leaf powder on growth performance and lipid metabolism of common carp (Cyprinus carpio) fed high-fat diet

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Abstract：This study examines the influence of mugwort leaf powder (MLP) on common carp growth and lipid metabolism when fed a high-fat die.Diets were established: control (CT) with 5% fat , high-fat (HF) with 10% fat and HF added with MLP at 0.6% (MLP1), 1.2% (MLP2), 1.8% (MLP3), and 2.4% (MLP4), common carp were fed them for 8 weeks. MLP1 and MLP2 groups significantly increased fish weight and growth rate, lowered FCR compared with the HF ($P < 0.05$). The MLP could reduce lipid levels in serum and hepatopancreas. Hepatopancreas histology showed cell vacuolation and adipocyte area were reduced. Serum ALT, AST levels decreased in MLP-fed fish, MDA levels decreased in MLP1 and MLP2. Adding appropriate amount of MLP could down-regulate the expression of lipogenesis genes in hepatopancreas and adipose tissue, The lipolysis genes in adipose tissue of MLP-added groups show an upward trend ($P < 0.05$). MLP2 and MLP3 groups enhanced intestinal villi height, and MLP2 group up-regulated the gene expression of il-10, while MLP4 group down-regulated the gene expression of tnf-α. In summary, high-fat diet with MLP could boost fish growth,regulate lipid metabolism, promote common carp health.

Key words:： Common carp; Mugwort leaf powder; Growth; Lipid metabolism

饲料脂肪水平对牛蛙蝌蚪的生长性能、饲料利用、脂肪代谢和变态率的影响

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摘要：为了探究饲料脂肪水平对牛蛙蝌蚪的生长性能、饲料利用、脂肪代谢和变态率的影响，本试验配制了 6 种等氮饲料，脂肪水平分别为 4.46%、6.95%、9.10%、10.90%、12.34%和 15.00%。每个处理设置 3 个重复，每个重复 50 只蝌蚪（初始均重约 0.007g），试验为期 75 天。结果表明：增重率、干物质和总能的表观消化率、肠道脂肪酶活性、肝脏脂蛋白脂酶和肉碱棕榈酰基转移酶-I 活性及变态率均随饲料脂肪水平的升高而升高，在 12.34%脂肪水平时达到最高，之后则呈下降趋势。蛋白质效率、蛋白质沉积率、脂肪沉积率、粗脂肪的表观消化率均随饲料脂肪水平的升高而升高，在 10.90%脂肪水平时达到最高，之后则呈下降趋势。以增重率和变态率为判据进行二次回归分析，得到当脂肪水平分别为 11.08%和 10.72%时，增重率和变态率有最大值。综上所述，牛蛙蝌蚪饲料的最适脂肪水平为 10.72%-11.08%。

关键词：牛蛙蝌蚪；生长；脂肪；变态

Effects of dietary lipid levels on growth, feed utilization, lipid metabolism and metamorphosis rate of bullfrog (Aquarana catesbeianus) tadpoles

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Abstract： This study aimed to evaluate effects of dietary crude lipid requirement on growth performance, feed utilization, lipid metabolism, and metamorphosis rate of bullfrog (Aquarana catesbeianus) tadpoles. Six iso-nitrogenous diets were formulated with 4.46%, 6.95%, 9.10%, 10.90%, 12.34%, and 15.00% crude lipid. Triplicate replicates of tadpoles (0.007g) were fed for 75 days. Weight gain (WG), specific growth rate (SGR), apparent digestibility of dry matter and gross energy, intestinal lipase capacity (LPS), lipoprotein lipase (LPL), and carnitine palmitoyltransferase-I (CPT-I) in the liver, and metamorphosis rate of bullfrog tadpoles all increased with increasing dietary lipid level from 4.46% to 12.34%, and then decreased. The protein efficiency ratio (PER), protein deposition rate (PDR), lipid deposition rate (LDR), the intestinal trypsin activity (TPS), apparent digestibility of the crude lipid, and the superoxide dismutase (SOD) and catalase (CAT) activities in the liver all increased with increasing dietary lipid level from 4.46% to 10.90%, and then decreased. Based on the second-order polynomial regression analysis of the weight gain and metamorphosis rate vs. dietary lipid level, the optimal dietary lipid level for bullfrog tadpoles was 11.08 and 10.72%, respectively. In conclusion, the optimal dietary lipid level of bullfrog tadpoles was estimated to be 10.72% -11.08% of diet.

Key words:：Bullfrog tadpoles; growth; lipid; metamorphosis

海水贝类网箱附着物的资源化利用研究—以仿刺参 Apostichopus japonicus 饵料为例

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摘要：网箱养殖是海水贝类养殖的主要方式之一，过程中产生的附着物会造成资源浪费和环境污染。本研究将附着物高温烘干后制成贝笼泥，结合自制酵素将其开发成新型饵料以替代海泥饲喂仿刺参，通过饲喂实验评估贝笼泥替代海泥用作仿刺参饵料的可行性。进行九周饲喂实验后，饲喂贝笼泥和大菜叶的 BD 组存活率和特定生长率与对照组相比无显著性差异，添加自制酵素后的 BDJ 组仿刺参相较于对照组存活率显著提高（$P<0.05$），特定生长率无显著性差异；各实验组粪便中具有相同的优势细菌门并结构比例相似，均为拟杆菌门、变形菌门和疣微菌门，优势细菌属均为 Lutibacter 和 Haloferula，表明仿刺参可能具有相近的肠道功能。五组养殖水体的理化性质无明显差异，饲喂自制酵素的实验组水体中可培养弧菌数显著低于对照组（$P<0.05$）。实验表明，贝笼泥可以作为仿刺参饵料使用，从而解决附着物大量堆积以及仿刺参刺参养殖中大量使用海泥带来的环境问题。

关键词：仿刺参；贝笼泥；附着物处理；细菌群落结构；自制酵素

Research on the resource utilization of marine shellfish cage attachments - taking the bait of Apostichopus japonicus as an example

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Abstract：Net cage culture is one of the main methods of marine shellfish farming. The attachments produced during the process will cause waste of resources and environmental pollution. In this study, the attachments were dried at high temperature to make shellfish mud, which was then developed into a new type of bait using homemade enzymes to replace sea mud for feeding Apostichopus japonicus. Feeding experiments were conducted to evaluate the feasibility of using cage mud as a bait for Apostichopus japonicus. After nine weeks of feeding experiment, the survival rate and specific growth rate of the BD group fed with shellfish mud and vegetable leaves were not significantly different from those of the control group . The survival rate of the BDJ group with the addition of homemade enzymes was significantly improved compared with the control group ($P<0.05$), and the specific growth rate was not significantly different ； The feces of each experimental group had the same dominant bacterial phyla and similar structural proportions, all of which were Bacteroidetes, Proteobacteria and Verrucomicrobia, and the dominant bacterial genera were Lutibacter and Haloferula, indicating that the Apostichopus japonicus may have similar intestinal functions. There was no significant difference in the physical and chemical properties of the five groups of aquaculture water. The number of cultivable Vibrio in the water of the two experimental groups fed with homemade enzymes was significantly lower than that of the control group ($P<0.05$). Experiments have shown that shellfish mud can be used as bait for Apostichopus japonicus, thereby solving the environmental problems caused by the large accumulation of attachments and the large-scale use of sea mud in the Apostichopus japonicus farming process.

Key words:：Apostichopus japonicus，shellfish mud，attachments processing，bacterial community

外源性琥珀酸通过改善肝肠健康促进大口黑鲈对高糖饲料的利用

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摘要：为探究高糖饲料中琥珀酸对大口黑鲈生长和肝肠健康的影响，本研究分别配制标准饲料、高糖饲料以及高糖饲料中分别添加不同水平琥珀酸（0.5% 、1.0%、1.5%和 2.0%）的饲料，饲喂大口黑鲈（11.96±0.7g）10 周。本研究揭示了高糖饲料对大口黑鲈的不良影响，包括抑制生长和饲料利用、降低抗氧化力和免疫力以及造成糖脂代谢和肠道菌群的紊乱。随着琥珀酸添加水平的提高，饲料转化率、肝体比、脏体比、糖原含量、消化酶活力以及肝脏抗氧化力均呈现显著的线性和二次趋势。添加 0.5%的琥珀酸显著改善肠道屏障并缓解内质网应激。此外，外源性琥珀酸显著上调了糖酵解相关基因表达并抑制糖异生和脂肪合成相关基因的表达。综上，适宜的琥珀酸通过影响肝肠健康维持糖脂代谢稳态，提高对饲料碳水化合物的利用，从而促进大口黑鲈的生长。根据生长和饲料利用相关指标进行综合评价，本研究得出琥珀酸的适宜添加水平为 0.46% ~ 0.50%。

关键词：琥珀酸、高糖、糖脂代谢、肝肠健康

Exogenous succinic acid improved the utilization of a high-carbohydrate diet in largemouth bass (Micropterus salmoides) via enhancing enterohepatic health

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Abstract： A 10-week feeding trial was executed to illustrate the effects of succinic acid (SUA) in high carbohydrate diet (HCD) on growth performance and enterohepatic health of largemouth bass (Micropterus salmoides) (11.96 ± 0.7 g). Six diets with equal lipid content and energy level were formulated and presented as the standard diet containing 10% carbohydrate and 40% fish meal, the HCD containing 15% carbohydrate and 36% fish meal, and HCDs respectively supplemented with 0.5% (S0.5), 1.0% (S1.0), 1.5% (S1.5) and 2.0% (S2.0) SUA. The study revealed the adverse impacts of HCDs compared to standard diet including the feed utilization and growth hinderance, antioxidant capacity and immunity decline, and the metabolism and gut microbiota disturbance. Significant linear and quadratic trends were observed on feed conversion rate, hepatosomatic index, viscerosomatic index, glycogen content, activities of amylase and protease and liver antioxidant indicators with the increase of SUA supplementation. The addition of 0.5% SUA significantly improved intestinal morphology, the mRNA expression levels of tight junction proteins (ZO1 and Claudin4) and anti-apoptotic genes (Bcl2), and abundance of beneficial bacteria. The mRNA expression of endoplasmic reticulum stress key genes, including GRP78, PERK, IRE1, ATF6, eIF2α and Chopα, were also down-regulated. Besides, exogenous SA up-regulated the mRNA expression levels of anti-inflammatory factors (Nrf2, TGFβ1, IL10), glycolytic genes (PK, PFKL2, GK), β-oxidation gene (CPT1), anti-apoptotic gene (Bag) and glucose transporter (Glut2) in liver. The mRNA expression levels of pro-inflammatory factors (TNFα), gluconeogenesis key genes (PEPCK, G6Pase), fat synthesis genes (ACC1, FASN) and pro-apoptotic gene (Bad) were down-regulated. The optimal supplemental level of SUA was considered to be 0.46%-0.50% in the present study according to the comprehensive evaluation on growth and feed utilization. Overall, SUA repaired intestinal barriers, regulated gut microbiota, and alleviated oxidative stress and inflammation in the intestine and liver induced by HCDs. By influencing the enterohepatic health and maintaining glucose-lipid metabolism homeostasis, appropriate SUA enhanced the utilization of dietary carbohydrates and promoted the growth of largemouth bass.

Key words:： Succinic acid, high carbohydrate, glucolipid metabolism, enterohepatic health

鱼类免疫代谢学研究

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摘要：为解决我国饲料粮对外依存度高，大量新型原料逐渐被开发；研究表明养殖鱼类可逐渐适应新蛋白原料并有更高的生长潜力，然而病原感染后的炎症和死亡风险更高。考虑到健康、优质的水产品供给是渔业新质生产力的内在要求，应在解析鱼类免疫代谢机理的基础上，针对肝脏和鳃等关键器官开展精准地营养免疫调控。鱼类肝脏在病原感染早期产生强烈的先天免疫应答，并伴发有代谢重构，在感染后期淋巴细胞清除病原后，肝脏中代谢逐渐复原，伴随着 mTORC1 通路活性改变；后续研究表明 mTORC1 信号通过调控 B 细胞病原特异性 Igs 的产生，从而调节鱼类抵抗病原入侵。鱼类鳃在感染后发生明显病理改变，分别是由早期的细胞凋亡和后期的细胞焦亡所导致，伴随着 MAPK 通路活性改变；后续研究表明 p38MAPK 通路在调节病原感染后的细胞凋亡中发挥作用。因此，后续以 mTORC1 和 MAPK 通路等为靶点开展精准的营养免疫调控研究，将助推渔业高质量发展。

关键词：免疫代谢，蛋白原料，肝脏，鳃，细胞信号通路

Primary research on fish immunometabolism

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Abstract： In order to solve the high dependence of China's feed grain on foreign countries, plenty of new feed materials have been gradually developed. Our study showed that farmed fish can gradually be domesticated to new protein sources and exhibit higher growth potential, however higher risk of inflammation and mortality after pathogenic infection were detected. Considering that the supply of healthy and high-quality aquatic products is the intrinsic requirement for fishery new quality productivity, it is necessary to carry out precise nutritional immune regulation for key organs such as liver and gills on the basis of analyzing the mechanism of fish immunometabolism. In the early stage after pathogenic infection, fish liver elicited a strong innate immune response, accompanied by metabolic remodeling. Lymphocytes function in eliminating pathogens in the late stage of infection, resulting in the recovered hepatic metabolism, accompanied by the changed mTORC1 pathway activity. Subsequent studies have shown that mTORC1 signaling regulates fish resistance to pathogen invasion by regulating the production of B-cell pathogen-specific Igs. Fish gill underwent obvious pathological changes after infection, which were caused by early apoptosis and then pyroptosis, respectively, accompanied by changes in MAPK pathway activity. Follow-up studies showed that p38MAPK pathway plays a role in regulating apoptosis after pathogen infection. Therefore, the precise nutritional regulation of fish immunity targeting mTORC1 and MAPK pathway will promote the high-quality development of fisheries.

Key words:： immunomtabolism, protein sources, liver, gill, cell signaling pathway

不同碳水化合物水平对梭鲈幼鱼生长、肝脏和肠道健康以及肠道菌群的影响

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摘要：为确定梭鲈（1.20±0.01 g）对饲料碳水化合物的最佳需求，配置 3 种淀粉添加水平（8%、10%、12%）的饲料，开展 8 周养殖试验。结果表明，梭鲈在 12%组的增重率和存活率均显著下降。与 8%组相比，12%组肠道中α淀粉酶活性降低，肝脏中出现脂肪沉积。12%组显著增加丙二醛含量，降低谷胱甘肽活性和总抗氧化能力。随着碳水化合物水平增加，occludin-a、occludin-b 和 zo-2 表达量降低，促炎细胞因子（il1-β，il8，tnf-β）表达量升高，抗炎细胞因子（il10，tgf-β）表达量降低，肠绒毛高度和宽度均降低。此外，饲料碳水化合物摄入的增加会增加有害细菌丰度，减少有益细菌丰度，进而破坏肠道微生物组成结构。综上，适量添加淀粉可促进生长，但过量添加会对消化能力和免疫功能产生负面影响，建议淀粉添加量低于 10%。

关键词：梭鲈；碳水化合物；肝脏健康；肠道健康；肠道菌群

Effects of different levels of carbohydrates on growth performance, hepatic and intestinal health, and intestinal microflora of juvenile pikeperch (Sander lucioperca)

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Abstract： Pikeperch (Sander lucioperca) is a species with great potential for aquaculture in Eurasian countries, while feed costs limit the scale of pikeperch farming. Adding carbohydrates to the feed as an energy source is a viable approach to reduce costs, to improve the culture status of pikeperch. In this study, in order to determine the optimal carbohydrate requirement of pikeperch, three tapioca starch (8%, 10%, 12%) added feeds were produced with isonitrogenous (51%) and isolipidic (11%). For eight weeks, body weight was 1.20±0.01 g, were manually fed the trio of experimental diets until they seemed fully satisfied. The finding revealed that pikeperch can utilize dietary carbohydrate, but excessive dietary carbohydrate will adversely affect the growth performance. The growth and survival rate were decreased in pikeperch in the 12% group ($P<0.05$). The α-amylase activity of 12% group reduced in the intestine and lipid deposition was observed in the liver compared with the 8% group. In addition, pro-inflammatory cytokines (il1-β, il8, tnf-β) in the liver and intestine elevate and anti-inflammatory cytokines (il10, tgf-β) decrease with increasing dietary carbohydrate levels. Hepatic and intestinal antioxidant capacity were also adversely affected, with 12% group significantly increasing MDA contents and decreasing GSH and T-AOC ($P<0.05$). The intestinal barrier function is also damaged, the height and width of intestinal villi decreased, and the expression of occludin-a, occludin-b, and zo-2 genes were decreased. Elevated levels of starch intake led to harm to gut microflora, reducing bacterial populations, simultaneously boosting the presence of detrimental bacteria (Proteobacteria, Actinobacteriota, Achromobacter, and Rhodococcus) and diminishing the beneficial bacteria (Firmicutes). In conclusion, moderate addition of starch as an energy source can reduce feed costs, however, over addition can bring about organism damage and is recommended to be added at less than 10%.

Key words:：pikeperch; carbohydrate; hepatic health; intestinal health; intestinal microflora

饲料中添加 3 种不同小肽对大口黑鲈幼鱼生长、消化和免疫功能的影响

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摘要：为探究不同小肽对大口黑鲈幼鱼生长性能、消化酶活性、抗氧化能力和免疫功能的影响，试验选取平均体重 38.43 ± 3.17g 大口黑鲈 360 尾，随机分成 4 组，每组 3 个重复，每个重复 30 尾鱼。在基础日粮中分别添加 3 种不同小肽（第益肽产品 DI、DYT、KZ）和空白对照组进行为期 50 d 养殖试验。结果表明：DI 组增重率比对照组提升 12.05%，成活率提升 6.66%，饲料系数下降 1.27；DI 组胃蛋白酶、胰蛋白酶和脂肪酶活性最高，分别比对照组提升了 39.21%、18.18%和 20.40%；KZ 组α-淀粉酶活性最高，比对照组提升了 93.19%；DI 组超氧化物歧化酶活性和总抗氧化能力比对照组分别提升 35.59%和 61.86%；DYT 组丙二醛含量比对照组下降了 22.75%；DYT 组谷丙转氨酶比对照组下降了 75.27%；KZ 组谷草转氨酶对照组下降了 46.25%；

关键词：大口黑鲈；小肽；生长性能；消化酶活性；免疫功能

Effects of Three Different Small Peptides on Growth, Digestive and Immune Function of Micropterus Salmoides

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Abstract：To investigate the effects of different small peptides on the growth performance, digestive enzyme activity, antioxidant capacity, and immune ability of Micropterus salmoides, 360 experimental fishes with an average weight of 38.43 ± 3.17 g were selected for the experiment and randomly divided into 4 groups, with 3 replicates in each group and 30 fish in each replicate. Three different small peptides (Diyitai Products DI, DYT, KZ) were added to the basal diet of the experimental group and one control group was set for a 50-day experiment. The results showed that, compared to the control group, the weight gain rate of the DI group increased by 12.05% , the survival rate increased by 6.66%, and the feed coefficient decreased by 1.27; the activities of pepsin, trypsin, and lipase in the DI group were the highest, increasing by 39.21%, 18.18%, and 20.40% respectively compared to the control group, and the activity of alpha-amylase in the KZ group was the highest, increasing by 93.19% compared to the control group; the superoxide dismutase activity and total antioxidant activity in the DI group increased by 35.59% and 61.86% respectively compared to the control group, while the content of malondialdehyde in the DYT group decreased by 22.75% compared to the control group; the glutamic-pyruvic transaminase in the DYT group decreased by 75.27% compared to the control group, and the glutamic-oxalacetic transaminase in the KZ group decreased by 46.25%; the acid phosphatase and alkaline phosphatase in the DI group increased by 58.65% and 179.61% compared to the control group, respectively. In conclusion, the experimental results of comparing three small peptides showed that the Diyitai product DI had the best effect, which could significantly improve the growth, digestion and immunity of Micropterus salmoides, and was suitable for large-scale production of Micropterus salmoides .

Key words:：Micropterus salmoides; small peptide; growth performance; digestive enzyme activity; immune function

虾青素对罗氏沼虾生长、体色、免疫及其相关基因表达的影响

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摘要：为研究虾青素对罗氏沼虾生长、体色与免疫等方面的影响。在基础饲料中分别添加 4 种不同含量的虾青素（0、50、100 和 200 mg/kg），开展了罗氏沼虾的生长性能、体色差异、免疫效果评估并检测相关基因表达水平。饲喂 20 周后结果显示，与对照组相比，饲喂虾青素均能提高罗氏沼虾的增重率和特定生长率、缩短蜕皮周期；体色方面：随着虾青素含量的增加红度（a*）和黄度（b*）显著提升（$p < 0.05$）。酶活检测表明：200 mg/kg 虾青素显著提高血淋巴中 MDA、AKP 和 SOD 活性。在基因表达方面，虾青素显著改变不同蜕皮时期 MIH、EcR 和 RXR 表达水平；100 mg/kg 虾青素显著提高 cat、sod、gsh-px 和 acp 基因表达量。因此，在饲料种添加 100 mg/kg 和 200 mg/kg 虾青素能显著改善罗氏沼虾的生长性能和体色，提高其免疫和抗氧化能力。本研究为虾青素在甲壳动物饲料中的应用提供参考。

关键词：罗氏沼虾；虾青素；生长性能；体色；免疫；基因表达

Effects of astaxanthin on the growth, body color, immunity, and related gene expression of Macrobrachium rosenbergii

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Abstract： To investigate the effects of astaxanthin on the growth, body color, and immunity of Macrobrachium rosenbergii, four different levels of astaxanthin (0, 50, 100, and 200 mg kg-1) were added to a basal diet. This study evaluated the growth performance, body color differences, immune effects, and related gene expression levels of Macrobrachium rosenbergii. After 20 weeks of feeding, the results showed that compared to the control group, astaxanthin supplementation increased the weight gain rate and specific growth rate of Macrobrachium rosenbergii and shortened their molting cycle. In terms of body color, the redness (a*) and yellowness (b*) significantly increased with the increase in astaxanthin content ($p < 0.05$). Enzyme activity assays revealed that 200 mg kg-1 of astaxanthin significantly enhanced the activities of malondialdehyde (MDA), alkaline phosphatase (AKP), and superoxide dismutase (SOD) in the hemolymph. Regarding gene expression, astaxanthin significantly altered the expression levels of molt-inhibiting hormone (MIH), ecdysone receptor (EcR), and retinoid X receptor (RXR) during different molting stages. Furthermore, 100 mg kg-1 of astaxanthin significantly upregulated the expression of catalase (cat), superoxide dismutase (sod), glutathione peroxidase (gsh-px), and acid phosphatase (acp) genes. Therefore, the inclusion of 100 mg kg-1 and 200 mg kg-1 of astaxanthin in the feed significantly improved the growth performance, body color, immune response, and antioxidant capacity of Macrobrachium rosenbergii. This study provides valuable insights for the application of astaxanthin in crustacean feeds.

Key words:： Macrobrachium rosenbergii; Astaxanthin；Growth performance；Body color; Immunity; Gene expression

温度和盐度对中国卤虫生长、繁殖、类胡萝卜素积累的影响及转录组分析

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摘要：以螺旋藻粉为饵料，在不同盐度（10、30、50、70 和 90）和不同温度（20℃、25℃和 30℃）下，探究温度、盐度对中华卤虫生长及体内类胡萝卜素积累及转录组的影响。结果表明，温度和盐度对卤虫成活率、体长和体内类胡萝卜素积累有显著的交互作用。盐度 70、温度 20℃条件下，存活率（83.7%）显著高于其他各组。盐度 30~90、温度为 25~30℃各组体长差异不显著。20°C 时，体长显著低于其他各组，且均无性成熟个体。在 25~30℃条件下，随着盐度的升高，性成熟的比例增加。卤虫体内主要积累的类胡萝卜素为海胆酮和角黄素，随着温度和盐度的升高，卤虫体内积累的胡萝卜素含量总体呈下降趋势。转录组分析显示，高温条件下“铁死亡”和“谷胱甘肽代谢”相关基因显著上调，“氧化磷酸化”等相关基因显著下调。在高盐度条件下，“离子转运”等相关基因显著上调。在低盐度条件下，差异基因主要富集在“核糖体”和“溶酶体”等通路上。

关键词：中华卤虫，温度，盐度，生长性能，性成熟，类胡萝卜素积累

Effects of temperature and salinity on the growth, reproduction, carotenoids accumulation in Artemia sinica, and transcriptome analysis

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Abstract：To better understand the metabolism of the brine shrimp (Artemia sinica) under different conditions, the growth, reproduction, and carotenoid accumulations in Artemia were evaluated via experiments encompassing five salinity levels (10, 30, 50, 70, and 90), and three temperature levels (20 ℃, 25 ℃, and 30 ℃). The results showed that temperature and salinity displayed significant interactions with survival, body length, and carotenoid accumulation in the body ($P < 0.05$). The survival rate for Artemia under conditions with salinity of 70 and temperature of 20°C was significantly higher than those in other groups ($P <0 .05$), reaching approximately 83.7%. There was no significant difference in body length among the groups maintained at temperatures ranging from 25-30 °C under salinities ranging from 30-90 ($P >0 .05$). However, the body length of Artemia at 20 °C remained significantly lower than those in other groups ($P <0 .05$). There was no sexually mature individual in any salinity group maintained at 20 °C. The proportion of sexual maturity increased with rising salinity under conditions ranging from 25-30 °C. The contents of echinenone, canthaxanthin, and total carotenoid in Artemia declined overall with increasing temperature and salinity, and the temperature effect decreased with rising salinity. Transcriptome analysis revealed that high-temperature exposure significantly up-regulated genes related to "ferroptosis" and "glutathione metabolism" and down-regulated genes associated with "oxidative phosphorylation" and other metabolic processes. Under high salinity conditions, up-regulated genes were significantly enriched in pathways on "ion transport". In the case of low salinity, the main differentially expressed genes were predominantly enriched in pathways on "ribosome" and "lysosome". The results of this study could be helpful for the high-quality culture of Artemia sinica.

Key words:：Artemia sinica, temperature, salinity, growth performance, sexual maturity, carotenoids accumulation

添加嗜粘蛋白阿克曼氏菌可改善斑马鱼肠道免疫和屏障

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摘要：Akkermansia muciniphila (Akk)是一种第二代益生菌，以其调节哺乳动物肠道功能的能力而闻名，但在水产养殖方面尚未完全了解。本研究旨在研究不同形式 Akk 对高脂饮食条件下斑马鱼肠道屏障功能和免疫反应的影响。结果表明，与高脂组相比，Akk 组和 P-Akk 组的绒毛数量和长度均显著增加。claudin 等基因表达水平显著上调，肠道促炎因子基因和蛋白表达水平显著下调。与高脂肪组相比，Akk 组显示更完整和保存完好的细胞核、线粒体和紧密连接结构。中、高浓度 Akk 组小肠上皮微绒毛形态完整、致密。转录组分析显示免疫相关基因 pigr 显著上调，stat3 显著下调，细胞间黏附分子 f11r 显著上调。由此可见，饲粮中添加 Akk 可减轻高脂肪斑马鱼肠道屏障损伤和免疫功能障碍。本研究为 Akk 在鱼类中的潜在应用提供了重要的见解，并为进一步研究其在鱼类免疫中的作用奠定了基础。

关键词：Akkermansia muciniphila；高脂；肠道屏障；免疫

Supplementation with Akkermansia muciniphila improved intestinal barrier and immunity in Zebrafish (Danio rerio)

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Abstract： Akkermansia muciniphila (Akk), a second-generation probiotic known for its ability to regulate intestinal function in mammals, is not yet fully understood in the context of aquaculture. This study aims to investigate the effects of different forms of Akk on intestinal barrier function and immune response in zebrafish (Danio rerio) under high-fat diet conditions. The experimental groups included a control group, a high-fat diet group, an Akk group, and a group receiving various concentrations of pasteurized Akkermansia muciniphila (P-Akk) along with a high-fat diet. Evaluation methods included histological examination with hematoxylin and eosin staining, ultrastructural analysis using transmission electron microscopy, real-time fluorescence quantitative analysis, and transcriptome sequencing technology. The results showed that both the Akk and P-Akk groups exhibited a significant increase in villi number and length compared to the high-fat group. Furthermore the expression levels of claudin, claudin-2, occludin A, occludin B, and other genes were significantly upregulated, while the expression levels of intestinal proinflammatory factors genes and proteins were significantly downregulated. Compared to the high-fat group, the Akk group showed a more complete and well-preserved nucleus, mitochondria, and tight junction structures. Additionally, the morphology of intestinal epithelial microvilli in the medium and high concentration Akk group was complete and dense. The expressions of tlr2 and nf-κb were upregulated, while the expressions of myd88 and nod2 were downregulated in the medium- and high-concentration Akk groups. Akk may improve immune dysfunction in high-fat fed zebrafish through the TLR2/NF-κB signaling pathway, which requires further study. Transcriptome analysis revealed significant upregulation of the immune-related gene pigr, significant downregulation of stat3, and significant upregulation of the intercellular adhesion molecule f11r. In conclusion, dietary Akk supplementation alleviated intestinal barrier damage and immune dysfunction in high-fat zebrafish. This study provides important insights into the potential use of Akk in fish and lays the foundation for further studies on its role in fish immunity.

Key words:： Akkermansia muciniphila, high-fat feed, intestinal barrier, immunity.

在高植物蛋白日粮中添加植酸酶可促进牛蛙生长和营养物质吸收并缓解肠道功能紊乱

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摘要：为了探究高植物蛋白饲粮中添加植酸酶对牛蛙生长性能、消化吸收和肠道健康的影响，本实验配制正常磷(NP)、低磷高植物蛋白(LP0)、在 LP0 饲料中分别添加 750（LP750）、1500（LP1500）、2250（LP2250）和 3000 （LP3000）Fytase Unit (FTU) / kg 植酸酶，共 6 种实验饲料。牛蛙(33.21 ± 0.12 g)分别饲喂 6 种饲料，试验期 56 d。LP2250 和 LP3000 组牛蛙比 LP0 组牛蛙表现出更高的增重率、磷表观消化率、蛋白质效率以及胰蛋白酶活性。与 LP0 组相比，LP2250 和 LP3000 组牛蛙白细胞介素- 1 β和肿瘤坏死因子α基因表达量显著降低，白细胞介素- 10、闭合蛋白和闭合小环蛋白- 1 基因表达量显著升高。综上所述，在高植物蛋白饲粮中添加 2250 ~ 3000 FTU / kg 植酸酶可促进牛蛙生长、营养物质吸收和肠道健康。

关键词：牛蛙；生长；植酸酶；肠道健康

Addition of phytase to a high plant protein diet increases growth and nutrient absorption and alleviates intestinal dysfunction in bullfrogs (Aquarana catesbeianu)

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Abstract： Bullfrogs (33.21 ± 0.12 g) were fed with 6 kinds of feeds for 56 days. Bullfrogs fed LP2250 and LP3000 diets showed higher weight gain rate, phosphorus apparent digestibility, protein efficiency and trypsin activity than bullfrogs fed the LP0 diet. Compared with bullfrogs fed the LP0 diet, the gene expression levels of interleukin-1β and tumor necrosis factor-α in bullfrogs fed LP2250 and LP3000 diets were significantly decreased, and the gene expression levels of interleukin-10, occludin and occludin-1 were significantly increased. In summary, adding 2250 ~ 3000 FTU / kg phytase to a high plant protein diet can promote the growth, nutrient absorption and intestinal health of bullfrogs.

Key words:：Bullfrog ; growth ; phytase ; intestinal health

基于内质网应激和线粒体功能障碍探讨鱼类营养性脂肪肝形成的分子机制

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摘要：内质网（ER）在蛋白质合成和脂类代谢中发挥重要作用。当鱼类摄入高脂饲料时，ER 超负荷诱发内质网应激（ERS）。本研究通过构建黑鲷和黑鲷原代肝细胞的体内（高脂，HFD）和体外（油酸，OA）高脂模型，探讨 ERS 在营养性脂肪肝中的作用。结果显示，HFD/OA 引发了 ERS，导致炎症反应和细胞凋亡，而 ERS 抑制剂 4-PBA 能有效缓解这些脂毒性损伤，表明 ERS 在脂肪肝形成中具有关键作用。研究进一步发现，ERS 中的 Ire1α通路在调控脂肪肝过程中起重要作用，并通过 Sirt1 去乙酰化 Ire1α的 K61 位点，缓解肝脏损伤。同时，Perk 通路也参与了高脂引发的肝脏脂毒性损伤。此外，研究发现 HFD/OA 通过促进 Perk/Alcat1 在线粒体相关内质网膜（MAM）间相互作用，抑制 Pink1/Parkin 通路，导致线粒体功能障碍。综上，ERS 与线粒体功能障碍及 MAM 共同介导鱼类营养性脂肪肝的形成。

关键词：内质网应激，脂毒性损伤，线粒体相关内质网膜，线粒体自噬

The molecular mechanism of nutritional fatty liver formation in fish based on endoplasmic reticulum stress and mitochondrial dysfunction

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Abstract：The endoplasmic reticulum (ER) plays a crucial role in protein synthesis and lipid metabolism. When fish consume high-fat diets, ER overload induces ER stress (ERS). This study investigated the role of ERS in nutritional fatty liver disease by establishing in vivo (high-fat diet, HFD) and in vitro (oleic acid, OA) high-fat models using juvenile black seabream and primary hepatocytes. The results showed that HFD/OA triggered ERS, leading to inflammation and apoptosis, while the ERS inhibitor 4-PBA effectively alleviated these lipotoxic injuries, indicating the critical role of ERS in fatty liver formation. Further research revealed that the Ire1α pathway of ERS plays an important regulatory role in fatty liver development, with Sirt1 deacetylating the K61 site of Ire1α to mitigate liver damage. Additionally, the Perk pathway was found to be involved in high-fat-induced hepatic lipotoxicity. Moreover, HFD/OA promoted interactions between Perk and Alcat1 at the mitochondria-associated membranes (MAM), inhibiting the Pink1/Parkin pathway and causing mitochondrial dysfunction. In conclusion, ERS, mitochondrial dysfunction, and MAM interactions collectively mediate the formation of nutritional fatty liver in fish.

Key words:：Endoplasmic reticulum stress, lipotoxic injury, MAM, Mitophagy

不同脂肪源对大口黑鲈（ Micropterus salmoides ）生长性能、 脂质沉积、 抗氧化能力和炎性反应的影响

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摘要：本研究通过在饲料中添加不同的脂肪源（鱼油 FO，豆油 SO，亚麻油 LO 和椰子油 CO）， 探究其对对大口黑鲈生长性能、脂质沉积、 抗氧化能力和炎症反应的影响。结果表明， FO 组的增重率和特定生长率显著高于 LO 组和 CO 组。SO 组肝脏甘油三酯含量显著高于其他处理组。 转录水平上，SO 组 脂肪合成和分解相关的基因表达量显著高于 FO 组。 LO 和 SO 替代鱼油显著降低了大口黑鲈肝脏 MDA 含量并提高了 CAT 和 T-SOD 活力。然而，植物油替代鱼油会显著提高大口黑鲈肝脏炎性反应和内质网应激相关基因的表达。综上所述，豆油可能作为大口黑鲈饲料脂肪源。

关键词：脂肪源；脂肪沉积；抗氧化能力；炎性反应；大口黑鲈

Dietary lipid sources affect growth performance, lipid deposition, antioxidant capacity and inflammatory response of largemouth bass (Micropterus salmoides)

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Abstract： The present study explored the effects of different lipid sources replacing fish oil on growth performance, lipid deposition, antioxidant capacity, inflammatory response and disease resistance of largemouth bass (Micropterus salmoides). Four isonitrogenous (crude protein 50.46%) and isolipidic (crude lipid 11.12%) diets were formulated to contain 7% of different oil sources including fish oil (FO) (control), soybean oil (SO), linseed oil (LO) and coconut oil (CO). Largemouth bass with initial body weight of 36.0 ± 0.2 g were randomly distributed into 12 tanks, with 30 fish per tank and 3 tanks per treatment. The fish were fed the experiment diets twice daily for 8 weeks. The results indicated that the weight gain of largemouth bass fed the FO diet was significantly higher than that of fish fed the LO and CO diets. The liver crude lipid content in FO group was significantly higher than LO and CO groups, while the highest liver triglyceride content was showed in SO group and the lowest was detected in LO group. At transcriptional level, expression of lipogenesis related genes (pparγ, srebp1, fas, acc, dgat1 and dgat2) in the SO and CO group were significantly higher than the FO group. However, the expression of lipolysis and fatty acids oxidation related genes (pparα, cpt1, and aco) in vegetable oils groups were significantly higher than the FO group. As to the antioxidant capacity, vegetable oils significantly reduced the malondialdehyde content of largemouth bass. Total antioxidant capacity in the SO and LO groups were significantly increased compared with the FO group. Catalase in the LO group was significantly increased compared with the FO group. Furthermore, the ER stress related genes, such as grp78, atf6α, atf6β, chop and xbp1 were significantly enhanced in the vegetable oil groups compared with the FO group. The activity of serum lysozyme in vegetable oil groups were significantly higher than in FO group.

Key words:： Lipid sources; Lipid deposition; Antioxidant capacity; Inflammation response; Largemouth bass

一株仿刺参致病菌 Shewanella sp.B9 的分离筛选

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摘要：本研究以化皮病仿刺参为试验材料，从患病组织分离可培养细菌，通过哥伦比亚血平板从中筛选可产生β-溶血环的菌株，对菌株进行形态学观察、生理生化检测以及分子鉴定，进一步通过注射攻毒回接至健康仿刺参，筛选仿刺参致病菌。结果表明：从化皮病仿刺参的患病组织共分离获得可培养细菌，有 4 株能产生β-溶血环。注射攻毒试验表明这 4 株细菌中仅菌株 B9 对仿刺参有致病性，在细菌浓度为 2.5×104 cell/g、2.5×105 cell/g、2.5×106 cell/g 和 2.5×107 cell/g 的试验中，5 d 死亡率分别为 17%、47%、47%和 100%，而空白对照组 5 d 死亡率为 0%。菌株 B9 对仿刺参的半致死浓度 LC50[T1] 为 6.28×105 cell/g。从菌株 B9 注射攻毒的发病仿刺参患病组织中又分离出菌株 B9，试验结果符合科赫法则。

关键词：仿刺参；致病；组织病理学；细菌；攻毒；Shewanella

Isolation and screening of Shewanella sp. B9，a bacterial strain pathogenic to Apostichopus japonicus

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Abstract： In this study, the disease as test material, isolated from the diseased tissue can culture bacteria, through the Columbia blood plate screening can produce β -hemolytic ring strains, strains of morphological observation, physiological and biochemical detection and molecular identification, further through injection challenge back to health, screening of pathogenic bacteria. The results showed that the diseased tissue of Conghua skin disease obtained the cultured bacteria, and 4 strains could produce β -hemolytic ring. The injection challenge test showed that only strain B9 was pathogenic to the four bacterial strains, with 5 d mortality of 17%, 47%, 47%, 105 cell / g, 2.5106 cell / g, and 2.5107 cell / g, respectively, compared with 0% in 5 d. The semi-lethal concentration of LC50was 6.28105 cell / g. Strain B9 was isolated from the diseased tissue of strain B9 injection, and the test results complied with Koch's rule.

Key words:： Apostichopus japonicus;pathopoiesia;histopathology;bacterium;challenge;Shewanella

肠道原籍益生菌能够提高花鲈对天虫优饲料的利用

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摘要：天虫优(TC)是一种新型饲料原料，由黄粉虫及其生长过程中转化的培养基组成。实验室前期研究发现，花鲈(Lateolabrax maculatus)对饲料中 TC 的利用有限。因此本研究旨在探讨肠道原籍益生菌能否提高花鲈对 TC 的利用。试验分为对照组(TC，饲喂基础饲料)和 5 个处理组，分别饲喂在基础饲料(TC)中添加地衣芽孢杆菌 BL（Bacillus licheniformis）、盐枝芽孢杆菌 VS（Virgibacillus salarius）、克劳斯碱性卤杆菌 AC（Alkalihalobacillus clausii）、泛酸枝芽孢杆菌 VP（Virgibacillus pantothenticus）和沙福芽孢杆菌 BS（Bacillus safensis subsp. safensis）的饲料。结果表明：VS 组和 VP 组花鲈的终末体重、增重率和特定生长率均显著高于 TC 组($P < 0.05$)。与 TC 组相比

关键词：花鲈，天虫优，鱼粉替代，生长性能，肠道健康

Autochthonous potential probiotics improve the Tianchongyou feed utilization in spotted seabass (Lateolabrax maculatus)

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Abstract： Tianchongyou (TC), is a new feed ingredient that contains yellow mealworm and the medium transformed during their growth. Our previous research found that TC utilization of spotted seabass (Lateolabrax maculatus) was limited. This research was conducted to examine whether indigenous intestinal probiotics can improve the utilization of TC in spotted seabass. The experiment includes a control group (TC, fed basal diet) and five treated groups, fed the diets prepared by supplementing the basal diet (TC) with Bacillus licheniformis (BL), Virgibacillus salarius (VS), Alkalihalobacillus clausii (AC), Virgibacillus pantothenticus (VP), and Bacillus safensis subsp. safensis (BS). The results indicated that the final body weight, weight gain, and specific growth rate of spotted seabass in both the VS and VP groups exhibited a significant increase compared to those in the TC group ($P < 0.05$). There were no statistically significant alterations observed in the levels of serum AKP, LZM, and complement 3 among the treated groups when compared to the TC group ($P > 0.05$). Intestinal health of spott

Key words:： Lateolabrax maculatus, Tianchongyou, fish meal replacement, growth, intestinal health

P-AKK 对高糖饲喂大口黑鲈糖代谢紊乱及肝脏和肠道损伤的改善作用

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摘要：鱼类摄入过多糖类会引起糖代谢紊乱、肝脏及肠道损伤。在哺乳动物的研究中发现经巴氏灭活的嗜黏蛋白阿克曼菌(P-AKK)对高糖导致的糖代谢紊乱具有良好的改善作用。本研究以经济鱼类大口黑鲈作为研究对象，探究 P-AKK 对高糖诱导下大口黑鲈的糖代谢紊乱及肝脏和肠道损伤的改善作用。选用 480 尾健康大口黑鲈，分为 4 个组。对照组饲料中添加 9% α淀粉组为 C 组，对照组饲料基础上添加 P-AKK（1×109cfu/g）为 CP 组，高糖组饲料中添加 18%淀粉组为 H 组，高糖饲料基础上添加 P-AKK（1×109cfu/g）为 HP 组。室内循环水养殖 60 天，并于第 1 周、第 2 周、第 4 周、第 6 周和第 8 周分别取样，检测大口黑鲈血糖和血脂水平。对 P-AKK 改善效果最显著的时间点进一步探究 P-AKK 对肝脏损伤和肠道炎症的改善效果。高糖饲料中添加 P-AKK 对大口黑鲈的糖代谢紊乱和肝脏损伤有较好的改善作用，且在饲养第 4 周时效果较好。

关键词：嗜黏蛋白阿克曼菌；大口黑鲈；糖代谢

Ameliorating effect of P-AKK on glucose metabolism disorder and liver and intestinal damage of largemouth bass fed with high glucose

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Abstract： Excessive intake of polysaccharides by fish can cause disorders of glucose metabolism, liver and intestinal damage. In mammalian studies, it has been found that P-AKK, inactivated by Pasteurella, has a good effect on glucose metabolism disorder caused by high glucose. In this study, the economic fish largemouth bass was taken as the research object to explore the effect of P-AKK on the glucose metabolism disorder and liver and intestinal injury of largemouth bass induced by high glucose. A total of 480 healthy largemouth bass were selected and divided into 4 groups. The group supplemented with 9% α starch was group C, the group supplemented with P-AKK (1×109cfu/g) was group CP, the group supplemented with 18% starch was group H, and the group supplemented with P-AKK (1×109cfu/g) was group HP. The blood glucose and blood lipid levels of largemouth bass were measured at week 1, week 2, week 4, week 6 and week 8, respectively. The time point at which the improvement effect of P-AKK was most significant was further explored to explore the improvement effect of P-AKK on liver injury and intestinal inflammation. The addition of P-AKK in high glycemic diet can improve the glucose metabolism disorder and liver injury of largbass, and the effect is better at the 4th week of feeding.

Key words:：Akkermansia muciniphila；Micropterus salmoides；glycometabolism

不同生物饵料组合对中华绒螯蟹幼体生长发育的影响

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摘要：为了探究不同生物饵料组合对中华绒螯蟹蚤状幼体生长发育的影响，本试验以中华绒螯蟹蚤状幼体Ⅴ期幼体为研究对象，随机将蚤状幼体分为三个组别，即纯轮虫饵料组、纯丰年虫饵料组和轮虫+丰年虫饵料组，测定了幼体免疫、抗氧化、消化酶指标以及体内微生物群落变化情况。试验结果表明：在生化方面，混合饵料组 TP 含量显著高于其他两组；免疫指标混合饵料组属于较低水平，轮虫组最高；在抗氧化指标上丰年虫组与轮虫组相对偏高，混合饵料组相对较低一些；混合饵料组的消化酶指标指标均处于较低水平。在微生物方面，试验发现有 4 个细菌门共同组成了中华绒螯蟹幼体肠道菌群的主要结构，分别是：厚壁菌门，变形菌门，拟杆菌门和放线菌门，其中轮虫组的变形菌门丰度显著高于其他两组。在数水平上志贺氏菌属、普雷沃氏菌属、弧菌属、活泼瘤胃球菌组、丛毛单胞菌属和梭杆菌属三组有显著差异。

关键词：中华绒螯蟹；蚤状幼体；轮虫；丰年虫；微生物

Effects of different food combinations on the growth and development of Eriocheir sinensis larva

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Abstract： In order to investigate the effects of different food combinations on the growth and development of Eriocheir sinensis larva, the larvae of Eriocheir sinensis flea stage V were divided into pure rotifer feed group, pure harvest worm feed group and rotifer + harvest worm feed group. In terms of biochemistry, TP content in the mixed diet group was significantly higher than that in the other two groups. The level of immune indexes was lower in the mixed diet group and the highest in the rotifer group. The antioxidant indexes of the two groups were higher than those of the two groups, but lower in the mixed diet group. The digestive enzyme indexes in the mixed diet group were at a lower level. In terms of microorganisms, four bacterial phyla were found to constitute the main structure of the intestinal flora in the larva of Eriocheir sinensis, namely Firmicutes, Proteobacteria, Bacteroidetes and actinobacteria. The abundance of Proteobacteria in the rotifer group was significantly higher than that in the other two groups.

Key words:：Eriocheir sinensis; Flea-like larva; Rotifer; The harvest worm; microorganism

一株刺参(Apostichopus japonicas)肠道有益细菌 Bacillus flexus 的分离筛选及应用研究

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摘要：为筛选对刺参生长有益的细菌，本研究从健康刺参肠道分离可培养细菌，通过点种法分别接种至选择性培养基，从中筛选出产蛋白酶、产脂肪酶、产淀粉酶的菌株，进一步检测其对抗菌药物的敏感性及对酸和胆盐的耐受性，基于产酶菌株细胞形态及 16S rDNA 序列对其进行鉴定，通过安全性试验和养殖试验检测其对幼参的益生效果。结果表明：从健康刺参肠道筛选出两株可以产多种酶的细菌，编号分别为 AC20、AC27，均不产生β-溶血环；AC20 对多种抗菌药物有抗性，而 AC27 对多种抗菌药物表现为高度敏感；在 pH 为 3.0、胆盐质量浓度为 0.7%的环境条件下，AC27 仍可生长。选择 AC27 作为刺参潜在益生菌菌株，基于形态学观察和 16S rDNA 序列分析鉴定其可能为弯曲芽孢杆菌；注射攻毒试验显示菌株 AC27 对刺参无致病性，养殖试验表明菌株 AC27 可提高刺参增重率及特定生长率，降低体降低体重变异系数研究结果丰富了刺参肠道有益细菌研究。

关键词：刺参；潜在益生菌；蛋白酶；脂肪酶；淀粉酶；芽孢杆菌

Bacillus flexus isolated from the intestine of Apostichopus japonicas: Identification of a potential probiotic for Apostichopus japonicas culture

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Abstract：To screen for bacteria beneficial to sea cucumber growth, culturable bacteria were isolated from the gut of healthy sea cucumbers and inoculated onto selective media by spot seeding. Bacterial strains producing lipase, amylase and protease were then screened and tested for antimicrobial susceptibility and acid/bile tolerance, and the probiotic effects of the enzyme-producing strains were demonstrated in juvenile sea cucumbers using their cell morphology and 16S rDNA sequences. Two bacterial strains, designated AC20 and AC27, were isolated from the gut of healthy cucumbers and tested; neither strain was able to form the β-hemolytic ring; while AC20 showed broad resistance to antimicrobials, AC27 showed significant susceptibility to a variety of antimicrobials and maintained growth at pH 3. AC27 was selected as a potential probiotic for sea cucumbers and identified as Bacillus flexus. Tests showed that AC27 was not harmful to sea cucumbers and could help it grow. This study added to our knowledge of beneficial bacteria in sea cucumbers intestines.

