2025年中国水产学会青年学术年会

—— 渔业创新　青年担当 ——

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河南·新乡
2025年9月16–19日

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甲壳对克氏原螯虾（*Procambarus clarkii*）贮藏期间肌肉品质的影响机制解析

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摘要：本研究旨在探讨煮熟的克氏原螯虾（*Procambarus clarkii*）在冷冻存储过程中质量变化，重点分析了在−20℃下存储 120 天期间，虾肉的理化特性和代谢变化。研究还比较了去壳与保壳样品的差异，评估外骨骼去除对虾肉质量的影响。结果表明，随着存储时间的延长，去壳组和保壳组的虾肉水分含量、持水能力（WHC）及 pH 值均显著下降（$P < 0.05$）。去壳处理加速了虾肉的质量劣化，表现为 TBARS 和 TVB-N 值的显著升高。保壳组在储存过程中表现出更好的质地保持、湿度保持及整体质量，且其感官特性，如硬度、咀嚼性和弹性等优于去壳组。代谢组学分析表明，去壳组的氧化稳定性相关代谢物发生显著变化，进一步支持了去壳样品质量恶化的现象。微观结构分析显示，保壳组的肌原纤维蛋白结构保持较好，表明外骨骼对冰晶形成所引起的结构损伤具有保护作用。综上所述，外骨骼的存在显著提升了克氏原螯虾肉质在冷冻存储过程中的质量保持，强调了保留外壳在优化存储条件、维持产品质量方面的重要性。

关键词：克氏原螯虾；甲壳；肉质；氧化稳定性；代谢组学

Unraveling of the effect on crayfish (*Procambarus clarkii*) muscle quality affected by shell among the storage

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Abstract: This study focused on the quality changes of cooked crayfish (*Procambarus clarkii*) during frozen storage, analyzing key physicochemical and metabolic alterations under the storage conditions of −20 °C for 120 days. The impact of shell removal on the quality of crayfish meat was also examined by comparing shell-intact and shell-removed samples. The results indicated that with the extension of storage time, the moisture content, water-holding capacity (WHC), and pH of crayfish meat decreased significantly ($P < 0.05$) in both the shelled and unshelled groups. The removal of the exoskeleton accelerated the deterioration of the meat, as evidenced by increased TBARS and TVB-N levels. The shell-intact group exhibited superior preservation of texture, moisture retention, and overall quality during storage, with better sensory attributes, including hardness, chewiness, and resilience, compared to the shell-removed group. Metabolomic analysis revealed significant shifts in oxidative stability-related metabolites, further supporting the accelerated quality deterioration in the shell-removed samples. Additionally, microstructural analysis showed that the integrity of myofibrillar proteins was better maintained in the shell-intact group, reflecting the protective role of the exoskeleton in mitigating the structural damage caused by ice crystal formation. In conclusion, the presence of the exoskeleton significantly improves the quality preservation of crayfish meat during frozen storage, emphasizing the importance of shell retention for optimizing storage conditions and maintaining product quality.

Key words: cooked crayfish (*Procambarus clarkii*); shell retention; meat quality; oxidative stability; metabolic profiles

预制淡水鱼制品中的腥异味形成途径与消减策略

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摘要：近年来，淡水鱼作为预制鱼制品原料受到广泛关注。然而，淡水鱼通常被认为比海水鱼具有更明显的腥味和土腥味，这限制了其进一步发展和消费者接受度。因此，需通过有效控制腥味来提升淡水鱼在预制鱼制品中的应用价值及消费者接受度。本汇报将综述预制淡水鱼制品（调理鱼片和鱼糜制品）中的主要腥味物质、其形成机制及控制方法，并深入探讨了全面理解腥味形成机制及实施有效控腥策略面临的挑战。研究认为，异味物质主要由微生物作用、蛋白质降解和脂质氧化产生。通过减少原料中的风味前体物质（净化或漂洗处理）及采用适当加工方法（添加外源物质、热加工与非热加工技术、食品包装），可显著降低调理鱼片和鱼糜制品的腥味。此外，需重点关注异味物质的浓度与阈值对淡水鱼及其制品风味特性的影响，以及水产品体系中香气释放的体内动态。本研究将为控制淡水鱼制品腥味提供理论支持，并推动相关产业的创新发展。

关键词：预制鱼制品；鱼糜制品；鱼腥味；风味形成与释放；风味调控

Fishy odorants in pre-processed freshwater fish products: Formation mechanism and control methods

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Abstract: Freshwater fish are generally considered to have a heavier fishy and earthy smell than marine fish, thus restricting their further development and consumer acceptance. This suggests that the fishy odor should be effectively controlled to enhance the application of freshwater fish in pre-processed fish products as well as improve consumer acceptability. The compounds associated with off-flavors are mainly generated by microbial action, protein degradation, and lipid oxidation. Fishy smell reduction for pre-processed fish fillets and surimi products can be largely achieved by decreasing flavor precursors in raw materials (purifying or rinsing treatment) and adopting appropriate processing methods (adding exogenous substances, thermal and non-thermal, and using food package). Additionally, more attention should be paid to the influence of the concentration and threshold of odor substances on the odor properties of freshwater fish and their products, and the effects of in vivo aroma releases in aquatic-based food systems.