Key words:：Apostichopus japonicus; potential probiotic; protease; lipase; amylase; Bacillus

发酵饲料对刺参生长性能、消化及非特异性免疫能力的影响

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摘要：为研究碳源对刺参(Apostichopus japonicus)配合饲料发酵效果的影响以及发酵饲料对刺参生长、消化以及非特异性免疫能力的影响，在发酵过程中添加 2%的葡萄糖、蔗糖、麦芽糖、可溶性淀粉和低聚果糖为碳源，选择最优发酵效果的配合饲料以不同的比例替代基础饲料，配制成发酵饲料含量分别为 0(D1)、5%(D2)、10%(D3)、20%(D4)、30%(D5)和 40%(D6)的 6 组实验饲料，饲喂初始体质量为(27.03± 0.12)g 的刺参 8 周。结果显示，在刺参配合饲料发酵过程中添加低聚果糖作为碳源发酵效果最佳，可溶性淀粉发酵效果最差；以增重率为评价指标，经一元二次回归分析得出，体质量 27.03 g 的刺参饲料中发酵饲料的最适替代比例为 24.69%。

关键词： 刺参；发酵饲料；生长；消化；非特异性免疫

Effects of fermented feed on growth performance, digestion and non-specific immunity of sea cucumber (Apostichopus japonicus)

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Abstract： In order to study the effects of fermented feed on the growth, digestion and non-specific immunity ofA. japonicus, fermented feed with different proportions was used to replace the basic diet, and six groups of experimental diets with fermented feed contents of 0 (D1), 5% (D2), 10% (D3), 20% (D4), 30% (D5) and 40% (D6) were prepared.A. japonicus with an initial body weight of (27.03 ± 0.12) g was feed for 8 weeks.The results showed that: the appropriate substitution ratio of fermented feed in the feed could improve the growth performance of A. japonicus, promote the secretion of digestive enzymes, and enhance the non-specific immunity of A. japonicus. Taking the weight gain rate as the evaluation index, analysis by a linear regression equation showed that the optimal substitution ratio of fermented feed for A. japonicus(initial body weight 27.03 g) was 24.69%.

Key words:： Apostichopus japonicus; fermented feed; growth; digestion; non-specific immunity

美洲大蠊粉替代鱼粉对大口黑鲈生长、代谢、肠道健康及对嗜水气单胞菌抵抗力的影响

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摘要：为探究美洲大蠊粉部分替代鱼粉对大口黑鲈生长性能、体成分、血清生化指标、肠道健康和对嗜水气单胞菌抵抗力的影响，开展为期 8 周的养殖实验。选取初始体重为(14.55±0.09)g 的健康大口黑鲈 450 尾，随机分为 5 组。分别用美洲大蠊粉替代基础饲粮中 0% (P0)、15% (P15)、30% (P30)、45% (P45)和 60% (P60)的鱼粉配制 5 种实验饲料。结果表明，P15 组和 P30 组的终末体重、增重率和特定生长率与对照组相比无显著差异。各美洲大蠊粉组全鱼粗蛋白均显著升高，粗脂肪均显著降低。P30 组抗氧化酶活性显著高于对照组和其他实验组，丙二醛显著降低。注射嗜水气单胞菌后，各组大口黑鲈均出现死亡，但 P30 组的累积死亡率最低。综上所述，美洲大蠊粉可以部分替代大口黑鲈日粮中的鱼粉，替代水平不超过 30%不会对其生长性能产生不利影响，且可提高鱼体粗蛋白，有利于肠道健康。

关键词：美洲大蠊粉，大口黑鲈，生长性能，体成分，肠道健康

Effects of dietary fish meal replacement by Periplaneta americana meal on growth, metabolism, intestinal health and resistance against Aeromonas hydrophila of Micropterus salmoides

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Abstract： Strong El Niño has serious consequences for environmental conditions in Peru, reducing production of high-quality fishmeal （FM) and fish oil. This study aimed to explore the effects of different levels of Periplaneta americana meal (PAM) (0%, 15%, 30%, 45% and 60%, as a substitute for FM) on the growth performance and intestinal health of largemouth bass (14.55±0.09) g. The results showed that final body weight (FBW), weight gain rate (WGR), and specific growth rate (SGR) were no significant difference in P15 and P30 compared with the control group ($P > 0.05$). Replacing FM with 15% and 30% PAM can increase the activity of intestinal digestive enzymes without affecting intestinal villus height and crypt depth, which is beneficial to intestinal health. In addition, replacing FM with 30% PAM can increase liver antioxidant enzyme (SOD, CAT, and GPx) activity and reduce malondialdehyde content. In summary, replacing FM with 30% PAM benefits the growth and intestinal health of largemouth bass.

Key words:： Periplaneta americana meal, Largemouth bass, Growth performance, Body composition, Intestinal health

低磷通过 Drp1 介导的线粒体分裂诱导花鲈肝脏脂肪沉积

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摘要：本研究旨在探究花鲈长期投喂低磷饲料诱导肝脏脂肪沉积的具体机制。在活体实验中，花鲈分别投喂磷水平为 0.36%（低磷组，S-LP）和 0.72%（正常磷组，S-AP）的饲料，养殖周期为 10 周。结果显示：S-LP 组花鲈的肝脏脂肪含量显著高于 S-AP 组。电镜结果显示，S-LP 组花鲈的肝脏线粒体多呈现为短小的形态。并且，相较于 S-AP 组花鲈，S-LP 组的肝脏线粒体分裂相关蛋白（Drp1）蛋白表达升高，伴随着肝脏 ATP 含量降低。在细胞实验中，将花鲈肝脏细胞分别在适宜磷培养基（磷水平 35 mg/L，AP），低磷培养基（磷水平 7.7 mg/L，LP）和抑制剂培养基（LP+50 μM Mdivi-1，DRP1 抑制剂，LPM）中孵育 72 小时。结果显示，AP 和 LPM 组细胞的甘油三酯含量显著低于 LP 组；同时，AP 和 LPM 组细胞的 ATP 含量升高。综上，本试验发现低磷通过 Drp1 介导的线粒体分裂诱导肝脏脂肪沉积。

关键词：磷；花鲈；脂肪沉积；线粒体

Low phosphorus induces hepatic fat deposition through Drp1-mediated mitochondrial fission in spotted seabass (Lateolabrax maculatus)

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Abstract：This study was to investigate the mechanism underlying hepatic fat deposition induced by fish fed low phosphorus diets. In vivo, spotted seabass (Lateolabrax maculatus) (initial weight: 7.54 ± 0.07 g) were fed low phosphorus diets (phosphorus levels: 0.36%, S-LP) and appropriate phosphorus diets (phosphorus levels: 0.72%, S-AP) for 10 weeks. The results indicated that hepatic fat content was higher in the S-LP group than that in the S-AP group. TEM revealed that hepatic mitochondria in the S-LP group were predominantly shorter in length compared to those in the S-AP group. Furthermore, Elevated Drp1 protein expression and reduced hepatic ATP content were also observed in the S-LP group, indicating that Drp1-mediated mitochondrial fission is key in LP-induced hepatic fat deposition. In vitro, hepatocytes were cultured in three different media: AP medium (phosphorus level of 35 mg/L), LP medium (phosphorus level of 7.7 mg/L), and LPM medium (LP medium + 50 μM Mdivi-1, a DRP1 inhibitor) for 72 hours. Triglyceride levels were lower and ATP levels higher in the AP and LPM-treated hepatocytes compared to the LP-treated hepatocytes. Together, these findings demonstrate that LP induces hepatic fat deposition via Drp1-mediated mitochondrial fission.

Key words:：Phosphorus; Lateolabrax maculatus; Fat deposition; Mitochondrial fission

EGCG 和 EC 通过 AMPK/Sirt1/PGC-1α信号通路增强黄河鲤脂质分解代谢和抗氧化能力

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摘要： (-)-表没食子儿茶素-3-O-没食子酸酯（EGCG）和 (-)-表儿茶素（EC）可调节黄河鲤抗氧化和脂质代谢，但其在高脂饲喂下作用机制尚不明确。本研究选取 360 尾黄河鲤幼鱼（9.75 ± 0.09 g）进行为期 84 天养殖实验，分为四组：对照组（CN，6.15%脂含量）、高脂组（HF，14.05%脂含量）、HF 添加 EGCG 组（HF + EGCG，14.05% 脂含量 + 50 mg/kg EGCG）和 HF 添加 EC 组（HF + EC，14.05% 脂含量 + 1000 mg/kg EC）。结果表明， EGCG 和 EC 能缓解由高脂饲喂引起的生肉剪切力和硬度下降以及肌肉脂肪和 ROS 过度积累。此外，EC 或 EGCG 可上调肌肉 AMPK 磷酸化水平、sirt1 和 PGC-1α表达水平。综上所述，EGCG 或 EC 可通过 AMPK/Sirt1/PGC-1α途径调节黄河鲤肌肉抗氧化和脂质代谢能力。

关键词：EGCG,EC，高脂饲料，AMPK/Sirt1/PGC-1α, 脂质代谢，黄河鲤

(-)-Epigallocatechin-3-O-gallate or (-)-epicatechin enhances lipid catabolism and antioxidant defense in Yellow River carp (Cyprinus carpio) fed a high-fat diet: Mechanistic insights from the AMPK/Sirt1/PGC-1α signaling pathway

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Abstract： (-)-Epigallocatechin-3-O-gallate (EGCG) and (-)-epicatechin (EC), have been found to regulate antioxidant ability and lipid metabolism. Furthermore, the underlying mechanisms remain unknown. In this study, a total of 360 carp (average weight: 9.75 ± 0.09 g) were provided with four experimental diets: a control diet (CN, 6.15% dietary lipids), a high-fat diet (HF, 14.05% dietary lipids), HF supplemented with EGCG (HF + EGCG, 14.05% dietary lipids + 50 mg/kg EGCG), and a HF diet supplemented with EC (HF + EC, 14.05% dietary lipids + 1000 mg/kg EC) for a duration of 84 days. The results indicated that EGCG or EC alleviate the decrease in shear force and hardness of raw meat and the excessive accumulation of muscle lipids and ROS caused by the HF diet. Further study showed that EGCG or EC facilitated the phosphorylation of AMPK and increased Sirt1 and PGC-1α expression in muscle. Taken together, the results of this study revealed that EGCG or EC enhance lipid metabolism and antioxidant capacity in the muscle of Yellow River carp (Cyprinus carpio) via the AMPK/Sirt1/PGC-1α pathway.

Key words:：(-)-Epigallocatechin-3-O-gallate; (-)-epicatechin; high-fat diet; AMPK/Sirt1/PGC-1α; lipid metabolism; Yellow River carp

黑水虻酶解物对四氯化碳致鲤急性肝损伤的保护作用

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摘要：为了探究黑水虻酶解物（ZBSF）对四氯化碳致鲤急性肝损伤的保护作用，本试验设置空白对照组（NC）、模型对照组（MC）、低剂量组（ZL，200 mg/kg ZBSF）、中剂量组（ZM，400 mg/kg ZBSF）、高剂量组（ZH，800 mg/kg ZBSF）和阳性对照组（PC，100 mg/kg 联苯双酯）6 个处理组，对鲤进行 7 天的灌喂及注射。结果表明，ZBSF 处理组的肝胰脏结构得到改善；与 MC 组相比，ZH 组血清 ALT 和 AST 活性显著降低，ZM 组的血清 AST 活性显著降低；ZH 组血清、肝胰脏、脾脏和头肾的 SOD、CAT 活性和 T-AOC 与 MC 组相比均显著升高；ZH 组脾脏和肾脏抗氧化基因表达量与 MC 组相比显著上调；与 MC 组相比，灌喂 ZBSF 组肝胰脏、脾脏及肾脏的促炎基因发生显著下调，ZH 组脾脏基因表达量显著上升。因此，ZBSF 可通过提高抗氧化能力和调节炎症反应缓解 CCl4 引起的鲤急性肝损伤。

关键词：黑水虻酶解物；鲤；抗氧化；免疫

ZBSF's protective effect on carbon tetrachloride (CCl4)-induced acute hepatopancreas injury in Carp

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Abstract：In order to investigate the protective effect of zymolytic black soldier fly (ZBSF) against carbon tetrachloride-induced acute hepatopancreas injury in carp, this experiment induced a blank control group (NC), a model control group (MC), a ZBSF low-dose group (ZL, 200 mg/kg), a ZBSF medium-dose group (ZM, 400 mg/kg), a ZBSF high-dose group (ZH, 800 mg/kg), and a biphenyl diester positive control group (PC, 100 mg/kg), all groups were infused and injected into the carp for seven days. The results show that: The hepatopancreatic structure of the ZBSF-treated group was improved; The serum alanine aminotransferase (ALT) activity and the aspartate aminotransferase (AST) activity in the ZH group was significantly decreased compared to the MC group , with a notable reduction in AST activity also observed in the ZM group ; The superoxide dismutase (SOD) activity, catalase (CAT) activity and total antioxidant capacity (T-AOC) in the serum, hepatopancreas, spleen, and head kidney were significantly increased in the ZH group compared to the MC group ; The antioxidant gene expressions in the spleen and kidney of the ZH group was significantly up-regulated compared with the MC group ; Compared to the MC group, the expressions of hepatopancreas, spleen and kidneys in the ZBSF groups were significantly down-regulated., while expression of spleenwas significantly increased in the ZH group. Therefore, ZBSF effectively alleviated CCl4-induced acute hepatopancreas injury by enhancing antioxidant capacity and modulating the inflammatory response.

Key words:：Zymolytic black soldier fly; Common carp; Antioxidation; Immunity

投喂南极磷虾对红螯螯虾幼虾生长性能、体成分、生理生化指标、免疫机能及肠道菌群结构的影响

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摘要：为研究投喂南极磷虾冰鲜肉对红螯螯虾生长性能等各方面的影响，实验设置了四种投喂组合，分别为：AKC（饲喂基础饲料，作为对照组）、AK1（每天饲喂南极磷虾）、AK2（1d 基础饲料+1d 南极磷虾）、AK3（2d 基础饲料+1d 南极磷虾鲜肉）。饲喂 10 周后，与对照组相比， AK2 组和 AK3 组的增重率和特定生长率显著提高（$p<0.05$），且 AK2 组的成活率最高。肌肉的脂肪酸分析发现 EPA 和 DHA 量与南极磷虾投喂量呈显著正相关，而与氨基酸组成无显著变化。在肌肉与虾壳的虾青素分析中发现 AK2 组虾青素含量最高。此外，投喂南极磷虾显著提高了肝胰腺中胰蛋白酶、脂肪酶活（$p<0.05$），而抗氧化和免疫相关酶活无显著影响。基因检测结果证实，饲喂南极磷虾显著上调了与蜕皮和免疫等相关基因表达水平。肠道菌落分析发现，饲喂南极磷虾增加了肠道菌群丰度，提升了其营养代谢功能。

关键词：南极磷虾；红螯螯虾；生长性能；肠道菌群；脂肪酸营养；

Effects of dietary supplementation of Antarctic Krill(Euphausia superba) on growth performance, body composition, physiological and biochemical indexes, immune function and Intestinal microbiota of Redclaw Crayfish(Cherax quadricarinatus.)

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Abstract： This study comprehensively examined the effects of feeding raw frozen Antarctic krill (Euphausia superba) on performance and other aspects of Redclaw Crayfish(Cherax quadricarinatus). Four feeding combinations were established for the experiment: AKC (fed basal diet, control group), AK1 (fed Antarctic krill daily), AK2 (1-day basal diet, 1-day Antarctic krill), and AK3 (2-day basal diet, 1-day Antarctic krill). After feeding for 10 weeks, compared with the control group, the weight gain rate and specific growth rate of AK2 and AK3 groups were significantly increased ($p < 0.05$), and the survival rate of AK2 group was the highest. The fatty acid analysis of muscle showed that EPA and DHA were positively correlated with krill feeding, but not with amino acid composition. The AK2 group had the highest astaxanthin content in muscle and shell. In addition, the activities of trypsin and lipase in hepatopancreas were significantly increased by feeding Antarctic krill ($p < 0.05$), but the activities of antioxidant and immune-related enzymes were not significantly affected. Gene expression analysis confirmed that feeding Antarctic krill significantly upregulated the expression levels of genes related to molting and immunity. Intestinal microbiota analysis demonstrated that feeding krill increased the abundance of intestinal microbiota, enhancing the nutritional metabolism function.

Key words:： Euphausia superba,Cherax quadricarinatus, Growth performance, Intestinal microbiota, fatty acid nutrition

山茱萸提取物改善氨氮胁迫诱导的鲤肝胰脏损伤和脂代谢

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摘要：本研究通过在鲤的基础饲料中添加山茱萸提取物（COE），分析 COE 在水体氨氮（Am，5 mg / L）胁迫下对鲤肝胰脏损伤和脂代谢的改善作用。结果表明，与 Am 组相比，COE 组鲤的生长性能显著提高且肝胰脏粗脂肪含量下降($P < 0.05$)；HE 染色结果显示，COE 组缓解了肝细胞的核偏移；与 Am 组相比，COE 组的血清、肝胰脏、肾脏和鳃组织的抗氧化酶活性均显著提高($P < 0.05$)；脂分解和转运以及抗氧化基因表达量也显著升高但促炎相关基因表达降低 ($P < 0.05$)。转录组学数据显示，添加 COE 组肝胰脏的差异基因主要富集在胆固醇代谢、PPAR 信号、脂质代谢、氧化应激和炎症等通路。综上，鲤饲料中添加 0.5 % COE 可改善氨氮胁迫下的生长性能、肝胰脏抗氧化能力，抑制炎症反应，并改善脂质代谢紊乱。

关键词：山茱萸提取物；肝胰脏损伤；抗氧化；脂质代谢；鲤

Dietary supplementary of Cornus officinalis extract alleviated hepatopancreas injury and lipid metabolism induced by ammonia nitrogen stress in common carp (Cyprinus carpio)

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Abstract： Cornus officinalis extract (COE) was added to the basic diet in common carp (Cyprinus carpio) to evaluate its effects on hepatopancreas injury and lipid metabolism under water ammonia nitrogen (Ammonia-N, 5 mg / L) stress. The results demonstrated showed that compared to the Am group, the growth performance of common carp in the COE group was significantly enhanced and the crude fat content of the hepatopancreas was reduced ($P < 0.05$), Histological analysis using HE staining showed that the COE group alleviated the nuclear deviation of hepatocytes; the activities of antioxidant enzymes in serum, hepatopancreas, kidney and gill were significantly increased ($P < 0.05$). The expression levels of genes associated with lipolysis, lipid transport and antioxidant genes were also significantly increased, while the expression of pro-inflammatory genes decreased ($P < 0.05$). The transcriptome data of hepatopancreas indicated that compared with Am group, the differential genes in COE group were mainly enriched in pathways related to cholesterol metabolism, endoplasmic reticulum, PPAR signaling, lipid metabolism, oxidative stress and inflammation. In summary, the addition of 0.5 % COE to diet of the common carp can improve the growth performance, antioxidant capacity of hepatopancreas, inhibit the inflammatory response, and ameliorate lipid metabolism disorders induced by chronic Ammonia-N stress.

Key words:： Cornus officinalis extract; hepatopancreas injury; antioxidation; Cyprinus carpio

斜带石斑鱼干扰素 IFNh 和 IFN 受体 CRFB3 CRFB4 对 NNV 复制的调节作用初探

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摘要：神经坏死病毒引起的病毒性神经坏死病给斜带石斑鱼(Epinephelus coioides)养殖产业造成了严重的经济损失。鱼类先天性免疫信号通路介导干扰素的产生，后者识别结合干扰素受体，诱导多种干扰素刺激基因，建立抗病毒状态。为了阐释斜带石斑鱼 IFN 和 IFNRs 对先天免疫信号的调控作用，我们从斜带石斑鱼脑细胞中克隆了 EcIFNh 和两个细胞因子受体家族 B(CRFB)成员。NNV 感染后，EcIFNh、EcCRFB3 和 EcCRFB4 mRNA 水平显著上调。EcIFNh 的启动子被 EcMDA5、EcMAVS、EcSTING、EcIRF3 和 EcIRF7 激活。EcIFNh 通过诱导 ISGs 的表达增强免疫应答并抑制 NNV 复制，而 EcCRFB3 和 EcCRFB4 通过抑制 ISGs 表达促进 NNV 复制。我们的发现揭示了 EcIFNh 作为新型免疫激活剂在抗 NNV 感染中的潜在应用价值，丰富了对 IFNRs 功能的认识。

关键词：斜带石斑鱼、神经坏死病毒、干扰素、干扰素受体

Preliminary Investigation on the Regulatory Effects of Interferon IFNh and IFN Receptor CRFB3 and CRFB4 on NNV Replication in Orange-spotted Grouper

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Abstract：Orange-spotted grouper (Epinephelus coioides) is an economically important aquaculture species which has faced serious economic losses due to the viral pathogen, NNV. On microbial invasion, PRRs detect the PAMPs, initiate a cascade of signaling events, and lead to IFN production. IFN-Is recognize and bind IFNR, inducing ISGs production to establish an antiviral state. To reveal the role of IFN and IFNRs in orange-spotted grouper, EcIFNh and two members of CRFB were cloned from GB cells. The mRNA levels of EcIFNh, EcCRFB3 and EcCRFB4 were upregulated after NNV infection. The promoter of EcIFNh was significantly activated by EcMDA5, EcMAVS, EcSTING, EcIRF3, and EcIRF7. Both intracellular overexpression and administration of recombinant protein of EcIFNh effectively inhibited NNV replication and enhanced the expression of ISGs. On the other hand, EcCRFB3 or EcCRFB4 exhibited contrasting effects. When overexpressed, they inhibited ISGs expression and facilitated NNV replication. Our findings suggest the potential application of EcIFNh as a novel immune activator, enrich the understanding of IFNRs functions, and will enhance our knowledge of the fish IFN system.

Key words:：Epinephelus coioides, IFNh, NNV, CRFB

神经坏死病毒蛋白 CP 和 ProA 动态调节鱼类 cGAS 介导的 IFN 信号通路以促进病毒免疫逃逸

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摘要：神经坏死病毒（NNV）是一种水生 RNA 病毒，能导致大量养殖幼鱼和子稚鱼的死亡，造成巨大的经济损失。cGAS 被广泛认为是 DNA 传感器，在抗 DNA 病毒中发挥关键作用, 但其在对抗水生 RNA 病毒中的作用尚不清楚。本研究发现，过表达斜带石斑鱼 cGAS（EccGAS）能抑制 NNV 复制，而 EccGAS 的沉默则促进 NNV 复制。EccGAS 通过激活 IFN 信号通路，包括 TBK1 磷酸化、IRF3 核转位及诱导 IFNc 和 ISGs 的表达，发挥抗 NNV 作用。有趣的是，NNV CP 和 ProA 与 EccGAS 相互作用，通过泛素-蛋白酶体途径调节其蛋白水平，从而动态调节 EccGAS 介导的 IFN 信号通路，促进病毒逃避。值得注意的是，NNV CP 通过泛素连接酶 EcUBE3C 促进了 EccGAS 的泛素化。这些发现揭示了水生 RNA 病毒逃避 cGAS 介导的先天免疫的一种新策略，加深了我们对病毒-宿主相互作用的了解。

关键词：神经坏死病毒，cGAS，CP，ProA，UBE3C，先天性免疫

Nervous necrosis virus capsid protein and Protein A dynamically modulate the fish cGAS-mediated IFN signal pathway to facilitate viral evasion

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Abstract：Nervous necrosis virus (NNV), an aquatic RNA virus, infects a variety of fishes, leading to massive mortality of cultured larvae and juveniles and substantial economic losses. The enzyme cyclic guanosine monophosphate-adenosine monophosphate synthase (cGAS) is well-known as a DNA sensor pivotal in antiviral responses against DNA viruses. However, little is known about the reaction of cGAS to aquatic RNA viruses. This study found that Epinephelus coioides cGAS (EccGAS) overexpression inhibited NNV replication, whereas EccGAS silencing promoted NNV replication. The anti-NNV activity of EccGAS was involved in interferon (IFN) signaling activation including TBK1 phosphorylation, IRF3 nuclear translocation, and the subsequent induction of IFNc and ISGs. Interestingly, NNV CP and ProA interact with EccGAS to modulate their protein levels through the ubiquitin-proteasome pathway, dynamically influencing the EccGAS-mediated IFN signaling pathway and enhancing viral evasion. Specifically, NNV CP enhances EccGAS ubiquitination via the ubiquitin ligase EcUBE3C. These findings uncover a new evasion strategy used by aquatic RNA viruses against cGAS-mediated innate immunity, advancing our understanding of virus-host interactions.

Key words:：nervous necrosis virus, cGAS, CP, ProA, UBE3C, innate immune response

大黄鱼 SOCS3 通过作用于转录因子 STAT1 负调控抗病毒免疫应答

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摘要：细胞因子信号传导抑制因子(SOCS)蛋白是 JAK-STAT 通路的重要调控因子。然而，关于 SOCS3 在调节鱼类 I 型干扰素(IFN)信号传导中的作用仍知之甚少。大黄鱼 SOCS3 具有 1 个 SH2 结构域、1 个 SOCS box、1 个 KIR 和 1 个扩展的 SH2 结构域。大黄鱼 SOCS3 mRNA 在所有器官或组织中均有表达，且在 poly(I:C)刺激后，其在头肾和脾组织以及原代头肾白细胞中的表达均显著升高。过表达大黄鱼 SOCS3 显著下调 EPC 细胞中 IFN 通路基因 IFN1、IRF7、ISG15、Viperin、PKR 和 Mx 的表达水平，促进鲤春病毒（SVCV）的复制；而沉默大黄鱼 SOCS3 相应上调了大黄鱼头肾细胞系中 IFNi、IFNh、PKR、Viperin 和 Mx 的表达水平。此外，证实 SOCS3 与 STAT1 相互作用可抑制 STAT1 蛋白磷酸化水平及转移到细胞核内的水平，从而负调控 I 型 IFN 信号传导，促进病毒复制。

关键词：抗病免疫，干扰素信号，大黄鱼，SOCS3，STAT1

SOCS3 acts as a potential negative regulator in the antiviral response of large yellow croaker (Larimichthys crocea) by interacting with STAT1

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Abstract： Suppressors of cytokine signaling (SOCS) proteins are important regulators of the Janus kinase-signal transducer and activator of transcription (JAK-STAT) pathway. Within the SOCS family, SOCS3 is one of the most potent inhibitors of cytokine signaling. However, there is limited knowledge regarding the function of SOCS3 on regulating type I interferon (IFN) signaling in fish. In this study, the complete open reading frame (ORF) of SOCS3 from the large yellow croaker (Larimichthys crocea, LcSOCS3) was cloned and characterized. The ORF of LcSOCS3 was 618 nucleotides in length and encoded a protein containing 205 amino acids. LcSOCS3 had the typical domain architecture of the SOCS family, including an SRC homology 2 (SH2) domain, a SOCS box, an additional kinase inhibition region (KIR), and an extended SH2 subdomain (ESS). Phylogenetic analysis revealed that LcSOCS3 was clustered with other fish SOCS3s and most closely related to the SOCS3 of Collichthy lucidus. LcSOCS3 mRNA was detected in all organs or tissues examined, and its expression was significantly increased in both head kidney and spleen tissues, and primary head kidney leukocytes after poly(I:C) stimulation. Overexpression of LcSOCS3 significantly promoted Spring viremia of carp virus (SVCV) replication, resulting in a more severe cytopathic effect, increased viral titer, enhanced copy number of the SVCV-G gene, and decreased expression levels of IFN1, IRF7, ISG15, Viperin, PKR, and Mx in epithelioma papulosum cyprinid (EPC) cells. Silencing of LcSOCS3 correspondingly up-regulated the expression of IFNi, IFNh, PKR, Viperin, and Mx in large yellow croaker head kidney (LYCK) cells. Additionally, LcSOCS3 was shown to interact with Signal Transducer and Activator of Transcription 1 (STAT1) which may inhibit STAT1 translocating into the nucleus. This speculation was supported by the increased phosphorylation level of STAT1 in head kidney leukocytes after LcSOCS3 silencing. These results indicated that LcSOCS3 functioned as a potential negative regulator of type I IFN signaling in large yellow croaker through its interaction with STAT1.

Key words:： Antiviral response, Interferon signaling, Large yellow croaker, SOCS3, STAT1.

乌鳢白细胞衍生趋化因子 LE CT2 互作蛋白的筛选与鉴定

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摘要：为了解乌鳢(Channa argus)白细胞衍生趋化因子 2 (CaLECT2)在抗菌免疫过程中所调控的配体蛋白，克隆获得 CaLECT2 基因，并对其表达特征进行了分析。利用体内注射试验分析了 CaLECT2 对乌鳢机体的免疫增强作用。利用 His-pull down 联合质谱、Co-IP 分析了 CaLECT2 的互作蛋白。结果显示，在感染鰤诺卡氏菌的乌鳢脾脏、肾脏和肝脏中，CaLECT2 mRNA 的表达量显著上调。利用原核表达系统表达纯化获得了 CaLECT2 重组蛋白。通过 Western Blot 证明 rCaLECT2 抗血清可以特异性识别 CaLECT2 重组蛋白。向乌鳢体内注射 CaLECT2 蛋白可以显著提高脾脏内巨噬细胞数量。Pull down 联合质谱鉴定得到 Fetuin-like protein、Serotransferrin 和 CD209 等 253 个潜在的互作蛋白。

关键词：白细胞衍生趋化因子 2；His-pull down；质谱；互作蛋白；乌鳢

SCREENING AND IDENTIFICATION OF INTERACTING PROTEINS OF LECT2 IN CHANNA ARGUS

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Abstract：Leukocyte-derived chemotaxin-2 (LECT2) is a multifunctional immunoregulator that plays a key role in immune regulation, cell growth, differentiation, self-damage repair, and tumorigenesis. We investigated the ligand protein regulated by snakehead LECT2 (CaLECT2) in the antibacterial immunity process. The sequence of the CDs region of the CaLECT2 gene was obtained through homology search and gene cloning technology. The immune-enhancing effect of CaLECT2 on snakehead was assessed through in vivo injection tests. Interacting proteins of CaLECT2 were analyzed using His-Pull down combined with mass spectrometry and Co-IP. The mRNA expression of CaLECT2 significantly increased in the spleen, kidney, and liver of snakehead fish after infection with Nocardia seriolae. The CaLECT2 recombinant protein was effectively expressed and purified using the pET-32a prokaryotic expression system. Western Blot analysis confirmed that the anti-rCaLECT2 polyclonal antibody specifically identified the recombinant CaLECT2 protein. Injection of the rCaLECT2 protein into snakehead fish significantly increased the number of macrophages in the spleen. Pull down assays combined with mass spectrometry identified 253 potential interacting proteins, including Fetuin-like protein, Serotransferrin, and CD209. Co-IP verification confirmed an interaction between CaLECT2 and CD209. This study lays the groundwork for further exploration into the roles of ligand proteins regulated by CaLECT2.

Key words:：LECT2; His-pull down; Mass spectrometry; Interacting protein; Channa argus

转录组比较分析揭示美国红鱼感染哈维氏弧菌后机体内基因以及免疫信号通路的潜在调控机制

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摘要：美国红鱼作为一种重要的海洋经济鱼类，近年来其产业发展受到各种细菌性病害的影响。哈维弧菌会在美国红鱼中引起致命的弧菌病，导致大量死亡，并对美国红鱼水产养殖行业造成严重影响。然而，美国红鱼对哈维氏弧菌感染反应的调控机制尚不清楚。因此，我们对感染哈维氏弧菌 12、36 和 48 小时后的美国红鱼肾脏组织样本进行了转录组比较分析，以揭示参与免疫和炎症反应的关键基因和信号通路。这一动态转录组分析为深入了解美国红鱼感染哈维氏弧菌后的基因表达调控和免疫相关途径提供了新的思路，为进一步研究美国红鱼以及其它硬骨鱼类的免疫防御机制提供了有效的理论基础。

关键词：美国红鱼；哈维氏弧菌；头肾组织；免疫反应；转录组

Comparative transcriptome analysis reveals potential regulatory mechanisms of genes and immune pathways following Vibrio harveyi infection in Red drum (Sciaenops ocellatus)

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Abstract： Red drum (Sciaenops ocellatus), as an important economical marine fish, has been affected by various bacterial diseases in recent years. Vibrio harveyi cause fatal vibriosis in S. ocellatus, leading to massive mortality and causing significant setbacks in aquaculture. However, the regulatory mechanisms of S. ocellatus response to V. harveyi infection are poorly understood. In this regard, we performed transcriptomic analysis with kidney tissues of S. ocellatus after V. harveyi infection from 12 h to 48 h to reveal genes, gene expression profiles, and pathways involved in immune and inflammation responses.This dynamic transcriptome analyses provided insights into gene expression regulation and immune related pathways involved in S. ocellatus after V. harveyi infection, and provides useful information for further study on the immune defense mechanisms in S. ocellatus as well as other teleost species.

Key words:： Sciaenops ocellatus; Vibrio harveyi; Head kidney; Immune responses; Transcriptome

RGNNV 感染诱导硬骨鱼脾脏中 Slc43a2+ T 细胞向脑转移

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摘要：虽然中枢神经系统(CNS)存在免疫特权被广泛接受，但是硬骨鱼脑中 T 细胞的来源尚不清楚。并且先前的研究表明，硬骨鱼中各器官中发挥重要作用 T 细胞是来自于胸腺而不是脾脏中。本研究中，我们通过单细胞测序分析鉴定了斜带石斑鱼胸腺和脾脏中的 9 个 T 细胞亚群。赤点石斑鱼神经坏死病毒(RGNNV)感染中枢神经系统后，脾脏和脑组织中 slc43a2+ T 细胞数量同步增加，而在无脾斑马鱼(tlx1▲斑马鱼模型)感染试验中，未观察到脑内 slc43a2+ T 细胞数量增加。进一步开展 slc43a2+ T 拟时分析发现，slc43a2+ T 细胞是在脾脏内成熟并进行功能分化，然后迁移到大脑中发挥免疫效应。该研究揭示了病毒感染期间 T 细胞从脾脏迁移到大脑的新途径。

关键词：中枢神经系统，slc43a2+T 细胞，RGNNV，T 细胞转移，硬骨鱼

Slc43a2+ T cell metastasis from spleen to brain in RGNNV infected teleost

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Abstract： The origin of T cells in the teleost's brain is unclear. While viewing the central nervous system (CNS) as immune privileged has been widely accepted, previous studies suggest that T cells residing in the thymus but not in the spleen of the teleost play an essential role in communicating with the peripheral organs. Here, we identified nine T cell subpopulations in the thymus and spleen of orange-spotted grouper (Epinephelus coioices) through single-cell RNA-sequencing analysis. After viral CNS infection with red-spotted grouper nervous necrosis virus (RGNNV), the number of slc43a2+ T cells synchronously increased in the spleen and brain. During the infection tests in asplenic zebrafish (tlx1▲ zebrafish model), no increase in the number of slc43a2+ T cells was observed in the brain. Single-cell transcriptomic analysis indicated that slc43a2+ T cells mature and functionally differentiate within the spleen and then migrate into the brain to trigger an immune response. This study suggests a novel route for T cell migration from the spleen to the brain during viral infection in fish.

Key words:：central nervous system， slc43a2+ T cell， RGNNV，T cell migration，teleost

鱼源副乳房链球菌前噬菌体裂解酶 Sply181 的功能研究

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摘要：副乳房链球菌病害造成水产养殖业严重的经济损失。本研究通过基因克隆、表达和纯化得到副乳房链球菌前噬菌体裂解酶 Sply181；浊度递减实验表明该酶能高效裂解其宿主菌；该酶的最适杀菌条件为酶浓度 50μg/mL、pH 6.2、温度 28℃、Ca2+浓度 10mM，且在 85℃处理 30 min 后仍保持较高的杀菌活性；结晶紫染色法证明该酶具有降解宿主菌生物被膜的能力；斑马鱼感染实验表明治疗后 72h 该酶对斑马鱼的保护力达到 46.6%。结构功能方面，利用定点突变构建的突变体 D32A、D40A 几乎无杀菌活性；通过截短构建的 Amidase-5 催化域对副乳房链球菌的杀菌活性与 Sply181 保持一致，但提升了对粪肠球菌和格氏乳球菌的杀菌活性；荧光检测结果表明构建的嵌合蛋白 GFP-SH3b 可特异结合副乳房链球菌。本研究阐明了裂解酶 Sply181 的杀菌活性及结构功能，为应用前噬菌体裂解酶防控水产链球菌病害奠定基础。

关键词：副乳房链球菌；前噬菌体裂解酶；杀菌活性；结构功能

Functional study of a prophage lysin Sply181 from fish-derived Streptococcus parauberis

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Abstract： Streptococcus parauberis disease causes serious economic losses in aquaculture. In this study, the prophage lysin Sply181 of S. parauberis was obtained by gene cloning, expression and purification; the turbidity decrease assay showed that Sply181 had the highest activity at enzyme concentration 50μg/mL, pH 6.2, 28℃ and Ca2+ concentration 10mM; crystal violet staining proved that the enzyme had the ability to degrade the biofilm of S. parauberis; the zebrafish infection experiment showed that protective effect of Sply181 on zebrafish reached 46.6% after 72h of treatment. In terms of structure function, mutants D32A and D40A constructed by site-directed mutagenesis had almost no bactericidal activity; the bactericidal activity of Amidase-5 constructed by truncation against S. parauberis was consistent with Sply181, but was improved against Enterococcus faecalis and Lactococcus garvieae; the results of fluorescence detection showed that the constructed chimeric protein GFP-SH3b could specifically bind to S. parauberis. This study clarified the bactericidal activity and structural function of Sply181, laying a foundation for the application of prophage lysin to control aquatic Streptococcal diseases.

Key words:： Streptococcus parauberis; prophage lysin; bactericidal activity; structure function

大黄鱼感染虹彩病毒后的黏膜免疫响应及其分子机制研究

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摘要：大黄鱼（Larimichthys crocea）是我国重要的海水养殖经济鱼类。然而，虹彩病毒感染导致的大黄鱼病害给养殖业带来了严重经济损失。研究鱼类对病原体激活的免疫反应可以为病害防治提供新的思路。本研究对健康与患虹彩病大黄鱼的肠道和鳃组织进行了组织病理学观察以及转录组和蛋白组分析。病理切片结果显示，患病组的各组织病理变化程度明显高于健康组。通过转录组和蛋白组联合分析发现，与健康组相比，患病组肠道中有 124 个因子在基因和蛋白水平上表达一致，其中 95 个因子上调，29 个因子下调；在患病鳃组织中，有 23 个因子表达一致，包括 16 个上调因子和 7 个下调因子。GO 和 KEGG 富集分析显示，在基因和蛋白水平上，补体途径和 Toll 样受体途径显著上调。这些结果为研究大黄鱼的免疫应答和病毒防控机制提供了参考依据。

关键词：大黄鱼；虹彩病毒；黏膜免疫；组织病理学；转录组学；蛋白质组学；

Mucosal Immune Responses and Molecular Mechanisms in Large Yellow Croaker Infected with Iridovirus

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Abstract： The large yellow croaker (Larimichthys crocea) is a crucial marine aquaculture species in China. However, iridovirus infections have caused significant economic losses in the aquaculture industry. Investigating the immune responses of fish to pathogens can provide new insights for disease prevention and control. In this study, histopathological observations, transcriptome, and proteome analyses were conducted on the intestinal and gill tissues of both healthy and iridovirus-infected large yellow croaker. Histopathological results showed that the degree of pathological changes in the infected group was significantly higher than that in the healthy group. Combined transcriptome and proteome analyses revealed that, compared to the healthy group, 124 factors were consistently expressed at both gene and protein levels in the intestines of the infected group, including 95 upregulated and 29 downregulated factors. In the gill tissues of the infected group, 23 factors were consistently expressed, with 16 upregulated and 7 downregulated. GO and KEGG enrichment analyses indicated that the complement pathway and Toll-like receptor pathway were significantly upregulated at both gene and protein levels. These findings provide valuable insights into the immune responses and mechanisms of virus prevention in large yellow croaker.

Key words:： Larimichthys crocea, iridovirus, mucosal immunity, tissue pathology, transcriptome, proteome

黄芪多糖联合传染性造血器官坏死病毒灭活疫苗对虹鳟的免疫反应和保护作用

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摘要：传染性造血器官坏死病毒（IHNV）是导致虹鳟幼鱼大量死亡的病原体之一。目前，我国还没有针对 IHNV 的有效治疗方法。本研究开发了一种以黄芪多糖（APS）为佐剂的灭活 IHNV 疫苗。在强毒力的 IHNV 感染后，对照组、疫苗组和 APS+疫苗组的存活率分别为 24%、62%和 78%。通过组织病理学和 TUNEL 分析发现，APS+疫苗可有效减少 IHNV 感染后的脾脏的损伤和凋亡。另外，APS+疫苗可显著增加血清中 SOD、CAT、T-AOC、AKP 和 ACP 活性。RNA-seq 结果显示，许多免疫相关途径被显著富集。TLR7、IRF7、IL-1β、CD4、CD8、IgM、IgT 和 IgD 基因在接种疫苗后被强烈诱导。总之，APS+疫苗成功诱导了有效的先天性和适应性免疫反应，这些反应比单一疫苗更强。这些结果表明，灭活疫苗与 APS 联合使用是对抗 IHNV 感染的有效方法，这可能有助于进一步控制虹鳟养殖中的 IHN 爆发。

关键词：疫苗；黄芪多糖；传染性造血器官坏死病毒

Immune response and protective effect of Astragalus polysaccharide combined with inactivated infectious haematopoietic necrosis virus vaccine on rainbow trout (Oncorhynchus mykiss)

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Abstract: IHNV is the cause of a massive mortality of salmon larvae, especially rainbow trout larvae, from the disease. Currently, there are no available treatments or vaccines for IHNV in China. Here, we developed an inactivated IHNV vaccine with Astragalus polysaccharide (APS) as an adjuvant and determined its efficacy. Safety testing showed that no abnormalities were observed at the animal and cellular levels after vaccination. After a serious IHNV challenge, survival rates were 24%, 62% and 78% in control, vaccine and APS+vaccine group, respectively. APS+vaccine was effective in reducing spleen damage and apoptosis after IHNV challenge by histopathological and TUNEL analyses. The APS+vaccine group performed better in enhancing non-specific immunity (increased activity of SOD, CAT, T-AOC, AKP and ACP). Moreover, RNA-seq revealed that many immune-related pathways were significantly enriched. TLR7, IRF7, IL-1β, CD4, CD8, IgM, IgT and IgD were identified as key genes in the immune response, which were strongly induced after vaccination. APS+vaccine induced effective innate and adaptive immune responses that were stronger than single vaccines after vaccination and IHNV challenged. These results suggest that inactivated vaccine combination with APS is an effective method against IHNV infection, which may help to further control IHN outbreaks in rainbow trout farming.

Key words:：Vaccine; Astragalus polysaccharide; Infectious hematopoietic necrosis virus

牙鲆细胞外纤维的释放及其在免疫防御中的作用

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摘要：血管内皮细胞与血液接触，是细菌、病毒感染的主要靶细胞。同时，中性粒细胞在机体受到病原感染后，通过内皮细胞外渗到感染部位，形成细胞外陷阱（ETs）俘获并杀死病原微生物。但是，牙鲆 ETs 以及内皮细胞在微生物感染中的应答特征尚不明晰。以牙鲆为试验动物，制备髓过氧化物酶（MPO）、血管性血友病因子（vWF）抗体。结果表明，MPO+细胞主要为中性粒细胞和巨噬细胞，在病原刺激腹腔后，可自前肾趋化到外周血和腹腔执行功能。MPO 存在于细胞外陷阱，起杀菌或抑菌作用。vWF+细胞主要为内皮细胞，在牙鲆弹状病毒（HIRRV）感染期间，病毒粒子可以侵染内皮细胞，诱导内皮细胞释放长链状 VWF 并俘获病毒粒子。同时，感染加速了中性粒细胞的募集。本文探究了两类细胞外纤维的基本特征，为鱼类病害中病原微生物与免疫细胞的病理、生理相互作用提供了重要信息。

关键词：髓过氧化物酶；细胞外陷阱；血管性血友病因子；内皮细胞；牙鲆

The release of extracellular fibers and their role in immune defense in flounder (Paralichthys olivaceus)

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Abstract：The vascular endothelium consists of a highly heterogeneous monolayer of endothelial cells which are the primary target for bacterial and viral infections due to endothelial cells constant and close contact with the bloodstream. Meanwhile, neutrophils are rapidly extravasated through the endothelial cells layer and recruited to infection and inflammation eliminating pathogenic microorganisms by phagocytosis, degranulation, and the formation of neutrophil extracellular traps (ETs). However, the extracellular traps of neutrophils and the response characteristics of endothelial cells in microbial infections in flounder are still unclear. This study used flounder as experimental animals and obtained antibodies against myeloperoxidase (MPO) and von Willebrand factor (vWF). The results showed that MPO positive cells were mainly neutrophils and macrophages, and we suggest a migration behavior of PoMPO+ cells – from the head kidney to blood and peritoneal cavity upon local inflammatory event. PoMPO is involved in the antibacterial effect of ETs. The vWF positive cells are mainly endothelial cells. During the infection of Hirame novirhabdovirus, virions can infect endothelial cells. Meanwhile, infection accelerates mediated recruitment of neutrophils into tissues by endothelial cells. After HIRRV infection in vitro, it can induce endothelial cells to release long-chain VWF and capture viral particles. The research results explored the basic characteristics of two types of extracellular fibers and provided a basic basis for the pathophysiological interaction between pathogenic microorganisms and immune cells in fish diseases.

Key words:：myeloperoxidase; extracellular traps; von Willebrand Factor; Endothelial cells; flounder

草鱼肾细胞对草鱼呼肠孤病毒和嗜水气单胞菌反应的 miRNA、mRNA 和蛋白质组比较分析

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摘要：草鱼出血性疾病由呼肠孤病毒和嗜水气单胞菌所引起是在水产养殖中最为广泛，但其感染机制尚不明确。在本研究中，分别用 PBS（对照组，N）、草鱼呼肠孤病毒（GCRV，NV）和嗜水气单胞菌（细菌，NB）感染的草鱼肾细胞（CIK），并对其 miRNA 组学、转录组和蛋白组联合分析，以了解其发病机制。与 N 组相比，NV 组分别鉴定出 99 个差异表达的 miRNAs（DEMs）、2132 个差异表达基因（DEGs）和 627 个差异表达蛋白（DEPs），NB 组分别鉴定出 92 个 miRNAs（DEMs）、3162 个差异表达基因（DEGs）和 712 个差异表达蛋白（DEPs）。此外，我们还分别从 NV/N 组和 NB/N 组之间的 DEGs/DEMs/DEPs 中筛选出特异性基因/miRNAs/蛋白。通过 KEGG 富集分析，NV 组中大多数差异表达基因主要参与细胞过程，NB 组中大多数差异表达基因参与代谢途径，阐明了草鱼 GCRV 感染与嗜水气单胞菌感

关键词：草鱼肾细胞，呼肠孤病毒，嗜水气单胞菌，转录组，蛋白质组

Comparative analysis of mRNA, microRNA of transcriptome and proteomics on CIK cells responses to GCRV and Aeromonas hydrophila

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Abstract： Grass carp haemorrhagic disease caused by Grass Carp Reovirus and Aeromonas hydrophila is the most widespread in aquaculture, but the mechanism of infection is not clear. In this study, grass carp kidney cells (CIK) infected with PBS (control group, N), Grass Carp Reovirus (GCRV, NV), and Aeromonas hydrophila (bacteria, NB) were analyses by miRNA, mRNA and proteome combination, respectively, in order to understand the pathogenesis. Compared with the N group, 99 differentially expressed miRNAs (DEMs), 2,132 differentially expressed genes (DEGs) and 627 differentially expressed proteins (DEPs) were identified in the NV group and 92 miRNAs (DEMs), 3,162 differentially expressed genes (DEGs) and 712 differentially expressed proteins (DEPs) in the NB group, respectively. In addition, we screened specific genes/miRNAs/proteins from DEGs/DEMs/DEPs between NV/N and NB/N groups, respectively. By KEGG enrichment analysis, most of the differentially expressed genes in the NV group were mainly involved in cellular processes, and most of the differentially expressed genes in the NB group were involved in metabolic pathways, which elucidated that the mechanism of GCRV infection in grass carp is different from that of Aeromonas hydrophila infection. An important regulatory network of miRNA-mRNA-protein was established by comprehensive analysis of transcriptome and proteome. Fourteen miRNAs and five differentially expressed genes were randomly selected, and qRT-PCR was used to validate miRNAomics and transcriptome data. This study not only provides data for understanding the pathogenesis of renal cell infection with GCRV and Aeromonas hydrophila in grass carp, but also provides reference value for other aquatic animal haemorrhagic diseases.

Key words:：Grass carp kidney cells, GCRV, Aeromonas hydrophila, transcriptome, proteome

腹腔细胞转录组分析揭示灭活鳗弧菌引起牙鲆的早期免疫应答

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摘要：鳗弧菌是一种严重危害牙鲆和其他养殖物种的细菌。疫苗是预防弧菌病的有效手段，主要通过腹腔注射接种。在免疫初期，有效的抗原处理对于引起适应性免疫应答和提高疫苗效果至关重要。为了了解灭活鳗弧菌引起牙鲆早期免疫应答，我们检测了灭活鳗弧菌免疫后腹腔细胞的转录组表达谱。我们获得了10亿多高质量的读数，其中89.33%匹配到牙鲆参考基因组。在免疫后48小时内共捕获到14534个差异表达基因。通过加权基因共表达网络分析，我们确定了与免疫时间相关的关键模块。GO和KEGG分析结果显示，关键模块的基因在多种免疫相关途径表达，包括：对刺激的反应、自噬、Th17细胞分化等。此外，我们还构建了与Th细胞分化相关的基因表达热图，这些基因构成了一个复杂的免疫调节网络，主要参与病原体识别、抗原加工和递呈以及Th细胞分化。本研究首次提供了与灭活鳗弧菌相关的牙鲆腹腔细胞转录组谱，为进一步研究高效的鳗弧菌疫苗奠定了坚实的基础。

关键词：腹腔细胞；RNA-测序；免疫应答；鱼

Transcriptome Analysis of Peritoneal Cells Reveals the Early Immune Response of Flounder (Paralichthys olivaceus) to Inactivated Vibrio anguillarum Immunization

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Abstract：Vibrio anguillarum (V. anguillarum) is a bacterium that seriously harms flounder and other aquaculture species. Vaccination is an effective means of preventing vibriosis and is mainly administered by intraperitoneal injection. Effective antigen processing at the initial stage of immunization is essential to elicit adaptive immune responses and improve vaccine efficacy. To understand the early immune response of flounder caused by inactivated V. anguillarum, we detected the transcriptome profiles of the cells in the peritoneal cavity (PoPerCs) after inactivated V. anguillarum immunization. More than 10 billion high-quality reads were obtained, of which about 89.33% were successfully mapped to the reference genome of flounder. A total of 14532 differentially expressed genes were captured within 48 h post immunization. The hub module correlated with the immunization time was identified by WGCNA. GO and KEGG analysis showed that hub module genes were abundantly expressed in various immune-related aspects, including the response to stimuli, autophagy, and Th17 cell differentiation. Additionally, genes related to Th cell differentiation are presented as heatmaps. These genes constitute a complex immune regulatory network, mainly involved in pathogen recognition, antigen processing and presentation, and Th cell differentiation. The results of this study provide the first transcriptome profile of PoPerCs associated with inactivated V. anguillarum immunity and lay a solid foundation for further studies on effective V. anguillarum vaccines.

Key words:：peritoneal cells; RNA-seq; immune response; fish

山药多糖诱导草鱼 IgM+B 细胞功能分化及其免疫保护作用

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摘要：山药多糖是一种有效的天然免疫增强剂，但其在草鱼中的免疫保护作用尚未明确。本研究首先通过流式细胞术和 RT-qPCR 检测山药多糖体外刺激草鱼头肾白细胞后的基因表达模式、IgM+B 细胞数量及抗体分泌水平，结果表明山药多糖可以促进草鱼头肾 IgM+B 细胞的增殖和功能分化以及 IgM 分泌。我们研究发现山药多糖还可以显著提高 IgM+B 细胞的吞噬功能。体内实验显示，进行山药多糖灌喂实验后，灌喂山药多糖组草鱼血清中 IgM 含量增加，与肽聚糖和脂多糖结合的能力也增加。此外，我们发现灌喂山药多糖组血清杀灭嗜水气单胞菌的能力也增强。在用嗜水气单胞菌攻毒后，山药多糖灌喂组的成活率高于对照组。同时，山药多糖能够显着调节草鱼肠道炎症因子的分泌，降低肠道致病菌负荷，这些结果表明山药多糖可以保护草鱼免受嗜水气单胞菌感染。我们的研究揭示了山药多糖对草鱼的免疫保护作用，为新型水生免疫增强剂的开发提供了理论基础。

关键词：IgM+B 细胞、山药多糖、草鱼

Chinese yam polysaccharide induces functional differentiation of grass carp IgM+ B cells to prevent Aeromonas hydrophila infection

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Abstract： Chinese yam polysaccharide (CYP) is an effective immunopotentiator, however, its efficacy in grass carp remains untested. Here, the objective of this study was to evaluate the effects of CYP on the immune cells in vitro and on humoral immunity and immune defense against A. hydrophila (Aeromonas hydrophila) infection in vivo. To assess antibody levels, grass carp head kidney leukocytes were isolated and then culture supernatants were collected 24 hours after stimulation with LPS and CYP. Flow cytometry and RT-qPCR (Reverse transcription-quantitative polymerase chain reaction) analysis of gene expression patterns and the number of IgM+ B cells in grass carp head kidney leukocytes after stimulation demonstrated that CYP induces IgM secretion and the proliferation and differentiation of head kidney IgM+ B cells. Meanwhile, CYP can stimulation boosts the phagocytic activities of IgM+ B cell. Further study revealed that CYP can protect grass carp from A. hydrophila infection. Grass carp were intragastric administration with CYP and then infected with A. hydrophila. Following gavage of CYP, the serum antibody level increased, as did the capacity of the serum to bind to peptidoglycan (PGN) and lipopolysaccharide (LPS). Additionally, the ability of serum bactericidal to kill A. hydrophila was enhanced. CYP can protect grass carp from A. hydrophila infection in vivo, because it significantly regulates the secretion of inflammatory factors and reduces intestinal bacterial load. Taken together, to our knowledge, our study reveals immune function of CYP in grass carp. Our study provides a theoretical basis for the development of new Aquatic immunopotentiators.

Key words:： IgM+ B cell, Chinese yam polysaccharide, Grass carp

SA-DME-EG/WPU 薄膜的制备及其对三文鱼鱼片的保鲜性能研究

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摘要：【目的】为减少贮藏中水产品渗出汁液对生物保鲜剂释放的负作用。【方法】以水性聚氨酯（WPU）为成膜基质，硅藻土（DME）为粗糙度构建因子，1H，1H，2H，2H-全氟辛基三氯硅烷（PFOTS）为低表面能改性剂，丁香酚（EG）为生物保鲜剂，以流延法制备了超双疏-硅藻土-丁香酚/水性聚氨酯薄膜(SA-DME-EG/WPU)。以腐败希瓦氏菌为抑菌对象，研究了薄膜的抗菌机理，以三文鱼鱼片为保鲜对象验证了其保鲜性能。【结果】EG 通过物理吸附包埋于 DME 中，PFOTS 改性后，DME 表面形成微纳米级结构，赋予了薄膜超双疏(SA)特性，缓释性能良好，抗菌性能优异。经薄膜处理后，菌体塌陷干瘪，细胞膜通透性增加，胞内外渗透压不平衡。保鲜实验进一步证明了薄膜可有效延缓鱼片的 TVC、pH 和 TVB-N 的升高及感官品质和质构的下降。【结论】该超双疏活性抗菌薄膜可有效防止贮藏过程中水产品渗出汁液对膜内抗菌剂释放的抑制。

关键词：水性聚氨酯；薄膜；超双疏；抗菌性；保鲜。

Preparation of SA-DME-EG/WPU film and its preservation performance on salmon fillets

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Abstract: [Objective] In order to improve the preservation properties of preservation films on aquatic products and reduce the negative effect of aquatic products' exudation juice on the release of biological preservative in the films during storage. [Methods] A series of films with different hydrophobic and oleophobic properties were prepared by tape casting method using waterborne polyurethane (WPU) as film-forming matrix, diatomite (DME) as roughness construction factor, 1H, 1H, 2H, 2H-perfluorooctane trichlorosilane (PFOTS) as low surface energy modification agent, and eugenol (EG) as active antibacterial agent. The antibacterial properties and mechanism of the films were studied by using Shewanella putrefaciens, which is the dominant spoilage bacterium aquatic products, as the antibacterial object. And the preservation properties of the films were verified by using Salmon fillets as the preservation object. [Results]The results show that EG is embedded in DME by physical adsorption, and the surface of DME formes a micro-nano structure giving the films superamphiphobic (SA) properties after PFOTS modification. Among the films, the SA-DME-EG/WPU film has excellent superamphiphobic properties, WCA>150 °, OCA>120 °, and the total release of EG in it is the highest, also has the best sustained release and antibacterial properties. After the composite film treatment, the Shewanella putrefaciens collapses and witheres, the cell membrane permeability increases, and the osmotic pressure is unbalanced. The preservation experiment of Salmon fillets further proves that the films can effectively delay the increase of TVC, pH, TVB-N, and the decrease of sensory quality and texture of fillets. Among them, the SA-DME-EG/WPU film has the best preservation performance for Salmon fillets. [Conclusion] The superamphiphobic active antibacterial films prepared in this study can effectively prevent the inhibition of the release of antibacterial agents in the film by exudation juice of aquatic products during storage, and has potential application value in the field of aquatic products preservation.

Key words:：Waterborne polyurethane; film; superamphiphobic; antibacterial; preservation

5 种水产药物对斑重唇鱼仔鱼的急性毒性及安全评价

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摘要：斑重唇鱼为国家Ⅱ级水生野生保护动物，其仔鱼培育时期易受疾病的侵扰。针对仔鱼不同疾病，开展其治疗药物甲醛、食盐和聚维酮碘、苯扎溴铵及亚甲基蓝对体质量（96.23±6.03）mg 斑重唇鱼仔鱼的 96 h 急性毒性实验，评价了药物的安全浓度。试验结果表明：甲醛对斑重唇鱼仔鱼的 96 h 半致死浓度为 89.27 mg/L，急性毒性为高毒；食盐对仔鱼的 96 h 半致死浓度为 89.27 mg/L，急性毒性为高毒；聚维酮碘对仔鱼的 96 h 半致死浓度为 89.27 mg/L，急性毒性为高毒；苯扎溴铵对仔鱼的 96 h 半致死浓度为 89.27 mg/L，急性毒性为高毒；亚甲基蓝对仔鱼的 96 h 半致死浓度为 89.27 mg/L，急性毒性为高毒，其安全浓度分别为：12.48 mg/L、3582.37 mg/L、8.47 mg/L。5 种药物对斑重唇鱼仔鱼的敏感性为：高聚碘＞ 甲醛＞ 食盐。

关键词：水产药物；斑重唇鱼；急性毒性；安全浓度

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Abstract：/

Key words:：/

转录组学和代谢组学联合分析揭示了铜暴露对虹鳟(Oncorhynchus mykiss)肝脏的影响

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摘要：铜是人体必需的微量元素之一，但过量的铜会产生毒性作用。我们研究了 75 μg/L、150 μg/L 和 300 μg/L Cu2+对虹鳟鱼肝脏的影响，转录组和代谢组的联合分析进一步揭示了铜胁迫下肝脏的调控机制。结果表明，Cu2+影响肝脏抗氧化指标，破坏肝脏正常组织结构。转录组和代谢组联合分析显示，胰岛素信号通路和脂肪细胞因子信号通路显著富集，Cu2+胁迫促进了机体糖酵解。此外，Cu2+胁迫通过降低丝氨酸和精氨酸含量，增加脯氨酸含量影响虹鳟鱼的氨基酸代谢；铜胁迫促进细胞凋亡，抑制自噬，影响机体的脂质代谢；综上所述，Cu2+胁迫影响虹鳟鱼的能量代谢和脂质代谢，丝氨酸和精氨酸的减少代表着抗氧化能力的降低，而脯氨酸含量的增加和细胞凋亡的促进可能是虹鳟鱼抗 Cu2+的重要策略。这些发现为虹鳟鱼在铜胁迫下的调控机制提供了见解，并为重金属污染的预防和生物标志物的选择提供了信息。

关键词：虹鳟，铜，转录组，代谢组，生理生化

rainbow trout; copper; transcriptomics; metabolomics; physiology and biochemistry

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Abstract：Copper is one of the essential trace elements for the body, but excessive Cu will produce toxic effects. We investigated the effects of Cu2+(75 μg/L, 150 μg/L and 300 μg/L) on the rainbow trout liver, and combined transcriptome and metabolome analysis further revealed the regulatory mechanism of liver under Cu stress. The results showed that Cu affects the antioxidant indexes and destroys the normal tissue structure of the liver. Combined transcriptome and metabolome analyses revealed significant enrichment of the insulin signaling pathway and the adipocytokine signaling pathway, and that Cu2+ stress promoted organismal glycolysis. In addition, Cu2+ stress affected the amino acid metabolism of rainbow trout by decreasing serine and arginine content and increasing proline content; Apoptosis is inhibited and autophagy and lipid metabolism are suppressed; In summary, Cu2+ stress affects energy and lipid metabolism, and the reduction of serine and arginine represents a decrease in the antioxidant capacity, whereas the increase in proline and the promotion of apoptosis may be an important strategy for Cu2+ resistance in rainbow trout. These findings provided insights into the regulatory mechanisms of rainbow trout under Cu2+ stress and informed the prevention of heavy metal pollution and the selection of biomarkers under Cu pollution.

Key words:：rainbow trout; copper; transcriptomics; metabolomics; physiology and biochemistry

吸水 3D 纤维棉的制备及其衬垫在海鲈鱼鱼片保鲜中的应用

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摘要：为延缓水产品腐败，具有吸水性能的抗菌保鲜衬垫是一个良好的选择。湿法静电纺丝无需外部设备的帮助，通过调节环境湿度即可轻松制备具有不同堆叠结构的 3D 纳米纤维材料，可大大降低运输成本。以聚苯乙烯、聚氨酯、聚氧化乙烯、聚乙烯吡咯烷酮为材料，通过调节环境湿度诱导相分离，利用同轴静电纺丝技术制备 3D 聚苯乙烯聚氨酯聚氧化乙烯-聚乙烯吡咯烷酮纺丝棉。对其进行表征，测定其热稳定性、机械性能和对水油的吸附性能。将 3D 纺丝棉作为吸水层制备保鲜衬垫，并研究衬垫对海鲈鱼鱼片的保鲜性能。结果表明，核壳不对称掺入聚氧化乙烯和聚乙烯吡咯烷酮能够在不影响三维结构和微观结构的同时，赋予纺丝棉更高的吸水性能。加入保鲜层的保鲜衬垫效果更优，可以抑制海鲈鱼鱼片内微生物的生长繁殖，延缓脂肪氧化和蛋白质降解，使海鲈鱼鱼片的货架期从 5.4 d 延长到 8.7 d。本研究提供了一种超轻吸水棉的简易制备方法，为保鲜衬垫在水产品中的应用提供依据。

关键词：3D 吸水棉；保鲜衬垫；同轴静电纺丝；海鲈鱼鱼片

Preparation of water-absorbing 3D spinning cotton and its application in the preservation of L. japonicus fillets

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Abstract：To delay the spoilage of aquatic products, antibacterial preservation pads with absorbent properties are a good choice. Wet electrospinning without the help of external equipment, by adjusting the ambient humidity can easily prepare 3D nanofiber materials with different stacked structures, which can greatly reduce transportation costs. Using polystyrene, polyurethane, polyoxyethylene and polyvinylpyrrolidone as materials, the 3D polystyrene polyurethane polyoxyethylene and polyvinylpyrrolidone spinning cotton was prepared by coaxial electrospinning technology through phase separation induced by adjusting ambient humidity. The thermal stability, mechanical properties and adsorption properties of water and oil were characterized. 3D spinning cotton was used as absorbent layer to prepare the preservation pad and the preservation performance of the pad on L. japonicus fillets was studied. The results show that the asymmetric core-shell incorporation of polyoxyethylene and polyvinylpyrrolidone can enhance the water absorption of spun cotton without affecting the three-dimensional structure and microstructure. The preservation pad added with f preservative layer has better effect, which can inhibit the growth and reproduction of microorganisms in L. japonicus fillets, delay fat oxidation and protein degradation, and extend the shelf life of L. japonicus fillets from 5.4d to 8.7d. This study provides a simple preparation method of ultra-light absorbent cotton, which provides a theoretical basis for the application of preservation pads in aquatic products.

Key words:：water-absorbing 3D spinning cotton; preservation pad;coaxial electrostatic spinning;L. japonicus

杂交鳢脾脏细胞系的建立及其对杂交鳢弹状病毒敏感性的探究

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摘要：杂交鳢是我国经济价值较高的淡水养殖鱼类，杂交鳢弹状病毒（HSHRV）给杂交鳢养殖业造成了严重的经济损失。建立基于稳定传代细胞系的病毒体外培养体系是分离，鉴定并研究鱼类病毒的必要技术手段。本研究以杂交鳢脾脏为材料，用胰蛋白酶消化组织方法，建立杂交鳢脾脏细胞系命名为CAMSp。启动原代培养以来传代超过80次。CAMSp能够在能含10%胎牛血清的Leibovitz’s 15培养基，28℃培养条件下快速增殖，1:3比例传代，24h可形成单层细胞。60代次的CAMSp细胞染色体众数为42，而杂交鳢体细胞染色体数目为44、45或46，染色体发生突变，表明CAMSp细胞已突变。以前期分离的杂交鳢来源的弹状病毒接种CAMSp单层细胞，可产生典型细胞病变效应，增殖病毒滴度可达10的8.33TCID50/mL，电镜观察可见大量子弹状病毒粒子。该细胞系的建立对后续研究HSHRV的致病机理有重要意义。

关键词：杂交鳢　脾脏　细胞系　杂交鳢弹状病毒

Establishment of spleen cell line of hybrid snakehead and its sensitivity to rhabdovirus

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Abstract： Hybrid snakehead is a freshwater fish with high economic value in China. Hybrid rhabvirus (HSHRV) has caused serious economic losses to the aquaculture of hybrid snakehead.The establishment of virus culture system based on stable cell line is a necessary technique to isolate, identify and study fish virus. In this study, spleen cell line CAMSp was established by trypsin digestion of the spleen of hybrid snakehead. More than 80 passages have been performed since the initiation of primary cell culture. CAMSp can rapidly prolificate in Leibovitz's 15 medium containing 10% fetal bovine serum at 28℃, and can form monolayer cells after 24h of 1:3 passage. The chromosome number of CAMSp cells in 60 generations was 42, while that of the somatic cells was 44, 45 or 46, indicating that CAMSp cells had mutated. The typical cytopathological effect (CPE) was produced by inoculating CAMSp monolamers with a titer of 108.33TCID50/mL, and a large number of bullet virus particles were observed by electron microscopy. The establishment of CAMSp cell line is of great significance for further studies on the pathogenesis of HSHRV, virus-host cell interaction, and disease prevention and control.

Key words:：Hybrid snakehead Hybrid snakehead rhabdovirus Spleen cell line

白斑综合征病毒和对虾内参基因双重荧光定量 PCR 检测方法的建立

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摘要：本研究旨在建立一种白斑综合征病毒（WSSV）和对虾内参基因双重荧光定量 PCR 检测方法，提高 WSSV 检测的灵敏度和特异性。首先，基于 WSSV 基因组保守序列设计合成特异性引物和 TaqMan 探针，建立 WSSV 单重荧光定量 PCR 检测体系，经特异性和重复性试验证实，该方法对 WSSV 具有良好的特异性和重复性。在此基础上，设计合成了凡纳滨对虾内参基因引物和探针，并对引物碱基进行优化替换，建立了 WSSV-对虾内参基因双重荧光定量 PCR 检测体系。敏感性试验结果显示，该双重检测体系对 WSSV 的检测下限可达 15 拷贝/μL，在 6.6×105~6.6 拷贝/μL 范围内，WSSV 质粒标准品的起始模板量对数值与 Ct 值呈良好的线性关系（R2=0.998）。同时，内参基因的引入可有效区分样本中由核酸提取或操作问题引起的假阴性结果。

关键词：白斑综合征病毒；荧光定量 PCR；TaqMan 探针；病毒检测；水产养殖

Development of a duplex real-time fluorescent quantitative PCR assay for simultaneous detection of white spot syndrome virus and shrimp reference gene

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Abstract：[Introduction]White spot syndrome virus (WSSV) is a highly infectious and lethal pathogen that poses a significant threat to the global shrimp farming industry. It belongs to the genus Whispovirus, family Nimaviridae, and is the sole member of the genus. WSSV has a wide host range, including all farmed and wild marine shrimp, crabs, crayfish, and freshwater prawns. The virus can spread rapidly through horizontal and vertical transmission, infecting various tissues such as gills, hepatopancreas, and exoskeleton, leading to white spot disease (WSD). Infected shrimp develop white calcified spots on the carapace and can experience cumulative mortality rates of up to 100% within 3-10 days post-infection, resulting in massive economic losses.Since its first outbreak in Taiwan in 1992, WSSV has quickly spread to major shrimp farming regions worldwide. In 1995, the World Organisation for Animal Health (OIE), the Food and Agriculture Organization (FAO), and the Network of Aquaculture Centres in Asia-Pacific (NACA) simultaneously listed WSSV as an important aquatic animal disease requiring monitoring. Due to the lack of effective prevention and treatment measures, developing rapid, accurate, and sensitive WSSV detection technologies is crucial for the timely diagnosis and implementation of control measures to prevent the spread of the disease. [Objective] This study aimed to establish a sensitive and specific duplex real-time fluorescent quantitative PCR (qPCR) method for the simultaneous detection of WSSV and an endogenous control gene in shrimp. [Methods] Firstly, specific primers and TaqMan probes were designed based on the conserved sequences of the WSSV genome, and a single WSSV qPCR detection system was established. The specificity and repeatability tests confirmed that the method had good specificity for WSSV without cross-reactivity, and the coefficient of variation for different gradients of plasmid standards was less than 1.5%, indicating high repeatability. Subsequently, primers and probes for the endogenous control gene of Litopenaeus vannamei were designed and synthesized, and the primer bases were optimized to establish a duplex qPCR detection system. [Results] The sensitivity test results showed that the detection limit of the duplex system for WSSV was 15 copies/μL, and there was a good linear relationship between the logarithmic value of the initial template amount and the Ct value of WSSV plasmid standards within the range of 6.6×105~6.6 copies/μL (R2=0.998).

Key words:： White Spot Syndrome Virus, real-time quantitative PCR, TaqMan probe, virus detection, aquaculture

噬菌体与副溶血弧菌的基因组学分析及其治疗效果评价

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摘要：副溶血弧菌的防治通常依赖抗生素，但抗生素的长期不当使用导致了多重耐药性（MDR）细菌的出现，使得防治变得十分棘手。噬菌体因其在替代抗生素治疗细菌性疾病方面的潜在可能而备受关注。本研究旨在分析我国东部沿海地区弧菌的流行情况，研究副溶血弧菌的毒力基因及耐药性，分析临床分离菌株的基因组学信息，并分离副溶血弧菌烈性噬菌体。我们研究了噬菌体的生物学特性、体外抑菌能力、清除生物膜能力以及比较基因组学分析。基于此，建立了副溶血弧菌 LCU-VP2（pirA+和 pirB+）感染红螯螯虾的实验动物模型，分析不同治疗方法对螯虾免疫基因的影响，综合评价单株噬菌体、噬菌体鸡尾酒（vB_VpaS_SD2 和 vB_VpaS_SD15）及抗生素（氟苯尼考）的治疗效果。结果显示，噬菌体鸡尾酒组的效果优于氟苯尼考组，能的效果优于氟苯尼考组，能够最大程度降低 86%的死亡率，并激活红螯螯虾的免疫基因的转录。

关键词：副溶血弧菌；噬菌体；生物学特性；基因组学；治疗效果

Genomic analysis of phage and Vibrio parahaemolyticus and evaluation of their therapeutic effects

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Abstract： Vibrio parahaemolyticus has emerged as a significant factor impeding the healthy development of the aquaculture industry. Additionally, it is a notable foodborne pathogenic bacterium that poses a serious threat to public health safety. While antibiotics are commonly employed to control Vibrio parahaemolyticus, the prolonged and unscientific use of these drugs has resulted in the emergence of multidrug-resistant (MDR) bacteria, complicating prevention and control efforts. Consequently, bacteriophages have garnered considerable attention due to their potential to serve as alternatives to antibiotics in the treatment of bacterial diseases. This study aims to analyze the prevalence of Vibrio in the eastern coastal regions of my country, investigate the virulence genes and drug resistance of Vibrio parahaemolyticus, and examine the genomic information of clinical isolates. Additionally, we seek to isolate virulent phages of Vibrio parahaemolyticus and assess their biological characteristics, including in vitro antibacterial ability, biofilm clearing capacity, and comparative genomics research. Based on these findings, an experimental animal model of red-clawed crayfish infected with Vibrio parahaemolyticus LCU-VP2 (pirA+ and pirB+) was established to evaluate the effects of different treatments on crayfish immunity. The influence of genes was examined to comprehensively assess the therapeutic effects of single phage strains, phage cocktails (vB_VpaS_SD2 and vB_VpaS_SD15), and antibiotics (florfenicol). The results indicated that the phage cocktail group was more effective than the florfenicol group, achieving a maximum reduction in mortality rate of 86% and activation of immune genes in red crayfish. Furthermore, the treatment effect of the florfenicol group surpassed that of single phage treatment, resulting in a 62% reduction in mortality rate. This study demonstrates the potential of phage therapy for treating red crayfish infected by Vibrio parahaemolyticus, suggesting that phage cocktail preparations could be further promoted and utilized as an alternative to antibiotics.

Key words:： Vibrio parahaemolyticus; bacteriophage; biological characteristics; genomics; therapeutic effect

对虾偷死野田村病毒（CMNV）反向遗传系统的构建及拯救病毒的感染能力研究

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摘要：对虾病毒性偷死病（VCMD）是一种新发的病毒性疾病，由对虾偷死野田村病毒（CMNV）引起。病毒反向遗传系统是深入研究病毒特性的关键技术，利用病毒基因组的全长 cDNA 拷贝产生具有感染性的病毒，即“感染性克隆”。本研究利用病毒反向遗传技术，成功构建了 CMNV 的感染性克隆。具体研究结果如下：通过将 CMNV 的全基因组 RNA1 和 RNA2 的全长 cDNA 克隆到基因表达载体中，构建了表达质粒 pIZ-RNA1 和 pIZ-RNA2，并共转染至昆虫 Sf9 细胞，实现了 CMNV 感染性克隆的“拯救”。“拯救”的 CMNV 感染性克隆（rCMNV）经透射电镜负染观察显示其平均直径为 38 nm，且在细胞敏感性检测中证实了其对对虾血淋巴原代培养细胞具有感染能力，并造成明显的细胞病变效应（CPE）。此外，本研究进一步发现 rCMNV 能够跨物种感染昆虫 Sf9 细胞和褐点石斑鱼鱼鳍细胞。本研究成果为深入研究 CMNV 病毒提供了重要工具。

关键词：对虾；对虾偷死野田村病毒（CMNV）；反向遗传系统；感染性克隆；Sf9 细胞

Construction of the Reverse Genetic System for the Shrimp Covert Mortality Nodavirus (CMNV) and Study on the Infectivity of the Rescued Virus

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Abstract：Viral Covert Mortality Disease (VCMD) is an emerging viral disease caused by the Covert Mortality Nodavirus (CMNV). The reverse genetics system is a crucial technique for studying viruses, which involves using the full-length cDNA copy of the viral genome to produce infectious viruses, known as "infectious clones." In this study, we successfully constructed infectious clones of CMNV using reverse genetic technology. By cloning the full-length cDNAs of CMNV into the pIZ-V5/His expression vector, we created the expression plasmids pIZ-RNA1 and pIZ-RNA2. These were co-transfected into Sf9 cells to "rescue" the CMNV infectious clones. Transmission electron microscopy (TEM) with negative staining revealed that the purified "rescued" CMNV particles (rCMNV) had a mean diameter of 38 nm. The rCMNV was confirmed to be capable of infecting shrimp primary cultured hemolymph cells, resulting in obvious cytopathic effects (CPE). Furthermore, we discovered that rCMNV could cross-species infect insect Sf9 cells and brown-marbled grouper fin cells. The establishment of the CMNV reverse genetics system provides a tool for studying CMNV.

Key words:：shrimp; Covert Mortality Nodavirus (CMNV); reverse genetics system; infectious clone; Sf9 cells

多组学联合探究鲤春病毒血症病毒（SVCV）诱导鲤科鱼类脑部炎症的具体机制

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摘要：鲤春病毒血症病毒（SVCV）对多种鲤科鱼类具有高度传染性和死亡率。SVCV 感染期间，患病鱼有眼球凸出、头部出血等典型临床症状，组织病理学检测结果表明，患病鱼脑组织出现明显炎性病变，这会导致患病鱼反应迟钝、游动失衡、摄食减少等异常行为，阻碍患病鱼对饲料及口服抗病毒药物的正常摄入，极大影响治疗效果。通过探究 SVCV 突破血脑屏障并诱导鱼脑组织炎症的具体机制，可以为 SVCV 防治策略的开发提供重要的理论依据。本研究利用斑马鱼活体感染模型及多组学联合分析方法，对斑马鱼脑组织进行了转录组和非靶代谢组测序，共筛选得到 1267 个与天然免疫、细胞死亡和代谢相关的差异表达基因（DEGs），以及 80 个与淀粉和蔗糖代谢、苯丙氨酸代谢、泛酸和辅酶 A（CoA）生物合成等相关的差异代谢物（DMs），并且共富集于与脑组织炎症高度相关的嘌呤代谢和苯丙氨酸代谢途径，为 SVCV 致病机制的进一步解析和防治策略的开发提供了新的视角。

关键词：鲤春病毒血症病毒；斑马鱼；脑组织炎症；血脑屏障；

Integrated transcriptomic and metabolomic analyses reveal the mechanism by which spring viremia of carp virus infects zebrafish brain tissue and induces inflammation

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Abstract：Spring viremia of carp virus is highly contagious and lethal to cyprinid fish. The SVCV-infected fish exhibit head hemorrhages and eyeball bulges. Histopathological results also showed inflammatory lesions in fish brains, which can lead to sluggish reactions, imbalanced swimming, and reduced feeding. These abnormal behaviors can hinder the intake of antiviral drugs and affect the therapeutic effect. The study of the specific mechanism by which SVCV breaks through the blood-brain barrier and induces brain inflammation can provide a theoretical basis for the control strategies development. In this study, transcriptomic and metabolomic analyses of zebrafish brains were performed. A total of 1267 differentially expressed genes (DEGs) were identified and mainly enriched in the pathways related to innate immunity, cell death, and metabolism. Besides, 80 differential metabolites (DMs) were identified and mainly involved in starch and sucrose metabolism, phenylalanine metabolism, and biosynthesis of pantothenic acid and coenzyme A. Both DMs and DEGs were co-enriched in purine metabolism and phenylalanine metabolism pathway and led to brain inflammation. These data provide a new perspective to further elucidate the pathogenic mechanism of SVCV.

Key words:：SVCV; zebrafish; brain inflammation; blood-brain barrier

鱼类神经坏死病毒新受体肌球蛋白轻链 3 的鉴定及功能研究

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摘要：神经坏死病毒是严重危害多种海淡水经济鱼类的病原之一，但其入侵机制仍未完全阐明。病毒受体是病毒成功入侵宿主的决定性因素之一。在此过程中，肌球蛋白，作为一类具有维持细胞形态、协助细胞内吞和胞吐功能的细胞骨架蛋白，参与了多种病毒的入侵过程。在本研究中，我们发现花鲈的肌球蛋白轻链 3 定位于细胞膜，且显著促进 RGNNV 入侵宿主细胞，提示 MYL3 可能是 RGNNV 的潜在受体。为了进一步验证其功能，以模式生物海水青鳉为研究对象，通过体外实验发现：海水青鳉 MYL3 能够与 NNV 的结构蛋白 CP 直接互作；敲降 MmMYL3 或通过 MYL3 抗体封闭细胞，均能显著抑制 RGNNV 入侵。此外，MmMYL3 能够介导 RGNNV 入侵非敏感细胞 HEK293T。体内实验结果表明在 RGNNV 感染的情况下注射 MmMYL3 重组蛋白能够提高海水青鳉的存活率，进一步证明 MYL3 在病毒感染中的重要作用。

关键词：神经坏死病毒；肌球蛋白轻链 3；受体

Identification and functional characterization of myosin light chain 3, a new receptor for fish nervous necrosis virus

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Abstract： Nervous necrosis virus (NNV) is one of the pathogens that seriously jeopardize a wide range of marine and freshwater economic fish, but its infection mechanism is still not fully elucidated. The viral receptor is one of the determining factors for the successful infection of the virus into the host. In this process, myosins, as a class of cytoskeletal proteins with the function of maintaining cellular morphology and assisting in cellular endocytosis and cytotranspiration, are involved in the infection process of a variety of viruses. In this study, we found myosin light chain 3 (MYL3) of the sea perch (Lateolabrax japonicus) was localized on the cell membrane and significantly promoted the infection of RGNNV into the host cells, suggesting that MYL3 may be a potential receptor for RGNNV. To further validate its function, the model organism, marine medaka, was used as a research object, and in vitro experiments revealed that MmMYL3 could directly interact with the only structural protein CP of RGNNV; knockdown of MmMYL3 or cell block by MYL3 antibody significantly inhibited the infection of RGNNV. In addition, ectopic expression of MmMYL3 facilitated the internalization of RGNNV into cells typically resistant to RGNNV infection. The results of in vivo experiments showed that the injection of MmMYL3 recombinant protein in the presence of RGNNV infection was able to improve the survival rate of marine medaka, further demonstrating the important role of MYL3 in viral infection. The above results suggest that MYL3 is a new receptor for RGNNV, which not only deepens the understanding of the pathogenic mechanism of NNV, but also provides a potential target for the development of receptor-blocking-based prevention and control strategies.

Key words:： Nervous necrosis virus;myosin light chain 3;receptor

NPY 参与罗非鱼不同组织免疫调节作用的初步研究

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摘要：神经肽 Y（Neuropeptide Y，NPY）是一种重要的神经递质与促食欲因子，广泛分布于脊椎动物神经系统。在哺乳动物中，NPY 具有多项功能，但在鱼类的 NPY 研究中，其是否参与鱼类的免疫调控和具体的作用还有待阐明。因此，在本研究中，我们在罗非鱼中构建了的 NPY 与无乳链球菌共注射模型，对不同组织的免疫水平进行检测。结果显示，单独的 NPY 注射对免疫组织的影响微弱，具有较好的生物安全性。而在无乳链球菌引起的炎症模型中，NPY 能够补偿 y8b mRNA 的表达水平，抑制细胞因子风暴、缓解头肾和脾脏组织的病理学变化及细胞凋亡水平。此外，我们还研究了 NPY 对罗非鱼胃肠道免疫的调控效果，结果发现 NPY 能够改善无乳链球菌引起的胃和后肠组织的组织损伤和炎症反应，对前肠和中肠没有显著调控作用。本研究关注了 NPY 在罗非鱼不同组织中的免疫调控效果，其结果可为 NPY 参与罗非鱼免疫调控的具体机制研究提供参考。

关键词：罗非鱼；神经肽 Y；无乳链球菌

A preliminary study on the involvement of NPY in the immuno-regulatory effects of different tissues in tilapia (Oreochromis niloticus)

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Abstract：Neuropeptide Y (NPY), an important neurotransmitter, is widely distributed in the nervous systems of vertebrates. Multiple functions of NPY in mammals include the regulation of brain activity, emotion, stress response, feeding, digestion, metabolism and immune function. In studies of NPY in fish, whether it is involved in immune regulation in fish and its specific role remains to be elucidated. Therefore, we conducted a preliminary study on the immunological role of NPY in different immune tissues of tilapia. In this study, we examined the immune levels of different tissues in a co-injection model of NPY with Streptococcus agalactiae constructed in tilapia. The results showed that NPY injection alone had a weak effect on immune tissues and had a good biosafety profile. Whereas, in a model of inflammation caused by Streptococcus agalactiae, NPY was able to compensate for the expression level of y8b mRNA. It also inhibited cytokine storm, alleviated pathological changes and apoptosis levels in head kidney and spleen. Combined with the analysis of RNA-seq results, the anti-inflammatory effect of NPY may mainly affect leukocyte differentiation and down-regulate the expression of inflammatory factors. In turn, it suppressed immune-related signaling pathways and apoptosis levels. In addition, we investigated the modulatory effects of NPY on gastrointestinal immunity in tilapia. The results revealed that NPY ameliorated tissue damage and inflammatory responses in gastric and hindgut induced by Streptococcus agalactiae, and did not have a significant modulatory effect on foregut and midgut. This study focused on the immunomodulatory effects of NPY in different tissues of tilapia. The results may provide a reference for the study of the specific mechanism of NPY involved in the immunoregulation of tilapia.

Key words:：Tilapia, Neuropeptide Y, Streptococcus agalactiae

监测三文鱼新鲜度的荧光探针的制备及应用

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摘要：水产品富含蛋白质、脂肪酸等多种营养物质，在贮藏与运输过程中极易发生腐败变质，产生胺类、醇类及硫类等挥发性物质。其中，生物胺是评价鱼类新鲜度的重要参数，生物胺是由蛋白质或氨基酸腐败产生，人类误食含生物胺类过高的水产品会危害自身健康。因此，监测水产品中的胺类物质对保障人类健康至关重要。本研究以噻吩醛为荧光基团，酯基作为识别基团，通过 Knoevenagel 缩合反应，设计并合成了荧光探针 PAC，并通过物理沉降法制备负载 PAC 的指示标签，用于实时监测三文鱼新鲜度。结果表明，PAC 具有较大的斯托克斯位移（125 nm），在 pH 4-11 对胺类物质响应良好，检测限低至 1.30 μM，具有较高的灵敏度。随着鱼肉新鲜度的下降，制备的指示标签表现出明显的比色和荧光变化，日光和荧光均呈现红色-橙红色-浅粉色的变化。本研究为实现水产品新鲜度的实时、无损、可视化监测提供了有力的技术支撑。

关键词：荧光探针；新鲜度；指示标签；噻吩醛

Preparation and Application of Fluorescent Probe for Monitoring Freshness of Salmon

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Abstract： Aquatic products are rich in a variety of nutrients such as proteins and fatty acids, which are highly susceptible to spoilage and deterioration during storage and transportation, producing volatile substances such as amines, alcohols, and sulfides. Among these, biogenic amines are an important parameter for evaluating the freshness of fish. Biogenic amines are produced by the spoilage of proteins or amino acids, and the consumption of aquatic products containing excessively high levels of biogenic amines can pose health risks to humans. Therefore, monitoring amine substances in aquatic products is crucial for ensuring human health. In this study, using thiophene aldehyde as the fluorescent group and an ester group as the recognition group, a fluorescent probe PAC was designed and synthesized through the Knoevenagel condensation reaction. An indicator label loaded with PAC was prepared by physical sedimentation method for real-time monitoring of salmon freshness. The results showed that PAC had a large Stokes shift (125 nm) and responded well to amine substances at pH 4-11, with a detection limit as low as 1.30 μM, demonstrating high sensitivity. As the freshness of the fish decreases, the prepared indicator label exhibits significant colorimetric and fluorescent changes, showing a transition from red to orange-red to light pink under both daylight and fluorescence. The correlation between the B/G value of the color change of the indicator label under daylight and the TVB-N value with the change in freshness is good. This study provides strong technical support for the real-time, non-destructive, and visual monitoring of the freshness of aquatic products.

Key words:： fluorescent probe; freshness; indicating label; thiophene aldehyde

我国鲑鳟疫病流行病学与疫苗研发

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摘要：传染性造血器官坏死病（Infectious hematopoietic necrosis，IHN）和传染性胰脏坏死病（Infectious hematopoietic necrosis，IPN）是主要威胁鲑鳟鱼的两种病毒性传染病，分别属于我国二类和三类动物疫病。团队通过十余年的流行病学调查，揭示了我国鲑鳟养殖环境现行 IHN 病毒和 IPN 病毒的基因型、分布及危害；基于系统进化分析及毒力分析结果，筛选获得疫苗候选毒株，创制了实验室保护效率高达 90%以上的 IHN 核酸疫苗，已完成该疫苗的转基因生物安全评价，获批我国首个水产核酸疫苗转基因生物安全证书；制备了保护期>9 个月、保存期 1 年以上的 IHN/IPN 二联灭活疫苗，正开展中间试制研究。该系列疫苗的产业化有望解决制约我国虹鳟产业的两大疫病难题。

关键词：鲑鳟鱼；疫病；传染性造血器官坏死病；传染性胰脏坏死病；分子流行病学；疫苗

Epidemiology and vaccine development for viral diseases of salmonids in China

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Abstract：Infectious hematopoietic necrosis (IHN) and Infectious hematopoietic necrosis (IPN) are two kinds of infectious diseases that mainly threaten salmon and trout. They belong to Class II and Class III animal epidemics in China, respectively. The genotypes, distribution and hazards of IHN virus and IPN virus in salmon culture environment in China were revealed through epidemiological investigation over the past ten years. Based on the results of phylogenetic analysis and virulence analysis, the vaccine candidate strains were screened and obtained, and the IHN nucleic acid vaccine with a laboratory protection efficiency of more than 90% was created. The GMO safety evaluation of the vaccine was completed, and the GMO safety certificate of was approved as the first aquatic nucleic acid vaccine in China. IHN/IPN vaccine with a protection period of more than 9 months and a shelf life of more than 1 year has been prepared. The industrialization of this series of vaccines is expected to solve the two major problems that restrict the rainbow trout industry in China.

Key words: ： Salmon and trout; Epidemic diseases; Infectious hematopoietic organ necrosis; Infectious pancreatic necrosis; Molecular epidemiology; Vaccine

监测三文鱼新鲜度的荧光探针的制备及应用

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摘要：水产品富含蛋白质、脂肪酸等多种营养物质，在贮藏与运输过程中极易发生腐败变质，产生胺类、醇类及硫类等挥发性物质。其中，生物胺是评价鱼类新鲜度的重要参数，生物胺是由蛋白质或氨基酸腐败产生，人类误食含生物胺类过高的水产品会危害自身健康。因此，监测水产品中的胺类物质对保障人类健康至关重要。本研究以噻吩醛为荧光基团，酯基作为识别基团，通过Knoevenagel缩合反应，设计并合成了荧光探针PAC，并通过物理沉降法制备负载PAC的指示标签，用于实时监测三文鱼新鲜度。结果表明，PAC具有较大的斯托克斯位移（125 nm），在pH 4-11对胺类物质响应良好，检测限低至1.30 μM，具有较高的灵敏度。随着鱼肉新鲜度的下降，制备的指示标签表现出明显的比色和荧光变化，日光和荧光均呈现红色-橙红色-浅粉色的变化。本研究为实现水产品新鲜度的实时、无损、可视化监测提供了有力的技术支撑。

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Abstract： Aquatic products are rich in a variety of nutrients such as proteins and fatty acids, which are highly susceptible to spoilage and deterioration during storage and transportation, producing volatile substances such as amines, alcohols, and sulfides. Among these, biogenic amines are an important parameter for evaluating the freshness of fish. Biogenic amines are produced by the spoilage of proteins or amino acids, and the consumption of aquatic products containing excessively high levels of biogenic amines can pose health risks to humans. Therefore, monitoring amine substances in aquatic products is crucial for ensuring human health. In this study, using thiophene aldehyde as the fluorescent group and an ester group as the recognition group, a fluorescent probe PAC was designed and synthesized through the Knoevenagel condensation reaction. An indicator label loaded with PAC was prepared by physical sedimentation method for real-time monitoring of salmon freshness. The results showed that PAC had a large Stokes shift (125 nm) and responded well to amine substances at pH 4-11, with a detection limit as low as 1.30 μM, demonstrating high sensitivity. As the freshness of the fish decreases, the prepared indicator label exhibits significant colorimetric and fluorescent changes, showing a transition from red to orange-red to light pink under both daylight and fluorescence. The correlation between the B/G value of the color change of the indicator label under daylight and the TVB-N value with the change in freshness is good. This study provides strong technical support for the real-time, non-destructive, and visual monitoring of the freshness of aquatic products.

Key words:： fluorescent probe; freshness; indicating label; thiophene aldehyde

感染溶藻弧菌的属于新病毒科的新型噬菌体的鉴定与基因组分析

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江苏海洋大学，厦门大学，深圳大学高等研究院，中国科学院南海海洋研究所，澳门大学，广西北部湾海洋资源、环境与可持续发展重点实验室/自然资源部

摘要： 本研究从养殖用水中分离得到一种能有效感染溶藻弧菌病原菌的新型噬菌体vB_ValC_RH1G，并对其进行了微生物学和基因组学分析。透射电镜显示RH1G具有肌尾病毒的形态。改噬菌体仅能感染宿主，潜伏期为20 min，爆发大小为218.1 PFU/cell。基因组测序结果显示，RH1G具有194,806 bp的双链DNA基因组，GC含量为34.91%。RH1G的基因组序列与Genebank数据库中记载的其他噬菌体的相似性在96.87%-88.51%。基于主衣壳蛋白等多个保守基因的系统发育分析显示，噬菌体RH1G与其他4个噬菌体归为同一个进化支，并与国际病毒分类委员会（ICTV）批准的所有已知的Caudoviricetes目的噬菌体不同，对Caudoviricetes目不同噬菌体的蛋白质组学比较支持这一聚类结果，并建议将RH1G与其他5个噬菌体归类为Caudoviricetes目的一个新的科。

关键词： 溶藻弧菌，噬菌体，生物学特性，基因组分析，噬菌体治疗

Identification and genomic analysis of a novel bacteriophage belonging to a new virus family infected with Vibrio alginolyticus

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Abstract： Vibriosis outbreak has caused huge economic losses to aquaculture industry, and the frequent use of antibiotics has led to the development of bacterial resistance, and phages have the conditions to replace antibiotics for the treatment of bacterial diseases. In this study, a new bacteriophage vB_ValC_RH1G, which can effectively infect the pathogenic bacteria of Vibrio alginolyticus, was isolated from aquaculture water and analyzed by microbiology and genomics. Transmission electron microscopy showed that RH1G had the form of Myoviridae virus. The phage can only infect the host, the incubation period is 20 min, and the burst size is 218.1 PFU/cell. The results of genome sequencing showed that RH1G had 194,806 bp double-stranded DNA genome with GC content of 34.91%. The similarity between RH1G genome sequence and other phages recorded in Genebank database was 96.87% to 88.51%. Phylogenetic analyses based on genomes and proteomics showed that, including the main capsid protein, showed that phage RH1G belonged to the same clade as four other phages, including phage Va1 (MK387337.2), phiKT1024 (OM249648.1), phiTY18 (MW451250.1), VB_VaC_TDDLMA (PP083315.1), and VB_VaC_SRILMA (PP083314.1), and unlike all known bacteriophages of the class Caudoviricetes approved by the International Committee on Taxonomy of Viruses (ICTV), Proteomic comparisons of different phages of the order Caudoviricetes support the clustering results and suggest that RH1G, together with five other phages, be classified as a new family of the class Caudoviricetes. Subsequent analysis of the core genes also revealed which genes were shared in this new cluster. Overall, these results provide a characterization of phage RH1G and support our proposal for a new family in Caudoviricetes.

Key words:： Myoviridae, Vibrio alginolyticus, phage, genome analysis

监测三文鱼新鲜度的荧光探针的制备及应用

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摘要：水产品富含蛋白质、脂肪酸等多种营养物质，在贮藏与运输过程中极易发生腐败变质，产生胺类、醇类及硫类等挥发性物质。其中，生物胺是评价鱼类新鲜度的重要参数，生物胺是由蛋白质或氨基酸腐败产生，人类误食含生物胺类过高的水产品会危害自身健康。因此，监测水产品中的胺类物质对保障人类健康至关重要。本研究以噻吩醛为荧光基团，酯基作为识别基团，通过 Knoevenagel 缩合反应，设计并合成了荧光探针 PAC，并通过物理沉降法制备负载 PAC 的指示标签，用于实时监测三文鱼新鲜度。结果表明，PAC 具有较大的斯托克斯位移（125 nm），在 pH 4-11 对胺类物质响应良好，检测限低至 1.30 μM，具有较高的灵敏度。随着鱼肉新鲜度的下降，制备的指示标签表现出明显的比色和荧光变化，日光和荧光均呈现红色-橙红色-浅粉色的变化。本研究为实现水产品新鲜度的实时、无损、可视化监测提供了有力的技术支撑。

关键词：荧光探针；新鲜度；指示标签；噻吩醛

Preparation and Application of Fluorescent Probe for Monitoring Freshness of Salmon

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Abstract： Aquatic products are rich in a variety of nutrients such as proteins and fatty acids, which are highly susceptible to spoilage and deterioration during storage and transportation, producing volatile substances such as amines, alcohols, and sulfides. Among these, biogenic amines are an important parameter for evaluating the freshness of fish. Biogenic amines are produced by the spoilage of proteins or amino acids, and the consumption of aquatic products containing excessively high levels of biogenic amines can pose health risks to humans. Therefore, monitoring amine substances in aquatic products is crucial for ensuring human health. In this study, using thiophene aldehyde as the fluorescent group and an ester group as the recognition group, a fluorescent probe PAC was designed and synthesized through the Knoevenagel condensation reaction. An indicator label loaded with PAC was prepared by physical sedimentation method for real-time monitoring of salmon freshness. The results showed that PAC had a large Stokes shift (125 nm) and responded well to amine substances at pH 4-11, with a detection limit as low as 1.30 μM, demonstrating high sensitivity. As the freshness of the fish decreases, the prepared indicator label exhibits significant colorimetric and fluorescent changes, showing a transition from red to orange-red to light pink under both daylight and fluorescence. The correlation between the B/G value of the color change of the indicator label under daylight and the TVB-N value with the change in freshness is good. This study provides strong technical support for the real-time, non-destructive, and visual monitoring of the freshness of aquatic products.

Key words:： fluorescent probe; freshness; indicating label; thiophene aldehyde

GCRV 病毒蛋白 VP6 利用自噬降解 TBK1 实现免疫逃逸

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摘要：干扰素（IFN）反应是鱼体抵御病毒侵袭的第一道免疫防线，但草鱼出血病病毒（GCRV）却可以逃避鱼体的免疫反应造成感染，其中的机制尚不清楚。本研究表明，GCRV-873 的 S8 节段编码蛋白 VP6 可以通过自噬途径降解 TANK 结合激酶 1（TBK1），阻断 IFN 反应从而实现免疫逃逸。首先，过表达 VP6 可以增强 GCRV 在细胞中的增殖，同时阻断 poly I:C 和 GCRV 诱导的 IFN 启动子的激活。在蛋白水平， VP6 与 TBK1 具有相互作用并抑制 TBK1 表达，自噬抑制剂处理能够恢复 VP6 对 TBK1 的降解，共表达 VP6 和 TBK1 后细胞中微管相关蛋白轻链 3（LC3）发生聚集，细胞自噬水平显著上升，表明 VP6 可能通过自噬途径降解 TBK1。此外，VP6 削弱了 TBK1 介导的细胞抗病毒功能。本研究揭示了 GCRV 病毒蛋白 VP6 利用自噬途径降解 TBK1 阻断宿主 IFN 反应的分子机制，为阐明 GCRV 的致病机理提供了理论依据。

关键词：草鱼出血病病毒、VP6、TBK1、自噬

Grass carp reovirus VP6 restricts interferon production by degrading TBK1 in the autophagy pathway

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Abstract： The interferon (IFN) response serves as a potent defense mechanism against viral infections in fish. However, grass carp reovirus (GCRV) virus is still capable of evading the IFN system, albeit the specific mechanisms remain unclear. In this study, we report that the VP6 of GCRV employs an immune evasion mechanism by degrading TANK-binding kinase 1(TBK1) through the autophagy pathway, thereby inhibiting IFN activation. Firstly, overexpression of VP6 facilitated GCRV virus replication, while, it impeded poly I:C and GCRV-induced IFN promoter activation. In addition, VP6 was observed to interact with TBK1 and suppressed TBK1 expression. Treatment with autophagy pathway inhibitors can restore TBK1 degradation, indicating that TBK1 is degraded by VP6 in the autophagy pathway. Furthermore, VP6 substantially attenuated the cellular antiviral response mediated by TBK1, consequently suppressing interferon production. These findings elucidate GCRV's exploitation of the host autophagy pathway for immune evasion. This study reveals the molecular mechanism by which GCRV evades from the host immune response.