Key words: Pre-processed fish products; Surimi-based products; Fishy odors; Formation; Flavor retention and release; Regulation

不同阶段黄河鲤肌肉 LC-PUFAs 和挥发性风味物质沉积特性研究

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摘要：为探究不同阶段黄河鲤（*Cyprinus carpio L.*）长链多不饱和脂肪酸（LC-PUFAs）和挥发性风味物质（VOCs）沉积特性，我们系统追踪了全周期养殖中小规格（SYRC，~100 g）、中规格（MYRC，~250 g）和大规格鱼（HYRC，~600 g）肌肉营养成分、质构特性及 VOCs 的动态变化。结果表明，与 SYRC 组相比，HYRC 组水分和脂质含量降低，蛋白质、羟脯氨酸和硬度增加（$P<0.05$）。MYRC 组 LC-PUFAs 及脂质品质低于 SYRC 和 HYRC（$P<0.05$）。HYRC 和 MYRC 组醇类和呋喃类物质含量高于 SYRC 组（$P<0.05$）。综上所述，SYRC 具有较高的 LC-PUFA 和较低的硬度；MYRC 具有较低的 LC-PUFAs；HYRC 展示了营养、质地和 VOCs 最佳窗口期，但需避免不良 VOCs 的过度积累。本研究为黄河鲤品质优化、加工及消费指南提供了理论依据和数据支持。

关键词：黄河鲤；养殖；LC-PUFA 沉积；挥发性风味化合物；营养价值与质构；个体发育

Deposition Characteristics of LC-PUFAs and Volatile Flavor Compounds in Muscle Tissue of Yellow River Carp at Different Growth Stages

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Abstract: To investigate the deposition of long-chain polyunsaturated fatty acids (LC-PUFAs) and volatile organic compounds (VOCs) in different growth stages of Yellow River carp (*Cyprinus carpio L.*), we systematically tracked the dynamic changes in nutritional composition, texture, and VOCs during the full-cycle aquaculture of small (SYRC, ~100 g), medium (MYRC, ~250 g), and large fish (HYRC, ~600 g). Compared to SYRC, HYRC exhibited decreased moisture and lipid content, while protein, hydroxyproline, and hardness increased ($P < 0.05$). MYRC had lower levels of LC-PUFAs and lipid quality compared to SYRC and HYRC ($P < 0.05$). The contents of alcohols and furans were higher in HYRC and MYRC than in SYRC ($P < 0.05$). In conclusion, SYRC demonstrated higher levels of LC-PUFA content and lower hardness; MYRC exhibited lower LC-PUFAs; HYRC presented represented the optimal stage in terms of nutrition, texture, and VOCs, though excessive accumulation of undesirable VOCs should be avoided. These results offer a foundation for quality improvement and consumption guidance.

Key words: Yellow river carp; cultivated; LC-PUFAs deposition; volatile flavor compounds; nutritional value and texture; ontogenetic development

氨氮应激对鱼肌肉品质的影响及调控措施

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摘要：氨氮是一类重要的应激源。氨氮暴露可显著诱发应激反应，表现为血液生化指标异常以及鳃、头肾、肾脏和肝脏等组织结构损伤；同时，随着氨氮浓度升高和暴露时间延长，鱼体肌肉的滴水损失显著增加，剪切力则逐渐下降。运输前实施短期禁食（2–3 天）能够有效缓解应激，皮质醇和超氧化物歧化酶水平分别降低 28.60%和 55.39%，并显著改善肌肉的持水性、剪切力和弹性。然而，禁食时间延长至 4 天会导致能量物质消耗加剧、氧化损伤增加，从而造成肌肉品质下降。为控制运输过程中水体氨氮的积累，将制备的壳聚糖负载镁生物炭微球（CS-Mg-SB-M）添加至运输水体中，可有效去除 33–53%的氨氮，使鱼体存活率提高 40–60%，并显著改善运输后肌肉品质。综上，氨氮暴露是造成运输过程中团头鲂肌肉品质劣变的重要因素，而运输前短期暂养和水体中添加氨氮吸附材料是缓解运输应激、提高成活和改善肌肉质量的有效策略。

关键词：氨氮暴露；肌肉品质；运输

Effects of Ammonia Nitrogen Stress on Fish Muscle Quality and Regulatory Measures

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Abstract: Ammonia nitrogen is a significant stressor. Exposure to ammonia nitrogen triggers pronounced stress responses, characterized by abnormal biochemical indicators and tissue structural damage in gills, head kidneys, kidneys, and liver. Additionally, as ammonia nitrogen concentrations rise and exposure time extends, fish muscle experiences increased drip loss and decreasing shear force. Implementing short-term fasting (2–3 days) prior to transportation effectively mitigates stress, reducing cortisol levels by 28.60% and superoxide dismutase levels by 55.39%. This improves muscle water retention, shear force, and elasticity. However, extending fasting to 4 days results in greater energy consumption and increased oxidative damage, leading to reduced muscle quality. To control ammonia nitrogen accumulation during transportation, adding chitosan-loaded magnesium biochar microspheres (CS-Mg-SB-M) to the transport water removes 33–53% of ammonia nitrogen, increasing survival rates by 40–60% and significantly improving post-transport muscle quality.

Key words: Ammonia nitrogen exposure；Fish muscle quality；Transportation

揭示中国内陆休闲渔业的空间分异：多源异构数据的新见解

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摘要：内陆休闲渔业在创造经济价值、提供就业及补充营养方面至关重要。本研究整合企业工商注册、地理兴趣点及垂钓应用程序数据，运用空间统计模型分析中国内陆休闲渔业的空间分异，重点关注垂钓点特征与分布、放养鱼类、垂钓活动水平及相关服务。主要结果：（1）垂钓点呈 “东密西疏、多核集聚” 格局，92.99% 位于胡焕庸线以东，高密度区在城市服务圈和水文丰富区；（2）池塘垂钓（66.77%）、旅游导向型垂钓、河湖水库垂钓空间异质，池塘垂钓占主导；（3）呈金字塔规模结构，小微企业（91.28%）填补城乡休闲空白，大中型企业沿主要经济走廊集中；（4）超 60% 站点放养鲫鱼、鲤鱼或草鱼，多物种高密度放养区在沿海省份（江苏、浙江、山东）及内陆水产养殖中心（湖北、湖南）；（5）垂钓活动水平空间集聚，四川、广东、江苏为热点，“垂钓 +” 模式融合餐饮、划船及社交娱乐，形成 “微度假” 范式。

关键词：休闲渔业；内陆休闲垂钓；空间分异；多源数据融合

Unveiling spatial differentiation of China’s inland recreational fishing: novel insights from multi-source data

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Abstract: Inland recreational fishing (IRF) matters for economy, employment and nutrition. This study integrates business registration, POI and angling app data, using spatial models to analyze China's IRF spatial patterns, examining sites, stocked fish, activity levels and related services.Key findings: (1) IRF sites show "east-dense, west-sparse, multi-core clustering"; 92.99% lie east of the Hu Line, with high-density cores in urban service circles and hydrologically rich areas. (2) Three types (pond, tourism-oriented, river-lake-reservoir angling) differ spatially; pond angling dominates (66.77%). (3) A pyramid structure: small/micro sites (91.28%) fill urban-rural leisure gaps, while medium/large ones cluster along major economic corridors. (4) Over 60% stock crucian carp, carp or grass carp; multi-species hotspots in coastal provinces (Jiangsu, Zhejiang, Shandong) and inland hubs (Hubei, Hunan). (5) Angling activity clusters spatially, with Sichuan, Guangdong and Jiangsu as hotspots. China's "angling+" model merges catering, boating and social recreation into single-day micro-vacations.

Key words: Recreational fisheries; Inland recreational fishing; Angling sites; Spatial differentiation; Multi-source data integration

全球休闲渔业的经济维度：基于 PRISMA 的系统综述

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摘要：休闲渔业在全球范围内发挥着至关重要的作用，创造了大量的就业机会和收入。然而，尽管有许多案例研究，但对休闲渔业经济的系统和比较理解仍然有限。基于综述，我们将论文分为三个关键领域——经济和消费者行为、资源利用和管理以及环境和生态效应。结果表明：（1）休闲渔业经济的发展呈现出全球两极分化，高收入国家在资源管理和政策支持方面表现出色，而中等收入和低收入国家则面临资源利用和基础设施不足的挑战。（2）环境保护支付意愿、消费者剩余和出行成本法估算是经济贡献和消费者行为分析的关键研究方向。（3）单位捕捞量和袋限值是减轻休闲渔业捕捞压力的基本管理工具。通过实施长期的资源保护措施，管理当局可以维持休闲渔业的经济可行性。（4）生态保护、恢复和环境治理产生直接的经济效益，这是政府管理机构越来越重视的一个因素。本文旨在综合全球休闲渔业经济研究成果，借鉴发达国家成功模式为欠发达地区提供参考。

关键词：休闲渔业；系统评价；经济影响；PRISMA；渔业管理

Economic dimensions of global recreational fisheries: A PRISMA-based systematic review

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Abstract: Recreational fisheries play a crucial role worldwide, generating substantial employment and income. Based on this review, we categorized the papers into three key domains—economic and consumer behavior, resource utilization and management, environmental and ecological effects. The results showed that (1) The development of the recreational fishery economy exhibits global polarization, with high-income nations excelling in resource management and policy support, while middle-income and low-income countries face challenges in resource utilization and inadequate infrastructure. (2) Willingness to pay for environmental protection, consumer surplus and travel cost method estimation represent key research directions in economic contributions and consumer behavior analysis. (3) Catch per unit effort and bag limits serve as fundamental management tools to mitigate fishing pressure in recreational fisheries. (4) Ecological protection, restoration, and environmental governance yield direct economic benefits.

Key words: Recreational fisheries; Systematic review; Economic impact; PRISMA; Fisheries management

水下声学技术在水下生物监测、预警与定位遥测中的关键技术及应用

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摘要：聚焦于声学技术在水下的优势，借助 NEO-SV 声呐与配套数据处理机、超声波遥测这三项技术实现海洋生物的监测、预警和定位。声呐作为基础感知手段，负责探测并获取原始水下目标信息，数据处理机对声呐回波进行高效分析，精确识别目标特征和位置；超声波遥测利用声波在水中传播的优势，实现目标的可靠定位、跟踪及数据的远程传输。三者紧密协作，构成了从数据获取、分析到应用与传输的完整链条，显著提升了水下生物监测系统的精准性和实时性，为江河湖海生态保护和资源管理提供了有力技术支持。

关键词：声呐；水下生物监测；水下目标定位

Key Technologies and Applications of Underwater Acoustics in the Monitoring, Early-Warning, and Remote Localization of Underwater Organisms

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Abstract: Leveraging the inherent strengths of underwater acoustics, we integrate NEO-SV sonar, a dedicated data-processing unit, and ultrasonic telemetry to monitor, warn, and localize marine organisms. The sonar serves as the primary sensor, detecting and capturing raw underwater target information. The data-processing unit rapidly analyzes the sonar echoes to accurately identify target characteristics and positions. Ultrasonic telemetry exploits the efficient propagation of sound in water to achieve reliable target localization and tracking while enabling remote data transmission. Together, these three components form a seamless chain—from data acquisition and analysis to application and transmission—greatly enhancing the precision and real-time capability of underwater biological monitoring systems and providing strong technical support for the conservation and resource management of rivers, lakes, and oceans.