Key words:：Grass carp reovirus, VP6, TBK1, autophagy

中华绒螯蟹 CDC42 基因特征及在螺原体感染中的作用研究

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河南师范大学

摘要：细胞分裂周期蛋白 42（Cdc42 ）是一类 Rho GTP 酶，作为信号调控枢纽，其在先天免疫中发挥着重要作用。然而，Cdc42 在中华绒螯蟹（Eriocheir sinensis）防御螺原体感染中的作用尚不清楚。本研究通过 RACE 技术克隆了河蟹 Cdc42 基因（EsCdc42），并通过体内和体外的 RNA 干扰以及果蝇 S2 细胞过表达实验， 研究其在螺原体侵染过程中的作用。结果表明，EsCdc42 进化上高度保守，其在河蟹的多种组织中广泛表达，在肠和血淋巴细胞中表达量较高。螺原体刺激后，EsCdc42 在河蟹血淋巴细胞的表达水平显著上调。沉默 EsCdc42 会加快螺原体的侵染，血淋巴细胞凋亡率和个体累积死亡率明显增加。在果蝇 S2 细胞中过表达 EsCdc42，共聚焦显微镜分析表明，其在 S2 细胞核质中均有分布，且会抑制螺原体的侵染。这些结果表明，EsCdc42 参与了河蟹抵御螺原体感染的免疫应答。

关键词：中华绒螯蟹，Cdc42，螺原体，先天免疫

Characterization of Eriocheir sinensis CDC42 and its role in Spiroplasma eriocheiris infection

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Abstract：Cdc42 is a class of Rho GTPases that serves as a signaling hub and plays an important role in innate immunity. However, the role of Cdc42 in the defense against Spiroplasma eriocheiris infection in the Chinese mitten crab (Eriocheir sinensis) is not clear. In this study, we cloned the E. sinensis Cdc42 gene (EsCdc42) using RACE technology and studied its role in S. eriocheiris infection using in vivo and in vitro RNA interference and overexpression expression in Drosophila S2 cells. The results showed that EsCdc42 is highly conserved and is widely expressed in various tissues of the E. sinensis, with high expression levels in the gut and hemocytes. S. eriocheiris infection resulted a significant upregulation of EsCdc42 expression in hemocytes. Silencing of EsCdc42 could accelerated S. eriocheiris infection, and the rate of hemocyte apoptosis and individual cumulative mortality were significantly increased. Overexpression of EsCdc42 in Drosophila S2 cells was analyzed by confocal microscopy, showing that it was distributed in both the nucleus and cytoplasm of S2 cells. And overexpression the EsCdc42 will enhance the ability of S2 cell against S. eriocheiris infection. These results suggested that EsCdc42 plays a role in the crab's defense against S. eriocheiris infection.

Key words:：Eriocheir sinensis, Cdc42, Spiroplasma eriocheiris, innate immunity

监测三文鱼新鲜度的荧光探针的制备及应用

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渤海大学食品科学与工程学院

摘要：水产品富含蛋白质、脂肪酸等多种营养物质，在贮藏与运输过程中极易发生腐败变质，产生胺类、醇类及硫类等挥发性物质。其中，生物胺是评价鱼类新鲜度的重要参数，生物胺是由蛋白质或氨基酸腐败产生，人类误食含生物胺类过高的水产品会危害自身健康。因此，监测水产品中的胺类物质对保障人类健康至关重要。本研究以噻吩醛为荧光基团，酯基作为识别基团，通过 Knoevenagel 缩合反应，设计并合成了荧光探针 PAC，并通过物理沉降法制备负载 PAC 的指示标签，用于实时监测三文鱼新鲜度。结果表明，PAC 具有较大的斯托克斯位移（125 nm），在 pH 4-11 对胺类物质响应良好，检测限低至 1.30 μM，具有较高的灵敏度。随着鱼肉新鲜度的下降，制备的指示标签表现出明显的比色和荧光变化，日光和荧光均呈现红色-橙红色-浅粉色的变化。本研究为实现水产品新鲜度的实时、无损、可视化监测提供了有力的技术支撑。

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Abstract： Aquatic products are rich in a variety of nutrients such as proteins and fatty acids, which are highly susceptible to spoilage and deterioration during storage and transportation, producing volatile substances such as amines, alcohols, and sulfides. Among these, biogenic amines are an important parameter for evaluating the freshness of fish. Biogenic amines are produced by the spoilage of proteins or amino acids, and the consumption of aquatic products containing excessively high levels of biogenic amines can pose health risks to humans. Therefore, monitoring amine substances in aquatic products is crucial for ensuring human health. In this study, using thiophene aldehyde as the fluorescent group and an ester group as the recognition group, a fluorescent probe PAC was designed and synthesized through the Knoevenagel condensation reaction. An indicator label loaded with PAC was prepared by physical sedimentation method for real-time monitoring of salmon freshness. The results showed that PAC had a large Stokes shift (125 nm) and responded well to amine substances at pH 4-11, with a detection limit as low as 1.30 μM, demonstrating high sensitivity. As the freshness of the fish decreases, the prepared indicator label exhibits significant colorimetric and fluorescent changes, showing a transition from red to orange-red to light pink under both daylight and fluorescence. The correlation between the B/G value of the color change of the indicator label under daylight and the TVB-N value with the change in freshness is good. This study provides strong technical support for the real-time, non-destructive, and visual monitoring of the freshness of aquatic products.

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监测三文鱼新鲜度的荧光探针的制备及应用

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摘要：水产品富含蛋白质、脂肪酸等多种营养物质，在贮藏与运输过程中极易发生腐败变质，产生胺类、醇类及硫类等挥发性物质。其中，生物胺是评价鱼类新鲜度的重要参数，生物胺是由蛋白质或氨基酸腐败产生，人类误食含生物胺类过高的水产品会危害自身健康。因此，监测水产品中的胺类物质对保障人类健康至关重要。本研究以噻吩醛为荧光基团，酯基作为识别基团，通过 Knoevenagel 缩合反应，设计并合成了荧光探针 PAC，并通过物理沉降法制备负载 PAC 的指示标签，用于实时监测三文鱼新鲜度。结果表明，PAC 具有较大的斯托克斯位移（125 nm），在 pH 4-11 对胺类物质响应良好，检测限低至 1.30 μM，具有较高的灵敏度。随着鱼肉新鲜度的下降，制备的指示标签表现出明显的比色和荧光变化，日光和荧光均呈现红色-橙红色-浅粉色的变化。本研究为实现水产品新鲜度的实时、无损、可视化监测提供了有力的技术支撑。

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两株中华绒螯蟹源二尖梅奇酵母的生物学特性及其致病力比较

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摘要：旨在比较两株中华绒螯蟹源酵母菌分离株的生物学特性和致病力差异，本试验采用多基因序列分析进行物种鉴定，结合人工感染试验、形态学观察、生理生化反应检测及生长曲线测定进行比较分析。基于基因序列分析，2 菌株均被鉴定为二尖梅奇酵母；人工感染试验结果表明，2 菌株能够导致中华绒螯蟹“牛奶病”，且致病力存在明显差异，菌株 Y1 相较于菌株 W1 导致中华绒螯蟹更高死亡率（100% VS. 46.67%）；相同培养条件下呈现明显表型差异，其中，菌株 W1 菌落呈白色，细胞卵圆形、表面圆润光滑，而菌株 Y1 菌落呈淡黄色，细胞椭圆形、表面粗糙，且菌株 Y1 细胞大于菌株 W1 细胞；生理生化特征显示生理生化指标基本相同；而生长曲线显示菌株 Y1 更早进入对数生长期、到达平台期。因此，本文明确了两株致“牛奶病”二尖梅奇酵母在相同条件下的生物学特性和致病力差异，丰富了二尖梅奇酵母分子分类学研究，为深入研究二尖梅奇酵母致病机制提供理论依据。

关键词：二尖梅奇酵母；牛奶病；生物学特性；多基因序列分析；致病力

Characterizing the Biological Traits and Comparing the Pathogenicity of Two Metschnikowia bicuspidata Strains Isolated from Eriocheir sinensis

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Abstract：In the study, polygenic sequence analysis was used to determine the taxanomic position of yeast strains W1 and Y1 isolated from Eriocheir sinensis. In addition, artificial challenge tests, morphological observation, physiochemical tests, and growth curves were conducted to characterize and compare their biological traits and pathogenicity. Both the strains were identified as Metschnikowia bicuspidate, according to the sequence analyses using ITS, 26S and 18S rRNA genes. Results of experimental challenge tests showed apparent difference in virulence between the two strains, which could cause the emulsification disease of E. sinensis. Strain Y1 caused higher mortality of E. sinensis (100% VS. 46.67%) in comparison to that of strain W1. Obvious phenotypic differences were also observed for the two strains under the same culture conditions. Strain W1 formed white colonies, of which cells were oval and smooth, while strain Y1 formed pastel yellow, and the cells were ellipsoidal and rough. Cells of strain Y1 were relatively larger in size than strain W1. Strains W1 and Y1 shared generally consistent physiochemical traits. However, strain Y1 earlier entered the logarithmic growth stage and reached the platform stage than strain W1. Therefore, the present study determined the biological characteristics and virulence differences of the two M. bicuspidate isolates, which were causative agents of the emulsification disease, under the same conditions. These results enrich the molecular taxonomic studies of M. bicuspidata, and provide theoretical basis for insights into the pathogenic mechanism of M. bicuspidata and technical supports for the prevention and control of the emulsification disease of E. sinensis.

Key words:：Metschnikowia bicuspidata; emulsification disease; biological characteristics; polygenic sequence analysis; pathogenicity

簇生蟹奴内体寄生组织和外体发育过程研究

丰程程，曹旭，杜明会，姜宏波，李晓东
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摘要：簇生蟹奴寄生在中华绒螯蟹体内导致宿主蟹生长缓慢甚至死亡，严重损伤中华绒螯蟹的食用价值和繁殖能力。本研究发现簇生蟹奴寄生导致雄蟹的 6 个腹节的节宽变化趋势显著雌性化，可作为簇生蟹奴病早期诊断的依据。簇生蟹奴寄生在中华绒螯蟹的多个组织中，表达量从高到低依次为肝胰腺、精巢、卵巢、眼柄神经节、胸神经节、肠、脑、肌肉、心脏、血、鳃和胃。在肝胰腺、性腺、神经节等组织中簇生蟹奴内体呈结构高度致密的分支根状形态，压迫各组织细胞，导致细胞破碎并出现大量空腔。簇生蟹奴外体发育分为未成熟期、卵黄生成期、胚胎发育期和虫体排放期四个时期，最后萎缩脱落。主要细胞类型按照分期依次是卵原细胞、卵母细胞、受精卵和眼胚胎期以及附肢期。随后附肢期挣脱外层卵膜通过外体排放口排放到水体中发育成营自由生活的无节幼体。建议在蟹奴病高发期，定期检测养殖水体中是否存在簇生蟹奴无节幼体，以便迅速抑制蟹奴病的传播。

关键词：簇生蟹奴，寄生，外体，中华绒螯蟹

Study on the parasitic tissue of interna and the development process of the externae of Polyascus gregaria

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Abstract： Polyascus gregaria, a parasite that infests the Chinese mitten crab (Eriocheir sinensis), causes slow growth and even death of the host crab, significantly compromising its edible value and reproductive capability. This study discovered that P. gregaria infestation leads to a notable feminization in the width variation trend of the six abdominal segments of male crabs, which can serve as a basis for early diagnosis of P. gregaria infestation. The parasite was found to infest multiple tissues of E. sinensis, with expression levels ranging from high to low in the hepatopancreas, testis, ovary, eyestalk neuroganglion, thoracic neuroganglion, intestine, brain, muscle, heart, blood, gill, and stomach. In tissues like the hepatopancreas, gonads, and neuroganglia, the interna of P. gregaria exhibits a dense, branched root-like structure, compressing tissue cells and resulting in cell rupture, tissue atrophy, and the formation of numerous cavities. The development of the externae of P. gregaria is categorized into four distinct stages: immature stage, vitellogenesis stage, embryo development stage, and parasite emission stage, followed by atrophy and shedding. The primary cell types, in sequential stages, are oogonia, oocytes, fertilized eggs and eye embryos， and appendage embryos. Subsequently, the appendage embryos break free from the outer egg membrane and are released into the seawater through the mantle opening, developing into free-swimming nauplius larvae. We recommend regular testing of aquaculture water for the presence of P. gregaria larvae during peak parasite disease periods to swiftly halt the spread of the infestation.

Key words:：Polyascus gregaria; parasite；externae ;Eriocheir sinensis

草鱼呼肠孤病毒利用硫酸乙酰肝素作为其吸附受体

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摘要：草鱼呼肠孤病毒（GCRV）引起的草鱼出血病，对我国的草鱼养殖业造成了重大的经济损失，出血病防控及抗病品系培育是亟待研究的课题。病毒感染起始于病毒组分与受体之间的特定相互作用，但 GCRV 感染所需的受体尚不清楚。在本研究中，我们发现细胞表面的硫酸乙酰肝素是 I 型及 II 型 GCRV 的吸附受体。酶解细胞表面的硫酸乙酰肝素能够导致 GCRV 的吸附及感染效率显著降低。硫酸乙酰肝素以及同源物肝素能够显著抑制 GCRV 吸附到细胞表面。敲降硫酸乙酰肝素合同通路关键基因能显著降低 GCRV 的吸附和感染效率，而过表达上述基因却能够促进 GCRV 的吸附和感染效率。纯化的 GCRV 病毒颗粒以及 GCRV 外衣壳蛋白均能够结合硫酸乙酰肝素。此外，用肝素预先孵育 GCRV 病毒液，或在饲料中添加肝素，均能够显著降低草鱼感染 GCRV 后的死亡率。总之，本研究证明了硫酸乙酰肝素是 GCRV 的吸附受体，为出血病防控及抗病品系培育提供了重要的分子靶标。

关键词：草鱼出血病，受体，吸附，硫酸乙酰肝素，肝素，外衣壳蛋白

Cell surface heparan sulfate is an attachment receptor for grass carp reovirus

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Abstract： Grass carp reovirus (GCRV) induces hemorrhagic disease, resulting in significant economic losses to the aquaculture industry of grass carp, a vital commercial fish species in China. Virus infection begins with specific interactions between virion components and cellular receptors, however, the cellular receptors responsible for the initiation of GCRV infection remain unclear. In this study, we demonstrated that cell surface heparan sulfate (HS) acts as an attachment receptor for both GCRV subtype I and subtype II. Removal of cell surface HS by heparinase led to a significant reduction in GCRV attachment and subsequent infection. We found that both HS and its homologue, heparin, inhibit the attachment of GCRV to cells. Moreover, knockdown of HS expression in cells had a notable impact on GCRV attachment and infection, whereas increasing HS biosynthesis showed the opposite trend. Furthermore, we confirmed that the outer capsid proteins from GCRV subtype I and GCRV subtype II, as well as purified GCRV virions, bind to the HS. Importantly, pretreatment of GCRV with heparin or feeding grass carp with feed containing heparin remarkable reduced fish mortality caused by GCRV infection. Collectively, these results highlight the crucial role of HS as an attachment receptor for GCRV and therefore provide a promising target for the prevention and control of this virus.

Key words:：grass carp reovirus; receptors; attachment; heparan sulfate; heparin; outer capsid proteins

鳜肠道抗菌肽 hepcidin 对嗜水气单胞菌感染的防御模式

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摘要：细菌性败血症是鳜养殖中最为常见的细菌性疾病之一。Hepcidin 抗菌肽参与机体免疫以防御病原体。为研究鳜肠道 hepcidin 的防御模式，检测了嗜水气单胞菌感染的鳜肠道中铁代谢和免疫基因表达变化，体外抗菌实验检测 hep 合成肽抗菌活性。结果表明（1）Hep 合成肽可抑制嗜水气单胞菌、柱状黄杆菌和副溶血弧菌生长，对迟缓爱德华氏菌未见明显抑制作用。（2）嗜水气单胞菌感染后，hep 表达显著上调，48 hpi（115.01）。具转运 Fe2+作用的 fpn（2.75）和储存 Fe2+的 ftn（4.16）在 24 hpi 和 72 hpi 表达呈峰值。（3）Hep 可通过 TNF 和 Toll-like 信号通路分别诱导 il-1β和 socs3，il-8 和 tlr2，参与免疫调节。研究表明，感染早期（0-48 hpi），hep 可调节铁代谢使肠道内短期限铁以防御病原菌；晚期（48-96 hpi），hep 可通过诱导免疫因子参与免疫调节。

关键词：鳜，hepcidin，铁代谢，免疫作用，抗菌活性

Hepcidin defense patterns in intestine of mandarin fish (Siniperca chuatsi) against Aeromonas hydrophila infection

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Abstract： Mandarin fish (Siniperca chuatsi) aquaculture production is challenged by bacterial septicaemia, which is one of the most common bacterial diseases. Hepcidin antimicrobial peptide involved in immune defense when infected by kinds of pathogens. To understand the defense pattern of the hepcidin in the intestine of mandarin fish, the expression changes of iron metabolism-related genes (hepcidin, fpn, ftn, tf, and tfr1) and immune-related genes (il-1β, il-6, il-8, il-10, tnf-α, socs3, NF-κB activating protein, tlr1, and tlr2) were assessed after Aeromonas hydrophila (LC50-4d) challenge, as well as by detection of antibacterial activity of the hepcidin synthetic peptide in vitro. The results showed that (1) the hepcidin synthetic peptide inhibited the growth of A. hydrophilus, Vibrio parahaemolyticus, and Flavobacterium cloumnare, but no inhibitory effect on growth of Edwardsiella tarda. (2) After A. hydrophilus challenge, hepcidin gene expression increased and then decreased, with peak expressions of 115.01 at 48 hpi. The fpn (2.75), which functions as a transporter of Fe2+, and the ftn (4.16), which stores Fe2+, showed peak expression at 24 hpi and 72 hpi, respectively. (3) After pathogen challenge, il-1β, il-8, socs3, tlr2, and hepcidin with peak expression at 72 hpi (5.13, 37.05, 3.08) and 48 hpi (5.35, 115.01), respectively. Hepcidin may involved in the immunomodulatory by inducing il-1β and socs3 through the TNF signaling pathway while inducing il-8 and tlr2 by the Toll-like receptor signaling pathway. In summary, the results revealed that hepcidin could be directly involved in bacterial inhibition through regulating iron metabolism to short-term iron restriction against pathogen in the intestine at the early stages of A. hydrophila infection (0-48 hpi), and at the later stages of A. hydrophila infection (48-96 hpi), hepcidin may participated in immunomodulatory by inducing immune genes.

Key words:：Siniperca chuatsi, hepcidin, iron metabolism, immune regulation, antibacterial activity

草鱼抗原处理相关转运体因子的系统进化及其响应 SVCV 感染的转录表达分析

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摘要：TAP 蛋白是 MHC I 通路的抗原相关转运体，以 ATP 依赖的方式协助胞质肽装配至 MHC I 分子上呈递给 CD8+T 细胞。本研究克隆了草鱼 TAP1、TAP2t、TAP2a 基因，发现草鱼 TAP 基因结构非常保守，与鲤科鱼类亲缘关系最近。草鱼 TAP 基因在肾脏和头肾组织中表达量较高；草鱼感染嗜水气单胞菌 72h 后，TAP1、TAP2t、TAP2a 表达显著上调。此外，细胞因子 IFNγ和 IL-1β上调 TAP1 和 TAP2t 的表达。EPC 细胞在 SVCV 感染 12h、24h 和 36h 后 TAP1 的表达量显著升高，TAP2t 表达在 12h 上调，随后明显下调。我们进而在 EPC 细胞中过表达 SVCV N、P、M 或 G 蛋白 36h TAP2t 表达下调效果显著，与之相比，与之相比，过表达 SVCV N 或 G 蛋白上调 TAP1，而过表达 SVCV M 或 P 蛋白则抑制 TAP1 的表达。实验结果提示，草鱼 TAP 基因参与应答细菌和病毒感染的免疫反应。

关键词：抗原处理相关转运体、MHC I 、草鱼、转录表达分析，细菌，病毒

Phylogenetic evolution of transporter associated with antigen processing factors in grass carp(Ctenopharyngodon ideals) and their transcriptional expression analysis in response to SVCV infection

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Abstract：Transporter associated with antigen processing proteins are antigen-associated transporters of the MHC I pathway that assist in assembling cytoplasmic peptides onto MHC I molecules for presentation to CD8+ T cells in an ATP-dependent manner. In this study, we cloned the grass carp TAP1, TAP2t, and TAP2a genes and found that the grass carp TAP genes are structurally very conserved and have the closest affinity to carp family fishes. Grass carp TAP genes were highly expressed in kidney and cephalic kidney tissues; TAP1, TAP2t, and TAP2a were significantly up-regulated in grass carp after 72h of infection with Aeromonas hydrophila. In addition, the cytokines IFNγ and IL-1β up-regulated the expression of TAP1 and TAP2t. EPC cells showed significantly higher expression of TAP1 after 12h, 24h, and 36h of SVCV infection, and the expression of TAP2t was up-regulated at 12h and then significantly down-regulated. We then overexpressed SVCV N, P, M, or G proteins in EPC cells for 36h The downregulation of TAP2t expression was significant, compared to the upregulation of TAP1 by overexpression of SVCV N or G proteins, while overexpression of SVCV M or P proteins inhibited the expression of TAP1. The results suggest that grass carp TAP genes are involved in the immune response in response to bacterial and viral infections.

Key words:：transporter associated with antigen processing, MHC I, grass carp, transcriptional expression analysis, bacterial, viral

ELMO1 调控灿烂弧菌吞噬的分子机制探究

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摘要：ELMO1 在哺乳动物中被鉴定为 RAC 信号通路的一个新型、进化保守的上游调控因子，该因子对细胞的多种生理和病理过程至关重要。然而，在无脊椎动物中，它的功能及其潜在机制普遍了解较少。在本研究中，我们通过组学分析发现，敲降 AjELMO1 的刺参体腔细胞中调控内吞作用和 GTP 活性蛋白显著富集。此外，AjELMO1 的过表达或干扰显著改变了由灿烂弧菌 AJ01 诱导的体腔细胞吞噬水平。进一步的功能分析发现用不同的内吞抑制剂处理结果表明其主要依赖于肌动蛋白依赖的内吞途径。通过共免疫沉淀和 GST 下拉实验结合质谱鉴定，我们发现 AjDOCK180 是它的相互作用蛋白。进一步的功能分析还表明，其也是通过肌动蛋白内吞途径促进体腔细胞的吞噬作用。此外，我们发现 AjELMO1 促进的体腔细胞吞噬活性可以通过干扰 AjDOCK180 来阻断。综上所述，我们的数据表明 AjELMO1 通过介导肌动蛋白依赖的内吞途径抵御病原感染。

关键词：刺参，吞噬运动蛋白，先天免疫，灿烂弧菌

ELMO interacts with DOCK180 to enhance coelomocyte phagocytosis in Vibrio splendidus challenged Apostichopus japonicus

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Abstract： Engulfment and cell motility protein (ELMO) was identified as a novel, evolutionarily conserved upstream regulator of the RAC signaling pathway in mammals, which was essential for diverse physiological and pathological processes of cells, such as phagocytosis and cell migration. However, the functions and the underlying mechanisms of ELMO1 are generally poorly understood in invertebrates. In this study, we found that the endocytosis and GTP activity were significantly enriched in AjELMO1-interfered coelomocytes of Apostichopus japonicus by RNA-seq. Moreover, overexpression or interference of AjELMO1 significantly altered the coelomocyte phagocytosis levels induced by Vibrio splendidus AJ01, leading to an increase and decrease in the intracellular AJ01 burden by flow cytometry and bacteriophage plate counting in vivo and in vitro. Further functional analysis with different endocytosis inhibitors treatment revealed that AjELMO1 mediated AJ01 internalization via the actin-dependent endocytic pathways through the changes of F-actin/G-actin, but not the clathrin-, macropinocytosisi-, and dynamin-dependent endocytic pathways. The dedicator of cytokinesis protein 1 (AjDOCK180) was identified as an interacting protein of AjELMO1 using co-IP and GST-Pull down followed by mass spectrometry identification. Further function analysis also revealed that AjDOCK180 promotes coelomocyte phagocytosis through the actin endocytosis pathway via the changes in the phagocytosis levels, the intracellular AJ01 burden, and the ratio of F-actin/G-actin in coelomocytes. Additionally, we found that the phagocytic activity in sea cucumber coelomocytes promoted by AjELMO1 can be blocked by interference with AjDOCK180. Altogether, our data demonstrate that AjELMO1-AjDOCK180 is involved in resisting AJ01 infection via medicating coelomocyte phagocytosis through the actin dependent pathway.

Key words:：Phagocytosis, Engulfment and cell motility protein, Dedicator of cytokinesis protein 1, Innate immunity, Apostichopus japonicus

定向导流 LCONE-SPI/CS 薄膜保鲜衬垫的制备及保鲜性能研究

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摘要：为缓解水产品贮藏期间汁液滞留及微生物污染带来的腐败问题，以大豆分离蛋白(SPI)和壳聚糖(CS)为成膜基质，山苍子油(LCO)及其主成分柠檬烯(LM)和柠檬醛(CT)为保鲜剂，纳米乳液(NE)为缓释载体，采用流延法制备了精油纳米乳液-SPI/CS 复合薄膜。以吸水纸、脱脂棉、尼龙网纱为基材，膨润土为吸水材料，制备了定向导流精油纳米乳液-SPI/CS 保鲜衬垫，以海鲈鱼鱼片为作用对象，研究了其保鲜机制。结果表明，SPI/CS 膜具有一定抗菌性能，且 DPPH 清除率 26.1%，包埋 LM、CT、LCO 后，DPPH 清除活性增加到 35.7%、44.3%、49.6%，且复合薄膜对荧光假单胞菌和腐败希瓦氏菌的抗菌性能均有所提高，体现了 LM 和 CT 的协同增效作用。经 SPI/CS、LMNE-SPI/CS、CTNE-SPI/CS 和 LCONE-SPI/CS 保鲜衬垫处理的鱼片菌落总数、pH、TBA 值、TVB-N 值等鲜度指标。

关键词：定向导流；衬垫；山苍子油；膨润土；海鲈鱼鱼片

Preparation and preservation properties of unidirectional diversion LCONE-SPI/CS coatings preservation pads

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Abstract： In order to alleviate the problem of corruption caused by juice retention and microbial contamination during the storage of aquatic products, soybean protein isolate (SPI) and chitosan (CS) were used as coating-forming matrix, litsea cubeba oil (LCO) and its main components limonene (LM) and citral (CT) were used as preservatives, and nanoemulsion (NE) was used as sustained-release carrier, essential oil NE-SPI/CS composite coatings were prepared by flow casting method. Directional diversion essential oil nanoemulsion-SPI/CS preservation pads was prepared by using absorbent paper, absorbent cotton, nylon mesh yarn as the base material and bentonite as the absorbent material. The preservation mechanism of Lateolabrax japonicus fillets was studied. The results show that the SPI/CS film has certain antibacterial properties, and the DPPH scavenging rate is 26.1 %. After embedding LM, CT, and LCO, the DPPH scavenging activity increase to 35.7 %, 44.3 %, and 49.6 %, and the antibacterial properties of the composite film against Pseudomonas fluorescens and Shewanella putrefaciens are improved, reflecting the synergistic effect of LM and CT. The preservation indexes such as the total number of colonies, pH, TBA value and TVB-N value of fish fillets treated with the SPI/CS, LMNE-SPI/CS, CTNE-SPI/CS and LCONE-SPI/CS preservation pads are lower than those of the untreated group, and the addition of essential oil delays the fat oxidation and protein degradation in the fish fillets, and maintain the color, texture characteristics and muscle tissue microstructure of the fillets better. The shelf life of fillets are extended from 6.5 days to 13 d. This study can provide theoretical guidance and technical support for the development and application of antibacterial unidirectional water-conducting preservation pads.

Key words:： unidirectional diversion; pads; litsea cubeba oil; bentonite; Lateolabrax japonicus fillets

缢蛏抗菌肽 Theromacin 的分子鉴定与抗菌机制研究

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摘要：抗菌肽作为天然的免疫效应分子，能保护宿主免受病原微生物的侵害，在先天性免疫系统中发挥着重要作用。本研究通过 RACE 技术克隆了缢蛏中的抗菌肽基因，并确定其编码 Theromacin（命名为 ScTm）。ScTm 全长 720bp，其中 297bp 开放阅读框，编码 99 个氨基酸。ScTm mRNA 在所有测试组织中均有表达，其中性腺中的表达量最高。副溶血性弧菌感染后，ScTm mRNA 在血细胞和肝胰腺中的表达均显著增加。此外，重组 ScTm 蛋白（rScTm）对革兰氏阳性菌和革兰氏阴性菌具有明显的抗菌活性。与 0.64μg/μL rScTm 孵育后，8 种被测菌在 12 h 内生长受到完全抑制。此外，rScTm 还能与 LPS、PGN 和 MAN。此外，rScTm 还能破坏副溶血弧菌的膜并与细菌基因组 DNA 结合，从而显示出抗菌活性。更重要的是，ScTm 沉默导致受感染的缢蛏中副溶血弧菌显著增加。在这种情况下，缢蛏的存活率显著降低。

关键词：Theromacin， 分子特征，抗菌活性，副溶血弧菌，抑菌机制。

Molecular characterisation and immunological functions of the antimicrobial peptide Theromacin from razor clam Sinonovacula constricta

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Abstract： Antimicrobial peptides (AMPs), as natural immune effector molecule, which protected the host from pathogenic microorganisms and played an important role in the innate immune system. In this study, the AMP gene was identified as encoding Theromacin from the razor clam Sinonovacula constricta (designated as ScTm), which was cloned by RACE-PCR. The full-length cDNA of ScTm contained 720 bp, with a 297 bp open reading frame that encoded 99-amino acids. The predicted signal peptide cleavage site was between ser23-Gly24, and the mature peptide sequence contains 71 amino acids. ScTm mRNA was expressed in all tested tissues, with the highest level in gonads. After Vibrio parahaemolyticus challenge, the ScTm mRNA expression was significantly increased both in hemocytes and hepatopancreas. Moreover, The recombinant ScTm protein (rScTm) showed obvious antimicrobial activities against Gram-positive and Gram-negative bacteria. After incubated with 0.64 μg/μL rScTm, The growth of the eight bacteria under test could be inhibited thoroughly within 12 h. Besides rScTm was not hemolytic against sheep erythrocytes. In addition, rScTm dislayed binding ability to PAMPs including LPS, PGN and MAN. Furthermore, rScTm showed antimicrobial activity by disrupting the membrane and binding to the bacterial genomic DNA of V. parahaemolyticus. More importantly, ScTm silencing led to a significant increase in V. parahaemolyticus in the infected S. constricta. Under this condition, the survival rate of S. constricta was significantly reduced. Our current study demonstrated that ScTm had an important function in host defense against invasive pathogens, and achieved antimicrobial activity by disrupting the membrane and binding to the bacterial genomic DNA of V. parahaemolyticus.

Key words:：Theromacin; Molecular characteristics; Antimicrobial activity; V. parahaemolyticus; Bactericidal mechanism.

H2O2 胁迫对中华绒螯蟹鳃组织氧化应激、渗透调节、细胞凋亡和自噬的影响

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摘要：为探明氧化损伤对中华绒螯蟹鳃组织的影响，实验使用不同浓度 H2O2 对幼蟹进行胁迫，在蟹体暴露不同时间进行取样，测定鳃组织的相关指标。结果显示：H2O2 胁迫期间，MDA 和 H2O2 浓度及 SOD、CAT 和 GSH-Px 活性等在胁迫后发生不同程度的改变，降低鳃组织的抗氧化能力，促进了脂质过氧化；渗透调节指标如离子转运酶液泡型 ATP 酶、Na+-K+-2Cl 协同转运蛋白-1、Na+/K+-ATP 酶亚基α和钙通道蛋白、氨通道蛋白 2 等基因的相对表达水平受到不同程度影响；MAPK 信号通路（jnk、p38、erk）、细胞凋亡（Caspase8、Caspase3、Bc12、P53 等）和自噬（ATG7、ampkβ等）相关基因相对表达水平不同程度变化，推测 H2O2 可诱导鳃组织发生细胞凋亡和自噬。综上，H2O2 胁迫会影响中华绒螯蟹抗氧化能力、渗透调节和离子调控能力，可能通过 MAPK 通路引起鳃细胞凋亡和自噬的发生。

关键词：中华绒螯蟹；氧化应激；抗氧化；细胞调亡；自噬

无

无
无

Abstract：无

Key words:：无

核酸适配体在水生动物病毒检测及成像中的应用

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摘要：核酸适配体 (aptamer) 是通过指数富集的配基系统进化技术从随机文库中筛选得到的单链核酸分子，可以形成独特的二级或三级结构与靶标进行特异性的结合，在疾病的诊断、分子成像、药物递送等领域有着良好的应用前景。我们实验室已针对水生动物病毒筛选获得了一系列特异性核酸适配体，并系统开展了其在病毒检测和感染机制等方面的研究。例如，基于特异性识别石斑鱼神经坏死病毒（red-spotted grouper nervous necrosis virus, RGNNV）的核酸适配体并结合等温链置换扩增反应和纳米胶体金技术，建立了一种简单、灵敏的侧向流生物传感器（lateral flow biosensor, LFB），可快速检测 RGNNV。此外，利用荧光分子修饰的核酸适配体荧光标记 RGNNV 病毒粒子，在活细胞水平研究了 RGNNV 诱导细胞空泡化的过程与机制。这些结果有助于我们发展新的抗病毒策略。

关键词：核酸适配体，水生动物病毒，检测技术，感染机制

Application of aptamers in detection and imaging of aquatic animal viruses

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Abstract： Aptamer is a single stranded nucleic acid molecule screened from random library by systematic evolution of ligands by exponential enrichment (SELEX). Due to its specific three-dimensional structure, aptamer can specifically bind to the target, suggesting its potential applications in many fields such as disease diagnosis and treatment, living cell imaging and drug delivery. In our laboratory, a series of aptamers targeting aquatic animal viruses have been selected, and applied in developing virus detection methods and investigating the infection mechanism. For example, based on the aptamers against red-spotted grouper nervous necrosis virus (RGNNV), a simple and sensitive lateral flow biosensor (LFB) has been developed for the rapid detection of RGNNV by combining with isothermal strand displacement amplification (SDA) and colloidal gold nanoparticles. Besides, the formation mechanisms of RGNNV-induced vacuolization in living cells were studied by labeling RGNNV with fluorescent molecules modified aptamers. These results contribute to the development of new antiviral strategies.

Key words:：aptamer, aquatic animal virus, detection technology, infection mechanism

传染性造血器官坏死病毒（IHNV）的反向遗传操作系统的建立及其应用

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摘要：传染性造血器官坏死病毒(IHNV)对大多数鲑科鱼类易感，严重威胁鲑鳟鱼健康养殖。本研究构建表达 IHNV-Sn1203 毒株全长 cDNA 的质粒,其与辅助质粒共转染至 BHK-21-T7 细胞中，拯救出具有感染性的重组病毒 rIHNV-Sn1203。该重组病毒与野生型病毒保持着极其相近的生物学特性，说明 IHNV 反向遗传操作系统建立成功。将 GFP 插入到 IHNV 病毒载体的不同位置，通过测定 GFP 蛋白荧光强度发现，P/M 基因之间是 IHNV 作为载体表达外源基因的最佳位置。以 IHNV-Blk94 毒株为载体，将 IPNV 病毒的 VP2 基因插入到 P/M 基因之间，构建表达 VP2 蛋白的重组二联弱毒疫苗 rBlk94-VP2，其免疫后的虹鳟在感染 IHNV 时的相对存活率为 86%，且组织中 IPNV 载量显著降低。此外，利用反向遗传学方法构建多株 IHNV 减毒或无毒疫苗，其免疫后对虹鳟的相对保护率可达 70%-83.33%。

关键词：传染性造血器官坏死病毒 反向遗传学 重组病毒 减毒疫苗

Establishment and application of reverse genetic operating system of infectious hematopoietic necrosis virus (IHNV)

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Abstract： Infectious haematopoietic necrosis virus (IHNV) is susceptible to most salmonids and poses a serious threat to the healthy culture of salmon and trout. In this study, a plasmid expressing the full-length cDNA of IHNV-Sn1203 strain was constructed and co-transfected with the helper plasmids into BHK-21-T7 cells to rescue the infectious recombinant virus rIHNV-Sn1203. The recombinant virus maintained very similar biological characteristics to the wild type virus, indicating that the IHNV reverse genetic operating system was successfully established. GFP was inserted into different positions of IHNV vector, and the fluorescence intensity of GFP protein was measured. It was found that the best position for IHNV to express foreign genes was between P/M genes. Using IHNV-BLK94 strain as carrier, the VP2 gene of IPNV virus was inserted between P/M genes to construct recombinant attenuated vaccine rBlk94-VP2 expressing VP2 protein. The relative survival rate of rainbow trout infected with IHNV after immunization was 86%, and the IPNV load in tissues was significantly reduced. In addition, IHNV attenuated or non-toxic vaccines were constructed by reverse genetics method, and the relative protection rate of IHNV against rainbow trout after immunization could reach 70%-83.33%.

Key words:： Infectious hematopoietic necrosis virus, reverse genetic, recombinant virus, attenuated vaccine

应用于肉品保鲜的羧甲基壳聚糖基涂膜/薄膜的研究进展

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摘要：随着经济的快速发展和人们生活水平的持续提高，对食品包装材料的需求也日益增长。传统的石化资源虽然在一定程度上满足了这一需求，但其过度使用却对环境造成了严重的影响。因此，人们开始转向对新型、环保的食品包装材料和包装方式的探索。羧甲基壳聚糖(carboxymethyl chitosan，CMCS)因其独特的性质而备受关注。羧甲基壳聚糖不仅具有良好的水溶性、生物相容性和生物降解性，而且还具有出色的成膜性和抗菌活性，这些特性使其成为了一种理想的聚合物基质。为了进一步提升羧甲基壳聚糖的性能，研究人员开始在其基础上添加各种功能性成分。这些添加物不仅能改善复合膜的理化性能，还能增强其保鲜效果。因此，开发羧甲基壳聚糖基涂/薄膜对于食品包装行业来说具有重大的意义。本文旨在对羧甲基壳聚糖的结构和理化特性进行详细的阐述，并总结近年来羧甲基壳聚糖基复合涂/薄膜在肉品保鲜方面的研究进展。

关键词：羧甲基壳聚糖; 复合膜; 食品包装

Progress of carboxymethyl chitosan-based coating/films for meat preservation applications

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Abstract： With the rapid development of the economy and the continuous improvement of people's living standards, the demand for food packaging materials is also increasing. Although traditional petrochemical resources have met this demand to a certain extent, their excessive use has caused serious impact on the environment. Therefore, people are turning to the exploration of new, environmentally friendly food packaging materials and packaging methods. Carboxymethyl chitosan (CMCS) has attracted much attention because of its unique properties. Carboxymethyl chitosan not only has good water solubility, biocompatibility and biodegradability, but also has excellent film-forming and antimicrobial activities, and these properties make it an ideal polymer matrix. In order to further enhance the performance of carboxymethyl chitosan, the researchers have begun to add various functional components to its base. These additions not only improve the physicochemical properties of the composite film, but also enhance its freshness retention. Therefore, the development of carboxymethyl chitosan-based coatings/films is of great significance to the food packaging industry. The aim of this paper is to provide a detailed description of the structure and physicochemical properties of carboxymethyl chitosan, and to summarise the research progress of carboxymethyl chitosan-based composite coatings/films in meat preservation in recent years.

Key words:： carboxymethyl chitosan; laminated film; food packaging

GCRV-II 主要外壳蛋白 VP4 调控 VDAC2 通过钙通路促进细胞凋亡

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摘要：草鱼呼肠孤病毒（GCRV）因其流行广泛、致死率高而倍受学者的关注。病毒蛋白 VP4 是 GCRV 重要的外衣壳蛋白之一，但现有的研究对 VP4 的功能性研究较少。本研究通过转录组分析发现，在 VP4 转染细胞后，电压依赖性阴离子通道 2（VDAC2）表达上调。GO/KEGG 富集分析表明 VP4 高度参与调控细胞内离子跨膜转运体活性和钙信号通路。透射电镜和共聚焦显微镜证明 VP4 能引起内质网应激，导致细胞内钙浓度异常；同时，VP4 导致线粒体膜电位丧失，大量钙离子通过 VDAC2 进入线粒体，导致线粒体损伤和细胞凋亡。Western blot（WB）、实时荧光定量 PCR（qRT-PCR）及流式细胞术检测均显示，随着 VP4 转染浓度的增加，VDAC2 mRNA 表达量增加，细胞凋亡程度加剧。敲低 VDAC2 可降低细胞内钙离子浓度，减少 VP4 引起的细胞凋亡发生。综上所述，VP4 能上调 VDAC2 的表达，通过钙离子通路促进细胞凋亡。

关键词：草鱼呼肠孤病毒（GCRV）；外衣壳蛋白 VP4;电压依赖性阴离子通道 2;钙离子；凋亡

GCRV-II Major Outer Capsid Protein VP4 Regulates VDAC2 to Promote Cell Apoptosis by Calcium Pathway

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Abstract：Grass Carp Reovirus (GCRV) is widely concerned by scientific researchers because of its widespread prevalence and high mortality. Viral protein (VP4) is one of important major outer capsid protein of GCRV. However, the functional study of VP4 is rare. In this study, transcriptomic analysis revealed an up-regulation of voltage-dependent anion channel 2 (VDAC2) in VP4 transfection cells. GO/KEGG enrichment analysis indicted that VP4 is highly involved in regulation of the ion transmembrane transporter activity and calcium signaling pathway in cell. Transmission electron microscopy and confocal microscope were utilized to prove that VP4 can cause endoplasmic reticulum (ER) stress and lead to abnormal calcium concentration in cells. Also, VP4 cause the loss of mitochondrial membrane potential. This allows a large amount of calcium ions to enter the mitochondria by VDAC2, which lead to mitochondrial damage and apoptosis. Western blot (WB), quantitative real-time PCR (qRT-PCR) and flow cytometry showed that the mRNA expression of VDAC2 increase when the concentration of VP4 transfection increased and the degree of cell apoptosis intensified. Knocking down VDAC2 can reduce the concentration of calcium and decreased occurrence of apoptosis caused by VP4 in cells. In conclusion, the result demonstrates that VP4 can up-regulate VDAC2 through cell apoptosis enhancement by calcium pathway. This study provides a theoretical basis for subsequent scholars to prevent GCRV infection in grass carp.

Key words:：Grass Carp Reovirus (GCRV); major outer capsid protein VP4; VDAC2; Ca+; Apoptosis

双酚 S 诱导淡水小龙虾氧化应激、脂质代谢紊乱和自噬功能障碍的机制研究

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摘要：双酚 S（BPS）广泛应用于塑料制品、食品包装、电子产品等领域。近年来，BPS 的排放对水生生态系统的影响越来越大。本研究旨在探讨不同浓度 BPS（0、1、10 和 100 μg/L）暴露对克氏原螯虾脂质代谢、氧化应激和自噬功能的影响。结果表明，BPS 暴露可提高活性氧水平并抑制抗氧化酶的活性来引发氧化应激。此外，BPS 暴露导致血清和肝胰腺中脂质含量增加，这与脂质相关酶活性升高和相关基因表达增加有关。此外，BPS 暴露会降低磷脂酰胆碱(PC)和磷脂酰肌醇(PI)的水平，扰乱甘油磷脂代谢(GPI)，并导致肝胰腺脂质沉积。这可能是由于脂肪酸转运减少及肝胰腺中 PC 和 PI 合成受阻，进而抑制了 PI3K-AMPK 通路。综上所述，BPS 暴露会导致淡水小龙虾肝胰腺氧化应激，促进脂质积累。总之，我们的研究结果证明环境相关水平的 BPS 暴露可通过多种途径导致肝胰腺脂质沉积，引起人们对 BPS 和双酚类似物对人群的潜在影响的担忧

关键词：内分泌干扰物，环境污染物，甘油磷脂代谢，肝胰腺毒性，克氏原螯虾

Mechanisms Insights into Bisphenol S-induced Oxidative Stress, Lipid Metabolism Disruption, and Autophagy Dysfunction in Freshwater Crayfish

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Abstract：Bisphenol S (BPS) is widely used in plastic products, food packaging, electronic products, and other applications. In recent years, BPS emissions have increasingly impacted aquatic ecosystems. The effects of BPS exposure on aquatic animal health have been documented; however, our understanding of its toxicology remains limited. This study aimed to explore the mechanisms of lipid metabolism disorders, oxidative stress, and autophagy dysfunction induced in freshwater crayfish (Procambarus clarkii) by exposure to different concentrations of BPS (0 μg/L, 1 μg/L, 10 μg/L, and 100 μg/L) over 14 d. The results indicated that BPS exposure led to oxidative stress by inducing elevated levels of reactive oxygen species (ROS) and inhibiting the activity of antioxidant-related enzymes. Additionally, BPS exposure led to increased lipid content in the serum and hepatopancreas, which was associated with elevated lipid-related enzyme activity and increased expression of related genes. Furthermore, BPS exposure decreased levels of phosphatidylcholine (PC) and phosphatidylinositol (PI), disrupted glycerophospholipid (GPI) metabolism, and caused lipid deposition in the hepatopancreatic. These phenomena may have occurred because BPS exposure reduced the transport of fatty acids and led to hepatopancreatic lipid deposition by inhibiting the transport and synthesis of PC and PI in the hepatopancreas, thereby inhibiting the PI3K-AMPK pathway. In conclusion, BPS exposure induced oxidative stress, promoted lipid accumulation, and led to autophagy dysfunction in the hepatopancreas of freshwater crayfish. Collectively, our findings provide the first evidence that environmentally relevant levels of BPS exposure can induce hepatopancreatic lipid deposition through multiple pathways, raising concerns about the potential population-level harm of BPS and other bisphenol analogues.

Key words:：Endocrine disruptors, Environmental pollutants, Glycerophospholipid metabolism, Hepatopancreatic toxicity, Procambarus clarkii

华绒螯蟹β-连环蛋白在螺原体感染过程中的作用研究

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摘要：本文研究了中华绒螯蟹（Eriocheir sinensis）β-连环蛋白（Esβ-Catenin）在响应螺原体感染时的作用。首先通过克隆 Esβ-Catenin 的全长 cDNA 序列并对其序列特点进行分析，发现其在进化上高度保守保守。qRT-PCR、Western Blot 以及激光共聚焦实验显示螺原体感染后，Esβ-Catenin 表达水平显著下调，且核转移受到显著抑制。其次，个体水平 RNA 干扰 Esβ-Catenin 表达后，宿主抵抗病原感染能力显著下调。激活剂处理体外培养血淋巴细胞后，Esβ-Catenin 在细胞核和细胞质中的表达均显著上调，宿主细胞抵抗病原感染能力显著增强。最后，转录组分析发现干扰 Esβ-Catenin 后，与 Toll 样受体相关的基因显著下调。上述结果初步说明，宿主 Esβ-Catenin 可能通过与 Toll 样受体相关信号通路相互作用，进而影响河蟹应对螺原体的感染。

关键词：关键词：中华绒螯蟹；β-Catenin；螺原体；免疫响应

The Role of β-Catenin in the process of Eriocheir sinensis response Spiroplasma eriocheiris infection

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Abstract： Abstract: To study the role of β-Catenin in the process of Eriocheir sinensis response Spiroplasma eriocheiris infection. Firstly, the full-length sequence of Esβ-Catenin was obtained by RACE, and it was found that Esβ-Catenin was highly conserved in evolution by sequence characteristics analysis. qRT-PCR, Western blot and confocal experiment found that after S. eriocheiris infection the expression level of Esβ-Catenin was significantly decreased, and its nuclear translocation was inhibited. Secondly, knocking down Esβ-Catenin in crab hemocytes in vivo could accelerate the infection of S. eriocheiris. Consistent with this result, activated the Esβ-Catenin by pretreating hemocytes with Esβ-Catenina ctivator (SB-216763) in vitro could reduce S. eriocheiris infection by increasing the stability and nuclear translocation of Esβ-catenin. Finally, further transcriptome analysis showed that crab β-catenin could crosstalk with Toll pathway to positive regulate hemocytes antibacterial peptides transcription, and then involved in the host's response to the infection of S. eriocheiris.