Key words: Sonar; Underwater Biological Monitoring; Underwater Target Localization

Hox 基因 Abd-A 调控拟穴青蟹（*Scylla paramamosain*）幼体腹肢发育的分子机制

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摘要：螃蟹广泛分布于从珊瑚礁、热液喷口到陆地栖息地等多种生态系统中。尽管其在生态系统中具有重要地位，但关于其发育过程背后的遗传机制仍了解有限。本研究采用超长读长测序技术对青蟹进行了系统的基因组分析，成功构建了一个高质量的染色体水平基因组组装体。优化后的基因组大小为 1.21Gb，Contig N50 长度达到 11.45Mb，为后续的遗传与进化研究提供了宝贵的基因组资源。基因家族分析结果显示，与发育相关的信号通路呈现扩张趋势，而代谢相关通路则表现出收缩特征，这可能反映了青蟹对其生态环境的适应性演化。值得注意的是，Hox 基因家族的调控机制分析揭示了其在腹肢发育过程中的关键作用，其中 Abd-A 基因被鉴定为调控腹肢发育的核心因子。此外，miR-1317 介导的转录后调控机制被发现对 Abd-A 基因的表达具有负调控作用。

关键词：基因组；拟穴青蟹；早期发育

Molecular Mechanism of Hox Gene Abd-A in the Development and Regulation of Pleopods in Mud Crab (*Scylla paramamosain*) Larvae

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Abstract：Crabs thrive in diverse ecosystems, from coral reefs to hydrothermal vents and terrestrial habitats. Here, we report a comprehensive genomic analysis of the mud crab using ultralong sequencing technologies, achieving a high-quality chromosome-level assembly. The refined 1.21 Gb genome, with an impressive contig N50 of 11.45 Mb, offers a valuable genomic resource. Gene family analysis shows expansion in development-related pathways and contraction in metabolic pathways, indicating niche adaptations. Notably, Investigation into Hox gene regulation sheds light on their role in pleopod development, with the Abd-A gene identified as a linchpin. Posttranscriptional regulation involving novel-miR1317 negatively regulates Abd-A levels.

Key words: whole genome; Scylla paramamosain; early development

GRP94 介导的内质网应激调控及其在小黄鱼肝脏高温应激中的保护机制

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摘要：为阐明高温胁迫对小黄鱼(*Larimichthys polyactis*)肝脏基因表达的影响及其分子机制。本研究对高温(32℃)处理 6 h 的小黄鱼肝脏进行转录组和蛋白质组联合分析，结果显示，大多数显著差异表达的基因/蛋白都富集在内质网蛋白质加工通路。利用 qPCR 技术进一步分析了该通路关键基因(grp94, ire1α)在高温胁迫下不同时间点的 mRNA 表达规律。结果表明，grp94 和 ire1α 随着 32℃高温处理时间的延长，呈先升高后下降的变化趋势。为进一步阐明该通路关键基因的响应机制，在成功建立小黄鱼肝细胞体系的基础上，发现高温显著抑制肝细胞的增殖。通过调控肝细胞中 grp94 的表达，发现这种干预在高温条件下显著影响了细胞活力、氧化应激水平、凋亡进程以及 ire1α的表达。本研究揭示了高温胁迫后内质网应激通路中关键调控因子的响应机制，为深入理解鱼类热适应机制提供了重要理论依据。

关键词：小黄鱼；高温应激；内质网应激；细胞凋亡相关基因

GRP94-Mediated Endoplasmic Reticulum Stress Regulation Modulates Hepatic Heat Stress Response in *Larimichthys polyactis*

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Abstract： To elucidate the impact of high-temperature stress on hepatic gene expression in Larimichthys polyactis and its molecular mechanisms, we performed combined transcriptomic and proteomic analysis on liver samples from fish subjected to 32°C for 6 hours. Results showed significant enrichment of differentially expressed genes/proteins in the endoplasmic reticulum protein processing pathway. Subsequent qPCR analysis of key genes (grp94, ire1α) revealed their expression initially increased and then decreased over time under 32°C stress. Using an established hepatocyte model, we observed that high temperature markedly suppressed cell proliferation. Modulation of grp94 expression significantly influenced cell viability, oxidative stress, apoptosis, and ire1α levels under thermal stress. These findings reveal key regulatory mechanisms of the endoplasmic reticulum stress response to high temperature, providing a theoretical basis for understanding thermal adaptation in fish.

Key words: *Larimichthys polyactis*; High-temperature stress; Endoplasmic reticulum stress; Apoptosis-related genes

变形假单胞菌感染期间小黄鱼（*Larimichthys polyactis*）肝脏损伤及凋亡通路的时间动态变化

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摘要：小黄鱼是一种具有重要经济价值的海水鱼类，然而目前对其响应变形假单胞菌感染的防御机制尚不清楚。本研究整合组织病理学、生物化学、转录组学和蛋白质组学分析方法，旨在揭示变形假单胞菌注射感染后小黄鱼肝脏响应的时间动态变化规律。组织病理学结果显示，在感染后 72 小时和 96 小时，受感染的肝脏中出现肉芽肿性结节。生物化学检测表明，感染过程中肝脏损伤呈渐进性发展，且机体持续处于氧化应激状态。TUNEL 检测显示，感染后 72 小时和 96 小时肝脏组织存在显著的细胞凋亡现象。转录组学和蛋白质组学分析筛选出不同感染阶段特异性的分子应答特征。利用 RT-qPCR 和 WB 进一步验证结果表明，内质网应激诱导的细胞凋亡在小黄鱼抵抗细菌感染过程中发挥关键作用。本研究结果有助于深入理解小黄鱼抵御变形假单胞菌感染的分子机制，同时为减轻海水鱼类养殖过程中由该病原菌引发的感染损失提供理论参考。

关键词：小黄鱼；内脏白点病；全基因组关联分析；转录组；干扰素基因刺激因子 1

Temporal dynamics of liver injury and apoptotic pathways in small yellow croaker (*Larimichthys polyactis*) during Pseudomonas plecoglossicida infection

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Abstract： The small yellow croaker is an economically significant marine fish species that faces substantial threats from Pseudomonas plecoglossicida. This study integrated histopathological, biochemical, transcriptomic, and proteomic analyses to reveal the temporal dynamics of the liver response in L. polyactis following injection with P. plecoglossicida. Histopathological examination revealed granulomatous nodules in the infected liver at 72 and 96 hours post-infection (hpi). Biochemical assays indicated progressive liver injury and sustained oxidative stress. TUNEL assays conformed significant apoptosis at 72 and 96 hpi. Transcriptomic and proteomic profiling identified stage-specific molecular responses. Further validation using RT-qPCR and Western blot highlighted the critical role of endoplasmic reticulum stress (ERS)-induced apoptosis in resisting bacterial infection. These findings enhance our understanding of the molecular mechanisms underlying host defense against P. plecoglossicida and provide insights for mitigating infection-related losses in marine fish aquaculture.

Key words: *Larimichthys polyactis*, Pseudomonas plecoglossicida, liver, transcriptome, proteome, apoptosis

克氏原螯虾前列腺素 E2 合成酶（PGES）基因的 cDNA 克隆及其在卵巢发育中的功能分析

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摘要：为了揭示了克氏原螯虾（*Procambarus clarkii*）前列腺素 E_2合成酶基因（PcPGES）调控其卵巢发育的分子机制，本研究通过 RACE 技术克隆获得了该基因的 1678 bp 的全长 cDNA 序列，其开放阅读框编码一种由 410 个氨基酸组成的具有 TRX 和 GST 结构域的胞质型蛋白。qRT-PCR 分析表明 PcPGES 基因在肌肉、心脏及卵巢中高表达，且在 V 期卵巢中表达量最高。荧光原位杂交与免疫组化证实其 mRNA 及蛋白均定位于卵原细胞、卵母细胞及滤泡细胞的细胞质中。RNA 干扰表明 PcPGES 沉默抑制 PcCOX 及卵黄合成关键基因 PcVg 和 PcVgr 的表达以及 PGE_2的合成，并延缓卵母细胞发育。注射外源 AA 或 PGE_2激活 AA-COX-PGES-PGE_2通路促进卵黄沉积，而注射 DEX 则相反。上述结果证实 PcPGES 通过催化 PGE_2合成来调控克氏原螯虾的卵巢发育过程。

关键词：克氏原螯虾，前列腺素 E_2合成酶，卵巢发育，RNA 干扰，信号通路

Prostaglandin E2 synthetase (PGES) gene from *Procambarus clarkii*: cDNA cloning and functional analysis in ovarian development

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Abstract： To reveal the molecular mechanism by which prostaglandin E_2 synthase gene (PcPGES) regulates ovarian development in Procambarus clarkii, the full-length PcPGES cDNA (1678 bp) was cloned via RACE technology, with its open reading frame encoding a 410-amino acid cytosolic protein containing TRX and GST domains in this study. qRT-PCR analysis showed that the gene was highly expressed in muscle, heart and ovary, with the highest expression in stage V ovary. Fluorescence in situ hybridization and immunohistochemistry confirmed the localization of its mRNA and protein to cytoplasm of oogonia, oocytes, and follicular cell. RNA interference indicated that PcPGES silencing inhibited the expressions of PcCOX as well as vitellogenesis-related genes PcVg and PcVgr, reduced the synthesis of PGE_2, and delayed oocyte development. The injection of exogenous AA or PGE_2 activated the AA-COX-PGES-PGE_2 pathway to promote vitellin deposition, while DEX injection had the opposite effect. These results confirm that PcPGES regulates ovarian development in Procambarus clarkii by catalyzing PGE_2 biosynthesis.

Key words: *Procambarus clarkii*; Prostaglandin E2 synthetase; Ovarian development; RNA interference; Signaling pathway

许氏平鲉(*Sebastes schlegelii*)卵干细胞的原代培养：形态和转录组研究

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摘要：许氏平鲉（Sebastes schlegelii）是一种海洋卵胎生硬骨鱼，具有明显的性别二态性，雌性生长速度更快且体型更大。建立稳定的卵原干细胞体外培养体系（OSCs）对于理解生殖系干细胞的动态变化以及实现全雌性繁殖至关重要。在本研究中，我们成功地从许氏平鲉中分离并培养了 12 代的卵原干细胞。这些细胞表现出碱性磷酸酶活性，表达生殖细胞标记基因（ddx4、cdh1、klf4），并保持二倍体核型（2n = 48）。早期（P3）和晚期（P12）传代细胞的转录组比较显示，晚期传代细胞存在显著的代谢功能障碍和细胞周期停滞。具体而言，谷胱甘肽相关和糖酵解相关基因（gstm3、gstt1、mgst3、gsta1、gsta4、gsto1、gapdh）以及关键有丝分裂调节因子（cdk1、chk1、cdk4、e2f3、ccne2、ccnb1）的下调表明代谢失衡导致氧化应激，从而抑制细胞周期并最终导致衰老。