Key words:：Keywords: Eriocheir sinensis; β-Catenin; Spiroplasma eriocheiris; Immune response

MiRNA-mRNA 联合分析揭示
菲律宾蛤仔抗鳗弧菌感染的免疫调节

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摘要：菲律宾蛤仔简称蛤仔，蛤仔的规模化养殖经常受到鳗弧菌的影响造成大面积死亡。然而，鳗弧菌的制病原理等方面的探究尚不清楚。在本研究中，我们发现菲律宾蛤肝胰脏载菌量在感染后 2 d 达到峰值，随后逐渐下降，而溶菌酶活性在 12 h 达到峰值。组织切片观察显示，感染后的肝胰脏细胞失去正常结构并伴随部分坏死。此外，利用蛤仔肝胰腺细胞构建了 6 个小 RNA 文库。感染后 48 h 共检测到 15 个差异表达 microRNA，其中 8 个表达上调，7 个表达下调。同时，GO 和 KEGG 富集结果显示，共预测出 48 个已知的 miRNAs 和 127 个新的 miRNAs，共对应 2171 个靶基因。功能注释表明内吞通路，对外来细菌的识别蛋白，泛素介导的蛋白水解，FoxO 通路和 mTOR 通路等多个信号通路发生显著改变。测序结果与 qRT-PCR 验证基本一致，说明数据的准确性。本研究为探讨鳗弧菌感染后菲律宾蛤仔的免疫调节机制提供了新的思路。

关键词：菲律宾蛤仔、鳗弧菌、高通量测序、免疫应答

Integrated miRNA-mRNA analysis reveals the immune regulatory mechanisms of the Ruditapes philippinarum 's resistance to Vibrio anguillarum infection

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Abstract：Manila clam (Ruditapes philippenarum) is an important shellfish aquaculture product. The large-scale breeding of clams is often affected by V. anguillarum and causes large-scale death. However, the pathogenesis, immune response and metabolic pathway of V. anguillarum are still unclear. In this study, we found that the bacterial load in the hepatopancreas of R. philippinarum peaked at 2 d after V. anguillarum infection, and then gradually decreased, while the activity of lysozyme reached the peak at 12 h. Tissue section observation reveals that the infected hepatopancreas cells lost normal structure or necrosis. Additionally, six small RNA libraries were constructed using hepatopancreas of clams. A total of 15 differentially expressed (DE) microRNA (miRNA) were identified at 48 h after V. anguillarum infection, including 8 upregulated and 7 downregulated miRNAs. GO and KEGG enrichment results indicated the prediction of 48 known miRNAs and 127 new miRNAs, corresponding to 2,171 target genes. Functional annotations indicate significant changes in several signaling pathways, including endocytosis, bacterial recognition proteins, ubiquitin-mediated protein degradation, the FoxO pathway, and the mTOR pathway. The sequencing results were basically consistent with the qRT-PCR validation, indicating the accuracy of the data. This study provides a new idea to explore the immune regulation mechanism of shellfish after V. anguillarum infection, which brings important reference significance for modern immunological research.

Key words:：Ruditapes philippinarum; Vibrio anguillarum; High-throughput sequencing; Immune response

黄芩素抗鲤春病毒血症病毒的研究

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摘要：鲤科鱼类在我国淡水鱼养殖品种中占据重要位置，占淡水鱼总产量的 60%以上，鲤春病毒血症是鲤春病毒血症病毒（spring viremia of carp virus，SVCV）引起的一种鲤鱼易感的急性出血性病毒病，从鲤科鱼类中分离出来，农业农村部 573 号公告《一、二、三类动物疫病病种名录》（2022）将其列为二类动物疫病。由于传播速度快、致死率极高，因此急需针对鲤春病毒开发绿色无公害鱼药。本研究证实使用不同浓度的黄芩素处理后，能够有效抑制 SVCV 在 EPC 细胞中的增殖。利用 Real-Time PCR 技术分析培养上清中 SVCV 病毒量的差异,定量结果显示，随着实验组中黄芩素浓度的增加,上清中 SVCV 病毒拷贝数呈明显下降趋势。通过 Western-blot 技术检测发现 SVCV 病毒蛋白表达量呈明显下降趋势。本研究表明黄芩素作为一种植物来源小分子抑制物，对防控 SVC 具有广阔的应用前景。

关键词：鲤春病毒血症；黄芩素；鲤鱼；SVCV

Study on the Antiviral Activity of Baicalein Against Spring Viremia of Carp Virus

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Abstract：Cyprinid fish play a crucial role in China's freshwater aquaculture, comprising over 60% of total production. Spring viremia of carp (SVC), caused by the spring viremia of carp virus (SVCV), is a severe hemorrhagic disease affecting carp. According to China's Ministry of Agriculture and Rural Affairs (Announcement No. 573, 2022), SVC is classified as a Category II animal disease. Due to its rapid spread and high mortality rate, there is an urgent need for eco-friendly and effective treatments against SVCV. This study demonstrates that baicalein, at varying concentrations, effectively inhibits SVCV proliferation in EPC cells. Real-Time PCR analysis showed a significant reduction in viral load with increasing baicalein concentrations. Western blot analysis further confirmed a marked decrease in SVCV protein expression. These results suggest that baicalein, a plant-derived small molecule inhibitor, holds great promise for the prevention and control of SVC.

Key words:：SVC；Baicalein；Carp；SVCV

合浦珠母贝抗菌肽 pfMacin1 的克隆、重组表达和抑菌机制

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摘要：广西和广东养殖的合浦珠母贝抵抗力下降及养殖水体恶化是限制南珠养殖的产量、质量和效益的主要原因之一。因此，提高合浦珠母贝免疫力是合浦珠母贝养殖和育种中的重点工作。抗菌肽是由基因编码的一类小分子蛋白，是生物免疫效应分子的重要组成部分，其研究和应用对于增强合浦珠母贝的免疫能力具有重要意义。我们从合浦珠母贝中基因组鉴定并克隆了一个新的 Macin 家族成员 pfMacin1。pfMacin1 在合浦珠母贝外套膜、鳃和血淋巴中呈组成型表达，微生物侵染后 pfMacin 表达显著升高，抑制其表达导致合浦珠母贝对病原微生更加敏感。重组表达 pfMacin (rpfMacin 1)可有效抑制和 5 种革兰氏阴性菌(副溶血性弧菌、嗜水气假单胞菌、大肠杆菌、鳃弧菌和溶藻弧菌)的生长，最低抑制浓度为 1~ 4 μM。分子动力学模拟、细菌结合实验和电镜观结果表明，pfMacin 通过与细菌及细菌表面成分结合并破坏细菌膜以杀灭细菌。

关键词：合浦珠母贝; 抗菌肽;Macin; 表达模式; 重组表达; 抗菌机制;

Cloning, recombinant expression and bacteriostatic mechanism of the antimicrobial peptide pfMacin1 in Pinctada fucata

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Abstract： The decline in resistance and deterioration of aquaculture water are among the primary factors limiting the yield, quality, and economic benefits of pearl culture in China. Therefore, enhancing the immunity of pearl oyster is crucial for breeding and cultivation. Antimicrobial peptides, small molecular proteins encoded by genes, play a significant role as biological immune effector molecules. Researching and applying antimicrobial peptides holds great importance in boosting the immune capacity of pearl oyster. We have identified and cloned pfMacin1, a new member of the Macin family, from the genome and transcriptome of Pinctada fucata. The constitutive expression of pfMacin1 was observed in the mantle, gill, and hemolymph of P. fucata. It’s expression significantly increased following microbial infection. Inhibition of Pfmacin1 expression rendered the P. fucata more susceptible to pathogenic microorganisms. Furthermore, we expressed recombinant pfMacin1 (rpfMacin 1), which effectively inhibited the growth of four Gram-negative bacteria (Aeromonas hydrophila, Escherichia coli, Vibrio anguillarum, Vibrio alginolyticus) with a minimum inhibitory concentration of 1-4 μM. Nevertheless, its efficacy in inhibiting two types of Gram-positive bacteria was limited. PfMacin1 can bind to bacteria, Pathogen-associated molecular patterns and damage bacterial cell membranes. This study can provide a basis for the development of disease control measures and breeding of disease-resistant varieties of pearl oyster.

Key words:：Pinctada fucata martensii; Antimicrobial peptides; Macin; Gene Expression analysis; Recombinant expression; Antibacterial mechanism;

p38MAPK 通路抑制剂对副溶血性弧菌感染后马氏珠母贝的作用及影响

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摘要：SB203580 抑制剂是一种 p38MAPK 通路的阻断剂，为了探究其对副溶血弧菌刺激后马氏珠母贝的免疫效果，本研究克隆了马氏珠母贝 p38MAPK 通路下游关键基因 PmMKK6 和 PmCREB，分析感染副溶血弧菌以及感染后注射抑制剂后的表达情况，通过分子生物学技术酶活检测、ELISA 蛋白定量和组织学观察，分析 SB203580 抑制剂对马氏珠母贝的作用。本研究发现，在副溶血弧菌刺激下 PmMKK6 和 PmCREB 的基因表达量、酸性磷酸酶（ACP）和碱性磷酸酶（AKP）酶活力以及 p38 蛋白含量发生了显著性变化，注射抑制剂后发生的表达量和活性的显著性变化符合分子调控机制。感染后肝胰腺发生水肿和受损病变，而注射抑制剂后的肝胰腺水肿表征有所缓解，且受损细胞被结缔组织填充。结果表明，SB203580 抑制剂能成功阻断马氏珠母贝的 p38MAPK 通路，以此降低其对副溶血弧菌免疫应激反应，达到对马氏珠母贝的免疫保护作用。

关键词：马氏珠母贝，p38MAPK 通路，SB203580 抑制剂，副溶血弧菌刺激，MKK6，CREB

Role and effects of p38MAPK pathway inhibitors on Pinctada fucata martensii after Vibrio parahaemolyticus infection

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Abstract：SB203580 inhibitor is a blocker of the p38MAPK pathway. To explore its immune effect on Pinctada fucata martensii after stimulation by Vibrio parahaemolyticus, this study cloned key genes of the p38MAPK pathway in P. f. martensii, PmMKK6 and PmCREB, analyzed their expression after infection with V. parahaemolyticus and subsequent injection of the inhibitor. Molecular biological techniques, including enzyme activity detection, ELISA protein quantification, and histological observation, were used to analyze the effects of the SB203580 inhibitor on P. f. martensii. The study found that under V. parahaemolyticus stimulation, the gene expression levels of PmMKK6 and PmCREB, the ACP and AKP, the content of p38 protein, changed significantly. The significant changes in expression and activity after inhibitor injection were consistent with molecular regulatory mechanisms. After infection, the hepatopancreas showed edema and damaged lesions, but the edematous characteristics of the hepatopancreas were alleviated after inhibitor injection. The results indicate that the SB203580 inhibitor can successfully block the p38MAPK pathway in P. f. martensii, thereby reducing its immune stress response to V. parahaemolyticus and providing immunoprotection to P. f. martensii.

Key words:：Pinctada fucata martensii; p38MAPK pathway; SB203580 inhibitor; Vibrio parahaemolyticus stimulation

致对虾急性肝胰腺坏死病副溶血性弧菌外膜囊泡(VpAHPND-OMVs)免疫调控机制研究

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摘要：副溶血性弧菌（Vibrio parahaemolyticus）是引发急性肝胰腺坏死病（VpAHPND）的重要病原菌，严重威胁凡纳滨对虾（Litopenaeus vannamei）的养殖。革兰氏阴性菌的外膜囊泡（OMVs）在宿主免疫应答中发挥重要作用。本研究通过差速超速离心分离 VpAHPND-OMVs，并通过质谱鉴定了包括 PirA 和 PirB 在内的多种毒素蛋白。VpAHPND-OMVs 可与对虾血淋巴细胞融合，饲喂实验表明不同剂量 OMVs（30 和 60 μg/kg）对对虾生长和肝胰腺结构无影响，但第 7 和 14 天免疫相关酶活性显著升高，暗示 OMVs 诱导了快速免疫应答。转录组和蛋白质组分析表明，28 天后免疫相关分子在转录和蛋白水平上显著下调，差异基因和蛋白富集于细胞凋亡、吞噬体等先天免疫通路，表明饲喂的后期免疫抑制更为显著。研究结果为病害防治和对虾抗病育种提供了新思路。

关键词：凡纳滨对虾；副溶血性弧菌；急性肝胰腺坏死病（AHPND）；外膜囊泡；免疫反应

The immunomodulatory mechanisms of outer membrane vesicles from Vibrio parahaemolyticus causing acute hepatopancreatic necrosis disease

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Abstract： Vibrio parahaemolyticus (Vibrio parahaemolyticus) is an important pathogen causing acute hepatopancreatic necrosis (VpAHPND), which seriously threatens the culture of Litopenaeus vannamei. Outer membrane vesicles (OMVs) of Gram-negative bacteria play important roles in host immune response. In this study, VpAHPND-OMVs were isolated by differential ultracentrifugation, and a variety of toxic proteins, including PirA and PirB, were identified by mass spectrometry. It was demonstrated that VpAHPND-OMVs could fuse with shrimp hemocytes. Feeding experiments showed that different doses of OMVs (30 and 60 μg/kg) had no effect on shrimp growth and hepatopancreas structure, but the activities of immune-related enzymes increased significantly on the 7th and 14th day, suggesting that OMVs induced a rapid immune response. Transcriptome and proteome analysis showed that after 28 days, immune-related molecules were significantly down-regulated at the transcriptional and protein level, and differential genes and proteins were enriched in innate immune pathways such as apoptosis and phagosomes, indicating that immunosuppression was more significant in the later stage of feeding. The results provide a new idea for disease control and disease resistance breeding of shrimp.

Key words:： Litopenaeus vannamei, Vibrio Parahaemolyticus, Acute hepatopancreatic necrosis disease (AHPND), Immune response

灿烂弧菌 VI 型分泌系统蛋白 Hcp 介导刺参免疫应答的分子机制研究

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摘要：灿烂弧菌是刺参的主要病原，灿烂弧菌有与其它革兰氏阴性菌类似的 T6SS。在我们的研究中，我们发现灿烂弧菌 T6 SS 的的关键分泌蛋白——溶血素共调节蛋白（hemolysin-coregulated protein，Hcp）能够定位到刺参体腔细胞内，为了探究该蛋白是否会参与到对刺参免疫通路的调控中。于是我们构建了 Hcp 缺失突变体（△Hcp)和 ClpV 缺失突变体（△ClpV），通过 GST-pull down 实验，我们发现 Hcp 蛋白能够与刺参 MYP1 蛋白接合。结合前期的研究，MYP1 蛋白参与调控 NF-kB 通路。因此，我们通过 qPCR 和 WB 实验明确了 Hcp 的缺失抑制 NF-kB 通路炎症因子的激活。通过切片观察与 NO、TNOS、iNOS 测定，明确 Hcp 的缺失显著降低了宿主炎症反应水平。综上所述，我们的研究结果表明灿烂弧菌 Hcp 蛋白与刺参 MYP1 蛋白相互作用，抑制宿主炎症水平，增强自身胞内存活能力和毒力。

关键词：灿烂弧菌；VI型分泌系统；溶血素共调节蛋白；主要卵黄蛋白 1；炎症

The molecular mechanism of V.splendidus type VI secretion system protein Hcp-mediated immune response in Apostichopus japonicus

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Abstract：Vibrio splendidus is the main pathogen of Apostichopus japonicus. Vibrio splendidus has T6SS similar to other Gram-negative bacteria. In our study, we found that the key secretory protein of V.splendidus T6 SS, hemolysin-coregulated protein (Hcp), which is localized to the coelomocytes of A.japonicus. In order to explore whether this protein is involved in the regulation of the immune pathway of A.japonicus. Therefore, we constructed Hcp deletion mutant (△ Hcp) and ClpV deletion mutant (△ ClpV). Through GST-pull down experiment, we found that Hcp protein could bind to MYP1 protein of Apostichopus japonicus. Combined with previous studies, MYP1 protein is involved in the regulation of NF-kB pathway. Therefore, we confirmed that the absence of Hcp inhibited the activation of inflammatory factors in the NF-kB pathway through qPCR and WB experiments. Through slice observation and NO, TNOS, iNOS determination, it was clear that the deletion of Hcp significantly reduced the level of host inflammatory response. In summary, our results show that V.splendidus Hcp protein interacts with MYP1 protein to inhibit host inflammation and enhance its intracellular survival and virulence.

Key words:：vibrio splendidus ; type VI secretion system ; hemolysin-coregulated protein ; major yolk protein 1 ; inflammation

基于主成分分析法建立罗非鱼一般抗病力模型

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摘要：为建立尼罗罗非鱼的一般抗病力评估模型，综合评价不同罗非鱼品系、群体及个体的一般抗病力，对 5 个不同尼罗罗非鱼群体的免疫指标（SOD、ACP、AKP、补体 C3、TNF-α、IFN-γ、IgM、IgT）共检测 8 个免疫指标，并进行主成分分析和聚类分析。结果表明，各免疫指标在不同群体中差异明显，变异系数在 10.18 ~ 78.17 %之间。选取前 5 个特征值作为主成分时的累计贡献率达到 85.422 %，基本反应了 8 项免疫指标包含的全部信息。5 个群体的主成分综合得分为 E> D> C> A > B；系统聚类分析结果表明，D 和 E 群体聚为一支，A、B 和 C 群体聚为一支。说明 D 和 E 群体的一般抗病力较强，免疫指标的相似性较高。无乳链球菌攻毒试验结果表明，各群体的累计死亡率 E< C< D< A< B，说明有较高的可信度和稳定性。本研究建立尼罗罗非鱼的一般抗病力评估模型并进行了初步验证，可为罗非鱼抗病选育工作提供参考。

关键词：主成分分析（PCA），罗非鱼，一般抗病力，综合评价

Based on principal component analysis, the general disease resistance model of tilapia was established

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Abstract： In order to establish a general disease resistance evaluation model for Nile tilapia and comprehensively evaluate the general disease resistance of different tilapia strains, populations and individuals, a total of 8 immune indexes (SOD, ACP, AKP, complement C3, TNF-α, IFN-γ, IgM, IgT) of five different Nile tilapia populations were detected, and principal component analysis and cluster analysis were performed. The results showed that the immunization indexes were significantly different in different groups, and the coefficient of variation ranged from 10.18 ~ 78.17%. When the first five eigenvalues were selected as principal components, the cumulative contribution rate reached 85.422%, which basically reflected all the information contained in the eight immunization indicators. The composite scores of principal components in the five groups were E> D> C> A > B. The results of systematic cluster analysis showed that groups D and E were clustered into one branch, and groups A, B and C were clustered into one branch. The results indicated that the general disease resistance of groups D and E was stronger, and the similarity of immune indexes was higher. The results of Streptococcus agalactiae challenge test showed that the cumulative mortality rate of each group was E<C<D< A< B, indicating high reliability and stability. In this study, a general disease resistance evaluation model of Nile tilapia was established and preliminarily verified, which could provide a reference and basis for the disease resistance breeding of tilapia.

Key words:： Principal component analysis (PCA), tilapia, general disease resistance, comprehensive evaluation

马氏珠母贝中 TNFR16 在外来刺激和 RNA 干扰下的表征、功能分析及表达研究

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摘要：本研究调查了马氏珠母贝中肿瘤坏死因子受体（TNFR）基因的免疫功能。克隆得到 PmTNFR16 cDNA 序列长度为 1675 bp，编码 406 个氨基酸残基。序列分析显示 PmTNFR16 包含一个信号肽域、四个 TNFR 域、一个跨膜域和一个死亡域。表达分析揭示 PmTNFR16 在外套膜中高度表达，并在外来刺激后显著上调。通过使用 PmTNFR16 的 RNA 干扰探针进一步探索了 PmTNFR16 对 NF-κB 信号通路中免疫效应分子的影响。在植核前用 dsRNA-PmTNFR 对珍珠贝进行预处理，结果在 24 小时时 PmTNFR16 的表达减少了 53%（$p<0.01$）。同样，NF-κB 信号通路中免疫相关基因的表达在 24 小时时显著下降。表明 PmTNFR16 成功被沉默，下游 NF-κB 信号通路中的免疫相关基因的表达也成功下调。这些结果表明 PmTNFR16 可能通过介导 NF-κB 信号通路参与宿主生物的免疫反应。

关键词：肿瘤坏死因子；NF-κB ；RNA 干扰；植核；马氏珠母贝

Characterization, functional analysis, and expression of TNFR16 from Pinctada fucata martensii in response to exogenous stimuli and RNA interference

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Abstract： Marine pearls from Pinctada fucata martensii are valuable for decoration, skin care, and health care, but their quality and yield can be threatened by diseases, pearl nuclei transplantation rejection, and other external factors. The present study investigated the immune function of the tumor necrosis factor receptor (TNFR) gene in P. f. martensii to better understand immune responses related to nuclei rejection. The PmTNFR16 cDNA sequence obtained from cloning was 1,675 bp in length and encoded 406 amino acid residues. Sequence analysis revealed that PmTNFR16 comprises one signal peptide domain, four TNFR domains, one transmembrane domain, and one death domain. Expression analysis revealed PmTNFR16 was highly expressed in the mantle and significantly up-regulated after exogenous stimuli. The effects of PmTNFR16 on immune effector molecules within the NF-κB signaling pathway were further explored using RNA interference probes for PmTNFR16. Pre-treatment of pearl oysters with dsRNA-PmTNFR before nucleus-insertion resulted in decreased expression of PmTNFR16 by 53% at 24 h ($p<0.01$). Similarly, the expression of the NF-κB signaling pathway immune-related genes TRAF2, TRADD, IKK, NIK, and NF-κB significantly decreased at 24 h. The results indicated that PmTNFR16 was successfully silenced as were the expression of immune-related genes in the downstream NF-κB signaling pathway. Overall, these results indicate that PmTNFR16 may be involved in the immune response of the host organism by mediating the NF-κB signaling pathway. These observations provide a framework for future studies of the immune mechanisms of pearl oysters.

Key words:： Tumor necrosis factor receptor; NF-κB; RNA interference; Nucleus insertion; Pinctada fucata martensii

嗜水气单胞菌感染显著上调草鱼 CD3γ/δ T 细胞和巨噬细胞中 IL-26 的表达

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摘要：白细胞介素-26（IL-26）是 IL-10 家族的重要成员，具有多种生物学功能。迄今，鱼类 IL-26 的功能研究十分有限。在本研究中，我们获得草鱼 IL-26 蛋白，制备 CiIL-26 的单克隆抗体。Western blot 结果显示，CiIL-26 单抗可以特异识别在大肠杆菌和 293 细胞中表达的重组 CiIL-26 蛋白，但不识别斑马鱼 IL-26。利用共聚焦显微镜分析感染 A.h 后草鱼组织中产生 IL-26 的阳性细胞，结果显示，后肠、鳃、头肾和脾脏中 IL-26+细胞数量明显增多。有趣的是，我们首次发现大多数表达 IL-26 的为 CD3γ/δ+ T 细胞和 MCSFR+ 巨噬细胞，而且，CD3γ/δ+/IL-26+ 和 MCSFR+/IL-26+ 细胞在 A.h 感染后显著上调。我们的研究结果表明，CD3γ/δ+/ IL-26+ 和 MCSFR+/IL-26+ 细胞在应答细菌感染反应中发挥重要作用。

关键词：白细胞介素-26（IL-26）；单克隆抗体；T 细胞； 巨噬细胞；细菌感染

A.hydrophila infection significantly upregulated IL-26 expression in grass carp CD3γ/δT cells and macrophages

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Abstract：Interleukin-26 (IL-26) is an essential member of the IL-10 family with various biological functions that play a crucial role in regulating the response of TH17 cells (T helper cell type 17). To date, there has been limited research on the function of IL-26 in fish. In this study, we obtained and purified the recombinant grass carp (Ctenopharyngodon idella, Ci) IL-26 protein and prepared and identified a monoclonal antibody (mAb) to CiIL-26. Western blot results showed that CiIL-26 mAb specifically recognized recombinant CiIL-26 protein expressed in E. coli and HEK293T cells, not zebrafish IL-26. Flow cytometry showed that CiIL-26 mAb detected HEK293-positive cells expressing CiIL-26. Confocal microscopy was used to analyze the positive cells producing IL-26 in grass carp tissues after infection with A. hydrophila, and the results showed that the number of IL-26+ cells in the hindgut, gills, head kidney, and spleen was significantly increased. Interestingly, for the first time, we found that the majority of IL-26-expressing cells were CD3γ/δ+ T cells and MCSFR+ macrophages and that CD3γ/δ+/IL-26+ and MCSFR+/IL-26+ cells were significantly upregulated after A. hydrophila infection. Our findings suggest that CD3γ/δ+/ IL-26+ and MCSFR+/IL-26+ cells are vital in responding to bacterial infection.

Key words:：Interleukin-26; monoclonal antibodies; T cells; macrophages; Bacterial infections

II 型干扰素激活 MHC-I 通路增强 GCRV 疫苗的呈递

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摘要：由草鱼呼肠孤病毒引发的出血病是威胁草鱼健康的最严重疾病之一。研究表明，DNA 疫苗可有效提升宿主抵御抗病毒感染的能力，但其免疫保护率有待进一步提高。本研究以 II 型干扰素（IFN）IFNγ和 IFNγ-rel 为分子佐剂，比较分析其对 VP35DNA 疫苗的免疫效果，为研发高效分子佐剂提高参考。利用免疫荧光法检测了在肌肉注射部位的 VP35、IFNγ和 IFNγ-rel 的表达情况，结果显示，VP35、IFNγ和 IFNγ-rel 在注射部位均可表达至少 5 周以上，并且促进脾脏中抗病毒基因（Mx1 和 Isg15）的表达。同样，接种 5d 后脾脏和肌肉中注射 IFNγ和 IFNγ-rel 混合质粒组中 IgM 表达水平增加最显著，在 IFNγ-rel 组中 IgM 表达水平在第 5 周时上调最高。有趣的是，我们的研究结果提示 II 型 IFNs 促进 VP35DNA 疫苗经 MHC-I 通路进行呈递，激活适应性免疫系统，具有作为分子佐剂提高免疫保护率的潜力。

关键词：草鱼呼肠孤病毒（GCRV）；DNA 疫苗；II 型干扰素；免疫佐剂

Type II IFN activates the MHC-I pathway to enhance the presentation of GCRV vaccines

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Abstract： Hemorrhagic disease caused by grass carp reovirus (GCRV) is one of the most severe diseases threatening the health of grass carp (Ctenopharyngodon idella). Studies have shown that DNA vaccines can effectively improve the host's ability to resist viral infection, but their immune protection rate needs further improvement. In this study, type II interferon (IFN) (including IFNγ and IFNγ-rel of grass carp) was used as molecular adjuvants to compare and analyze its immune effect on GCRV-VP35 DNA vaccine, which was a reference for the development of efficient molecular adjuvants. The expression plasmids of pcDNA3.1-VP35, pcDNA3.1-IFNγ and pcDNA3.1-IFNγ-rel were injected into the muscle of grass carp. Immunofluorescence detected the expressions of VP35, IFNγ and IFNγ-rel at the intramuscular injection site. The results showed that VP35, IFNγ and IFNγ-rel were expressed at the injection site and could last at least five weeks. Both IFNγ and IFNγ-rel plasmid injection promoted the expression of antiviral genes (mx1 and isg15) in the spleen, and the expression levels of mx1 and isg15 induced by IFNγ and IFNγ-rel mixed plasmid injection were more significant than those in IFNγ or IFNγ-rel plasmid groups. Similarly, the most significant increase in IgM expression levels was observed in the IFNγ and IFNγ-rel mixed plasmid groups injected into the spleen and muscle five days after vaccination, and the highest up-regulation of IgM expression levels was observed in fish inoculated with IFNγ-rel adjuvant at five weeks of vaccination. Interestingly, our findings suggest that type II IFNs promote the presentation of VP35 DNA vaccines through the MHC-I pathway, activate the adaptive immune system, and have the potential to improve immune protection as molecular adjuvants.

Key words:：Grass carp reovirus (GCRV); DNA vaccine; Type II IFNs; Adjuvant

斑马鱼 TRIM2a 负调控 IRF3 介导的干扰素反应

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摘要：干扰素（IFN）介导的免疫反应对宿主防御病毒感染必不可少，受到多水平调节。然而，其精确的分子调控机制不明确。本研究发现 E3 泛素连接酶（TRIM 2a）是调控斑马鱼和人细胞中干扰素产生的关键因子。斑马鱼感染鲤鱼春季病毒血症病毒（SVCV）后 TRIM 2a 的表达显著上调。敲除 TRIM 2a 基因可显著上调抗病毒基因的表达，增强斑马鱼幼鱼对 SVCV 的抗病力。我们发现，TRIM 2a 可激活 IRF 3 的 K11/K27/K48/K29 位点的泛素化，促进 IRF 3 降解，并稳定 SVCV 磷蛋白，从而有利于病毒复制。此外，在斑马鱼鱼和人细胞中，TRIM 2a 对 IFN 产生的抑制作用均被 IFN 抵消。总的来说，我们的研究表明，TRIM 2a 是一种病毒诱导因子，通过促进 IRF 3 降解下调 IFN 反应，具有减轻由 RLR 激活诱发的过度 IFN 反应的药物靶点潜力。

关键词：TRIM2a；IRF3；IFN；泛素化

Virus inducible TRIM2a is a negative regulator of IRF3 mediated interferon response

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Abstract：A balanced interferon (IFN) response is essential for host defense against viral infection and is tightly regulated at multiple levels. Here, we show that a virus inducible TRIM2 homolog acts as a negative regulator for IFN production in zebrafish. Zebrafish Trim2a was upregulated in response to spring viremia of carp virus (SVCV) infection, and knockout of Trim2a significantly increased the expression of antiviral genes, leading to enhanced resistance to SVCV. Overexpression of Trim2a resulted in pronounced ubiquitination of IRF3 via K11, K27, K29 and K48, promoting IRF3 degradation and stability of SVCV phosphoprotein to favor viral replication. Furthermore, the inhibitory effects of Trim2a on IFN production could be impaired by IFN in fish and human cells, suggesting that the regulatory functions of Trim2a are evolutionarily conserved. Collectively, our findings demonstrate that Trim2a is a negative regulator of IFN production, and could serve as a potential target for mitigating exacerbated IFN response triggered by aberrant RLR activation.

Key words:：TRIM2a; IRF3; interferon; ubiquitination

基于 RAA-CRISPR/Cas12a 水产病毒性病原核酸快速检测技术研发

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摘要：为建立一套特异性强、灵敏度高、操作便捷的水产病毒性病原检测技术，本研究基于密度梯度分相的原理，将重组酶介导链置换核酸扩增技术(Recombinase-aid amplification, RAA)与规律间隔成簇短回文重复序列及其关联蛋白(CRISPR/Cas)系统结合，建立了一套可视化“一步式”RAA-CRISPR/Cas12a 快速检测方法。使用该方法可进一步提高反应特异性，并且可在 37 ℃条件下于 60 min 内完成检测。此外，本方法荧光信号可直接肉眼观察，对仪器兼容性更高，更适用于现场检测。目前，本研究已开发出 CyHV-2 与 GCRV-Ⅱ两种病原检测方法，检测限分别为 10 copies/μL、100 copies/μL，两种方法与多种常见鱼类病原无交叉反应、且阳性检出率高于现行国标 PCR 法。综上，该技术较现有技术检测效率更高、操作更便捷，未来可将该技术作为一线即时检测的候选技术进行推广。

关键词：RAA；CRISPR/Cas12a；快速检测

Development of rapid nucleic acid detection technology based on RAA-CRISPR/Cas12a in aquatic viral pathogens

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Abstract： In order to establish an aquatic viral pathogen detection technique with high specificity, high sensitivity and convenient operation, high sensitivity and convenient operation, this study combined recombinase-aid amplification (RAA) with clustered regularly interspaced short palindromic repeats/CRISPR-associated proteins system (CRISPR/Cas) based on the principle of density-gradient phasing, and established a visualized “one-pot” RAA-CRISPR/Cas12a rapid detection method. The specificity of the reaction could be further improved by using this method, and the detection could be completed within 60 min at 37 ℃. In addition, the fluorescence signal of this method could be directly observed by naked eyes, which is more compatible with instrumentation and more suitable for field diagnosis. Currently, two pathogen detection methods, CyHV-2 and GCRV-II, have been developed in this study, with detection limits of 10 copies/μL and 100 copies/μL, respectively. The two methods have no cross-reactivity with a variety of common fish pathogens, and the positive detection rate is higher than the current national standard PCR method. In summary, this technology is more efficient and convenient to detect than the existing technology, and it could be promoted as a candidate technology for field diagnosis in the future.

Key words:：RAA; CRISPR; Field diagnosis

鲤疱疹病毒Ⅱ型（CyHV-2）的 ORF67 通过竞争性阻断 STING 的磷酸化 阻断 IFN 表达的分子机制研究

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摘要：鲤疱疹病毒 II 型（Cyprinid herpesvirus 2，CyHV-2）引起的鲫造血器官坏死症给鲫养殖业造成了巨大的经济损失。干扰素（IFN）反应是鱼体抵抗 CyHV-2 感染的一道重要防线，但 CyHV-2 往往能够突破这一防线造成鱼体损伤，甚至引起大量死亡，而 CyHV-2 是通过哪种机制突破鱼体 IFN 抗病毒反应还不甚清楚。本文以 CyHV-2 为研究对象，首先从分子水平探究其 ORF67 蛋白通过结合并竞争性阻断 TBK1-A/B 对 STING-A/B 的磷酸化从而抑制 IFN 表达的机制，其次从细胞水平阐述 ORF67 对细胞抗病毒功能的影响。综上所述，本研究解析了 ORF67 通过抑制宿主 IFN 表达实现免疫逃逸的分子机制，丰富了 CyHV-2 致病机理研究，同时有望为鲫造血器官坏死症的防治提供理论参考。

关键词：鲤疱疹病毒Ⅱ型；ORF67；IFN；磷酸化；免疫逃逸

Cyprinid herpesvirus 2 (CyHV-2) ORF67 inhibits IFN expression by competitively obstructing STING phosphorylation

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Abstract：Cyprinid herpesvirus 2 (CyHV-2) caused hematopoietic necrosis in crucian carp (Carassius auratus) has resulted in huge economic losses to the crucian carp aquaculture. Interferon (IFN) response serves as a crucial line of defense for fish against CyHV-2 infection; however, CyHV-2 frequently overcomes this defense, resulting in damage and even substantial mortality. The mechanism through which CyHV-2 avoids elimination of the fish IFN antiviral response remains unclear. In this study, we focused on CyHV-2 as our research target, initially investigating how its ORF67 protein inhibits IFN expression by binding to and competitively blocking the phosphorylation of STING-A/B by TBK1-A/B at the molecular level. Then, we elaborated on the effect of ORF67 on the antiviral function of cells at the cellular level. In summary, this study has clarified the molecular mechanism of immune evasion by ORF67 through the inhibition of host IFN expression, enriching the understanding of the pathogenesis of CyHV-2 and providing theoretical references for the prevention and treatment of hematopoietic necrosis.

Key words:：cyprinid herpesvirus 2 (CyHV-2); ORF67; IFN; phosphorylation; immune escape

基于智能手机 APP 辅助的荧光探针用于鱼肉新鲜度检测

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摘要：食品安全问题已经越来越受到人们的重视，为了确保食品安全和人类健康，开发免仪器化、准确可靠、可视化智能读取的鱼肉新鲜度检测方法至关重要。本文合成了一种基于酚噻嗪的荧光探针 MPZ，可以实现双通道快速（7 s）检测生物胺。自主开发了用于视觉便携式检测鱼肉新鲜度的 APP（Visual evaluation），APP 将拍摄图像、可编辑式扫描 RGB 值、数据分析拟合、数据储存及验证等功能集成于一体。更重要的是，APP 与负载 MPZ 的传感标签 MPZ/FPS 组成的智能检测平台可以定量检测鱼肉 TVB-N 值，通过中国国家标准方法证实了其准确性和可靠性。该智能检测平台有望为便携化视觉检测领域提供新的思路，同时也为消费者、商家和监管者检测鱼肉新鲜度时提供一种免仪器化和智能读取的新型工具。

关键词：荧光探针; 生物胺; 智能手机 APP; 鱼新鲜度

Fluorescent Probes Assisted by Smartphone Apps for the Detection of Fish Meat Freshness

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Abstract：People are paying increasing attention to aquatic product safety. In order to ensure both food safety and human health, developing portable, accurate, reliable, visual, and intelligent fish freshness detection methods is very important. In this paper, a fluorescence probe MPZ ((E)-5-((10-ethyl-2-methoxy-10H-phenothiazin-3-yl)methylene)thiazolidine-2,4-dione) with phenothiazine as a fluorophore was synthesized. Through deprotonation, MPZ enables the rapid (7 s) detection of biogenic amine by colorimetric fluorescence dual-mode. We developed an application (App) called Visual evaluation for the portable detection of fish freshness. This App integrates several functions, including image capture, editable scanning of red, green, and blue (RGB) values, data analysis fitting, data storage, and verification. More importantly, the smart detection platform composed of the App and the load MPZ sensing tag MPZ/FPS, enables the quantitative measurement of the total volatile basic nitrogen (TVB-N) value of fish meat, and its accuracy and reliability have been confirmed by the national standard methods of China. This intelligent detection platform is expected to provide new ideas for the field of portable visual inspection, and also to offers consumers, merchants, and regulators a new type of tool for non-instrumental and intelligent reading of the freshness of fish meat.

Key words:：Fluorescent probe; Biogenic amines; Smartphone App; Fish freshness

水产养殖环境中农兽药物残留及其风险评价

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摘要：为了确定水产养殖环境中农兽药物残留会产生的安全隐患，本研究选取了上海地区的主要水产养殖场开展采样调查。利用超高压液相色谱-静电场轨道离子阱质谱对养殖池塘中的养殖水体、底泥以及使用的投入品进行农兽药物筛查，并利用风险商值法对水产养殖环境的农兽药物污染进行评价。结果表明：采集于上海地区的 100 家水产养殖场的 380 个样品中共筛查出 16 种农兽药物。三类样品在鱼、虾和蟹养殖场中都筛查出了 11 种农兽药物，而风险商值法发现筛查出的大部分农兽药物对水产养殖环境表现出中高生态风险。建议加强养殖环境的农兽药物的监管。

关键词：养殖环境；药物残留；风险评估

Residue and Risk Impact Assessment of Pesticides and Veterinary Drugs in Aquaculture Environment

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Abstract：In order to determine the safety hazards of pesticide and veterinary drug residues in the aquaculture environment, major aquaculture farms in Shanghai were selected for sampling and investigation in this study. The ultrahigh-performance liquid chromatography–quadrupole-Orbitrap mass spectrometry (UHPLC-Q/Orbitrap MS) was utilized to screen the water, sediment, and inputs used in the aquaculture ponds for pesticide and veterinary drugs, and risk quotient (RQ) method was utilized to evaluate the pesticide and veterinary drug contamination in the aquaculture environment.The results showed that 16 pesticide and veterinary drug residues were screened out in 380 samples collected from 100 aquaculture farms in Shanghai area.Eleven pesticide and veterinary drugs were screened in all three types of samples from fish, shrimp and crab farms, and the RQ method found that most of the screened pesticide and veterinary drugs showed medium to high ecological risk to the aquaculture environment. Recommends strengthening the regulation of pesticide and veterinary drug in the aquaculture environment.

Key words:：aquaculture environment;drug residue;risk assessment

盐酸小檗碱对魁蚶抗牡蛎疱疹病毒(OsHV-1)感染的调控机制

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摘要：牡蛎疱疹病毒 (OsHV-1) 感染是导致全球双壳类病害死亡的重要原因，目前尚缺乏有效的治疗手段。小檗碱对多种病毒具有潜在的抗病毒作用，但其对 OsHV-1 的抗病性能及调控机制尚不明确。在本研究中，我们对魁蚶进行 OsHV-1 注射感染和盐酸小檗碱（BBH）药物暴露实验，采用 HPLC-MS/MS 进行药代动力学分析，并通过转录组学和代谢组学联合分析了 BBH 调控魁蚶抗 OsHV-1 感染的信号通路。研究结果显示，3mg/LBBH 药物浓度对魁蚶的治疗效果最佳，药物暴露 96h 后魁蚶的死亡率为 60%，而对照组死亡率为 100%。药代动力学分析显示，鳃组织是 BBH 富集最多的器官。组学联合分析结果显示，药物暴露前期（12h），通过上调氧化磷酸化、柠檬酸循环、蛋白酶体等信号通路抵抗病毒感染；药物暴露后期（96h），通过 Notch、TGF-beta、Wnt 等信号通路以及自噬抑制病毒复制，从而提高了魁蚶的存活率。

关键词：牡蛎疱疹病毒，盐酸小檗碱，抗病毒调控，转录组学，代谢组学

The regulatory mechanism of berberine hydrochloride on the resistance of Scapharca broughtonii to OsHV-1 (Oyster herpesvirus 1) infection.

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Abstract：Oyster herpesvirus 1 (OsHV-1) infection is an important cause of disease-related deaths in bivalves worldwide, and currently there is a lack of effective treatment methods. Berberine has potential antiviral effects on various viruses, but its disease resistance performance and regulatory mechanism against OsHV-1 are still unclear. In this study, we conducted OsHV-1 injection infection and berberine hydrochloride (BBH) drug exposure experiments on Scapharca broughtonii. HPLC-MS/MS was used for pharmacokinetic analysis. The signal pathways of BBH regulating the resistance of Scapharca broughtonii to OsHV-1 infection were jointly analyzed by transcriptomics and metabolomics. The research results show that a BBH drug concentration of 3 mg/L has the best therapeutic effect on Scapharca broughtonii. After 96 hours of drug exposure, the mortality rate of Scapharca broughtonii is 60%, while that of the control group is 100%. Pharmacokinetic analysis shows that gill tissue is the organ with the most abundant enrichment of BBH. The results of combined omics analysis show that in the early stage of drug exposure (12 hours), virus infection is resisted by up-regulating signal pathways such as oxidative phosphorylation, citric acid cycle, and proteasome. In the later stage of drug exposure (96 hours), virus replication is inhibited through signal pathways such as Notch, TGF-beta, Wnt, and autophagy, thereby improving the survival rate of Scapharca broughtonii.

Key words:：OsHV-1;BBH;Antiviral regulation;Ranscriptomics;Metabolomics

识别胺类物质的荧光探针在三文鱼新鲜度监测中的应用

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摘要：水产品在运输和储存过程中时极易发生腐败变质，会释放多种胺类化合物如三甲胺、二甲胺等有害物质。这不仅影响鱼肉质量，还会对人体造成危害。因此对水产品的新鲜度进行监测尤为重要。随着科技的发展，新型无损检测技术更加简单，快速，方便。本研究基于“质子化-去质子化”的原理，以噻吩醛为荧光团，通过 Knoevenagel 缩合反应，引入强吸电子基团，设计合成荧光探针 PTD，制备负载探针 PTD 的指示标签。探针 PTD 具有长波发射（675 nm）。对生物胺具有比色荧光双通道识别、灵敏度高（2.75 μM）、响应时间快（＜3 s）等优点。对鱼肉新鲜度监测时，指示标签表现出由橙黄色-黄色-浅粉的比色和荧光变化，将指示标签的比色和荧光与新鲜度指标相对应，验证指示标签的可行性，其可以成为食品安全领域中更具吸引力的新鲜度监测平台。

关键词：荧光探针；新鲜度；生物胺；指示标签；噻吩醛；

Application of fluorescent probe for identification of amines in freshness monitoring of salmon

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Abstract：Abstract: Aquatic products are prone to corruption and deterioration during transportation and storage, and will release a variety of amine compounds such as trimethylamine, dimethylamine and other harmful substances. This not only affects the quality of fish, but also causes harm to the human body. Therefore, it is particularly important to monitor the freshness of aquatic products. With the development of science and technology, the new non-destructive testing technology is simpler,faster and more convenient. Based on the principle of "protonation-deprotonation", the fluorescent probe PTD was designed and synthesized by Knoevenagel condensation reaction using thiophenal as fluorophore and introducing strong electron-withdrawing groups, and the indicator label of loaded probe PTD was prepared. The probe PTD has the advantages of colorimetric fluorescence dual recognition for bioamines with long wavelength emission (675 nm), high sensitivity (2.75 μM) and fast response time (< 3 s). When monitoring the freshness of fish, the indicator label shows the colorimetric and fluorescent chan

Key words:：fluorescent probe; freshness; biological press; indicating label; thiophenal;

棘皮动物 IL-1 样基因的发现：一种新的 IL-1 家族成员作为炎症的保守调节因子

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摘要：白细胞介素-1 （IL-1） 是脊椎动物免疫和炎症反应的中枢调节因子。由于 IL-1 结构域的保守性不高所以在无脊椎动物中迟迟没有被鉴定，其中调控炎症的机制也不明。本研究在获得了刺参 IL-1 受体（IL-1R1）和 IL-1 受体辅助链（IL-1RAcP）的基础上，通过分泌蛋白组学，GST-pull down 获得了一个 IL-1 like 类似物，并通过细胞趋化、增殖实验明确了 IL-1 like 在功能上的保守性，通过激光共聚焦明确了 IL-1 like 类似物与 IL-1R1 和 IL-1RAcP 的互作关系，通过 RNA 干扰及回补实验证实了 IL-1R1 和 IL-1RAcP 可以正向调控炎症反应。

关键词：白介素；仿刺参；炎症反应；趋化

Discovery of the IL-1 like Gene from Echinodermata: A Novel IL-1 Family Member Serving as a Conserved Regulator of inflammation

Interleukin；Apostichopus japonicus；Inflammatory response；chemotaxis
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Abstract：Interleukin-1 (IL-1) is a central regulator of the immune and inflammatory responses in vertebrate. Because of the low conservation of IL-1 domain, it has not been identified in invertebrates, and its role in inflammatory regulation remains unclear. In this study, an IL-1like analogue was obtained through secretomic analysis and GST-pull down, on the basis of obtaining the IL-1 receptor (IL-1R1) and the IL-1 receptor accessory protein (IL-1RAcP) in Apostichopus japonicus. The results of cell chemotaxis and proliferation experiments suggest that the functional conservatism of IL-1 like. Through immunofluorescence colocalization the interaction among AjIL-1 like, AjIL1R1 and AjIL-1RAcP was confirmed. AjIL1R1 and AjIL-1RAcP have been shown to positively modulate the inflammatory response via RNA interference and rescue experiments.

Key words:：Interleukin；Apostichopus japonicus；Inflammatory response；chemotaxis

夏季西南大西洋阿根廷无须鳕异尖线虫幼虫感染情况研究

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摘要：阿根廷无须鳕(Merluccius hubbsi)是西南大西洋最主要的捕捞物种之一, 近年来其捕捞产量持续上升, 异尖线虫幼虫(Anisakid larvae)是寄生于阿根廷无须鳕最常见的寄生虫之一, 本研究为了解西南大西洋阿根廷无须鳕感染异尖线虫幼虫的情况, 于 2022 年 10 月至 2023 年 2 月夏季阿根廷及马尔维纳斯群岛(福克兰群岛)专属经济区外的公海海域共捕获 435 尾阿根廷无须鳕, 对其进行生物学实验, 采集寄生虫进行形态学鉴别, 最后记录数据并进行分析。结果显示, 阿根廷无须鳕感染异尖线虫幼虫的数量与样本鱼的性腺成熟度和不同感染部位有关, 并且感染数量与叉长和体重具有相关性。本研究可为阿根廷无须鳕生长特征和影响因素提供研究基础。

关键词：阿根廷无须鳕; 异尖线虫幼虫; 感染强度; 性成熟度

Infections of anisakid larvae in Merluccius hubbsi from the southwes- tern Atlantic Ocean in summer

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Abstract：This study showed that the abundance and intensity of M. hubbsi infection by anisakid larvae in the Southwest Atlantic was high, which was related to the stable ecosystem of its living sea area, large host population size, and suitable environment for survival. As the host matures, the range and number of feeding objects increase, and the parasite accumulates in the host during this process; it mainly parasitizes the abdominal cavity where the environment is suitable and the area of parasitism is large, and the liver and stomach, which have high nutritional value, are suitable for its growth, development, and stable parasitism. In summary, the number of M. hubbsi infected with anisakid larvae was related to sexual maturity and different infection sites in the sample fish, and the number of infections was correlated with fork length and body weight. This study provides a basis for understanding the growth characteristics and factors influencing anisakid larval infection of M. hubbsi.

Key words:：Merluccius hubbsi; anisakid larvae; infection intensity; sexual maturity

益生菌对水生动物生长和免疫水平的影响

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摘要：益生菌是指定植在宿主体内，通过改变宿主体内菌群组成而对宿主产生有益作用的活性微生物。因具有安全无残留和绿色环保的优点，益生菌被认为是最有希望控制或治疗水产养殖动物疾病的饲料添加剂，因此，益生菌已广泛用于水产养殖中。益生菌具有促进水生动物对饲料的利用率，提升水生动物免疫水平，维持肠道稳态，抑制病原微生物等诸多优点。本文简要回顾了近年来关于益生菌对水生动物生长、免疫机能影响的研究进展，以期为今后益生菌在水产养殖中的规范使用和水产健康养殖提供理论基础。

关键词：水生动物，益生菌，免疫，益生作用

Effect of probiotics on growth and immune function of aquatic animals

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Abstract： Probiotics refers to the active microorganisms which are planted in the host and have a beneficial effect on the host by changing the composition of the microflora. With the advantages of safety, residue free and environmental protection, probiotics are considered to be the most promising feed additives to control or treat diseases of aquaculture animals. Therefore, probiotics have been widely used in aquaculture. Probiotics have many advantages, such as promoting feed utilization rate, improving host immune level, maintaining intestinal homeostasis, and inhibiting pathogenic microorganisms. This paper briefly reviewed the research progress on the effects of probiotics on the growth and immune function of aquatic animals in recent years, with a view to providing a theoretical basis for the standardized use of probiotics in aquaculture.