关键词：许氏平鲉；卵原干细胞；原代培养；细胞代谢；细胞周期

The Primary Cultivation of Oogonial Stem Cells from Black Rockfish (*Sebastes schlegelii*): Morphology and Transcriptome Landscape

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Abstract： Black rockfish (*Sebastes schlegelii*) is a marine ovoviviparous teleost that exhibits significant sexual dimorphism, with females growing faster and reaching larger sizes than males. Establishing stable oogonial stem cells (OSCs) is critical for understanding germline stem cell dynamics and facilitating all-female breeding. In this study, we successfully isolated and cultured OSCs from S. schlegelii for 12 passages. These cells exhibited alkaline phosphatase activity, expressed germline marker genes (ddx4, cdh1, klf4), and maintained a diploid karyotype (2n = 48). Transcriptomic comparisons be-tween early (P3) and late (P12) passages revealed significant metabolic dysfunction and cell cycle arrest in the late-passage cells. Specifically, the down-regulation of glu-tathione-related and glycolysis-related genes (gstm3, gstt1, mgst3, gsta1, gsta4, gsto1, gapdh) and key mitotic regulators (cdk1, chk1, cdk4, e2f3, ccne2, ccnb1) suggested that metabolic imbalance contributes to oxidative stress, resulting in cell cycle inhibition and eventual senescence.

Key words: *Sebastes schlegelii*; oogonial stem cell; primary cultivation; cell metabolism; cell cycle

水产动物循环免疫细胞吞噬与凝血功能的演化与保守机制

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摘要：先天免疫的细胞组成与防御机制在原口与后口动物谱系中呈现多样性分化，以应对不同环境压力。吞噬作用与凝血反应是先天免疫防御的核心机制。本研究通过构建涵盖多个不同进化节点水生生物的血细胞图谱，追溯了双侧对称动物中具有吞噬与凝血功能的细胞谱系进化历程。在水生无脊椎动物中(包括南美白对虾、香港巨牡蛎和玻璃海鞘)鉴定的吞噬样细胞群与脊椎动物髓系细胞共享 TFE/MiT 转录因子家族及其协调的吞噬功能基因网络，该程序可能是吞噬能力遗传的核心调控程序。值得注意的是，我们在无脊椎动物中定义了与血小板功能相当的特定细胞类型。尽管这些细胞表达独特的凝血分子，但展现出广泛的凝血响应能力，体现了功能的趋同性。该研究揭示了吞噬与凝血机制在双侧对称动物谱系中的进化保守性，既保留了共同的分子框架，也呈现出谱系特异性的适应性变化，为理解水产生物免疫系统的功能维持机制提供了重要依据。

关键词：循环免疫细胞；单细胞转录组测序；吞噬作用；凝血作用

Evolutionary conservation and divergence of phagocytic and coagulation programs across bilaterian circulating immune cells

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Abstract： Innate immunity's cellular components and defenses diversify across protostome and deuterostome lineages to adapt to environmental challenges. Phagocytosis and coagulation are core immune mechanisms. By constructing a cross-species cellular hierarchy of hemolymph/blood, we reconstructed the evolution of phagocytic and coagulative cell lineages in bilaterians. In invertebrates, phagocytic-like cells shared a TFE/MiT transcription factor network and phagocytic program with vertebrate myeloid cells, indicating a conserved regulatory basis for phagocytosis. We also defined invertebrate cell types functionally equivalent to platelets. Although these cells express unique coagulation molecules, they exhibit extensive coagulation responses, indicating functional convergence. This study reveals evolutionary conservation of phagocytic and coagulative mechanisms across bilaterians, involving both conserved and lineage-specific adaptations that maintain essential immune functions.

Key words: Circulating immune cells, Phagocytosis, Coagulation

克氏原螯虾前列腺素内过氧化物合酶（PTGS）基因的分子鉴定及其在卵巢发育中的作用

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摘要：前列腺素内过氧化物合酶（PTGS）是前列腺素合成的关键酶。为了研究 PTGS 基因对克氏原螯虾卵巢发育的作用，本研究克隆出了克氏原螯虾 PTGS（PcPTGS）基因 cDNA 序列（3262 bp），其开放阅读框 1830 bp，编码 609 个氨基酸组成的具有表皮生长因子结构域和动物血红素过氧化物酶结构域的蛋白。qRT-PCR 结果表明，在 I-VI 期的卵巢中，PcPTGS 基因在Ⅴ期卵巢中的表达量最高。免疫组化实验表明，PcPTGS 蛋白主要定位于 I–V 期卵巢的卵原细胞和卵母细胞的胞质中，以及Ⅵ期卵巢中的滤泡细胞中。功能分析表明，注射体内 AA 和 PGE2 可使克氏原螯虾卵巢中 PcPTGS 基因表达水平、PGE2 的含量、Vg 和 Vgr 基因表达水平均升高，而注射 DEX 和 PcPTGS 基因沉默则产生相反的结果。综上所述， PcPTGS 基因可通过调控 PGE2 的合成影响其卵黄生成，从而调控其卵巢发育。

关键词：克氏原螯虾；卵巢发育；前列腺素内过氧化物合酶；RNA 干扰

Molecular identification of prostaglandin-endoperoxide synthase (PTGS) gene of *Procambarus clarkii* and its role in ovarian development

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Abstract：Prostaglandin-endoperoxide synthase (PTGS) is a key enzyme in prostaglandin synthesis. To investigate the role of the PTGS gene from *Procambarus clarkii* (PcPTGS) in ovarian development, the full-length cDNA of PcPTGS was cloned in this study, which is 3,262 bp in length. Its open reading frame is 1,830 bp, encoding a protein composed of 609 amino acids with an epidermal growth factor-like domain and an animal heme peroxidase domain. qRT-PCR results showed that PcPTGS expression was highest in stage V ovary among ovaries at stages I-VI. Immunohistochemistry revealed that PcPTGS protein was mainly localized in the cytoplasm of oogonia and oocytes in stage I–V ovaries, and in follicular cells in stage VI ovary. Functional analysis indicated that AA and PGE2 injections upregulated the expression of PcPTGS, Vg and Vgr genes, as well as PGE2 content in the ovary, while DEX injection and PcPTGS gene silencing had the opposite effect. In conclusion, the PcPTGS gene can regulate vitellogenesis by controlling the synthesis of PGE2, thereby influencing the ovarian development of P. clarkii.

Key words:：*Procambarus clarkii*, ovarian development, prostaglandin-endoperoxide synthase, RNA interference

基于全基因组重测序的中国东南沿海野生拟穴青蟹遗传多样性、群体结构和连续性纯合片段模式分析

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摘要：青蟹（*Scylla paramamosain*）是我国重要的养殖海水蟹类之一。为了了解我国青蟹当前的种质资源和种群历史，基于中国东南沿海 4 个地理种群的 146 只青蟹的全基因组重测序数据，开展遗传多样性、群体遗传结构和连续性纯合片段（ROH）分析。结果表明，核苷酸多样性范围为 0.00157 至 0.00160，观察杂合度（0.248-0.257）近似期望杂合度（0.260-0.265），仍接近 Hardy-Weinberg 平衡。PCA、种群结构、系统发育树和 LD 分析的结果一致表明不同地理种群之间的遗传分化较弱。通过 ROH 检测发现青蟹基因组存在 47142 个 ROH，其中 60%以上的 ROH 小于 0.1 Mb。基于 ROH 估计的平均基因组近交系数为 0.0293，表明野生青蟹的近交程度低。此外，在 ROH 岛中鉴定出 29 个候选基因，包括 IARS 和 UNC79。总的来说，研究结果将青蟹种质资源的保护和开发提供理论依据。

关键词：拟穴青蟹、全基因组重测序、遗传多样性、连续性纯合片段

Whole-genome resequencing provides novel insights into the genetic diversity, population structure, and patterns of runs of homozygosity in mud crab (*Scylla paramamosain*)

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Abstract： Mud crab (*Scylla paramamosain*) is an economically important aquaculture crustacean species in China. To understand their current genetic resources and population history, a total of 146 mud crabs from the southeast coast of China were collected for analysis. Results showed that the nucleotide diversity ranged from 0.00157 to 0.00160, with observed heterozygosity (0.248-0.257) approximately equal to expected heterozygosity (0.260-0.265), indicating they were near Hardy-Weinberg equilibrium, albeit with low polymorphism. The results of PCA, population structure, phylogenetic tree, and LD analysis indicated weak genetic differentiation among four populations. ROHs detection revealed 47,142 ROHs in mud crabs, with over 60% shorter than 0.1 Mb. Moreover, the average genomic inbreeding coefficient estimated by ROHs (0.0293) and homozygous sites (0.0389) suggested low inbreeding. Notably, 29 candidate genes were identified in ROH islands, including IARS and UNC79. Overall, our results would provide valuable insights for conserving, managing, and improving the genetic resources of mud crabs.

Key words: *S. paramamosain*; Whole genome resequencing; Genetic diversity; Runs of homozygosity.

酸化对大黄鱼的影响

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摘要：海洋的持续酸化成为全球共同面临的重大生态问题之一，尤其是在近海。水产养殖是人类粮食安全的重要保障，而近海是主要的养殖场所。然而，有关酸化对经济鱼类的研究还相对匮乏。本研究以养殖大黄鱼为对象，分别暴露于三种 pH 梯度环境（LA-7.4、MA-7.8 和 HA-8.1）中养殖 30 天，然后通过生长、存活、组织结构、生理稳态以及先天免疫等方面系统评估酸化对大黄鱼的影响。结果表明，LA 组显著抑制大黄鱼生长，其应激水平显著升高，抗氧化酶活性以及先天免疫酶活性降低，组织学分析显示其各组织均出现明显病理损伤。值得注意的是 MA 组生长状况良好，同时存活未受影响且先天免疫酶活性较高。综上，长期暴露于 pH 7.4 的酸化环境会通过破坏氧化还原平衡、诱发应激反应及造成组织结构损伤等多重途径，对大黄鱼健康产生显著负面影响。本文有助于揭示未来海洋酸化可能对大黄鱼养殖造成不利影响。

关键词：海洋酸化；大黄鱼；存活率与生长；组织学；抗氧化能力；先天免疫

Effects of Acidification on *Larimichthys crocea*

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Abstract： Ocean acidification threatens ecosystems, particularly coastal areas supporting critical aquaculture. Farmed yellow croaker (*Larimichthys crocea*), an important economic fish, is understudied in acidified environments. This study tested 30-day exposure to three pH levels—LA (7.4), MA (7.8), HA (8.1)—on the fish's growth, survival, tissue health, physiological balance, and innate immunity.Results showed LA-group fish had notably reduced growth, higher stress, lower antioxidant enzyme activity, and weaker innate immunity. Histology showed severe multi-organ damage. MA-group fish had strong growth, normal survival, and better innate immunity. HA acted as a control with no harm.In short, long-term exposure to pH 7.4 harmed yellow croaker by disrupting redox balance, causing stress, and damaging tissues. These findings reveal ocean acidification risks to coastal aquaculture and stress the need for adaptive management.