Key words:： Aquatic Animals, Probiotics, Immunity, beneficial effect

微塑料联合铅离子暴露对厚壳贻贝的毒性作用研究

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摘要：本研究探讨了微塑料（microplastics，MPs）与铅离子（Pb2+）单独或联合暴露对厚壳贻贝的毒性作用。结果显示，MPs 单独暴露或联合 Pb2+暴露显著降低了贻贝的呼吸率和过滤率。MPs 单独或联合 Pb2+暴露诱导厚壳贻贝鳃和消化腺组织氧化应激损伤，组织中 H2O2 和 MDA 含量显著增加，抗氧化酶活性显著下降。此外，MPs 联合 Pb2+暴露对贻贝的免疫系统产生了负面影响，增加血细胞中活性氧（ROS）积累，并通过 TLR/MyD88/NFκB 信号通路抑制血细胞中自噬作用，同时诱导血细胞凋亡。本研究为微塑料与重金属联合暴露对海洋动物的毒性机制提供了新见解。

关键词：贻贝；微塑料；重金属；氧化应激；免疫响应

Simultaneous exposure to microplastics and heavy metal lead induced oxidative stress, histopathological damage, and immune dysfunction in marine mussel Mytilus coruscus

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Abstract： The increasing deposition of microplastics (MPs) in aquatic ecosystems is a worldwide issue of concern. MPs have the ability to interact with other environmental pollutants, such as heavy metals, and change their toxicity. In the present study, we focused on the effects of microplastics (MPs) and lead (Pb), as toxic metal, on marine mussel Mytilus coruscus under separate and co-exposure situations at environmentally relevant concentrations: MPs (1 mg/L) and Pb (50 μg/L). Results showed that MPs alone or co-exposure with Pb significantly decreased the respiration rate and filtration rate of the mussels. Histological observations have revealed varied extents of damage to the gill and digestive gland caused by single exposure to MPs, which was aggravated by co-exposure with Pb. In addition, the co-exposure induced a higher level of oxidative stress, which was reflected by increase of hydrogen peroxide and malondialdehyde content and decrease of antioxidant enzyme activities. Meanwhile, co-exposure poses a great threat to immune function of the mussels, as evidenced by inducing hemocytes

Key words:： Mussel; Microplastics; Heavy metal; Oxidative stress; Immune response

中华大蟾蜍流行疫病监测

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摘要：中华大蟾蜍（学名：Bufo gargarizans）为蟾蜍科蟾蜍属的两栖动物，俗名癞蛤蟆，是国家“三有”保护动物，同时是重要的中药材来源。中华大蟾蜍人工增养殖技术尚在探索中，为了掌握人工养殖中华大蟾蜍的疫病流行情况。2024 年，本研究综合利用常规病原鉴定技术、养殖环境病原分离技术和 16sRNA、微生物组学等对山东某养殖基地进行疫病监测和生物安保技术的探索。养殖周期内共检测 332 个样品，结果显示：未检出病毒性病原（蛙病毒 3 型、蛙虹彩病毒）、壶菌以及蛙脑膜炎败血伊丽莎白菌；检出气单胞菌（62/332）、蜡样芽孢杆菌（10/332）、柠檬酸杆菌（9/332）、不动杆菌（17/332）及线虫（65/84）;伴随降雨增多，不动杆菌检出率和蟾蜍死亡数激增。研究表明，实施标准化的生物安保技术，在开展人工中华大蟾蜍养殖过程中能有效预防流行疫病的发生，但应密切关注天气等因子的变化引起的中华大蟾蜍应激减产。

关键词：中华大蟾蜍；流行病学；生物安保；人工繁育

Epidemiological Surveillance of Bufo gargarizans

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Abstract：Bufo gargarizans ,commonly known as the toad, which is the “three animal”of China and an important source of Chinese medicinal materials. The artificial breeding of the toad is still immature. To grasp the epidemic situation of the process, in 2024, we used the conventional pathogen identification technology, environmental pathogen isolation technology, 16sRNA, and microbiome to explore the disease monitoring and biosecurity technology at a base in Shandong. The 332 samples tested showed that no Frog virus 3, Rana grylio virus, Batrachochytrium dendrobatidis and Elizabethkingia meningoseptica. Aeromonas (62/332), Bacillus cereus (10/332), Citrobacter (9/332), Acinetobacter (17/332) and Nematode (65/84) were detected; with increased rainfall, the detection rate of Acinetobacter and the toad deaths have surged. The results show that the implementation of standardized biosecurity technology can effectively prevent the occurrence of epidemic diseases in the breeding of toad, but we should focus on the stress and yield reduction of toad caused by changes in weather and other factors.

Key words:：Bufo gargarizans; epidemiology; biosecurity；artificial breeding

aroA 和 ppk1 在维氏气单胞菌致病性中的作用以及突变株 AV-ΔaroA/ppk1 作为减毒活疫苗的效力评估

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摘要：维氏气气单胞菌是一种对水产养殖和人类健康造成巨大威胁的条件致病菌，因此迫切需要绿色高效的方法来应对其感染。本研究构建了可稳定遗传的单基因缺失株和双基因缺失株（AV-ΔaroA、AV-Δppk1、AV-ΔaroA/ppk1）。与野生株相比，AV-Δppk1、AV-ΔaroA 和 AV-ΔaroA/ppk1 的 LD50 分别增加了 1.38、1.62 和 6.99 倍。致病性下降可能与突变株运动、生物膜形成能力、毒力相关基因表达水平降低有关。安全性评估表明，3×107 CFU/mL 浓度的 AV-ΔaroA/ppk1 是安全的，不会诱发明显的病理变化，且能有效增强宿主特异性和非特异性免疫水平。用野生菌株攻毒后，AV-ΔaroA/ppk1 的 RPS 为 67.85%明显高于灭活疫苗组。由此可知，aroA 和 ppk1 在致病过程中发挥重要作用，AV-ΔaroA/ppk1 是一种有效预防维氏气感染的减毒活疫苗。

关键词：维氏气单胞菌；致病性；减毒活疫苗；免疫反应

The role of aroA and ppk1 in Aeromonas veronii pathogenicity and the efficacy evaluation of mutant strain AV-ΔaroA/ppk1 as a live attenuated vaccine

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Abstract：Aeromonas veronii is an opportunistic pathogen that poses great threat to aquaculture and human health, so there is an urgent need for green and efficient methods to deal with its infection. In this study, single and double gene deletion strains (AV-ΔaroA, AV-Δppk1 and AV-ΔaroA/ppk1) that can be stably inherited were constructed. Pathogenicity test showed that the toxicity of AV-ΔaroA and AV-ΔaroA/ppk1 was significantly lower compared to wild-type A. veronii. Biological characterization analysis revealed that the decrease in pathogenicity might be due to the declined growth, motility, biofilm formation abilities and the expression of virulence-related genes in mutants. Subsequently, we evaluated the efficacy of AV-ΔaroA/ppk1 as a live attenuated vaccine (LAV). Safety assessment experiments showed that AV-ΔaroA/ppk1 injected at a concentration of 3 × 107 CFU/mL was safe for C. carassius. The relative percentage survival of AV-ΔaroA/ppk1 was 67.85 %, significantly higher than that of the inactivated A. veronii, which had an RPS of 54.84 %. This improved protective effect was mainly attributed to the increased levels of A. veronii specific IgM antibody, enhanced alkaline phosphatase, lysozyme and superoxide dismutase activities, as well as higher expression levels of several immune related genes. Together, these findings deepen our understanding of the functional roles of aroA and ppk1 in A. veronii pathogenicity, provide a good candidate of LAV for A. veronii.

Key words:：Aeromonas veronii; Pathogenicity; Live attenuated vaccine; Immune response

三种不同类型佐剂灭活疫苗免疫效果的研究与应用

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摘要：为研究 4%氢氧化铝凝胶、黄芪多糖和弗式完全佐剂三种不同类型佐剂灭活疫苗对于斑马鱼的免疫效果，实验分为将三种不同佐剂分别与美人鱼发光杆菌灭活疫苗按一定比列混合，与阴性对照、阳性对照和灭活疫苗组。免疫后 1d、3d、7d、14d、21d 分别取肝脏等组织测定其 AKP、ACP、SOD、CAT、LZM 等酶活。结果表明 ACP、AKP、CAT 活性表达最高的是黄芪多糖加灭活疫苗组，LZM 与 SOD 活性表达最高的是 4%氢氧化铝凝胶加灭活疫苗组，但与黄芪多糖组相差无几。研究表明三种不同类型佐剂对于灭活疫苗的免疫效果都具有促进效果，其中黄芪多糖效果最明显。本研究可为拓展佐剂灭活疫苗在水产疾病防控上的应用提供数据参考。

关键词：佐剂、灭活疫苗、酶活

Research and Application of the Effectiveness of Three Types of Adjuvant Inactivated Vaccines

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Abstract： In order to study the immune effects of three different types of adjuvant inactivated vaccines, namely 4% alumina hydroxide gel, Astragalus polysaccharide and Fulvish complete adjuvant, on zebrafish,The experiment was divided into three different adjuvants mixed with inactivated Bacillus mermaidii vaccine, negative control group, positive control group and inactivated vaccine group.AKP, ACP, SOD, CAT, LZM and other enzyme activities of liver tissues were measured on day 1, day 3, day 7, day 14 and day 21 after immunization.The results showed that the highest activity expression of ACP, AKP and CAT was in the Astragalus polysaccharide plus inactivated vaccine group, and the highest activity expression of LZM and SOD was in the 4% aluminum hydroxide gel plus inactivated vaccine group, which was similar to that in the Astragalus polysaccharide group.The results showed that three different types of adjuvants had promoting effect on the immune effect of inactivated vaccine, and the effect of Astragalus polysaccharide was the most obvious.

Key words:：Adjuvant, Inactivated vaccine, Enzyme activity

黑斑原鮡不同组织微生物群落特征及致病性研究

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摘要：黑斑原鮡是一种特有于西藏雅鲁藏布江的鱼类，现已被列为国家二级保护动物。本文通过对健康和病死黑斑原鮡不同组织可培养微生物的培养、组织学观察、不同组织及不同养殖水体进行 16S rRNA 基因的 V3-V4 可变区测序，比较了健康和病死黑斑原鮡不同组织病理组织学差异、微生物群落差异及致病性。结果显示健康和病死黑斑原鮡肠道绒毛高度无显著差异，皮肤和鳃在病理分析上存在差异。皮肤菌群之间 Shannon 和 Simpson 指数存在显著差异，鳃菌群在 PCoA 上存在显著差异。肠道、皮肤和鳃优势菌门均为厚壁菌门、拟杆菌门、变形菌门，但各菌门丰度不同。不同组织有大量菌属未被鉴定。综上病死黑斑原鮡不同组织中，放线菌门、绿弯菌门丰度均增加，疣微菌门丰度均减少，猜测放线菌门可能是此次疾病的主要致病菌。本研究分析了病死黑斑原鮡不同组织微生物群落特征及其致病性，以期为了解黑斑原鮡不同组织菌群结构、健康养殖中疾病的定向防控提供参考。

关键词：黑斑原鮡；微生物；鳃；皮肤；肠道；高通量测序

Investigation of microbial community characteristics and pathogenicity across various tissues of Glyptosternum maculatum

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Abstract：Glyptosternum maculatum, a Tibet Yarlung Zangbo River endemic fish, is a second-class protected species. This study cultured microbes from healthy and deceased Glyptosternum maculatum tissues, observed histology, and sequenced the 16S rRNA gene V3-V4 region. No significant intestinal villus height difference was found between healthy and deceased fish. Skin microbiota showed Shannon and Simpson index differences, and gill microbiota varied on PCoA. Firmicutes, Bacteroidetes, and Proteobacteria were dominant in intestine, skin, and gills, with varying abundances. Many bacterial genera remain unidentified. Actinomycete and chloromycete abundances increased, while verrucomicrobial abundance decreased, suggesting actinomycetes' role in disease. The study offers insights for targeted prevention in aquaculture.

Key words:：black spot bream; microorganisms; gills; skin; intestines; high-throughput sequencing

微囊藻毒素-LR 对吉富罗非鱼肠道损伤及肝脏脂代谢的影响

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摘要：本研究通过腹腔注射 MC-LR 对吉富罗非鱼进行急性胁迫实验。结果表明，MC-LR 显著影响血清生化指标，如 AST、ALT、C3、LYZ、AKP、TC 及 TG，表明其对肝功能、免疫及脂质代谢有急性毒性。肝脏抗氧化系统被激活，CAT、SOD 活性增加，MDA 累积，反映 MC-LR 诱导的氧化应激。肠道微生物α多样性及 p__Firmicutes 和 p__Bacteroidota 的相对丰度显著下降。Sphingobium 和 Sphingomonas 的相对丰度显著下降，而 Brevundimonas 的相对丰度显著上升，表明 MC-LR 改变肠道菌群结构。靶向代谢组分析显示短链脂肪酸减少，影响肠道代谢。研究揭示 MC-LR 扰乱免疫系统、损伤肝脏、改变肠道菌群及代谢，导致脂质代谢异常。这一发现为理解 MC-LR 对水生生物毒性机制提供了新视角。

关键词：吉富罗非鱼，脂质代谢，SCFAs，肠道微生物

Effects of Microcystin-LR Exposure on Intestinal Injury and Hepatic Lipid Metabolism in GIFT Tilapia

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Abstract： In this study, acute stress experiments were conducted on GIFT tilapia (Oreochromis niloticus) by intraperitoneal injection of microcystin-LR (MC-LR). The results demonstrated that MC-LR significantly affected serum biochemical indices, including AST, ALT, C3, LYZ, AKP, TC, and TG, indicating its acute toxicity on liver function, immunity, and lipid metabolism. The hepatic antioxidant system was activated, as evidenced by increased CAT and SOD activities and MDA accumulation, reflecting MC-LR-induced oxidative stress. Additionally, significant decreases were observed in the α-diversity of intestinal microbiota and the relative abundance of p__Firmicutes and p__Bacteroidota. Notably, the relative abundances of Sphingobium and Sphingomonas declined markedly, while that of Brevundimonas increased significantly, suggesting that MC-LR alters the intestinal microbiota composition. Targeted metabolomic analysis further revealed a reduction in short-chain fatty acids, impacting intestinal metabolism. This study unveils that MC-LR disrupts the immune system, damages the liver, alters the intestinal microbiota and metabolism, ultimately leading to abnormal lipid metabolism. These findings provide novel insights into the toxic mechanisms of MC-LR in aquatic organisms.

Key words:：GIFFT tilapia, lipid metabolism, SCFAs, gut microbiology

饲料中添加石榴皮水提物对仿刺参肠道微生物多样性的影响

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摘要：通过 16S rRNA 高通量基因测序技术研究了石榴皮投喂后仿刺参肠道微生物的种群结构特征，并比较不同添加水平（1%、3%、5%）的石榴皮水提物对仿刺参肠道微生物群落结构的影响。研究结果为：从门水平上分析，各组中肠道中微生物核心菌群均为变形菌门（Proteobacteria）、疣微菌门（Verrucomicrobiota）和拟杆菌门（Bacteroidota）；变形菌门占比总体呈升高趋势，疣微菌门和拟杆菌门的相对丰度逐渐降低，各组间变化趋势相似；从属水平分析，主要的菌属为 Persicirhabdus 和盐杆菌属（Haloferula）,各组中 Persicirhabdus 占比大幅度降低，盐杆菌属相对丰度随着石榴皮添加水平的升高总体呈现逐渐升高的趋势。综上所述，石榴皮作为饲料添加剂可影响仿刺参肠道菌群物种多样性，以 3%为最适宜添加量。

关键词：仿刺参；石榴皮水提物；肠道微生物；群落结构

Effects of aqueous extract of pomegranate peel on gut microbial diversity of Apostichopus japonicus

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Abstract：16S rRNA high-throughput gene sequencing was used to study the microbial community structure of A.japonicus fed with pomegranate peel, and to compare the effects of pomegranate peel aqueous extract at different levels (1%,3%,5%) on the microbial community structure of A.japonicus. Analysis at phylum level showed that the microbial core flora in each group belonged to Proteobacteria Proteobacteria, verrucous microflora (Verrucomicrobiota) and Bacteroides (Bacteroidota). The proportion of Proteobacteria increased, while the relative abundance of Verrucomicrobacteria and Bacteroides decreased gradually. At the subordinate level, Persicirhabdus and Haloferula were the main genera. The proportion of Persicirhabdus decreased greatly in each group, and the relative abundance of Haloferula increased gradually with the increase of pomegranate peel addition level. In conclusion, pomegranate peel as a feed additive can affect the intestinal flora species diversity of A.japonicus, and 3% is the most suitable addition.

Key words:：Apostichopus japonicus; Pomegranate peel aqueous extract; gut microbiome; Community structure

大黄鱼干扰素 h 抗病毒信号通路研究

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摘要：大黄鱼（Larimichthys crocea）是我国重要的海水经济鱼类。随着大黄鱼养殖业的快速发展，病源性疾病日益严重，造成了巨大的经济损失。然而迄今为止，尚无有效的防治手段。干扰素（Interferon，IFN）是一类可以引起宿主建立抗病毒状态的细胞因子，是脊椎动物抵御病毒感染的第一道防线。我们前期研究发现 LcIFNh 既具有抗病毒功能，但具体调控机制仍不清楚。本文利用荧光素酶报告基因系统、Western blot 等技术，揭示了 LcIFNh 与受体 CRFB1、CRFB5 结合的胞外段存在相互作，LcIFNh 不仅可上调 JAK-STAT 信号通路关键分子 STAT1、STAT2、JAK1、IRF9 及抗病毒效应基因 MxA、PKR 和 viperin 的转录水平，rLcIFNh 还可上调大黄鱼 STAT1 和 STAT2 的磷酸化水平。

关键词：大黄鱼；干扰素；信号通路

Study on the antiviral signaling pathway of interferon h in yellow croaker

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Abstract：Large yellow croaker (Larimichthys crocea), a perciform fish, is an economically important mariculture species in China. With the rapid development of large yellow croaker farming, diseases caused by various pathogens are becoming more severe and causing economic losses. However, there are no effective prevention and control measures. Interferons (IFNs) are a broad class of cytokines that can induce the host's antiviral state, which is the first line of defense against invasion of the virus in vertebrates. Previous studies revealed that large yellow croaker IFNh had antiviral biological activity, while the regulation mechanism was not clear. Studies on the mechanism of antiviral immunity of IFNh in large yellow croaker has been promoted by luciferase reporter assay and western blot. The results showed that the corresponding receptors of LcIFNh were CRFB1/CRFB5. The expression levels of Jak1, STAT1, STAT2, and IRF9, were significantly upregulated in head kidney leukocytes stimulated by rLcIFNh, suggesting that LcIFNh could upregulated the expression levels of key molecules involved in the JAK-STAT signaling pathway. LcIFNh could promote the phosphorylation levels of STAT1 and STAT2. Furthermore, rLcIFNh upregulated the expression levels of antiviral genes in the primary head kidney leukocytes, such as MxA, PKR and viperin. In conclusion, it demonstrated that LcIFNh could bind to corresponding receptors and induce the transcription of antiviral genes by activating the JAK-STAT signaling pathway. This paper laid a good theoretical foundation for understanding the mechanism of fish antiviral immunity and preventing viral disease with interferon genes in the future.

Key words:： Large yellow croaker (Larimichthys crocea); Type I interferon; The signaling pathway.

基于转录组学分析自噬通过调节细胞代谢和免疫途径增强罗氏沼虾的免疫防御

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摘要：自噬在抵抗入侵微生物的先天免疫和适应性免疫中起着至关重要的作用。然而，罗氏沼虾自噬的机制在很大程度上仍然未知。在本研究中，我们发现嗜水气单胞菌可以诱导罗氏沼虾的自噬激活，同时，激活自噬可以抑制嗜水气单胞菌对罗氏沼虾的感染。更进一步的，我们对雷帕霉素处理的罗氏沼虾鳃组织进行了 RNA-seq 分析。我们鉴定出 1684 个上调的 DEGs 和 1500 个下调的 DEGs，其中大多数 DEGS 主要负调控代谢途径。此外，我们结合了嗜水气单胞菌刺激的转录组数据，进行了综合分析，分别鉴定出 15 个和 25 个同时上调和下调的 DEGs，这些基因通过负调控代谢和促进免疫途径来增强罗氏沼虾的免疫防御。我们的研究结果将为进一步探索罗氏沼虾的抗菌感染机制提供一定的理论依据。

关键词：罗氏沼虾，自噬，代谢，免疫防御

Comparative transcriptomic analysis of autophagy enhances the immune defense of Macrobrachium rosenbergii by regulating cellular metabolism and immune pathways

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Abstract： Autophagy plays a vital role in innate and adaptive immunity against invading microorganisms. However, the mechanism underlying autophagy in Macrobrachium rosenbergii remains largely unknown. Here we report that Aeromonas hydrophila can induce autophagy activation in M. rosenbergii, which could inhibit the infection of A. hydrophila. Furthermore, we conducted high-throughput RNA-seq analysis from the gill tissue of M. rosenbergii treated by rapamycin. 1684 upregulated and 1500 downregulated DEGs were identified, most of which mainly negatively regulate metabolic pathways. In addition, we combined the transcriptome data stimulated by Aeromonas hydrophila and conducted a comprehensive analysis, identifying 15 and 25 DEGs that were simultaneously upregulated and downregulated, respectively. These genes enhance the immune defense of Macrobrachium rosenbergii by negatively regulating metabolic pathways and promoting immune pathways. Our results will provide a theoretical basis for further exploring the antibacterial infection mechanism of M. rosenbergii.

Key words:：Macrobrachium rosenbergii, Autophagy, Metabolism, Immune defense

鲍疱疹病毒体外培养及其与杂色鲍血淋巴细胞互作机制

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摘要：鲍疱疹病毒（HaHV-1）上世纪 90 年代以来引起中国大陆、台湾与澳大利亚养殖鲍大规模死亡。HaHV-1 主要侵染鲍神经组织和血淋巴细胞，由于缺乏软体动物细胞系，对 HaHV-1 入侵与宿主免疫机制的认识非常欠缺。本研究使用体外悬浮培养的杂色鲍血淋巴细胞，建立 HaHV-1 体外培养平台。使用实时定量 PCR 对血淋巴细胞感染 HaHV-1 后的病毒载量进行监测，使用转录组技术对 HaHV-1 与血淋巴细胞的互作机制进行分析。结果显示，病毒在感染后 60h，载量最高可达到 4.0×107 copies/ng 总 DNA；感染 72h 时载量开始下降。转录组分析结果显示，血淋巴对病毒的免疫集中在感染早期，感染后 24h 内吞、TNF、mTOR、P13K-AKt 等免疫信号通路显著上调，神经损伤相关信号通路显著下调。在感染后期，细胞代谢相关信号通路显著上调。本研究对 HaHV-1 体外感染平台建立和病毒-宿主互作机制研究提供了重要参考。

关键词：杂色鲍； HaHV-1； 血淋巴细胞； 体外培养； 转录组

In vitro culture of abalone herpes virus and its interaction mechanism with mixed abalone blood lymphocytes

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Abstract：The abalone herpes virus (HaHV-1) has caused mass deaths in Chinese mainland, Taiwan and Australia since the 1990s. HaHV-1 mainly infects abalone nerve tissue and blood lymphocytes and is known as abalone neuritis. The lack of molluscan cell lines. In this study, in vitro suspension culture of lymphocytes were used to culture the HaHV-1. The viral load was monitored after HaHV-1 infection using real-time quantitative PCR, and the interaction mechanism between HaHV-1 and hemolyphocytes was analyzed using transcriptome technology. The results showed that the virus could load reached up to 4.0107 copies / ng total DNA at 60h after infection; the load began to decrease at 72h of infection. The results of transcriptome analysis showed Hemolymph immunity to virus was concentrated in the early stage of infection, with TNF, mTOR, and P13K-AKt significantly upregulated, while those related to nerve injury were significantly downregulated. Cell metabolism-related signaling pathways were significantly upregulated later late infection. This study provides an important reference for the establishment of HaHV-1 infection platform and the mechanism of virus-host interaction.

Key words:：haliotis diversicolor Reeve ;HaHV-1;Blood lymphocytes; Culture in vitro ; Transcriptome

IV 型菌毛蛋白 PilA/Q 介导杀鱼爱德华氏菌感染机制及牙鲆白介素-8/血红蛋白抗菌免疫功能研究

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摘要：杀鱼爱德华氏菌是一种强毒力的水产病原菌。在本研究中，IV 型菌毛 PilA/PilQ 的缺失或封闭可抑制杀鱼爱德华氏菌的运动、生物膜、抗酸抗氧化、黏附/侵入细胞能力。rPilA/Q 可激活牙鲆巨噬细胞的 ROS/ACP 活性、IL8 等免疫基因表达，促进血清的抑菌能力。亚单位疫苗 rPilA/Q 对牙鲆具有显著的相对保护率。研究发现 rPilA 可结合 rIL8s，rIL8s 可结合、抑制、杀死多种细菌。rIL8s 可结合 PBLs 并激活其活性，并可促进中性粒细胞释放 NETs。rIL8s 或敲降可显著影响细菌的侵染能力。研究发现 rPilA 可结合 rHb-β，rHb-β具有抗菌的活性，rHb-β可激活巨噬细胞的趋化、增殖、ACP/ROS 和吞噬活性。细菌可调控 Hb-β的表达量，rHb-β可促进鱼体增强抗菌能力。研究结果将加深细菌菌毛与硬骨鱼免疫系统互作的认识，为牙鲆疾病的绿色健康防控奠定理论基础。

关键词： 牙鲆，杀鱼爱德华氏菌，Ⅳ型菌毛，白介素-8，血红蛋白

Mechanistic Study of Edwardsiella piscicida infection mediated by Type IV Pili Proteins PilA/Q and the antimicrobial immune function of Interleukin-8 and Hemoglobin in Paralichthys olivaceus

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Abstract：Edwardsiella piscicida is a highly virulent aquatic pathogen. In this study, the deletion or inhibition of Type IV pili proteins PilA/PilQ significantly suppresses the motility, biofilm formation, acid and oxidative stress resistance, and the ability of E. piscicida to adhere to and invade host cells. rPilA/Q can activate ROS and ACP activities in flounder macrophages, induce the expression of immune-related genes such as IL-8, and enhance the antibacterial capacity of serum. The subunit vaccine rPilA/Q provides a significant relative protection rate in flounder. The study found that rPilA can bind to recombinant rIL8s, and rIL8s are capable of binding to, inhibiting, and killing various bacteria. Additionally, rIL8s can bind to PBLs and activate their functions, while also promoting NETs. The upregulation or knockdown of rIL8s can significantly affect the bacterial infection capacity. The study found that rPilA can bind to rHb-β, which exhibits antimicrobial activity. rHb-β can activate macrophage chemotaxis, proliferation, ACP/ROS, and phagocytic activities. Bacteria can regulate the expression levels of Hb-β, and rHb-β can enhance the antimicrobial capacity of the fish.

Key words:：Paralichthys olivaceus, Edwardsiella piscicida, Type IV Pili, Interleukin-8, Hemoglobin

玫瑰精油对乌鳢源维氏气单胞菌的抑菌活性及其机理研究

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摘要：维氏气单胞菌（A. veronii）是一种水生人畜共患病原体，宿主范围很广，会造成水生动物的死亡和渔业的巨大经济损失。随着细菌耐药性的发展，天然植物提取物被认为是一种有效的替代抗菌剂。结果表明，玫瑰精油（REO）对 A. veronii 的 MIC 和 MBC 均为 1.25 μL/mL，表明 REO 具有显著的抑菌活性。电子显微镜和活死细胞染色发现，REO 会严重破坏细胞形态并增加细胞膜的通透性。此外，REO 处理还导致细菌内蛋白质和核酸等生物大分子的泄漏。代谢组学分析表明，REO 处理后共筛选到了 190 种差异代谢物（118 个下调，72 个上调），主要富集在生物素代谢、精氨酸生物合成、谷胱甘肽代谢、赖氨酸降解、组氨酸代谢等代谢途径，表明 REO 严重干扰了 A. veronii 代谢。这些结果为了解 REO 对 A. veronii 的抗菌机制提供了理论依据，并支持 REO 作为一种潜在的抗菌剂用于预防和治疗水产养殖中的细菌性疾病。

关键词：维氏气单胞菌、玫瑰精油、抗菌活性、代谢组学

Antibacterial Activity and Mechanism of Rose Essential Oil (REO) against Aeromonas veronii isolated from Northern snakehead (Channa argus)

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Abstract： Aeromonas veronii (A. veronii) is a zoonotic aquatic pathogen with a wide host range, causing significant mortality in aquatic animals and economic losses in fisheries. With rising bacterial resistance, natural plant extracts, such as rose essential oil (REO), are considered effective alternative antimicrobials. The study found that the MIC and MBC of REO against A. veronii were 1.25 μL/mL, showing strong bacteriostatic activity. Electron microscopy and live-dead cell staining revealed that REO severely damaged cell morphology and increased membrane permeability, leading to leakage of proteins and nucleic acids. Metabolomics analysis identified 190 differential metabolites (118 down-regulated, 72 up-regulated) after REO treatment, affecting key pathways like biotin metabolism, arginine biosynthesis, glutathione metabolism, lysine degradation, and histidine metabolism, indicating major metabolic disruption. These results suggest that REO is a promising antimicrobial agent for controlling bacterial diseases in aquaculture.

Key words:： Aeromonas veronii, Rose essential oil, Antibacterial activity, Metabolomics analysis

tapP 基因在调节嗜水气单胞菌毒力中的功能及其作用机制

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摘要：目的 研究 tapP 基因对嗜水气单胞菌的致病力、生物学特性及相关毒力因子基因表达的影响。方法 利用同源重组法构建嗜水气单胞菌 tapP 缺失突变株（ΔtapP-AH），比较突变株和野生株的毒力、生物学特性差异以及其他相关毒力因子基因的表达情况。结果 成功构建一株遗传稳定的、毒力明显减弱的 tapP 突变株。透射电子显微镜下观察ΔtapP-AH 的菌毛，仅见短而稀疏的Ⅰ型菌毛。ΔtapP-AH 黏附能力和生物被膜形成能力显著下降。qRT-PCR 结果表明 tapP 的缺失影响了Ⅳ型菌毛、Ⅱ型分泌系统、Ⅵ型分泌系统和鞭毛相关基因的表达，而不影响Ⅰ型菌毛相关基因表达。结论 tapP 参与调控嗜水气单胞菌的Ⅳ型菌毛组装、黏附能力和生物被膜形成能力，并影响其他相关毒力因子基因的表达，对嗜水气单胞菌的致病力至关重要。

关键词：tapP 基因；毒力；黏附能力；嗜水气单胞菌；Ⅳ型菌毛

The role and function mechanism of tapP in modulating the virulence of Aeromonas hydrophila

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Abstract：Aeromonas hydrophila (A. hydrophila) is a widespread pathogen capable of infecting most freshwater fish and causing septicemia. Type IV pili are one of the major virulence factors of A. hydrophila and play a key role in virulence and adhesion to the host. TapP is known to be involved in the synthesis of type IV pili. However, the effect and molecular mechanism of the tapP in A. hydrophila remain unknown. In this study, we constructed a genetically stable tapP deletion mutant strain of A. hydrophila (ΔtapP-AH), the median lethal dose (LD50) value of the ΔtapP-AH in Carassius auratus gibelio was 3.1-fold higher than that of the wild-type strain (WT-AH). The transmission electron microscopy (TEM) results showed that ΔtapP-AH exhibited sparser pili. The ability of adhering to gill tissues and biofilm formation was significantly reduced in ΔtapP-AH. For motility, the swimming ability of ΔtapP-AH was significantly higher, no significant difference was found in twitching and swarming abilities. We further investigated the effect of tapP gene deletion on the expression of virulence related factor genes to explore the molecular mechanisms of attenuated virulence and altered biological characteristics. The results indicated that deletion of the tapP directly affected the expression of genes related to type IV pili, type II secretion system, type VI secretion system and flagellum, but had no effect on the genes related to type I pili. In conclusion, this study provides new insights into the function of the tapP and the pathogenic mechanism in A. hydrophila.

Key words:：tapP gene; Virulence; Adhesion; Aeromonas hydrophila; type IV pili

印度洋长鳍金枪鱼不同生命阶段栖息地时空分布研究

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摘要：本研究利用印度洋海洋环境数据, 构建了印度洋长鳍金枪鱼不同生命阶段的栖息地模型, 通过对比模型预测的适宜栖息地位置与实际渔获量分布的关系对模型准确性进行了验证, 并在此基础上分析了不同生命阶段长鳍金枪鱼适宜栖息地的年际变动, 探究了海洋环境变动对长鳍金枪鱼栖息地时空分布的影响。结果表明: (1)渔获量大值区与模型预测的适宜栖息地基本重合, 性未成熟与性成熟长鳍金枪鱼栖息地模型月平均 AUC 值分别为 0.79 和 0.73, 预测准确率较高, 性未成熟长鳍金枪鱼栖息地的预测效果略好; (2)模型预测的性未成熟长鳍金枪鱼适宜栖息地在 1 月~6 月位于 25°S~40°S 海域, 7 月~12 月位于 20°S~40°S 海域; 性成熟长鳍金枪鱼适宜栖息地在产卵期位于 10°S~25°S 马达加斯加岛以东海域, 非产卵期位于 25°S~45°S 海域; (3)性未成熟与性成熟长鳍金枪鱼适宜栖息地都呈逐年南移趋势。

关键词：印度洋; 长鳍金枪鱼; 栖息地指数; 年际变动

Research on the spatial-temporal distribution of habitat of Indian Ocean albacore tuna at different life stages

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Abstract： In this study, we used environmental data from the Indian Ocean to construct a habitat model for different life stages of albacore tuna and their corresponding environmental requirements. We validated the accuracy of the model by comparing the predicted suitable habitat locations with the actual distribution of catch quantities. We evaluated the model using the area under the receiver operating characteristic curve and analyzed the inter-annual variations of suitable habitat at different life stages of albacore tuna, investigating the impact of marine environmental changes on the spatial-temporal distribution of habitat. The results indicate that: (1) The high catch areas largely overlap with the model-predicted suitable habitat, with monthly average AUC values of 0.79 for immature and 0.73 for mature albacore tuna habitat models, showing high prediction accuracy. The prediction performance for the habitat of immature albacore tuna is better; (2) The model predicts that suitable habitat for immature albacore tuna is located between 25°S and 40°S in the Indian Ocean from January to June, and between 20°S and 40°S from July to December. For mature albacore tuna, the suitable habitat during spawning period is situated east of Madagascar Island between 10°S and 25°S, while during non-spawning period, it is found between 25°S and 45°S in the sea; (3) Both the suitable habitat for immature and mature albacore tuna show a year-on-year trend of southward migration.

Key words:：Indian Ocean; Thunnus alalunga; Habitat suitability index; Inter-annual variability

基于稳定同位素分析法研究日本鲐与远东拟沙丁鱼之间的营养关系

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摘要：日本鲐和远东拟沙丁鱼广泛分布于日本沿海、西北太平洋海域，两个物种是重要的捕捞对象。为了研究两个物种之间的营养关系，本研究根据 2021 年 6～7 月在西北太平洋公海采集的（38°59′N～43°00′N，150°30′E～161°48′E）日本鲐和远东拟沙丁鱼肌肉样本，应用稳定同位素示踪技术，分析了在不同体长和性别的日本鲐、远东拟沙丁鱼种间和种内稳定同位素的差异性。对于种内差异，日本鲐和远东拟沙丁鱼的δ13C、δ15N 值在雌、雄个体间均无显著差异（P＞0.05）；日本鲐的δ15N 值在不同体长组间无显著差异（P＞0.05），δ13C 值差异显著（P＜0.05），远东拟沙丁鱼δ13C、δ15N 值在不同体长组间的差异均显著（P＜0.01）。对于种间差异，日本鲐和远东拟沙丁鱼的δ13C、δ15N 值在对应体长组间均存在显著差异（P＜0.01）。

关键词：日本鲐；远东拟沙丁鱼；摄食生态；稳定同位素；生态位；营养关系

Assessing the trophic interactions between two pelagic fishes in the northwestern Pacific based on stable isotopes

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Abstract： Scomber japonicus (S. japonicus) and Sardinops melanostictus (S. melanostictus) are widely distributed off the coast of Japan and in the northwestern Pacific. To investigate the trophic interactions between these two species, samples of S. japonicus and S. melanostictus were taken from the high seas of the northwestern Pacific Ocean (38°59′N–43°00′N, 150°30′E–161°48′E) from June to July 2021. We utilized stable isotope analysis to study the intraspecific and interspecific differences of them. For intraspecific variability, there was no significant difference in δ13C or δ15N values between females and males for either S. japonicus or S. melanostictus (P > 0.05). Significant differences in the δ13C and δ15N values of S. melanostictus were found among the body length groups (P < 0.01). The δ13C values of S. japonicus significantly differed among body length groups (P < 0.05). However, there was no significant difference in the δ15N values of S. japonicus (P > 0.05). For interspecific variability, there were significant differences in the δ13C and δ15N values between S. japonicus and S. melanostictus (P < 0.01). According to the GAM results, both the δ13C and δ15N values of S. japonicus gradually increased with body length, whereas both the δ13C and δ15N values of S. melanostictus tended to decrease and then increase. The niche overlap between S. japonicus and S. melanostictus decreased with increasing growth. Compared to those of S. melanostictus, the δ15N levels of S. japonicus were greater, while the niche width was smaller. The intraspecific niche overlap and width for both S. melanostictus and S. japonicus tended to increase and then decrease with growth. We suggest that the average trophic level of S. japonicus is greater than that of S. melanostictus. However, S. melanostictus has a greater diversity of prey items, and these two species coexist by reducing inter- and intraspecific competitive pressures through dietary differentiation.

Key words:： trophic interactions; stable isotopes; feeding ecology; S. japonicus; S. melanostictus

碳氮稳定同位素揭示中国东海北部金乌贼（Sepia esculenta）的个体发育、性别和月间生态位分离

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摘要：金乌贼为中国近海重要渔业资源，在东、黄海食物网中作用显著。本研究基于 2021 年 9 月至 2022 年 3 月东海北部样本，采用稳定同位素技术分析其摄食生态。发现随生长，δ13C 与 δ15N 平均值递增，但生长至 101-120mm 后增速减缓；季节变化上，δ13C 值先降后升再降，δ15N 值秋冬降后趋稳。雌雄性生态位重叠率介于 17.64-30.39%，营养级范围为 2.98-3.53，随体长递增。此研究为东黄海食物网研究提供基础，助力金乌贼资源可持续开发。

关键词：金乌贼；稳定同位素；摄食生态；生态位

Ontogenetic, sexual, and monthly niche segregation of Sepia esculenta in the northern East China Sea revealed by stable carbon and nitrogen isotopes

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Abstract：Golden cuttlefish play a significant role in the food web of the East and Yellow Seas and are a valuable fisheries resource in Chinese coastal waters. Samples of golden cuttlefish were obtained from the northern East China Sea between September 2021 and March 2022, and stable isotope methods were utilized in this study to examine the variations in the forage ecology of golden cuttlefish among various life cycle stages and seasons. The results showed that the mean value of 13C increased with individual growth between 40 and 120 mm and remained steady between 120 and 160 mm; the mean value of δ15N showed an overall increasing trend, with more rapid growth in the early stages. The mean value of 13C showed a tendency of first dropping, then increasing, and then declining from September to March of the following year; the mean value of 15N displayed a trend of first decreasing from September to November, then increasing from November to December, and then stabilizing. The size and location of the niche changed continually in stages 1-6 of niche ontogeny. Stages 1-4 were characterized by habitat shifts and a rapid rise in trophic level; stages 4-6 were characterized by a high rate of niche overlap and a slow rise in trophic level. The overlap of the trophic niche between males and females ranged from 42.04% to 60.78% during ontogeny, and the δ15N values of females were higher than those of males in all stages other than stages 4 and 5. The trophic levels of golden cuttlefish ranged from 2.98-3.53 and trophic levels tended to increase with mantle length. This study indicated that the feeding ecology of golden cuttlefish varied among sexes, life history stages and seasons.

Key words:：Sepia esculenta; stable isotope; feeding ecology; trophic niche

中西太平洋重要金枪鱼群体
时空分布研究

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摘要：近年来在金枪鱼年捕捞量最高的中西太平洋海域，我国延绳钓捕捞能力仅约 100 吨/艘/年，不足高产国或地区的 50%。洄游性金枪鱼群体的时空分布特征是反映其不同生活史阶段环境偏好的重要指标。本研究基于中西太平洋渔业委员会公开的 1950-2019 年的金枪鱼延绳钓捕捞努力量数据，采用有限混合模型对黄鳍、长鳍、大眼金枪鱼进行无监督分类，结合 CPUE 时空分布，推演三种重要金枪鱼的种群生活史。分类结果显示，黄鳍、长鳍、大眼金枪鱼分别由 3 种、2 种以及 2 种组成，三种金枪鱼分布存在空间分化，但同种季节性差异不显著；黄鳍金枪鱼产卵地聚集在中西太平洋赤道两侧的群岛附近；长鳍金枪鱼洄游范围覆盖西北太平洋海域并在北回归线附近进行产卵；大眼金枪鱼洄游目的地主要聚集在太平洋中部，不同群体的洄游路径出现了纬度差异，这可能由于历年海水温度升高等环境因素造成了大眼金枪鱼的渔场北移现象。

关键词：金枪鱼 延绳钓 中西太平洋 时空分布 有限混合模型

Spatiotemporal distribution of Yellowfin (Thunnus albacares), Bigeye (Thunnus obesus), and Albacore Tunas (Thunnus alalunga) in the Western and Central Pacific

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Abstract： Tuna are highly valuable migratory fish found worldwide. In the Western and Central Pacific, where tuna catches are the highest, the average longline catch per vessel of Chinese fleet has dropped to about 100 tons annually—less than half of what high-yield countries or regions achieve. The migratory patterns of tuna reflect their environmental preferences at various life stages. Understanding their movement, habitat, and spawning behaviors is essential for improving fishing techniques and predicting fishing grounds. The present study analyzes tuna longline fishing data from 1950 to 2019, provided by the Western and Central Pacific Fisheries Commission. A finite mixture model was used to classify populations of yellowfin, bigeye, and albacore tunas, based on biological characteristics and catch-per-unit-effort (CPUE) data. The results show that 3 populations of yellowfin (Thunnus albacares), 2 of albacore (Thunnus obesus), and 2 of bigeye (Thunnus alalunga) are identified, respectively. There are distinct spatial distributions among three tunas but, the minimal seasonal variation of every tuna exists only. Yellowfin tuna primarily spawn near equatorial islands, albacore migrate across the northwest Pacific and spawn near the northern tropics, while bigeye tuna migrates in the central Pacific with northward shifts, which is likely influenced by rising sea temperatures.

Key words:：Tuna, Longline, Western and Central Pacific, Spatiotemporal distribution, Finite mixture model

东海剑尖枪乌贼砷、镉、铬、钴、铜和锌的生物富集

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摘要：本研究对采自东海的剑尖枪乌贼进行了微量元素(TEs)含量的测定。不同部位 TE 浓度之间存在显著差异。Cu、Zn 和 Cd 在消化腺中含量最高，Cr 和 Co 在鳃中含量最高。这些组织之间的浓度没有显著差异。在所分析的 4 种组织中，胴体的元素负荷比例最高，而消化腺和鳃的元素负荷比例最低。成熟后，胴体中的 TEs 没有显著差异。在消化腺中，除 Zn 外，所有元素的浓度均显著增加。性腺显示出明显的增加。

关键词：乌贼；微量元素；组织分布

Bioaccumulation of Arsenic, Cadmium, Chromium, Cobalt, Copper, and Zinc in Uroteuthis edulis from the East China Sea

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Abstract： In this study, the concentrations of trace elements (TEs) in Uroteuthis edulis caught from the East China Sea were determined. There were significant differences between TE concentrations in different body parts. Cu, Zn, and Cd were the most concentrated in the digestive glands and the concentrations of Cr and Co were highest in the gills. No significant differences in concentrations were shown between these tissues. In the four tissues analyzed, the mantle recorded the highest proportion of elemental load, while the digestive glands and gills had the lowest proportions. After maturity, TEs in the mantle showed no significant differences. In the digestive gland, the concentrations of all elements, except Zn, were significantly increased. The gonads illustrated apparent increases in the concentrations of Cr, Cu, and As. In the gills, the concentrations of Co and As were markedly increased.

Key words:： squids; trace elements; distribution in tissues

基于不同权重的印度洋北部鸢乌贼栖息地适宜性研究

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摘要：根据2017—2019年1—3月、10—12月印度洋北部鸢乌贼的渔获数据，结合海表面温度、风速和光合有效辐射环境因子，利用捕捞努力量与SST、WS和PAR建立适宜性指数模型，赋予不同环境因子不同的权重比例，采用算术加权法构建综合栖息地适宜性指数模型，通过分析HSI区间的产量、捕捞努力量占比和单位捕捞努力量，选取最佳模型，并用2019年的数据进行验证。结果表明，SST、WS、PAR的SI值权重比值为0.25：0.5：0.25时为最优权重方案，且最优权重方案的HSI模型可以精确预测印度洋北部鸢乌贼的渔场分布。研究表明，使用基于SST、WS和PAR的HSI模型探究并预测印度洋北部鸢乌贼渔场分布的效果良好；且在SST、WS和PAR中WS对印度洋北部鸢乌贼栖息地的分布影响最为重要。本研究通过分析海洋环境因子对印度洋北部鸢乌贼栖息地变动的影响，验证并预测印度洋北部鸢乌贼栖息地变动规律。

关键词：鸢乌贼；栖息地指数模型；环境因子；权重；印度洋北部

Habitat suitability of the squid Sthenoteuthis oualaniensis in northern Indian Ocean based on different weights

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Abstract： Data from the fishery of S.oualaniensis in the northern Indian Ocean from January to March and October to December 2017 to 2019, were modelled with sea surface temperature (SST), wind speed (WS), and photosynthetically active radiation (PAR). In this study, the fishing effort was used to evaluate the suitability index (SI) at SST, WS and PAR. An integrated Habitat Suitability Model (HSI) was developed with different weighting scenarios and weighting schemes. The optimal case was selected by calculating and comparing with the proportion of catch, effort and catch per unit effort (CPUE) in HSI interval (0~0.2, 0.2~0.6, 0.6~1), validation was performed using data from 2019. The weight of the optimal HSI model was 0.25 for sea surface temperature and photosynthetically active radiation, and 0.5 for wind speed. This model yielded the best performance and could accurately predict the fishing ground of S.oualaniensis in northern Indian Ocean. The findings suggest that the integrated HSI model can predict the distribution of S.oualaniensis commendably with wind speed as the most important factor as the most important factor affecting spatial distribution of S.oualaniensis habitat in the northern Indian Ocean. By analyzing habitat selection by S.oualaniensis, this study verified and predicted the distribution of squid in the northern Indian Ocean, which allow to model the distribution of squid resources and fishing grounds and sustainable use of squid fishery resources.

Key words:：Sthenoteuthis oualaniensis; habitat; marine environment; distribution

大辽河口秋季鱼类群落结构与生态位的研究

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摘要：为了解大辽河河口海域秋季鱼类群落结构，本研究根据2018年9、10、11月份的大辽河口鱼类资源调查数据，分析了大辽河口海域鱼类资源组成、多样性及其与群落结构的关系。研究结果显示，大辽河口秋季共计发现鱼类8目17科25种。优势种为矛尾复虾虎鱼、钟馗虾虎鱼，其中矛尾复虾虎鱼为秋季大辽河口海域的绝对优势种。多样性指数变化范围分别为Shannon－Wiener多样性指数H'(0.28~1.66)，Margalef丰富度指数D(0.19~1.88),Pielou均匀度指数J(0.17~0.76)。根据非度量多维标度排序分析显示秋季中9、10月份相似度较高。ABC曲线分析表明秋季大辽河口鱼类群落受到了较强干扰。相对重要性指数与生态位的分析显示大辽河口海域鱼类相对重要性指数与生态位宽度较高的鱼类呈现小型化，营养级较低的现象，各物种之间对资源利用较为相似。总体来说，大辽河口海域鱼类群落受到了较大的干扰。

关键词：大辽河河口；物种多样性；群落结构；生态位；

Study on the Fish Community Structure and Niche in the Daliao River Estuary in Autumn.

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Abstract：In order to understand the autumn fish community structure in the Daliao river estuary, the fish resource composition, diversity and their relationship with the community structure were analyzed according to the survey data in September, October and November 2018. Research results show that a total of 25 fish species belonging to 17 families across 8 orders were found in the Daliao river estuary during autumn. The dominant species include Synechogobius hasta and Triaenopogon barbatus, with Synechogobius hasta being the absolute dominant species in the Daliao river estuary during autumn. The variation range of the fish community diversity indices in the Daliao river estuary during autumn are as follows: the Shannon-Wiener diversity index H' (0.28 to 1.66), the Margalef richness index D (0.19 to 1.88), and the Pielou evenness index J (0.17 to 0.76). According to the NMDS (Non-metric Multi-Dimensional Scaling) analysis, the fish community similarity in September and October during autumn is relatively high. The ABC curve analysis indicates that the fish community in the Daliao River Estuary has experienced significant disturbance in autumn.The analysis of the relative importance index and ecological niche shows that fish species in the Daliao river estuary with a higher relative importance index and wider ecological niche tend to be smaller in size and belong to lower trophic levels. There is a similarity in resource utilization among different species in the marine area. Overall, the fish community in the Daliao river Estuary has been significantly disturbed.

Key words:：Daliao River Estuary; Species Diversity; Community Structure; Niche

基于贝叶斯剩余产量模型的东海剑尖枪乌贼资源评估

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摘要：剑尖枪乌贼是我国重要的海洋捕捞对象，在我国海洋渔业生产中占有重要地位，对其进行资源评估在资源可持续利用方面具有重要意义。本研究利用 2009—2021 年来自中国大陆、中国台湾及日本的渔获量数据和单位捕捞努力量渔获量数据，使用基于贝叶斯剩余产量模型 JABBA 中三种剩余产量模型对东海剑尖枪乌贼的资源状况进行评估。结果显示，使用 Schaefer 模型时，模型拟合效果最好。2021 年东海剑尖枪乌贼资源量为 135.0×104t，最大可持续产量 MSY 为 57.34×104t；Kobe 图显示资源有 43.2%的概率为健康，46.7%的概率为过度捕捞状态。回顾性分析结果显示，评估结果存在回顾性误差，F/FMSY 的值可能被低估，资源量可能被高估。预测性分析表明，当总允许可捕量 TAC 设置为小于等于 52.26×104t(即 2021 年渔获量)时，剑尖枪乌贼资源量呈现上升趋势，在 2033 年前资源能往可持续利用方向发展。

关键词：剑尖枪乌贼；资源评估；剩余产量模型；JABBA

Stock assessment for Uroteuthis edulis in the East China Sea based on JABBA

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Abstract：Uroteuthis edulis is one of the most important Marine fishing objects in our country and plays an important role in Marine fishery production. Stock assessment is of great significance in sustainable utilization of resources. Based on the catch data and CPUE data from Chinese Mainland, Taiwan, China, and Japan from 2009 to 2021, this study adopted a Bayesian state space residual surplus production model, three surplus production models in JABBA were used to assess the stock status of the East China Sea. The results showed that the model fits best when Schaefer model is used. In 2021, the biomass of the East China Sea Uroteuthis edulis are 1355.0×104t, the maximum sustainable yield MSY is 57.34×104t, and the Kobe plot showed that the resources have a 43.2% probability of being healthy, 46.7% is overfished. The results of retrospective analysis showed that there were retrospective problems in the evaluation assessment results, the value of F/FMSY may be overestimated, and the stock biomass may be underestimated. The predictive analysis showed that when the total allowable catch TAC was.

Key words:：Uroteuthis edulis; Resource Stock assessment; Surplus production model; JABBA

中西太平洋鲣鱼不同鱼群资源丰度的影响因子比较研究

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摘要：为了探究鲣鱼自由鱼群和随附鱼群资源丰度（CPUE）受环境与生物影响因子影响的差异。实验采用2011-2020年中西太平洋鲣鱼的生产统计数据，结合同时期海洋环境数据（SST、SSS、Chl-a），基于广义加性模型（Generalized addictive models, GAM）对两种鱼群的影响因素进行分析，并通过赤池信息准则进行模型比较。结果显示，生物因子是对两种鱼群影响最大的因子，解释偏差率分别达到了39.6%和82.6% 。对于自由鱼群而言，除生物因子之外，月和年影响较大，其解释偏差率分别为3.62%和3.51%；环境因子中SST最为重要，其次是SSS，Chl-a的影响相对较低；对于随附鱼群而言，除生物因子之外，月和经度影响较大，其解释偏差率分别为18.8%和12.1%；环境因子中SSS影响较大，Chl-a和SST影响较低。研究认为，未来的渔情预报模型中需要考虑生物因子的影响。

关键词：中西太平洋；鲣鱼；自由鱼群；随附鱼群；资源丰度CPUE

The relationship between different factors and abundance index of skipjack tuna(Kaisuwonus pelamis) in the Western and Central Pacific Ocean

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Abstract：The main objective of this study is to investigate the differences in the abundance of free-swimming school and associated school of Kaisuwonus pelamis influenced by environmental and biological factors. This study utilized the production statistics from 2011 to 2020, combined with marine environmental factors, a generalized additive model was used to analyze the two fish populations separately, and the final model was confirmed through the akaike information criterion. The results indicate that biological factors had the most significant influence on both school types, and the explanatory deviation rates were 39.6% and 82.6%. For free-swimming schools, month and year were significant besides biological factor. Among the environmental factors, SST was the most important, followed by SSS and Chl-a. For associated schools, month and longitude were significant. Among the environmental factors, SSS was the most influential, while Chl-a and SST had lesser impacts.It is concluded that the effects of biological factors should be considered in the future fishery forecasting models.

Key words:：Western and Central Pacific Ocean; Katsuwonus pelamis; free-swimming school; associated school; abundance

单齿螺对干露的转录响应机制

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摘要：潮间带环境的复杂性和多变性，特别是潮汐的周期性涨落，使单齿螺长期暴露在空气中。然而，目前的研究更多地关注温度和盐度的变化，而较少关注干露。本研究以潮间带软体动物单齿螺为研究对象，利用 RNA-Seq 技术分析了不同时间暴露在空气中的基因表达水平。研究结果表明，与未干露相比，干露 2 天(t1)有 33 个基因上调，17 个基因下调，主要参与调控 MAPK 信号通路和 PI3K-Akt 信号通路等，而干露 5 天(t2)有 368 个基因上调，572 个基因下调，改变真核生物内质网蛋白加工、核糖体合成等信号通路。与干露 2 天(t1)相比，干露 5 天(t2)有 364 个基因上调，331 个基因下调，差异表达基因主要参与细胞周期的调节。这些发现为研究干露对单齿螺的影响提供了理论依据和数据基础。然而，要更好地分析软体动物对干露后应激反应的分子机制，还需要对差异表达基因进行更深入的研究。

关键词：单齿螺；干露；转录组测序技术；信号通路

Transcriptional response mechanism of Monodonta labio to Air Exposure

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Abstract： The complexity and variability of the intertidal environment, particularly the cyclical rise and fall of the tides, exposes the M. labio to prolonged periods of air exposure. However, current research focuses more on changes in temperature and salinity, and less on air exposure. In this study, the intertidal mollusc M. labio was used as the research object, and the gene expression levels at different times of air exposure were analyzed by RNA-Seq technology. The results of the study showed that 33 genes were up-regulated and 17 genes were down-regulated in 2 days (t1) compared with that in no air exposure, which were mainly involved in the regulation of the MAPK signalling pathway and the PI3K-Akt signalling pathway, while 368 genes were up-regulated and 572 genes were down-regulated in 5 days (t2) of air exposure, which altered the signalling pathways of endoplasmic reticulum protein processing and ribosome synthesis of eukaryotic organisms. Compared with 2 days (t1), 364 genes were up-regulated and 331 genes were down-regulated on 5 days (t2), and the differentially expressed genes were mainly involved in the regulation of cell cycle. These findings provide a theoretical basis and data foundation for the study of the effects of air exposure on M. labio. However, more in-depth studies on DEGs are needed to better analyze the molecular mechanisms of mollusc responses to post-air exposure stress.

Key words:： Monodonta labio; air exposure; RNA-Seq; Pathways

盐度胁迫下弧边招潮蟹转录组分析

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摘要：弧边招潮蟹是一种分布广泛于世界各地的潮间带蟹类。目前，对弧边招潮蟹的盐度适应机制、功能基因和相关途径的研究还很有限。为了研究盐度胁迫下弧边招潮蟹基因表达水平的变化，对弧边招潮蟹鳃组织样本进行了转录组测序。结果显示，总共获得了63.83GB的clean reads。所有clean reads注释了125,462个unigene。N50长度为969bp，平均长度为688bp。与对照组相比，高盐组共获得52个差异表达基因，其中36个上调，16个下调；低盐组共获得1035个DEG，其中780个上调，255个下调。GO分析结果表明，DEGs在信号转导、酶活性和结合方面显著富集。KEGG分析表明，大多数途径与信号通路和代谢有关。随机选择6个差异表达基因进行RT-qPCR验证，结果表明转录组数据高度可靠。研究结果为弧边招潮蟹在盐度胁迫下的调控机制奠定了一定的基础，有利于在全球气候变化中保护和利用其资源。

关键词：弧边招潮蟹；盐度胁迫；转录组测序；差异表达基因

Transcriptome Analysis of Red Claw Crab Uca arcuata under Salinity Stress

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Abstract： The red claw crab, Uca arcuata, is a widely distributed intertidal crab species found in saline environments around the world. Limited research has been conducted on the salinity adaptation mechanisms, functional genes, and related pathways of U. arcuata. To investigate the changes in gene expression levels of U. arcuata under salinity stress, RNA-seq was performed on gill tissue samples of U. arcuata under experimental conditions. The results showed that a total of 63.83 GB clean reads were obtained. All clean reads were annotated 125,462 unigenes. The N50 length was 969 bp, and the mean length was 688 bp. Compared with the control group, the high-salt group obtained a total of 52 differentially expressed genes (DEGs), with 36 up-regulated and 16 down-regulated; The low-salt group obtained a total of 1,035 DEGs, with 780 up-regulated and 255 down-regulated. GO enrichment analysis results showed a significant enrichment of DEGs in signal transduction, enzymatic activity, and binding. KEGG enrichment analysis showed that the majority of pathways were related to signaling pathways, and metabolism. Six differentially expressed genes were randomly selected for RT-qPCR validation, and the results demonstrated that the transcriptome data was highly reliable. The research results had laid a certain foundation for studying the regulatory mechanism of U. arcuata under salinity stress, which was beneficial for the conservation and utilization of U. arcuata resources in global climate change.

Key words:： Uca arcuata; salinity stress; RNA-seq; differentially expressed genes

基于机器学习方法的头足类日龄预测初步研究：以剑尖枪乌贼为例

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摘要：了解头足类的生活史过程是合理开发生物资源的前提，年龄与生长是其中基础。目前头足类日龄获取仍依赖于传统轮纹判读法，但在实际操作中，平衡石的研磨耗时耗财且存在不可避免的人为误差，寻找相关替代且精确的方法也是重点研究内容。近年来随着现代统计方法和人工智能等理论和技术的发展，借助模型来合理预测头足类日龄有着较大的潜力。为了通过科学方法减少误差并提高读取效率，本研究利用 2017~2021 年捕捞的剑尖枪乌贼（Uroteuthis edulis）样本，基于机器学习方法，以 591 个平衡石样本读取的轮纹数据为因变量，生物学中的关键因子为自变量，建立随机森林模型、朴素贝叶斯模型、支持向量机模型进行模型拟合。研究分析表明，不同比例的训练组最优模型不同，根据最小赤池信息准则（AIC）和准确率选取最优模型，在选取 0.75 训练组时，选择支持向量机模型的 ML+date 组合，预测结果最为准确，达到 87.76%。

关键词：头足类；平衡石；日龄预测；机器学习；随机森林模型；朴素贝叶斯模型；支持向量机模型

Preliminary study on age prediction of Cephalopods based on machine learning methods: a case study of Uroteuthis edulis

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Abstract： The precondition of reasonable development of the biological resources is to understand the life history of the Cephalopods, age and growth is the foundation. At present, the methods to obtain the age of the Cephalopods depend on traditional daily ring interpretation. However, in actual operation, the grinding of statolith is time-consuming and costly and there are inevitable human errors, so it is also important to find relevant alternative and accurate methods. In recent years, with modern statistical methods and the development of the theory and technology such as artificial intelligence, machine learning method is gradually perfect, it has great potential to predict Cephalopod age reasonably with the help of models. In order to reduce errors and improve reading efficiency through scientific methods, this study used the samples of Uroteuthis edulis harvested from 2017 to 2021. Based on machine learning methods, the rim data read from 591 statolith samples were used as dependent variables, and the key factors in biology were used as independent variables. Random Forest model, Naive Bayes model, Support Vector Machine model for model fitting. The study analysis showed that the optimal model was different for different proportions of training groups, and the optimal model was selected according to the minimum Akaike information criterion (AIC) and accuracy. When the 0.75 training group was selected, the ML+date combination of the Support Vector Machine model was selected, and the prediction result was the most accurate, reaching 87.76%. Therefore, we suggest that Support Vector Machine model could be selected for Cephalopod age prediction in subsequent studies. This study provided a basis for the subsequent model-based fitting of Cephalopod age studies.

Key words:：Cephalopods; Statolith; Age prediction; Machine learning; Random Forest model; Naive Bayes model; Support Vector Machine model

条纹斑竹鲨不同组织线粒体 DNA 拷贝数差异分析

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摘要：线粒体 DNA(mitochondrial DNA, mtDNA)拷贝数在不同组织器官中存在一定差异，并与多种重要疾病的发生密切相关。mtDNA 拷贝数的稳定性对于维持线粒体功能和细胞代谢至关重要，因此，准确监测 mtDNA 拷贝数对生物学及生物医学研究具有重要意义。然而，目前常用的分析方法只能对 mtDNA 拷贝数进行相对定量分析，无法准确评估 mtDNA 含量。本研究尝试利用高通量测序数据和生物信息学分析软件 NOVOPlasty 建立了一种定量评估 mtDNA 拷贝数的方法，并采用该方法对条纹斑竹鲨肌肉与血液组织样品中 mtDNA 拷贝数开展比较分析。结果表明血液组织的 mtDNA 含量明显少于肌肉组织的含量。研究结果表明条纹斑竹鲨肌肉和血液的 mtDNA 含量存在明显的组织特异性，同时初步验证了本研究建立的 mtDNA 拷贝数定量分析方法的可行性。本研究可为 mtDNA 含量相关的生物医学和生理生态研究提供参考资料。

关键词：线粒体 DNA 拷贝数；条纹斑竹鲨；定量分析；组织特异性；高通量测序

Analysis of Mitochondrial DNA Copy Number Difference in Diverse Tissues of Chiloscyllium plagiosum

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Abstract：Mitochondrial DNA (mtDNA) copy number varies in different tissues and organs, and is closely related to the occurrence of many important diseases. The stability of mtDNA copy number is essential for maintaining mitochondrial function and cell metabolism. Therefore, accurate monitoring mtDNA copy number is important for biological and biomedical research. However, the current commonly used analytical methods can only perform relative quantitative analysis of mtDNA copy number, and cannot accurately quantify mtDNA content. In this study, a method for quantitative evaluation of mtDNA copy number was established by using high-throughput sequencing data and bioinformatics analysis software NOVOPlasty, and this method was used to quantitatively compare and analyze mtDNA copy number in muscle and blood tissue samples of Chiloscyllium plagiosum. The results showed that the mtDNA content of blood tissue was evidently less than that of muscle tissue. The results showed that the mtDNA content in the muscle and blood of C. plagiosum had obvious tissue specificity, and the feasibility of the mtDNA copy number quantitative analysis method established in this study was preliminarily verified. This study can provide reference materials for biomedical and ecophysiological studies related to mtDNA content.

Key words:：mitochondrial DNA copy number; Chiloscyllium plagiosum; quantitative analysis; tissue specificity; high-throughput sequencing

硬骨鱼类基因组重复序列比较分析

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摘要：重复序列是动植物基因组的重要组成部分，对基因组进化具有显著的影响。为探究重复序列对硬骨鱼类基因组大小差异及进化的影响，本研究收集了已报道的60种鱼类基因组数据及其重复序列比例信息并进行统计分析。统计结果显示硬骨鱼类基因组大小和重复序列比例存在较大的种间差异。相关性分析结果显示硬骨鱼类基因组大小与重复序列比例呈非线性的对数相关性，这与之前普遍认为的线性相关性存在差异。系统发育分析结果显示遗传关系较近的物种间具有相似的基因组大小及重复序列比例，表明硬骨鱼类基因组大小和重复序列比例呈现谱系特异性。然而在某些类群中也有例外，例如与近缘种相比，斑马鱼、多鳞白甲鱼等的基因组较小，但重复序列比例较高，提示遗传关系较近的物种间重复序列比例也存在异质性。本研究整理了多种硬骨鱼类基因组基本信息，并初步统计分析了其基因组大小的变化规律和进化模式，研究结果可为深入开展硬骨组进化研究提供参考资料。

关键词：硬骨鱼类；重复序列；基因组；系统进化

Comparative Analysis of Genomic Repetitive Sequences of Teleost Fish Species

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Abstract：Repetitive sequence is an important part of plant and animal genome, which has significant influence on genome evolution. As the oldest vertebrate group, fish is an ideal group for the study of vertebrate genome evolution due to its high species diversity and genome diversity. In order to explore the effect of repetitive sequences on the size difference and evolution of teleost fish genomes, we collected genome data and repetitive sequence ratio information for 60 species of fish and performed statistical analysis. The statistical results showed that there were large interspecific differences in genome size and proportion of repetitive sequences in teleost fish. The results of correlation analysis showed that the genome size of teleost fish had a nonlinear logarithmic correlation with the proportion of repeats, which was inconsistent with the previously reported linear relationship. Phylogenetic analysis showed that the genome size and repetitive sequence ratio were similar among closely related species, indicating that the genome size and repetitive sequence ratio of teleost fish were lineage specific. However, there are exceptions in some species, such as Danio rerio, Onychostoma macrolepis and Hippocampus abdominalis, which have smaller genomes but a higher proportion of repetitive sequences compared to their relatives. It is suggested that there is also heterogeneity in the proportion of repetitive sequence between species with close genetic relationship. In this study, we collated the genome size, repetitive sequence ratio, transposon composition and other information of a variety of teleost fish, and analyzed the variation rules and evolutionary patterns of the genome size of teleost fish. The research results can provide references for further research on the evolution of the genome of teleost fish.

Key words:：teleost fish; repetitive sequence; genome; phylogenetic evolution

基于 eDNA 技术的太湖鱼类多样性调查

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摘要：基于环境 DNA(environmental DNA, eDNA)技术开展太湖鱼类多样性调查，并结合传统形态学鱼类资源调查数据，初步探索 eDNA 技术在鱼类资源调查中的应用。结果显示：太湖 16 个点位共检出鱼类 8 目 20 科 47 属 54 种，其中鲫、蒙古鲌和刀鲚丰度相对较高；eDNA 与传统形态学调查共同检出鱼类 37 种，占 eDNA 检出鱼类序列总数的 91.89%；eDNA 检出的鱼类中有 45 种鱼类在太湖鱼类志中有记载，占检出鱼类序列数的 95.09%；2 种方法得出的鱼类多样性指数均为太湖东部和太湖南部相对较高、太湖北部和太湖西部相对较低，太湖鱼类的生态类型(洄游性、栖息水层和食性)也高度一致；eDNA 技术单个频次检出的鱼类物种数和单个点位的种类检出数均高于传统形态学方法，检出效率较高。综上，eDNA 技术可用于鱼类资源调查，且在鱼类物种检出效率上优于传统形态学，与传统检测相结合，可以进一步增加监测调查的可靠性。

关键词：eDNA；鱼类多样性；(宏)条形码技术；太湖

Investigation of Fish Diversity in Lake Taihu Based on eDNA Metabarcoding

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Abstract： In this study, the fish diversity survey based on environmental DNA (eDNA) technology was carried out in Lake Taihu, and combined the traditional morphological investigation for the survey data analysis. The application of eDNA technology in fish resource survey was preliminarily explored. A total of 54 species of fish were found at 16 sites in Lake Taihu belonging to 47 genera, 20 families, 8 orders. Carassius auratus, Chanodichthys mongolicus and Coilia nasus had relatively high abundance. 37 fish species were detected by both eDNA technology and traditional morphological investigation, accounting for 91.89% of the total number of fish sequences detected in eDNA; 45 species detected by eDNA technology were recorded in Fishes of the Taihu Lake, accounting for 95.09% of the fish sequences detected. The diversity index of fish obtained by the two methods were all relatively higher in the east and south of Lake Taihu, and lower in the north and west of Lake Taihu. The analysis of fish ecological types found that the migratory, habitat and feeding habits of fish obtained by the two methods were highly consistent. The number of fish species detected by eDNA technology at a single frequency and at each site were higher than those of traditional morphological investigation, showing higher detection efficiency of eDNA technology. In summary, eDNA technology can be used in fish resource surveys, and it is better than traditional morphology investigation in the number of species detected efficiency. It is a good strategy to combine them to increase the reliability of monitoring surveys.

Key words:： environmental DNA; fish diversity; (meta)barcoding; Lake Taihu

珠母贝不同地理种群形态与贝壳珍珠质特征分析

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摘要：国内的珠母贝珍珠质层颜色多为灰色或是彩虹色，导致所培育出来的黑色珍珠数量较少，选育出生长快、适宜环境能力强，珍珠质层颜色偏向黑色的群体对珠母贝产业优质发展尤为重要。本研究对海棠湾(HNHT)、三亚湾(HNSY)、春园湾(HNCY)和涠洲岛(GXWZ)这 4 个野生地理种群珠母贝的形态和贝壳珍珠质特性进行分析，结果表明，海棠湾种群的壳宽指数最大，涠洲岛种群的壳宽指数最小；海棠湾种群和涠洲岛种群珠母贝的外形偏向于长方形，三亚湾种群和春园湾种群珠母贝的外形偏向于正方形。海棠湾种群和三亚种群珠母贝的珍珠质层颜色呈现出较为明亮的浅蓝绿色；春园湾种群和涠洲岛种群珠母贝呈现出较暗的黄绿色，其中春园湾种群珠母贝外套膜区的颜色更偏向绿色。研究结果可为珠母贝育珠过程中“育珠母贝”和“小片贝”的选择提供科学依据。

关键词：珠母贝，珍珠质；颜色；形态

Analysis on the morphology of different geographical populations and the characteristics of shell narce

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Abstract：In the field of medical academia, it is important to select and breed populations of pearl oysters with fast growth rates, strong adaptability to the environment, and a tendency towards darker pearl nacre colors, as the domestic pearl oysters mostly have gray or rainbow-colored nacre layers, resulting in a limited number of black pearls. This study analyzed the morphological and shell pearl nacre characteristics of four wild geographic populations of pearl oysters in HNHT, HNSY, HNCY, and GXWZ, and the results showed that the shell width index of the HNHT population was the largest, while the index of the GXWZ population was the smallest. The morphology of the HNHT and GXWZ populations was more elongated in shape, while the morphology of the HNSY and HNCY populations was more square-shaped. The pearl nacre layer color of the HNHT and HNSY populations was brighter light green, while the color of the HNCY and GXWZ populations was darker yellow-green, with the mantle area of the HNCY population being more green-colored. The research results can provide scientific basis for the selection of "pearl mother oysters" and "small pieces" in the pearl cultivation process.

Key words:：Pinctada margaritifera, narce color, morphology

舟山海域海底垃圾组成与空间分布特征研究

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摘要：海底垃圾是海洋面源垃圾占比最大的组成部分，监测与评估工作是治理海底垃圾污染问题的首要举措。本研究选取浙江省舟山海域为采样区域，基于均匀采样法在 32 个站点使用单船底拖网开展平均拖曳时长 30 min，拖曳船速 4.0 kn 的海底垃圾采样调查。所获样品按照 ICES 分类标准进行整理分析。结果显示舟山海域海底垃圾中塑料数量占比达 80.92%，海底垃圾数量随尺寸呈现先增后减的趋势，可能与其滞留量和底拖网的采集效率有关；外消用品（65.57%）与海事活动（17.98%）是造成海底垃圾大量滞留舟山海域的主要来源。样本中未发现小于 2.5 cm 的垃圾。塑料垃圾滞留量密度空间分布随水深和离岸距离的增加而减少，非塑料垃圾滞留量密度高的站点主要集中在本岛外海处。表明此海域来往船舶并未严格遵守国际海事船舶垃圾可排规定排污。本研究结果有望完善海底垃圾本底调查监测与评估的理论与技术体系，为海底垃圾防治管理工作提供数据支撑。

关键词：海底垃圾，单船底拖网，组成与来源，空间分布

Assessment of seafloor litter composition and sources off the coast of Zhoushan City

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Abstract：Seafloor litter is the largest part of marine debris. Monitoring and evaluating seafloor litter is fundamental to manage marine pollution. The sampling region off the coast of Zhoushan city, Zhejiang Province was selected, with 32 stations designed on the uniform sampling method. A bottom otter trawl was used for sampling, with an average towing time of 30 min and a speed of 4.0 kn. Collected samples were categorized and analyzed following ICES classification standards. The results show that plastic makes up 80.92% of seafloor litter off the coast of Zhoushan city. The amount of litter first increases and then decreases with size, likely due to both the amount of litter present and the efficiency of the bottom trawl in collecting it. The main sources of litter are identified as take-out consumer (65.57%) and ocean and waterway (17.98%). Notably, there is no seabed litter whose size is less than 2.5 cm in the samples but it should be numerous. The quantity density of plastic litter decreases with greater water depth and distance from the shore, while high-density stations for other types of litter are concentrated in open sea areas around Zhoushan islands. It implies that ships passing through the region perhaps disobey the regulations on garbage disposal from the Marpol 73/78 appendix Ⅴ. These findings provide valuable data for pollution prevention and management efforts and enhance the framework construction of monitoring and evaluating seafloor litter.

Key words:：Seafloor litter, bottom otter trawl, composition and source, spatial distribution

海洋微塑料拖网法采集特性研究

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摘要：目前不同微塑料采样法的微塑料采集效率存在着数量级程度的差异，探究微塑料采集特性问题是分析海洋微塑料采样方法学差异的重要理论基础。本研究选取浙江宁波象山湾海域为采样区域，选取 4 种不同网目尺寸（50、150、330、500 μm）采集网进行船速 2 节、拖曳时间为 20 min（50-μm 采集网为 5 min）的表层水平拖曳对照试验。不同采集网得到的微塑料样品经室内检测、分类与数据汇总后，将 50-μm 采集网设为对照组，其他采集网为试验组。采用 SELECT 模型构建微塑料留存率模型，结合蒙特卡洛模拟推算微塑料遗失量与潜在赋存量。结果表明，不同采集网的微塑料样本多集中在 2000 μm 以内，纤维状数量占比 81%；相较于 50-μm 采集网的微塑料样本，500-μm 和 150-μm 采集网对于纤维微塑料采集效率差异不显著；与采水法相比拖网法下纤维微塑料的 l50 值小，选择区间（S.R.）波动小，筛分效果更佳，采集率更小。

关键词：微塑料，拖网法，采集特性，网目选择性，丰度标准化评估

Sampling efficiency of marine microplastics by towing net sampling

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Abstract： Standardizing sampling methods is essential for monitoring and assessing marine microplastics. However, even with identical mesh sizes, different sampling methods, such as water sieve sampling and towing net sampling, could result in significant variations in microplastic sampling efficiency. Understanding microplastic retention and loss during sampling is critical for improving and standardizing these methods. This study focused on towing net sampling in Xiangshan Bay, Ningbo, Zhejiang Province. Four towing nets with mesh sizes of 50, 150, 330, and 500 μm were tested, positioned two meters from the ship's side, with the ship moving at 2 knots for 20 minutes per sample (5 minutes for the 50-μm net). The 50-μm net served as the control, while the others were test groups. Data from the 330-μm net were excluded due to processing issues. After classification and analysis of microplastic samples, a retention model was developed using the SELECT method, and Monte Carlo simulations estimated the missed and potential microplastic quantities. Results indicated that most collected microplastics were smaller than 2000 μm, with 81% being fibrous. For fibrous microplastics, the 500-μm and 150-μm nets showed similar sampling efficiencies compared to the 50-μm net. Towing nets demonstrated worse efficiency in sampling fibrous microplastics compared to water sieve sampling, which is likely due to the oscillation of the net enhancing mesh selectivity. These findings provide a theoretical foundation and valuable data for standardizing marine microplastic sampling methods.

Key words:：Microplastics, towing net sampling, sampling efficiency, mesh selectivity, standardization assessment of the abundance

蚕丝制药-重组鲎 C 因子(rFC)替代鲎试剂保护鲎资源研究

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摘要：用于高灵敏检测细菌内毒素的鲎试剂由鲎血制备，但其长期以来面临着因鲎资源日渐濒危而停产的风险。利用重组鲎 C 因子(rFC)替代鲎试剂被认为是首选的解决方案，然而我国目前仍没有被药典认可的 rFC 产品，导致严重依赖进口。前期研究中，课题组利用源于蛛丝蛋白的增溶因子 sNT 技术，通过家蚕丝腺生物反应器实现了 rFC 在丝素层中的高活性表达，但存在 rFC 可溶性表达效率低而不易分离纯化的难题。为此，项目将(1)改变 rFC 在纤维化丝素层表达的模式，利用丝胶启动子使其表达在易溶于温水的丝胶层，以利温和条件下分离纯化蛋白；(2)同时选用具有较高启动子活性的 HKO“丝胶蚕”用于 rFC 的表达，以提高其表达效率；(3)进一步通过双位点法创建新型 sNT 元件，促使其介导 rFC 在丝腺酸性环境中仍能保持良好的可溶性胶束结构。项目旨在通过以上技术融合提高 rFC 在丝腺中的可溶性表达效率，为实现“蚕丝制备 rFC”产业化进行有益探索。

关键词：海洋无脊椎动物；海洋生物制品；海洋活性物质；海洋生物资源保护；基因表达

Preparation of pharmaceutical by silk industrialization——Study on the protection of Limulus resources by replacing limulus reagents with recombinant Limulus factor C (rFC)

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Abstract：Limulus reagents for highly sensitive detection of bacterial endotoxins are prepared from limulus blood, but they are facing the great risk of being discontinued due to the depletion of limulus resources. Using recombinant limulus factor C (rFC) instead of limulus reagents is considered to be an ideal solution. However, there are still no independent rFC products in our country, resulting in serious import dependence. The high-efficiency expression of rFC in silk fibroin by using the bombyx mori silk gland bioreactor, and successfully carried out trial production were realized by the solubilizing factor sNT technology derived from spidroin silk protein in our study. But, it is difficult to separate and purify rFC due to the low soluble expression rate of rFC. Herein, this project intends to carry out the following studies: (1) Change the expression pattern of rFC in the fibrotic silk fibroin layer, and use the sericin promoter to express it in the sericin layer that is easily soluble in warm water, so as to separate and purify the protein under mild conditions; (2) Select the "seric silkworm" HKO mutant with higher promoter activity for the expression of rFC to improve its expression rate; (3) Creat a novel sNT element by a two-site method, and make it mediate rFC to maintain an ideal soluble micellar conformation in an acidic silk gland environment. The project intends to realize the efficient and soluble expression of rFC in silk glands through technological integration and innovation, and conduct beneficial explorations for the characteristic scheme of "preparation of rFC by silk industrialization".

Key words:：marine invertebrate; Marine biological products; Marine active substances; Marine life resources protection; gene expression

长江口蟹类时空变化以及三疣梭子蟹生物学特性及资源利用评估

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摘要：为了解长江口禁捕后的蟹类的群落特征，本研究于 2022 年 8 月至 2023 年 11 月进行了 6 次拖网调查。结果表明蟹类共 14 种，优势种群随季节变化：2022 年夏季以红线黎明蟹和三疣梭子蟹为主，秋季以三疣梭子蟹、狭颚绒螯蟹和日本蟳为主；2023 年冬季以狭颚绒螯蟹和中华绒螯蟹为主，春季优势种群出现最多。整体丰度和生物量呈现冬季＜春季＜秋季＜夏季的趋势，蟹类群落的多样性指数、均匀度指数和丰富度指数也显示出季节性变化，冬季最低，春季最高。通过相关性和冗余分析，水体的溶解氧和盐度为影响蟹类群落变化的主要环境因子。其最大优势种群三疣梭子蟹共捕获 466 只，雌雄性比为 0.68，生长参数 $L\infty=183.75$。死亡系数（Z）分别为 2.60（雌性）和 2.64（雄性），自然死亡系数（M）为 1.05，资源开发利用率（E）为 0.596 和 0.602。表明其生长状况良好，资源利用率处于轻度开发水平。

关键词：长江口；蟹类；优势种；多样性；三疣梭子蟹，生长特性，资源

Temporal and Spatial Variations of Crab Species in the Yangtze River Estuary and Assessment of Biological Characteristics and Resource Utilization of Portunus Trituberculatus.**

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Abstract：Abstract: To understand the community characteristics of crab species after the fishing ban in the Yangtze River Estuary, this study conducted six trawling surveys from August 2022 to November 2023. The results indicated a total of 14 crab species, with dominant populations varying by season: in summer 2022, the dominant species were the Red Line Crab and the Portunus trituberculatus; in autumn, the dominant species shifted to Portunus trituberculatus, Charybdis japonica, and Japanese crab; in winter 2023, the dominant species were Charybdis japonica and Chinese mitten crab, while spring saw the highest diversity of dominant species. Overall abundance and biomass showed a trend of winter < spring < autumn < summer. The diversity index, evenness index, and richness index of crab communities also exhibited seasonal variations, with the lowest values in winter and the highest in spring. Correlation and redundancy analyses identified dissolved oxygen and salinity as the primary environmental factors influencing changes in crab communities. The most dominant species, Portunus trituberculatus, had a total catch of 466 individuals, with a sex ratio of 0.68 and growth parameters of $L\infty = 183.75$. The total mortality coefficients (Z) were 2.60 (female) and 2.64 (male), with a natural mortality coefficient (M) of 1.05, and resource exploitation rates (E) of 0.596 and 0.602. These findings indicate that the growth condition of Portunus trituberculatus is good, and the resource utilization rate is at a light exploitation level. This study reveals the changes in crab resources after the fishing ban in the Yangtze River Estuary and emphasizes the need for ongoing protection of Portunus trituberculatus resources, providing a scientific basis for future resource conservation and management.

Key words:：Keywords: Yangtze River Estuary; crab community; dominant species; Portunus trituberculatus; growth parameters; resources.

长江口刀鲚、凤鲚仔稚鱼的时空分布及其与环境因子的关系

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摘要：为比较研究长江口刀鲚(Coilia nasus)、凤鲚(Coilia mystus)仔稚鱼的时空分布特征及其与环境因子的关系。于 2022 年 7 月—2023 年 5 月在长江口南支、北支及崇明岛东滩各设置 10 个采样点，对刀鲚、凤鲚及环境因子按季度进行调查。利用广义相加模型(GAM)分析影响其时空分布的环境因子。结果表明：刀鲚仔稚鱼主要分布于长江口南支、北支口门内和崇明岛东滩附近水域；凤鲚产卵场存在于南支的长兴岛至九段沙水域和北支口门外水域，凤鲚仔稚鱼主要分布在南支口门外、北支和崇明岛东滩水域。GAM 模型分析结果表明，鱼类利用长江口作为产卵场、保育场有显著的季节性：夏季对刀鲚仔稚鱼的丰度有显著的正效应，夏季、春季对凤鲚仔稚鱼的丰度有显著的正效应，夏季显著高于春季。盐度对刀鲚的丰度影响显著，温度、盐度、pH 对凤鲚的丰度影响显著。

关键词：刀鲚；凤鲚；仔稚鱼；时空分布；广义可加模型

Spatiotemporal distribution of Larvae and Juveniles of Coilia nasus, Coilia mystus and its relationship with environmental in the Yangtze River Estuary

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Abstract: In order to comparatively study the spatial and temporal distribution characteristics of early fish resources of Coilia nasus and Coilia mystus in the Yangtze River Estuary and the relationship with environmental factors. From July 2022 to May 2023, 10 sampling stations were set up on each of the South Branch and North Branch of the Yangtze River Estuary and the waters of the East Beach of Chongming Island to conduct quarterly surveys of Coilia nasus, Coilia mystus and environmental factors. The generalized additive model (GAM) was used to analyze correlation between the abundance of larvae and juveniles and environment factor. The results showed that spring and summer were the main breeding periods for Coilia nasus and Coilia mystus in the Yangtze River estuary. Coilia nasus larvae and juveniles mainly distributed in the waters near the south branch and north branch of the Yangtze River estuary and the east beach of Chongming Island; the spawning grounds of Coilia mystus exist in the waters from Changxing Island to Jiuduansha in the South Branch and in the waters outside the entrance to the North Branch. Coilia mystus larvae and juveniles mainly distributed in the waters outside the entrance to the South Branch, the North Branch and the East Beach of Chongming Island. GAM analysis results showed that fish use the Yangtze River Estuary as spawning and nursery grounds with significant seasonality: summer had significant positive effect on the abundance of Coilia nasus larvae and juveniles, summer and spring had significant positive effect on the abundance of Coilia mystus larvae and juveniles. It was significantly higher in summer than in spring ($P<0.01$). Salinity had significant impact on the abundance of Coilia nasus ($P<0.01$). The suitable salinity for Coilia nasus larvae and juveniles was between 0 and 18, and the optimal salinity ranged from 0 to 8. The distribution of Coilia mystus larvae and juveniles was mainly affected by temperature, salinity, and pH($P<0.01$). The suitable temperature was 22~32 ℃, the suitable salinity was 2~24, the suitable pH was 7.3~8.4 and the suitable dissolved oxygen ranged from 6.0 to 9.0 mg/L.

Key words:：Coilia nasus; Coilia mystus; larvae and juveniles; Spatiotemporal distribution; generalized additive models

长江口水域仔稚鱼多样性与时空分布

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摘要：为探究禁渔开展后长江口鱼类早期资源情况，2022 年 7 月 18 日-8 月 14 日、2022 年 10 月 24 日-11 月 10 日、2023 年 2 月 8 日-3 月 8 日、2023 年 4 月 22 日-5 月 29 日在长江口南支与北支水域设置 42 个采样点，涨潮和退潮期间采用大型仔稚鱼网（口径 1.3m，网目 0.5mm）进行表层水平拖网调查。共采集到 20 目 23 科 82 种仔稚鱼，共计 89644 尾。鳀科鱼优势明显，占全年渔获总量的 82.13%。夏季仔稚鱼密度最大，达到 1.77ind./m³；春季次之，为 0.45ind./m³；秋季 0.12ind./m³；冬季最低，0.002ind./m³。除春季外，潮汐不改变单季节内仔稚鱼分布，夏季仔稚鱼北支多于南支，秋季仔稚鱼南支多于北支，春季涨潮期间仔稚鱼南支多于北支，退潮期间北支多于南支。除春季外，各季节涨潮期间仔稚鱼密度均高于退潮。

关键词：长江口；仔稚鱼；种类组成；多样性；时空分布

Diversity and spatiotemporal distribution of larvae and juveniles in the Yangtze River estuary

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Abstract：To explore the early fish resources in the Yangtze River Estuary after the ban on fishing, 42 sampling points were set up in the waters of the southern and northern branches of the Yangtze River Estuary from July 18 to August 14, 2022, October 24 to November 10, 2022, February 8 to March 8, 2023, and April 22 to May 29, 2023. The surface level trawling survey was conducted with large larvae and juveniles nets (diameter 1.3m, mesh 0.5mm) during high tide and low tide. A total of 89,644 larvae and juveniles of 82 species of 20 orders and 23 families were collected. Anchovy has a significant advantage, accounting for 82.13% of the total catch. The density of larvae and juveniles was the highest in summer, reaching 1.77ind./m³. Spring followed by 0.45ind./m³; Autumn 0.12ind./m³; Minimum in winter, 0.002ind./m³. Except in spring, tides did not change the distribution of larvae and juveniles in a single season. In summer, there were more larvae and juveniles in the north than in the south; in autumn, there were more larvae and juveniles in the south than in the north; in spring, there were more larvae and juveniles in the south than in the north during the high tide, and more larvae and juveniles in the north than in the south during the low tide. The density of larvae and juveniles was higher during high tide than low tide except spring. The richness index (D) and diversity index (H') were both highest in summer, followed by spring, lower in autumn and lowest in winter, but the evenness index (J') was slightly lower in summer than in autumn. CCA analysis of water temperature, salinity, pH and dissolved oxygen showed that salinity was significantly correlated with the distribution of larvae and juveniles during the whole season, while other environmental factors were significantly correlated with the distribution of larvae and juveniles only during the high tide or low tide in individual seasons.

Key words:：Yangtze River Estuary; larvae and juveniles fish; Species composition; Diversity; Spatiotemporal distribution

基于 eDNA 技术的辽宁地区刀鲚资源调查

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摘要：本研究针对辽宁地区 10 条主要的入海河流进行采样，每条河流设置河口、河口上游 5km 和 10km 三个采样点，共计 30 个采样点，每个采样点分别在 5 月、8 月采样两次。取得的水样通过环境 DNA 技术进行数据分析。结果显示：辽宁地区的刀鲚资源分布广泛，形成自西向东两大种群；辽西（葫芦岛、锦州、盘锦）流域种群洄游产卵的时间最早，辽南（大连）流域种群次之，辽东（丹东）流域最晚；河流流域内的水文特征及人工水利设施对刀鲚洄游产卵的影响很大。

关键词：eDNA；刀鲚；资源调查

Investigation of Coilia nasus resources in Liaoning region based on eDNA technology

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Abstract：In this study, 10 major rivers entering the sea in Liaoning were sampled. Three sampling points were set for each river estuary, 5km and 10km upstream of the estuary, with a total of 30 sampling points. Each sampling point was sampled twice in May and August respectively. The obtained water samples were analyzed by environmental DNA technology. The results showed that the Coilia nasus resources were widely distributed in Liaoning, forming two large populations from west to east. The time of migration and spawning was earliest in the western Liaoning (Huludao, Jinzhou, Panjin) basin, followed by the southern Liaoning (Dalian) basin and the latest in the eastern Liaoning (Dandong) basin. The hydrological characteristics and artificial water conservancy facilities in the river basin have great influence on the migration and spawning of anchovy.

Key words:：eDNA ；Coilia nasus；survey of resource

幼年罗氏沼虾暴露在微塑料环境中的毒性机制：来自多视角分析

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摘要：养殖水体中的微塑料不仅影响水产动物的正常生长和发育，而且也严重制约了水产养殖业的健康发展。本研究以 0.1mg/L 的微塑料浓度水体养殖饲养罗氏沼虾 42d，通过测定罗氏沼虾的生长性能、生理生化指标以及观察组织病理学和测定肠道菌落等方面进而评估微塑料对其的影响。结果表明，微塑料第 1d 即可在其鳃、胃及肠道等消化和吸收组织中迅速分布，即使经过 14d 水体净化仍有残留，更严重的是其还能显著抑制虾的生长。通过血液指标分析发现，其能进入幼虾的血液循环系统；组织病理学观察，同样证实微塑料对鳃和肠道的损害微结构产生了损伤，且细胞凋亡产生差异；酶活和基因表达检测揭示了微塑料对罗氏沼虾造成了一系列的氧化应激反应。最后，肠道菌群和转录组分析表明，微塑料不仅影响了肠道菌群中的厚壁菌门、不动杆菌属及乳球菌属的相对丰度，还导致了相关基因的表达差异。

关键词：微塑料；罗氏沼虾；生理生化指标；组织病理学；肠道菌落

Toxic mechanisms of nanoplastics exposure at environmental concentrations on juvenile Macrobrachium rosenbergii: From multiple perspectives

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Abstract： Microplastics in aquaculture water not only affect the normal growth and development of aquatic animals, but also seriously restrict the healthy development of aquaculture industry.This study cultured and raised M. rosenbergii in water with a microplastic concentration of 0.1mg/L for 42 days. The effects of microplastics on the growth performance, physiological and biochemical indicators, histopathological observation, and measurement of intestinal colonies of M. rosenbergii were evaluated by measuring their growth performance.The results showed that microplastics could rapidly distribute in the digestive and absorption tissues such as gills, stomach, and intestines on the first day, and even after 14 days of water purification, there were still residues. More importantly, it could significantly inhibit the growth of shrimp.Through analysis of blood indicators, it was found that it can enter the circulatory system of juvenile shrimp; Histopathological observation also confirms that microplastics damage the microstructure of gills and intestines, and there are differences in cell apoptosis; Enzyme activity and gene expression testing revealed that microplastics caused a series of oxidative stress responses in M. rosenbergii. Finally, gut microbiota and transcriptome analysis showed that microplastics not only affect the relative abundance of Firmicutes, Acinetobacter, and Lactococcus in the gut microbiota, but also lead to differential expression of related genes.This study clarified the impact of microplastics on the toxicity of M. rosenbergii, providing a scientific basis for future water pollution and environmental remediation.

Key words:： Microplastics; Macrobrachium rosenbergii; Physiological and biochemical indicators; Histopathology; Intestinal microbiota

暗纹东方鲀池塘养殖温室气体排放特征及其影响因素研究

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摘要：水产养殖的温室气体排放已引起全球关注。暗纹东方鲀是中国水产养殖中重要的高价值鱼种，池塘养殖是暗纹东方鲀最主要的养殖方式。我们采用漂浮静态箱-气相色谱法测量了暗纹东方鲀养殖池塘水-气界面的温室气体排放量。结果表明，三种温室气体 CO2、CH4 和 N2O 均为排放源。我们通过监测水质和气象因子，对影响温室气体排放的环境因子进行了相关性分析，发现叶绿素 a 和总氨氮是温室气体排放的主要环境驱动因素。我们对池塘底泥微生物的 16S rDNA 测序，发现 Proteobacteria 和 Desulfococcus 是 CO2 排放的主要贡献者，Proteobacteria 和 Synechococcaceae 是 CH4 排放的主要贡献者，而 Actinobacteria 则是 N2O 排放的主要贡献者。最后我们还对比了中国其他水体的温室气体排放，结果表明暗纹东方鲀池塘养殖产生的温室气体排放量低于内陆淡水池塘养殖。

关键词：暗纹东方鲀；池塘养殖；温室气体；排放通量；底泥微生物

Characteristics and influencing factors of greenhouse gas emissions from Takifugu fasciatus pond aquaculture

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Abstract： Greenhouse gas emissions from aquaculture have attracted global attention. Takifugu fasciatus is an important high-value fish species in aquaculture in China. During a 182-day study, GHG emissions from the water-gas interface of T. fasciatus aquaculture ponds were measured by the static floating chamber-gas chromatography. The results showed that three greenhouse gases, CO2, CH4 and N2O, were the emission sources. By monitoring water quality and meteorological factors, we conducted correlation analysis and discovered that chlorophyll a and total ammonia nitrogen were the primary environmental drivers of GHG emissions. 16S rDNA sequencing of pond sediment microorganisms indicated that Proteobacteria and Desulfococcus stand as the primary contributors to CO2 emissions, Proteobacteria and Synechococcaceae were found to be the main contributors to CH4 emissions, while Actinobacteria were mainly contributors to N2O emissions. The comparison results showed that the T. fasciatus aquaculture ponds produced less GHG emissions than the inland freshwater pond aquaculture.

Key words:：Takifugu fasciatus; Pond aquaculture; Greenhouse gas; Emission flux; sediment microorganisms

亚热带鉴江河口海洋保护区大型底栖动物：现状与生态质量分析

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摘要：本研究报道了粤西鉴江口海洋保护区大型底栖动物的种类组成、群落结构和多样性，并应用 3 种生物指数方法评价了该保护区的栖息地生态质量状况。本研究共鉴定出大型底栖动物 58 种，其中软体动物占比最高(48.28%)，其次是环节动物(27.59%)和节肢动物(18.97%)。春秋两季鉴江口大型底栖动物的密度和生物量变化较大，且 RDA 分析显示其群落受不同环境变量的影响。丰度生物量比较曲线(ABC 曲线)结果表明，大型底栖动物群落在春季处于未受扰动状态，但在秋季处于受干扰状态。AZTI 海洋生物指数(AMBI)表明，大多数站位的生态质量状况处于优或良好状态，且春季的生态质量总体高于秋季。M-AMBI 结果表明，春季鉴江口保护区的平均生态质量状况良好，高于秋季的中等状态。秋季鉴江口生态质量下降的原因可能与上游水库十年一遇的泄洪引起的扰动有关。本研究结果可为鉴江河口保护区的管理提供科学建议。

关键词：大型底栖生物，亚热带河口，保护区，生态健康，AMBI 指数

Macrobenthos in the marine protected area of the subtropical Jianjiang River Estuary, China: Current state and analysis of ecological quality

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Abstract： Macrobenthos composition, community and diversity in the marine protected area of Jianjiang Estuary was reported and three biotic indices were applied to evaluate the habitat ecological quality status (EcoQs) of the reserve. A total of 58 macrobenthos species were identified, of which Mollusca species accounted for the highest proportion (48.28%), followed by Annelida (27.59%), and Arthropoda (18.97%). The abundance and biomass of macrobenthos varied among the sites in different seasons, and macrobenthos community in spring and autumn were drove by different environmental variables. Abundance biomass comparison curves (ABC curve) combined with the W-statistic indicated that the macrobenthos community is undisturbed in the spring but disturbed in autumn. Second, the AZTI marine biotic index (AMBI) indicated that most sites have high or good EcoQs, with site quality generally being higher in the spring. Finally, the multivariate AMBI (M-AMBI) results showed that the average EcoQs in spring were good, compared to only moderate EcoQs in autumn. The lower EcoQs in autumn was largely due to sites near the river outflow that were disturbed primarily as a result of the 1-in-10-year flood discharge that occurred during our sampling year. In addition, the impact of assigning species ecological groups on the AMBI result was discussion. Overall, our results provide scientific suggestions for future management of the Jianjiang estuary reserve.

Key words:： Macrofauna, Subtropical estuary, Reserve, Ecological health, AMBI

头足类角质颚形态的系统发育相关性和分类地位

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摘要：头足类物种的摄食器官——角质颚，可以揭示重要的生态信息。本研究构建了来自 13 个属 5 个科的 24 个物种 1164 对角质颚的二维形态，采用几何形态测量方法探讨了角质颚侧面轮廓形状的系统发育相关性和分类效果。结合几何形态测量和分子生物学方法确认了它们的进化关系和分类地位。同时还评估了角质颚形状的系统发育信号。分析结果表明，角质颚的形状变异主要体现在喙部、头盖和侧壁。上颚和下颚的整体形状参数（所有主成分）对物种鉴定更有用。上下颚的形状表现出强烈的系统发育信号，并且基于角质颚形状的表型树基本反映了各科的分类地位。我们还假设头足类角质颚的形状变异可能归因于遗传和环境差异。总之，角质颚是分类头足类物种的可靠材料，几何形态测量方法是一种强有力的工具，能够揭示角质颚形状在头足类物种鉴定、系统发育相关性和表型多样性研究中的重要地位。

关键词：几何形态测量学；头足类角质颚；系统发育信号；形状识别；分类学

Geometric morphometrics casts light on phylogenetic relevance of cephalopod beak morphological

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Abstract： The feeding organ of cephalopod species, the beak, can be used to reveal important ecological information. In this study, geometric morphometric approaches were employed to investigate the phylogenetic relevance and classification effect of beak lateral profile shape. The two-dimensional beak morphologies of 1164 pairs of 24 species from 13 genera and 5 families were constructed, and their evolutionary relationships and taxonomic status were confirmed using geometric morphometrics and molecular biology approaches. We also assessed the phylogenetic signals of beak shape. The analysis results show shape variation in the beak mainly in the rostrum, hood, and lateral wall. The overall shape parameters (all PCs) of the upper and lower beak are more useful for species identification. The shapes of the upper and lower beak show a strong phylogenetic signal, and the phenogram based on the beak shape basically reflected the families' taxonomic positions. We also hypothesized that the shape variation in the beaks of cephalopods may be ascribed to genetic and environmental differences. In summary, beaks are a reliable material for the classification of cephalopod species. Geometric morphometric approaches are a powerful tool to reveal the identification, phylogenetic relevance and phenotypic diversity of beak shape in cephalopods.

Key words:： Geometric morphometrics; Cephalopod Beak; Phylogenetic signal; Shape Identification; taxonomy

基于美国哈德逊河条纹鲈的鱼类产卵策略的年代际变化研究

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摘要：了解产卵行为对于评估鱼类种群的生产力和对开发和气候变化的脆弱性至关重要。利用哈德逊河生物监测计划 (HRBMP) 收集的鱼类浮游生物数据，我们评估了条纹鲈 的产卵行为，条纹鲈是哈德逊河口 (HRE) 中一种具有高生育力的多次产卵溯河物种。我们开发了三个新的产卵最佳指数：热最佳指数 、时间最佳指数 和空间最佳指数 。我们的结果表明，条纹鲈喜欢在两个特定且不同的时间段在特定温度范围 产卵，但产卵地点在 HRE 的广泛地区。鲈鱼的产卵行为随着时间的推移发生了变化，在 1985 年和 1998 年发生了两次转变，导致在更普遍的策略下，有三个不同的时期采用不同的产卵策略。这些变化，包括最佳产卵温度范围变窄以及空间和时间产卵行为多样性降低，可能会对种群的稳定性和生殖弹性产生负面影响。研究表明，长期监测鱼卵的发生和丰度对于了解鲈鱼的长期产卵策略非常重要，并强调了在渔业管理中考虑产卵行为的重要性。

关键词：条纹鲈，产略策略，产卵行为，时空变化

Decadal-scale changes in fish spawning strategies: a case study of striped bass in the Hudson River

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Abstract： Understanding spawning behavior is critical in evaluating the productivity and vulnerability of fish populations to exploitation and climate change. Using the ichthyoplankton data collected in a long-term monitoring program, the Hudson River Biological Monitoring Program (HRBMP), we evaluated the spawning behavior of striped bass (Morone saxatilis), an iteroparous anadromous species with high fertility in the Hudson River estuary (HRE). We developed three novel spawning optimum indices: the Thermal Optimum Index (THOI), the Temporal Optimum Index (TEOI), and the Spatial Optimum Index (SOI). Our results showed that striped bass prefer to spawn at certain temperature ranges (14.5-17.5°C) during two specific and distinct time periods (May 13-30 and June 16-June 22) but in extensive locations in the HRE. We also found that the striped bass spawning behavior had changed over time, with two shifts occurring in 1985 and 1998 and resulting in three distinct periods with different spawning tactics under a more general strategy. These changes, including a narrower range of optimal spawning te

Key words:：striped bass, spawning temperature optima, spatio-temporal spawning behavior

禁渔期内湘江银鮈个体繁殖力与卵径研究

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摘要：为研究禁渔对鱼类个体繁殖力和卵径的影响，于 2023 年 5-6 月在湘江共采集 65 尾性成熟雌性银鮈，分析个体繁殖力和卵径，建立其与生物学指标的关系。结果表明：个体绝对繁殖力为（11160±7910）粒，体长相对繁殖力为（100.29±62.37）粒/mm，体重相对繁殖力为（421.86±240.20）粒/g。个体绝对繁殖力和体长相对繁殖力与体长、体重、卵巢重呈幂函数关系，体重相对繁殖力与体长、体重、卵巢重分别呈二次函数关系、线性函数关系、幂函数关系。卵径与个体绝对繁殖力和卵巢重呈幂函数关系，与体长、体重分别呈线性函数关系和幂函数关系。利用个体繁殖力和卵径与生物学指标关系，可预测湘江银鮈种群繁殖能力。比较不同水系银鮈繁殖力和卵径，发现纬度对银鮈繁殖力影响并不明显，繁殖力和卵径差异可能与鱼类栖息地稳定有关。

关键词：银鮈；繁殖力；卵径；湘江；禁渔

Individual fecundity and egg size of Xiangjiang Squalidus argentatus during the closed season

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Abstract：Abstract:In order to study the effects of the fishing ban on individual fecundity and egg diameter of the fish, a total of 65 sexually mature female Squalidus argentatus were collected in May-June 2023 in Xiangjiang River, and individual fecundity and egg diameter were analysed to establish their relationship with biological indicators. The results showed that the absolute fecundity of individuals was (11,160±7,910), the relative fecundity of body length was (100.29±62.37)/mm, and the relative fecundity of body weight was (421.86±240.20)/g. The absolute fecundity of individuals and the relative fecundity of body length showed a power function relationship with the body length, body weight and ovary weight, and the relative fecundity of body weight showed a quadratic, linear and quadratic function relationship with the body length, body weight and ovary weight, respectively. Body weight relative fecundity was quadratically, linearly and power functionally related to body length, body weight and ovary weight, respectively. Egg diameter was a power function of absolute individual fecundity and ovarian weight, and a linear and power function of body length and body weight, respectively. The relationships between individual fecundity and egg diameter and biological indicators can be used to predict the reproductive capacity of Xiangjiang River Squalidus argentatus populations. Comparing the fecundity and egg diameter of Squalidus argentatus in different water systems, it was found that the effect of latitude on the fecundity of Squalidus argentatus was not obvious, and the differences in fecundity and egg diameter might be related to the stability of the fish habitat. Habitat stabilisation during the closed season is of great significance for fishery resources conservation, and the study reveals the biological characteristics of Squalidus argentatus during the closed season, which will provide basic information for fishery resources management.

Key words:：Squalidus argentatus ; Fecundity; Egg diameter; Xiangjiang River; closed fishing

海洋牧场工程建设在驱动海洋碳储上的作用研究

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摘要：海洋牧场是一种环境友好型渔业方式，通过人工鱼礁等工程设施，能提升海洋初级生产力。虽然目前海洋牧场的碳汇理念已获认同，但目前对其碳储效应把控仍旧不足。本研究选取筏式养殖区、石块礁区、立方体礁区、上升流礁区、田字形礁区和自然礁区，探讨了不同鱼礁区海水和沉积物的储碳量及其驱动因素。结果表明：上升流礁区和田字形礁区的单个礁体后面形成的流场效应比立方体礁区更明显。随着培养时间的增加，类蛋白质组分减少，伴随着更易利用惰性溶解有机碳（RDOC）的微生物的相对丰度增加，并且上升流礁区具有较大的荧光负荷。在沉积物中，大部分站点总有机碳（TOC）含量随深度增加，虽然筏式养殖区 TOC 含量最高，但石头礁区碳水化合物的利用效率最高。研究结果表明，鱼礁产生的流场效应，营养盐含量及其营养盐通量会对海水和沉积物的碳储产生影响。

关键词：人工鱼礁 海洋牧场 溶解有机碳 总有机碳

Study on the Role of Marine Ranching Engineering in Driving Marine Carbon Sequestration

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Abstract： Marine ranching, an eco-friendly fisheries practice, enhances marine productivity using structures like artificial reefs. While its carbon sequestration potential is acknowledged, its effects on carbon storage are not well controlled. This study explored carbon storage in seawater and sediments across different artificial reef types: raft culture, rocky, cubic, upwelling, field-shaped, and natural habitats. Results showed that upwelling and field-shaped reefs have more pronounced flow field effects than cubic reefs. Over time, protein-like compounds decreased while microorganisms using recalcitrant dissolved organic carbon (RDOC) increased. Upwelling reefs had higher fluorescence. Sediment total organic carbon (TOC) generally rose with depth; raft culture had the highest TOC, but rocky reefs were most efficient in carbohydrate utilization. Findings indicate that flow fields and nutrient fluxes from artificial reefs significantly impact carbon sequestration in seawater and sediments.

Key words:： Artificial reef, Marine ranching, Dissolved organic carbon (DOC), Total organic carbon (TOC)

基于碳氮稳定同位素的中西太平洋中上层大型鱼类种间摄食生态分析

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摘要：大型鱼类作为食物链的顶端生物，通过捕食控制饵料生物种群的数量，维持海洋生态系统的平衡。为深入了解中西太平洋中上层大型鱼类的营养特征和摄食关系，本文通过分析鱼类肌肉的碳氮稳定同位素对大青鲨、帆蜥鱼、蛇鲭、大眼金枪鱼、凹尾长鳍乌鲂、剑鱼、异鳞蛇鲭、长鳍金枪鱼、紫色翼魟和蓝枪鱼的种间摄食生态进行分析。结果表明：10 个物种的 δ13C 值和δ15N 值存在显著性差异，δ13C 值最高的是蓝枪鱼，最低的是大青鲨；δ15N 值最高的是异鳞蛇鲭，最低的是紫色翼魟。生态位宽度最大的是剑鱼（3.425‰2），宽度最小的是异鳞蛇鲭（0.767‰2），通过生态位可以看出它们之间食性的差异。生态位重叠结果中出现生态位重叠度接近于 0 的情况，说明 10 个物种之间存在资源利用分离的现象。本文通过分析比较中上层大型鱼类的种间摄食竞争关系，为研究中西太平洋生态系统的稳定以及更好的利用和养护渔业资源提供更多资料。

关键词：大型鱼类；摄食生态；碳氮稳定同位素；中西太平洋

Inter-specific feeding ecological analyses of pelagic large fishes in the western and central Pacific Ocean based on carbon and nitrogen stable isotopes

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Abstract： As the top organisms in the food chain, large fishes control the population of bait organisms through predation and maintain the balance of marine ecosystems. The results showed that the δ13C and δ15N values of the 10 species were significantly different, with blue marlin having the highest δ13C value and great blue shark having the lowest, while the highest δ15N value was found in the isosceles mackerel and the lowest in the purple winged ray. The largest ecotope width was for swordfish (3.425‰2), and the smallest width was for heteroclitic snake mackerel (0.767‰2), and the differences in feeding habits between them could be seen through the ecotopes. The ecological niche overlap close to 0 appeared in the overlap results, which indicated that there was a phenomenon of resource utilisation separation among the 10 species. This paper analyses and compares the interspecific feeding competition among pelagic large fishes to provide more information for the study of the stability of the ecosystem in the western and central Pacific Ocean as well as for the better use and conservation of fishery resources.

Key words:： Large fishes; Feeding ecology; Carbon and nitrogen stable isotopes; Western and Central Pacific Ocean

基于 eDNA 技术的北部湾多营养级生物多样性及生态系统健康评价

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摘要：北部湾是一个资源丰富、生态多样的半封闭海湾，但由于人类活动的增加，其生态系统健康状况持续恶化。本研究于 2022 年至 2023 年间利用环境 DNA 宏条形码技术，对广西北部湾海域的多营养级生物群落进行了全面监测，共鉴定出 1339 个物种，包括哺乳动物 2 种、鱼类 214 种、无脊椎动物 195 种、原生动物 188 种、藻类 422 种和原核生物 318 种。结果表明，硝酸盐氮和水深是丰水期影响多营养级生物群落组成和多样性的关键环境因子，而盐度则在枯水期起主要作用。多样性指数（包括物种丰富度、香农多样性指数和系统发育多样性指数）随体型减小而逐渐增加，且群落组成呈现出显著的空间变异性。丰水期的食物网复杂度较高，由 472 个节点和 20766 条食物链构成，而枯水期则由 478 个节点和 18328 条食物链组成。基于生态系统完整性的综合评价，北部湾在丰水期和枯水期的生态健康等级均被评为“良”。

关键词：北部湾；eDNA；多营养级生物群落；食物网；水生态健康评价

Assessment of multi-trophic biodiversity and ecosystem health in Beibu Gulf based on eDNA technology

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Abstract：Beibu Gulf, a resource-rich and ecologically diverse semi-enclosed bay, faces deteriorating ecosystem health due to increased human activities. This study surveyed multi-trophic communities in Guangxi's Beibu Gulf from 2022 to 2023 using environmental DNA metabarcoding. A total of 1,339 species were identified, including 2 mammal species, 214 fish species, 195 invertebrate species, 188 protozoan species, 422 algal species, and 318 prokaryotic species. Nitrate nitrogen and water depth were key factors in community composition and diversity during the wet season, while salinity was crucial in the dry season. Diversity indices increased as body size decreased, showing significant spatial variability. The wet season had greater food web complexity, with 472 nodes and 20,766 trophic links, versus 478 nodes and 18,328 links in the dry season. A comprehensive evaluation of ecosystem integrity assigns a "Good" rating for both seasons.

Key words:：Beibu Gulf; eDNA; Multi-trophic communities; Food web; Water ecological health

海州湾紫菜养殖海域浮游植物时空分布特征及其对环境因子变化的响应

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摘要：为探究海州湾紫菜养殖是否改变海域的浮游植物群落结构，本研究于 2023 年在海州湾紫菜养殖海域及其邻近海域进行浮游植物四季采样调查。调查共鉴定出浮游植物 5 门 59 属 139 种（包括变种和变型），主要为硅藻和甲藻。浮游植物细胞密度平均值变化范围为 983.10×103（春季）- 367525.20×103 ind./m3（冬季）。通过聚类分析和相似性分析，结果表明不同季节的浮游植物群落组成有显著差异，在养殖区和对照区之间无显著差异。不同调查区域的优势种有不同的季节演替趋势；紫菜养殖区的浮游植物优势种组成更多样和稳定。近年来海州湾紫菜养殖规模缩减对浮游植物群落结构和多样性产生了重要影响。

关键词：浮游植物；海州湾；群落结构；紫菜养殖；CCA 分析

Spatiotemporal Distribution of Phytoplankton and Their Response to Environmental Variations in the Porphyra Cultivation Area of Haizhou Bay

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Abstract：To investigate whether Porphyra cultivation alters the phytoplankton community structure, we conducted seasonal sampling surveys of phytoplankton in the Porphyra cultivation area and adjacent areas of Haizhou Bay in 2023. A total of 139 species (including varieties and forms) from 59 genera across 5 phyla of phytoplankton were identified, primarily consisting of diatoms and dinoflagellates. The average abundance of phytoplankton varied from 983.10×103 ind./m3 (spring) to 367525.20×103 ind./m3 (winter). Cluster analysis and Non-Metric multidimensional scaling (NMDS) analysis revealed significant seasonal differences in the phytoplankton community composition, but no significant differences between the cultivation and control areas. Different survey areas exhibited distinct trends in the seasonal succession of dominant species, while the dominant species composition of phytoplankton in the Porphyra cultivation areas remained stable and diverse. The recent reduction in the scale of Porphyra cultivation in Haizhou Bay has shown a certain impact on the structure and diversity of phytoplankton communities. Correlation analysis and Canonical Correspondence Analysis (CCA) of the phytoplankton community indices with environmental factors indicated that the primary influencing factors of the phytoplankton community were temperature, dissolved oxygen (DO), salinity and nutrients (SiO32--Si, NO2---N).

Key words:：Phytoplankton; Haizhou Bay; Community structure; Porphyra cultivation; Canonical Correspondence Analysis (CCA)

澳洲鲭和日本鲭种间关系研究进展

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摘要：澳洲鲭和日本鲭广泛分布于太平洋、大西洋以及印度洋等海域，在海洋捕捞业中占有重要的地位，是世界上产量最高的经济种类。这两种鱼类每年在生殖和越冬季节进行远距离洄游，游泳能力强、速度快，作为连接海洋生物资源上、下营养级群体的纽带，在食物网中处于中等营养水平，它们可能会对低营养水平产生重要影响，主要食甲壳类、鱼类、桡足类等；同时可能会影响高营养级捕食者，它们是大型鱼类、头足类等的捕食对象，共享同一栖息地，生态位重叠，二者在分布、摄食等方面可能存在竞争关系。同一属不同种的鱼类生态位宽度和资源利用方式可能不同，应对环境胁迫的能力也不同，目前，对澳洲鲭和日本鲭不同群体的种群资源变动机制、竞争关系和共存机制的研究较少，为此，本文总结归纳了国内外对澳洲鲭和日本鲭关于种间关系以及摄食生态的最新发展趋势和研究进展，为探究两个物种的种间关系及合理开发渔业资源提供科学依据。

关键词：澳洲鲭；日本鲭；摄食生态；种间关系；资源利用

The progress of research on the interspecific relationship between Scomber australasicus and Scomber japonicus

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Abstract： Scomber australasicus and Scomber japonicus are widely distributed in the Pacific and Atlantic Oceans, as well as the Indian Ocean, where they play an important role in marine capture fisheries and are the most productive economic species in the world. These two species migrate long distances every year during the reproductive and overwintering seasons, with strong and fast swimming ability. As a link between the upper and lower trophic groups of marine living resources, they are at intermediate trophic levels in the food web, and they may have an important impact on the lower trophic levels, mainly feeding on crustaceans, fish, copepods, at the same time, they may affect the high trophic level predators, which are the prey of large fishes, cephalopods and so on. Sharing the same habitat and overlapping ecological niches, the two may have a competitive relationship in terms of distribution and feeding. Different species of the same genus may have different ecological niche widths and resource utilisation modes, as well as different abilities to cope with environmental stresses. Currently, there are fewer studies on the mechanisms of population resource changes, competition and coexistence of different groups of Scomber australasicus and Scomber japonicus, so this paper summarises the latest development trends and progress of domestic and international studies on the interspecific relationships and feeding ecology of Australian mackerel and Japanese mackerel, with the aim of investigating the interspecific relationships and rational development of these two species. This paper summarises the latest trends and progress of research on the interspecific relationship and feeding ecology of Scomber australasicus and Scomber japonicus, and provides scientific evidence for the investigation of the interspecific relationship between the two species and the rational development of fishery resources.

Key words:： Scomber australasicus；Scomber japonicus；feeding ecology；interspecific relationship；resource utilisation.

海洋牧场常年季节性低氧区沉积物-水界面 CO2 和 CH4 通量的时空驱动因素

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摘要：近海作为 CO2 和 CH4 的重要来源，正受到日益加剧的海底缺氧影响。由于近海缺氧在时空分布上的差异性，使其对温室气体生产和排放的具体影响尚不明确。自 2013 年以来，中国黄海北部海洋牧场区域在夏季出现连年季节性低氧现象。我们在 2023 年夏季于该区域采集了垂直分层水样和表层沉积物，以研究常年季节性低氧区对温室气体浓度及沉积物-水界面通量的影响。结果显示，在夏季，CO2 和 CH4 浓度及通量存在显著的时空差异。随着温度升高，CO2 和 CH4 含量增加。在空间上，常年低氧区的 CO2 和 CH4 浓度显著高于对照区，并与水体 DO 含量呈现负相关。此外，海底沉积物-水界面的 CH4 交换通量也显著高于对照区。研究表明，随着近海季节性低氧区域的扩大和低氧程度加剧，CH4 浓度和沉积物-水界面的交换通量显著增加，从而会对全球碳排放产生不可预见的变化。

关键词：海洋牧场，季节性低氧，CO2 和 CH4，沉积物-水界面，扩散通量

Spatial and Temporal Drivers of CO2 and CH4 Fluxes at the Sediment-Water Interface in the Seasonal Hypoxic Zone of Marine Ranching Areas

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Abstract： Coastal areas, key sources of CO2 and CH4, are increasingly impacted by deep-sea hypoxia. The spatial and temporal variability of coastal hypoxia makes its specific effect on greenhouse gas production unclear. Since 2013, northern Yellow Sea aquaculture areas have experienced seasonal hypoxia each summer. In summer 2023, we collected vertical water samples and surface sediments to examine how persistent seasonal hypoxia affects greenhouse gas concentrations and sediment-water interface fluxes. Results revealed significant temporal and spatial variations in CO2 and CH4 levels and fluxes. Higher temperatures led to increased CO2 and CH4. Hypoxic areas had notably higher CO2 and CH4 concentrations compared to control areas, with a negative correlation to DO levels. CH4 fluxes at the sediment-water interface were also higher in hypoxic regions. The study suggests that expanding and worsening hypoxic areas may significantly increase CH4 concentrations and fluxes, potentially affecting global carbon emissions unpredictably.

Key words:：Marine ranching,Seasonal hypoxia,CO2 and CH4, Sediment-water interface,Diffusive flux

PDA@Fe3O4-MNP
对三种亚历山大藻的吸附研究

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摘要：船舶压载水是亚历山大藻入侵的来源之一，进入水域后会引发有害藻华。本研究开展了不同 pH、盐度、藻细胞密度、磁性纳米颗粒浓度和孵育时间条件下，聚多巴胺修饰磁性纳米颗粒（Polydopamine@Fe3O4-magnetic nanoparticles，PDA@Fe3O4-MNP）对微小亚历山大藻（Alexandrium minutum）、链状亚历山大藻（Alexandrium catenella）和塔玛亚历山大藻（Alexandrium tamarense）吸附效率的研究。结果表明，PDA@Fe3O4-MNP 对微小亚历山大藻和塔玛亚历山大藻吸附的最适 pH 为 8.0，其吸附率为 0.991 和 0.884；对链状亚历山大藻的最适 pH 为 7.4，吸附率为 0.949。PDA@Fe3O4-MNP 对三种亚历山大藻的吸附率均随 PDA@Fe3O4-MNP 浓度增加而增大，最高值依次为 0.989、0.967 和 0.898。

关键词：聚多巴胺、磁性纳米颗粒、吸附、亚历山大藻

Study on the adsorption of polydopamine@Fe3O4-magnetic nanoparticles for Alexandrium

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Abstract： Ballast water contains a variety of microorganisms, including the harmful algal bloom species Alexandrium, the large-scale outbreak of which will endanger the aquatic ecological environment and human health. In this study, polydopamine@Fe3O4-magnetic nanoparticles (PDA@Fe3O4-MNP) was applied to separately adsorb Alexandrium minutum, Alexandrium catenella, and Alexandrium tamarense under varying conditions of pH, salinity, algal cell density, magnetic nanoparticle concentration, and incubation time. Thereafter, the adsorption rates were investigated and compared. The results showed that the optimal pH for the adsorption of A. minutum and A. tamarense by PDA@Fe3O4-MNP was 8.0, with adsorption rates of 0.991 and 0.884, respectively. The optimal pH for the adsorption of A. catenella was 7.4, with an adsorption rate of 0.949. The adsorption rates for all three Alexandrium species increased with the concentration of PDA@Fe3O4-MNP. The maximum adsorption rate was sequentially 0.989, 0.967, and 0.898. Salinity barely impacted the adsorption of A. minutum, while for the other two Alexandrium species, the adsorption rate decreased significantly with increasing salinity ($P<0.05$). The minimum adsorption rate for A. catenella and A. tamarense was 0.878 and 0.818, respectively. The adsorption rates of all three Alexandrium species decreased with increasing algal cell density, however, the adsorption rates for them remained over 0.89 even at a density of 1×10^6 cell/L. Prolonging the incubation time increased the adsorption rates of three species, and the maximum adsorption rate was 0.989, 0.978, and 0.913, sequentially. This study provides fundamental data support for constructing a ballast water treatment system for Alexandrium based on magnetic nanoparticles.

Key words:： polydopamine, magnetic nanoparticles, adsorption, Alexandrium

改善黄海北部沿海海洋环境：人工鱼礁对大型底栖生物群落和生态能质的作用

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摘要：投放人工鱼礁能够改善沿海生态环境并恢复生物资源，是近海海洋生物栖息地和渔业资源恢复的重要方法。大型底栖生物在海洋生态系统的生物类群中占据主要地位，也对环境变化尤为敏感。因此，认识大型底栖生物在不同礁区中的群落特征和热力学指标变化有助于理解人工鱼礁建设的生态效果。本研究基于黄海北部沿海区域采集的大型底栖生物数据，探讨了该地区不同类型的人工鱼礁及自然生境中大型底栖生物群落和生态能质差异。结果表明，季节和礁区类型对大型底栖生物群落的组成产生显著影响，鱼礁建设并未影响大型底栖生物优势种，但是改变了优势种的相对丰度。人工鱼礁区大型底栖生物群落的物种丰度、丰富度、生物多样性和生态能质均显著高于自然生境，其中以石头礁最为明显。研究显示，人工鱼礁可以增加附近海域的大型底栖生物的多样性以及生态能质。本研究可以为大型底栖生物群落对不同类型的人工鱼礁的响应提供基础数据，并加强对人工鱼礁建设生态效益的全面理解。

关键词：人工鱼礁生境，大型底栖生物，生物多样性，生态能质

Improving costal marine habitats in the northern Yellow Sea: The role of artificial reefs on macrobenthic communities and eco-exergy

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Abstract：The deployment of artificial reefs can significantly boost coastal ecosystems and restore biological resources, playing a crucial role in nearshore habitat and fishery recovery. Macrobenthos, key to marine ecosystems, are highly sensitive to environmental changes. This study, using data from the northern Yellow Sea, explores differences in macrobenthic community structure and ecological integrity across various artificial reef types and natural habitats. Findings reveal that seasonal changes and reef types greatly affect macrobenthic community composition. Although artificial reefs did not impact the dominant species, they altered their relative abundance. Artificial reef habitats showed notably higher species richness, abundance, biodiversity, and eco-exergy compared to natural habitats, with rock reefs showing the most significant differences. This study underscores that artificial reefs enhance macrobenthic diversity and ecological integrity, providing valuable insights into their responses to different reef types and the overall ecological benefits of artificial reef construction.

Key words:：Artificial reef habitats, Macrobenthos, Biodiversity, Eco-exergy

中华绒螯蟹生物扰动对跨营养梯度湖泊沉积物微生物群落的影响

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摘要：富营养化显著影响湖泊生态系统，改变水质与沉积物微生物群落。本研究聚焦于中华绒螯蟹（Eriocheir sinensis）在太湖不同营养区域（竺山湾、梅梁湾、鲤山湾）的生态作用，分析其对微生物群落结构与多样性的生物扰动效应。结果表明，蟹类活动重塑了沉积物微生物群落，与沉积物 pH 值、营养含量紧密相关。此扰动虽促进养分循环，但在高富营养区可能加速养分释放，威胁水质。LEfSe 分析显示，高富营养沉积物中细菌多样性增加，Bacteroides 与 Bacteroidaceae 占优，揭示其在极端环境的适应性。中性群落模型（NCM）模型强调随机过程在微生物群落构建中的重要性，特别是在低压力生态位，增强群落稳定性。综上，本研究揭示了中华绒螯蟹对太湖微生物群落的深刻影响，阐明了生物扰动、微生物生态学与富营养化的复杂关系，对底栖生物管理、水质提升及可持续水生生态系统构建具有重要指导意义。

关键词：富营养化湖泊;中华绒螯蟹;生物扰动;微生物群落

Effects of Chinese mitten crab (Eriocheir sinensis) bioturbation on microbial communities in lake sediment across nutrient gradients

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Abstract： Eutrophication profoundly affects lake ecosystems, shaping water quality and sediment microbial communities. In this study, we examined the influence of Chinese mitten crab (Eriocheir sinensis) across Taihu Lake's Zhushan, Meiliang, and Lishan Bays, each characterized by varying nutrient levels. Our findings revealed that crab bioturbation significantly altered microbial community composition and diversity, with changes closely linked tosediment properties such as pH and nutrient content. This bioturbation enhanced nutrient cycling but may also exacerbate nutrient release in eutrophic areas, potentially degrading water quality. LEfSe analysis illuminated that the higher eutrophication levels led to a significant increase in bacterial diversity, with the dominance of Bacteroides and Bacteroidaceae in heavily eutrophic sediments. Furthermore, Neutral Community Model (NCM) analysis emphasized the dominance of stochastic processes in microbial community assembly, particularly in less stressed habitats, contributing to the stability and persistence of microbial communities. These findings underscore the importance of understanding the intricate interplay between bioturbation, microbial ecology, and eutrophication. Such insights are essential for devising strategies to harmonize benthic populations, enhance water quality, and ensure sustainable aquatic ecosystem management.

Key words:：Eutrophic Lake；Chinese mitten crab；bioturbation；microbial communities

刺参体壁的超分子构造研究

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摘要：超分子构造是阐明食品加工与贮藏品质机理的关键基础。刺参是我国重要的经济水产品，体壁是其主要的可食部位。本研究运用蛋白组学及生物信息学技术，构建了刺参结构蛋白的分子列表，验证了 3 大类 16 亚类共 472 种结构蛋白的存在；采用定量蛋白组学，量化描述了胶原纤维组成的异质性，并阐明了原纤蛋白与胶原蛋白的化学计量学关系；基于抗原设计，制备出刺参原纤蛋白的特异性抗体，进而实现了原纤蛋白微纤维与胶原纤维组织构造关系的显微观察；基于碳水化合物结合结构域的基因挖掘，率先掌握了岩藻聚糖与岩藻糖基化硫酸软骨素的特异性结合蛋白，并构建出荧光融合蛋白作为探针，阐明了刺参中多糖分子的分布与组织构造。上述研究成果深化了刺参体壁超分子构造的认识、细化了刺参体壁微结构模型，有利于海参品质形成机理的深入研究及海参加工贮藏新技术的创新开发。

关键词：刺参；超分子构造；显微；组学；探针

Study on the Supramolecular Structure of Apostichopus Japonicus Body Wall

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Abstract： Supramolecular structure is a key foundation for elucidating the mechanisms of food processing and storage quality. Apostichopus Japonicus is an important economic aquatic food in China. This study utilized proteomics and bioinformatics techniques to construct a molecular list of structural proteins of A. japonicus and verified the existence of 472 structural proteins in 3 major categories and 16 subcategories. The heterogeneity of collagen fibril composition and the stoichiometric relationship between fibrillin and collagen fibril were elucidated by using quantitative proteomics. Based on antigen design, anti-A. japonicus fibrillin specific antibody was prepared. Thus, microscopic observation of the relationship between fibrillin microfibrils and collagen tissue structure was achieved. Based on carbohydrate binding domain gene mining, the specific binding proteins of sulfated fucan and fucosylated chondroitin sulfate were first mastered. The distribution and tissue structure of polysaccharide molecules were elucidated using the constructed fluorescent fusion protein as the probe. The results have deepened the understanding of the supramolecular structure and refined the microstructure model of A. japonicus body wall.

Key words:：Apostichopus Japonicus, Supramolecular Structure, microscopic, Omics, Probe

斩拌和食盐对僵直前鲢鱼肌肉特性的影响：代谢过程、蛋白质功能和超微结构

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摘要：斩拌和加盐是乳化肉制品中两个重要的加工环节。本研究目的是探究斩拌和加盐对僵直前鲢鱼肌肉代谢过程、蛋白质功能和超微结构的影响，以及这三个方面在僵直过程中是如何变化的。斩拌加速了 ATP 的损失，盐胁迫抑制了 HxR 和 Hx 的积累。同样，斩拌导致糖原下降更快，乳酸上升更快，食盐起到了抑制作用。与 ATP 和糖原分解一致，代谢组学显示斩拌和加盐改变了僵直过程中脂肪酸和氨基酸的代谢。僵直后，加盐斩拌导致自由基清除能力显著降低，同时伴随着更大的巯基损失。盐也促进蛋白质变性，表现为表面疏水性增加和内源荧光降低。斩拌或加盐斩拌后的鱼肉超微结构在僵直前和僵直后相似。上述发现可以为鱼类产品的生产提供有价值的见解。

关键词：僵直前；斩拌；加盐；代谢；超微结构

Effects of chopping and salting on the properties of pre-rigor silver carp muscle: Metabolic process, protein functionality, and ultrastructure

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Abstract： Chopping and salting are two important processing steps in emulsified meat products. Effects of chopping and salting on metabolic process, protein functionality, and ultrastructure of pre-rigor silver carp muscle, and how these three aspects changed during rigor transformation were explored. Chopping caused an accelerated loss of ATP, and salt addition inhibited accumulation of HxR and Hx. Similarly, chopping led to faster decrease of glycogen and increase in lactic acid, and salt exerted an inhibition effect. In agreement with ATP and glycogen breakdown, metabolic profiling revealed that chopping and salting altered the metabolism in fatty acids and amino acids during rigor transformation. After rigor transformation, chopping with salt led to significant reduction in radical scavenging ability, accompanied by greater loss of sulfhydryl groups. Salt also promoted protein denaturation, evidenced by increased surface hydrophobicity and decreased intrinsic fluorescence. The ultrastructure of fish muscle after chopping or chopping with salt was similar between pre- and post-rigor stages. The abovementioned findings can provide valuable insight into the production of fish products.

Key words:： pre-rigor; chopping; salting; metabolism; ultrastructure

高光谱成像技术在水产品品质检测应用研究进展

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摘要：高光谱成像（Hyperspectral Imaging, HSI）技术，融合了光谱分析与成像技术，能够同时捕捉样品的外部特征和内部分子结构及组成状态，达到对待测样品品质信息的可视化，从而实现在线检测的目的。因其无损、快速和精准的检测能力，HSI 技术已广泛应用于水产品品质检测等多个领域。本文阐述了 HSI 技术的基础原理和数据处理步骤，总结了该技术在水产品品质快速检测方面的国内外最新研究进展，涵盖了水产品种类鉴别与掺假鉴定、物理特性、化学指标、安全性以及冻融产品检测等五个方面。并且探讨了当前 HSI 技术在应用过程中所面临的瓶颈与挑战，对其在未来水产品品质检测中的潜在应用进行了展望,旨在能够实现水产品生产线上的自动化检测，从而推动水产品品质检测向更高层次的智能化和自动化发展。

关键词：高光谱；水产品品质；无损检测

Research Progress on The Application of Hyperspectral Imaging Technology in The Quality Detection of Aquatic products

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Abstract： Hyperspectral imaging (HSI) technology, which combines spectral analysis and imaging technology, can simultaneously capture the external characteristics of the sample and the internal molecular structure and composition state, to achieve the visualization of the quality information of the sample to be tested, achieve the purpose of online detection. Due to its non-destructive, rapid, and accurate detection capabilities, HSI technology has been widely used in many fields such as aquatic product quality detection. This paper expounds on the basic principle and data processing steps of HSI technology. It summarizes the latest research progress of this technology in the rapid detection of aquatic product quality at home and abroad, covering five aspects: species identification and adulteration identification of aquatic products, physical characteristics, chemical indicators, safety, and detection of freeze-thaw products.

Key words:： Hyperspectral ; Aquatic Product Quality ; Nondestructive Testing

基于机器学习的斑石鲷生长规律研究与视觉验证

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摘要：为了探究斑石鲷的生长规律，本研究从幼鱼早期阶段开始，对斑石鲷的长度、宽度和重量等生物量进行系统监测。在各个阶段生物量监测的同时，利用关键点检测模型、图像处理和三维重建算法获取精确的鱼体形态数据。通过长期监测和数据分析，研究斑石鲷在不同生长阶段的体长、体重及体型变化。此外，本研究将生长数据与喂养数据相结合，建立生长规律模型，并使用立体视觉获得的数据对模型进行验证。实验结果表明，立体视觉技术能够高效、准确地记录斑石鲷的生长数据，并揭示其在不同环境条件下的生长规律。这些发现为斑石鲷的养殖管理提供了科学依据，有助于优化养殖策略，提高养殖效率。研究还探讨了立体视觉技术在水产养殖中的应用前景，指出其在精准养殖、健康监测和生长评估等方面具有广泛的应用潜力。

关键词：立体视觉；生长规律；生物量；三维重建；关键点检测

Study and visual verification of growth rules of Maculatus maculatus based on machine learning

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Abstract： In order to explore the growth law of Porphyropleuron at all stages, this study systematically monitored the biomass of porphyropleuron, such as length, width and weight, starting from the early stage of juvenile fish. The key point detection model, image processing and 3D reconstruction algorithm were used to obtain accurate fish body morphology data during biomass monitoring at each stage. Through long-term monitoring and data analysis, the changes of body length, body weight and body shape in different growth stages were studied. In addition, this study combined growth data with feeding data to establish a growth law model, and verified the model using data obtained from stereo vision. The experimental results show that the stereo vision technology can record the growth data efficiently and accurately, and reveal its growth law under different environmental conditions. These findings provide scientific basis for the culture management of Porphyropomacris, and help to optimize the culture strategy and improve the culture efficiency. The paper also discusses the application prospect of stereovision technology in aquaculture, pointing out that it has a wide range of application potential in precision aquaculture, health monitoring and growth assessment.

Key words:：stereovision; growth law;biomass; three-dimensional reconstruction; keypoint detection

特定波长紫外线对投饵机料仓内饲料表面微生物灭菌效果研究

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摘要：试验旨在探究在高温高湿环境下，对比不同投饲机料桶密封程度的霉变情况，并通过不同紫外波长处理方式（180nm、254nm、270nm、395nm 和 270+395nm）研究饲料在投饲机内的长效保存方法。试验通过恒温恒湿箱提供 30℃、90%rh 的高温高湿环境，将四种密封程度的料仓模型（无开孔、顶部开孔、底部开孔、顶部和底部开孔）至于恒温恒湿箱一周，测量料仓顶部、底部表面菌落数量以及料仓内部湿度变化情况。结果表明：料仓内菌落数量随密封程度的增加而显著增长。在料仓无开孔和底部开孔时，料仓内湿度受密封程度影响不显著，而在顶部开孔和全开孔时，料仓内湿度受密封程度影响显著（$P<0.05$），全开孔时料仓内湿度接近环境湿度。紫外波长对饲料细菌杀菌能力为 185nm>254nm>365nm>270nm。紫外功率越大，杀菌速度越快。紫外照射距离 5-15cm 时，杀菌能力区别不显著，都具有良好的杀菌效果。

关键词：投饲机料仓；饲料；紫外；除湿

Study on bactericidal effect of specific wavelength ultraviolet light on feed surface microorganism in feed bin of feeder

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Abstract：The aim of this experiment was to compare the mildew of different sealing degree of feed barrel in feeders under high temperature and high humidity environment, and to study the long-term preservation method of feed in feeders by different ultraviolet wavelength treatments (180nm, 254nm, 270nm, 395nm and 270+395nm). The experiment provided a high temperature and humidity environment of 30℃ and 90%rh through a constant temperature and humidity chamber. Four types of sealed bin models (no openings, top openings, bottom openings, top and bottom openings) were placed in the constant temperature and humidity chamber for a week, and the number of colonies on the top and bottom surfaces of the silo and the changes in humidity inside the silo were measured. The results showed that the number of colonies in the silo increased significantly with the increase of sealing degree. The humidity in the bunker was not significantly affected by the degree of sealing when the bunker had no opening and the bottom opening, but was significantly affected by the degree of sealing when the bunker had the top opening and the full opening ($P<0.05$). The humidity in the bunker was close to the ambient humidity when the hole was fully opened. The bactericidal ability of ultraviolet wavelength to feed bacteria was 185nm>254nm>365nm>270nm. The higher the UV power, the faster the sterilization speed. When the UV irradiation distance is 5-15cm, the difference in bactericidal ability is not significant, and all have good bactericidal effect. The bactericidal effect of 185+254nm mixture is stronger than that of single wavelength. After irradiating the silo without opening holes for a week, the number of feed bacteria in the silo is always lower than the safety standard. In summary, under high temperature and high humidity environment, the silo should be sealed to the maximum extent, and regular ultraviolet disinfection can be taken in the silo to reduce the probability of feed mildew and avoid long-term storage.

Key words:：Feeder bin; Feed; Ultraviolet; dehumidification

基于 DEM-MBD 仿真的滩涂贝类振动采收设备设计与试验

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摘要：针对中国滩涂贝类采收机械化程度低、理论研究匮乏等问题，设计试制一种履带式滩涂贝类筛-刷协同振动采收设备。该研究以四角蛤蜊为研究对象，基于离散元法（Discrete Element Method）与多体动力学（Multi-Body Dynamics）耦合仿真方法开展滩涂贝类振动采收过程仿真研究。以设备的关键机构结构参数与运行参数为试验因素，以设备采收效率、贝类破碎率与漏采率为试验指标，完成滩涂贝类采收单因素与正交试验，求解得到设备最优值：滚刷螺旋升角为 40°、曲柄长度为 10mm、曲柄转速为 870rpm、一级螺旋滚刷转速为 65rpm、二级滚刷转速分别为 110rpm 时，设备采收效率为 938kg/h、贝类破碎率、漏采率分别为 5.25%、7.46%，采后滩涂底质有利于贝类可持续化养殖。该设备可满足滩涂贝类采收生产需求，为中国滩涂贝类机械化采收提供参考。

关键词：EDEM；ADAMS；机械化采收；滩涂；埋栖贝类

Design and testing of mudflat shellfish vibratory harvester based on DEM-MBD simulation

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Abstract：To tackle the low mechanization and limited theoretical research in shellfish harvesting on Chinese mudflats, a crawler-type device that coordinates screen and brush vibrations was designed and prototyped. This study centered on the White clam and used a coupled simulation method, combining the Discrete Element Method (DEM) and Multi-Body Dynamics (MBD), to model the vibrating shellfish harvesting process. Key structural and operational parameters of the device were considered as experimental factors. Harvesting efficiency, shellfish breakage rate, and missed harvest rate served as evaluation criteria. Single-factor and orthogonal experiments were conducted to determine the optimal device settings. The best performance was achieved with a spiral angle of 40° for the roller brush, a crank length of 10mm, a crank speed of 870 rpm, a first-stage roller brush speed of 65 rpm, and a second-stage roller brush speed of 110 rpm. Under these conditions, the device reached a harvesting efficiency of 938 kg/h, with a shellfish breakage rate of 5.25% and a missed harvest rate of 7.46%, thereby supporting sustainable shellfish farming. This device meets the production requirements for shellfish harvesting on tidal flats and offers a valuable reference for the mechanization of shellfish harvesting in China.

Key words:： EDEM; ADAMS; mechanized harvesting; mudflat; buried shellfish

立式螺杆内饲料颗粒随机运动与提升特性模拟与验证

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摘要：基于离散单元法，利用 EDEM 软件对立式螺杆内饲料颗粒运动的随机性与提升特性进行了模拟研究，分析了螺杆转速、拨杆旋转方向与速度对颗粒随机运动及提升特性的影响，并搭建实验样机进行性能验证。结果表明：螺杆转速的提高有利于改善饲料颗粒的随机运动过程，而且饲料颗粒的提升效果增强，提升速度加快。拨杆旋转方向对螺杆提料效果影响不显著，拨杆旋转速度低于螺杆转速时立式螺杆无法提料，拨杆速度必须大于等于螺杆转速才具有垂直提料效果。经样机现场验证，提料速度与仿真结果一致，出料误差低于 10%，能够实现垂直提升饲料功能。

关键词：饲料；立式螺杆；EDEM；随机运动；提升特性；模拟与验证

Simulation and verification of random motion and lifting characteristics of feed particles in a vertical screw

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Abstract： Based on the discrete unit method, the EDEM software was used to conduct a simulation study on the randomness and lifting characteristics of feed particles in the vertical screw. The effects of the screw speed, lever rotation direction and speed on the random movement and lifting characteristics of the particles were analyzed, and a Experimental prototype is used for performance verification. The results show that increasing the screw speed is beneficial to improving the random movement process of feed particles, and the lifting effect of feed particles is enhanced and the lifting speed is accelerated. The rotation direction of the lever has no significant effect on the screw lifting effect. When the lever rotation speed is lower than the screw speed, the vertical screw cannot lift materials. The lever speed must be greater than or equal to the screw speed to have a vertical material lifting effect. After on-site verification of the prototype, the feeding speed is consistent with the simulation results, the discharging error is less than 10%, and the feed function can be realized vertically.

Key words:： Fodder; Vertical screw; EDEM; Random motion; L:ifting characteristics; Simulation and verification

基于传统形态学和几何形态学的金乌贼内壳生长特性研究

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摘要：为了研究金乌贼内壳的生长特性，本文采用传统形态测量学与几何形态测量学两种方法，分析不同性别的金乌贼内壳生长的差异，传统形态测量结果显示，不同性别的金乌贼内壳形态参数存在显著差异，表现为雌性个体显著大于雄性个体，几何形态研究结果显示不同性别的金乌贼内壳形态不存在显著差异。对不同日龄的金乌贼内壳的生长进行分析，传统形态测量与几何形态测量的结果均显示不同日龄的内壳形态具有极显著差异，同时几何形态测量研究发现不同日龄组间的金乌贼内壳存在异速生长，该现象可能与乌贼内壳所具有的平衡力与浮力调节的作用有关。传统形态测量学可以直观地观察数据间的关系，几何形态测量学则可以更好的反映物体的形状变化规律，因此，本研究结合传统形态与几何形态两种形态测量学方法，可以更清晰地比较内壳形态的差异，能够更形象地从功能角度解读其差异性，为金乌贼的生物学研究提供基础。

关键词：金乌贼;内壳;传统形态;几何形态;生长特性

Characterization of the cuttlebone growth of Sepia esculenta based on traditional measurements and geometric morphometrics

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Abstract：In order to study the growth characteristics of the cuttlebone of the Sepia esculenta, this paper used two methods, traditional morphometrics and geometric morphometrics, to analyze the differences in the growth of the cuttlebone of the Sepia esculenta of different sexes.The results of the traditional morphometrics showed that there was a significant difference in the morphological parameters of the cuttlebone of the Sepia esculenta of different sexes, which manifested in the fact that the females were significantly larger than the males, and the results of geometric morphometrics study showed that there was no significant difference in the morphology of the cuttlebone between the sexes. The growth of the cuttlebone of the squid at different ages was analyzed, and the results of both traditional and geometric morphometric measurements showed that there were significant differences in the morphology of the cuttlebone at different ages, while the geometric morphometric study found that the cuttlebone of the squid at different ages had anisotropic growth, which may be related to the role of equilibrium and buoyancy regulation of the cuttlebone of the squid. Traditional morphometrics can visualize the relationship between data, while geometric morphometrics can better reflect the pattern of change in the shape of the object. Therefore, the present study combines the two morphometric methods of traditional morphometrics and geometric morphometrics, which can compare the differences in the morphology of the cuttlebone more clearly, and interpret the differences from a functional perspective in a more graphic manner, which can provide a basis for the study of the biology of the Sepia esculenta.

Key words:：Sepia esculenta;cuttlebone; traditional measurements; geometric morphometrics; growth characteristics

南海北部中国枪乌贼耳石日增量与环境因子关系

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摘要：根据 2016 年 4—6 月于南海北部采集的中国枪乌贼样本，采用梯度森林法筛选影响个体生长的关键环境因子，并通过广义加性模型(GAM) 建立耳石日增量与关键环境因子的关系，分析环境因子对个体生长的影响。结果表明: 研究中的中国枪乌贼孵化于 2015 年 10 月—2016 年 1 月，孵化高峰期为 11—12 月; 海表面温度(SST) 、25 m 水深温度(T25) 和海表面盐度 (SSS) 是影响枪乌贼产卵群体的关键环境变量。SST 为 23 ～ 28 ℃时，耳石日增量宽度随着 SST 的增加呈下降趋势。当 T25 为 23 ～ 28 ℃ 时，耳石日增量宽度随着 T25 的增加呈现逐渐下降的趋势。当 SSS 为 33． 2 ～ 33． 8 时，耳石日增量随着 SSS 的增加呈现逐渐下降的趋势。根据结果可以推断，水温和盐度对中国枪乌贼的生长影响显著。

关键词：中国枪乌贼; 南海北部; 耳石日增量; 环境因子

Relationship between statolith daily increment of Uroteuthis chinensis and environmental factors in the Northern South China Sea

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Abstract： According to the samples of Chinese squid (Uroteuthis chinensis) collected in the Northern South China Sea from April to June 2016，using the gradient forest method to screen the key environmental factors which affect individual growth，the relationship between daily increment of statolith and key environmental factors was established through the generalized additive model to analyze the impact of environmental factors on individual growth. The results showed that the squids hatched from October 2015 to January 2016，and the hatching peak was from November to December; sea surface temperature(SST) ，temperature of 25 m(T25) and sea surface salinity(SSS) are the key environmental variables affecting the spawning population of the squids . When SST changed in the range of 23 to 28 ℃ ， the daily increment width of statolith decreased with the increase of SST. When T25 changed in the range of 23 to 28 ℃，the daily increment width of statolith showed a gradual downward trend with the increase of T25 . When SSS changed in the range of 33． 2 to 33． 8，the daily increment of statolith decreased gradually with the increase of SSS . It can be inferred from the results that water temperature and salinity have significant effects on the growth of squids.

Key words:： Uroteuthis chinensis; Northern South China Sea; daily increment of statolith; environmental factor

绍兴市上虞区南美白对虾养殖 SWOT 分析及发展对策

林桢
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摘要：本文从养殖面积、养殖模式、养殖苗种、养殖群体四方面介绍了绍兴上虞南美白对虾养殖现状，并基于 SWOT 分析法对绍兴上虞南美白对虾产业发展的比较优势、相较劣势、当前机遇与存在威胁进行分析，认为上虞在南美白对虾产业化养殖发展中既拥有海涂资源丰富、产业配套完善、市场腹地广阔、营商环境良好、民间资本充足的优势，也存在养殖条件欠佳、发展起步较晚的劣势；既面临国产苗种技术突破、各级政策予以支持的机遇，也不可避免直面养殖成本急剧增加、无序竞争依旧存在、自贸协定巨大冲击、极端气候雪上加霜的威胁。基于此，研究从提升苗种质量、提高养殖技术、加强病害防治、延长产业链条对未来绍兴上虞南美白对虾养殖可持续发展提出意见建议。

关键词：绍兴上虞；南美白对虾；SWOT 分析法

SWOT Analysis and Development Strategies on the Aquaculture of Penaeus Vannamei in Shangyu District Shaoxing City

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Abstract： This article introduces the current situation of the aquaculture of Penaeus vannamei in Shangyu District Shaoxing City from four aspects: aquaculture area, aquaculture mode, aquaculture seedlings, and aquaculture groups. Based on the SWOT analysis method, it analyzes the comparative advantages, disadvantages, opportunities, and threats of the development of Penaeus vannamei industry in Shangyu District Shaoxing City. It is believed that Shangyu has the advantages of abundant coastal resources, complete industrial supporting facilities, broad market hinterland, good business environment, and sufficient private capital in the industrialization of Penaeus vannamei farming. However, it also has the disadvantages of inadequate aquaculture conditions and slow initial development. Moreover, it not only faces the opportunities of breakthroughs in domestic seedling technology and support from policies at all levels, but also inevitably faces the threats of sharp increases in breeding costs, the persistence of disorderly competition, the huge impact of free trade agreements, and extreme weather conditions. For the above-mentioned reasons, the study provides opinions and suggestions on the future sustainable development of Penaeus vannamei farming in Shangyu, Shaoxing from improving the quality of seedlings and aquaculture technology, strengthening disease prevention and extending the industrial chain.

Key words:： Shangyu District Shaoxing City, Penaeus vannamei, SWOT analysis method

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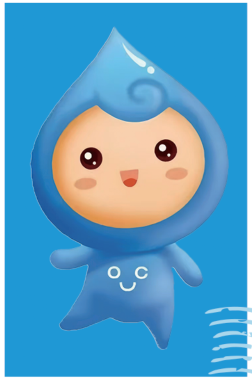

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