Key words: ocean acidification; Larimichthys crocea; survival and growth; histologic; antioxidant capacity; innate immunity

海带养殖群体的遗传同质化及其产业挑战

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摘要：海带（*Saccharina japonica*）是我国最重要的养殖藻类，其长期的大规模栽培促进了产业发展，但也导致了种质资源的遗传同质化风险。我们在山东荣成与福建两个核心产区，系统分析了主要养殖品系的遗传结构、农艺性状及化学成分。结果显示，不同品系在形态学指标上差异有限，遗传分化程度低，部分品系间存在明显同质化趋势。在十年的跟踪研究中，我们发现独立育苗场间普遍采用统一的亲本选择与育苗工艺，加之亲本共享与精子污染，显著加剧了群体间的遗传趋同。同时，杂交新品种（如205×B013后代）的引入能够有效增加群体的遗传复杂性，并在一定程度上改善产量与性状表现。然而，2021–2022年荣成海带灾害也提示遗传单一性使养殖群体易受环境胁迫。整体上，海带养殖正面临“高产稳定”与“遗传多样性保持”的双重挑战。我们建议加强核心种质收集与利用，优化育种策略，并建立长期的遗传监测体系，以支撑海带产业的可持续发展。

关键词：海带；遗传同质化；种质资源；杂交育种；可持续养殖

Genetic Homogeneity in *Saccharina japonica* Aquaculture: Challenges and Implications for Sustainable Kelp Farming

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Abstract： *Saccharina japonica* is the most important cultivated macroalga in China. While large-scale aquaculture has boosted production, it has also raised concerns about genetic homogeneity in farmed stocks. We investigated principal cultivars in Rongcheng (Shandong) and Fujian, combining microsatellite genotyping, agronomic traits, and chemical composition analyses.Results revealed limited morphological variation among cultivars and low genetic differentiation, with clear signs of homogenization. Standardized parental selection, uniform hatchery practices, parental stock sharing, and sperm contamination have collectively accelerated convergence across hatcheries.Nevertheless, hybrid breeding provided new opportunities. The 205 × B013 hybrid lineage introduced distinct genetic components, increased diversity, and improved productivity. Yet, the 2021–2022 mass mortality in Rongcheng, where uniform stocks collapsed under prolonged high transparency, highlighted the vulnerability of homogeneous populations. Only genetically distinct hybrids such as Zhongbao No.1 showed stronger resilience.

Key words: *Saccharina japonica*; genetic homogeneity; germplasm resources; hybrid breeding; sustainable aquaculture

全基因组重测序揭示大泷六线鱼（*Hexagrammos otakii*）的性别决定系统并开发可靠的性别特异性标记

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摘要：性别决定在水产养殖中至关重要，但六线鱼科的遗传机制尚不清楚。本研究通过大泷六线鱼全基因组重测序，发现第 9 号染色体为其雄性异配型（XY）性染色体，并界定了 3.11 Mb 的性别决定区，提出 TGF-β通路基因 gdf6a 为候选性别决定基因。结果显示，该性染色体与杜父鱼亚目其他物种不同源，揭示了至少两次独立的性染色体周转事件。同时，我们基于 99 bp 雄性特异性缺失建立了快速可靠的分子性别鉴定方法。

关键词：性染色体；性别决定系统；大泷六线鱼；性染色体周转；性别特异性标记

Whole-genome resequencing reveals the sex determination system and develops a reliable sex-specific marker in *Hexagrammos otakii*

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Abstract: Sex determination is crucial in aquaculture, yet the genetic mechanism remains unclear in Hexagrammidae. In this study, whole-genome resequencing of Hexagrammos otakii identified chromosome 9 as the male heterogametic (XY) sex chromosome and delineated a 3.11 Mb sex-determining region. We proposed the TGF-β pathway gene gdf6a as a candidate sex-determining gene. The results showed that this sex chromosome is non-homologous to those of other Cottioidei species, revealing at least two independent sex chromosome turnover events. Furthermore, we developed a rapid and reliable molecular sex identification method based on a 99 bp male-specific deletion.

Key words: sex chromosome; sex determination system; *Hexagrammos otakii*; sex chromosome turnover; sex-specific marker

日本沼虾核糖体蛋白 S6 激酶的鉴定及其在卵巢发育中的调控作用

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摘要：核糖体蛋白 S6 激酶（RPS6K）属于 Ser/Thr 蛋白激酶家族。为探究其在日本沼虾（*Macrobrachium nipponense*）卵巢发育中的作用，本研究克隆了 MnRPS6K 基因全长 cDNA（2993 bp，编码 932 个氨基酸），并通过 qRT-PCR 分析了其表达模式。MnRPS6K 有两个保守的 S_TKc 结构域，在雌性成虾和卵巢中高表达，且在 V 期卵巢达到峰值。免疫组化显示，MnRPS6K 主要分布于卵原细胞、卵母细胞及滤泡细胞的胞质。功能分析表明，注射重组 MnRPS6K 蛋白及 5-羟色胺显著上调 MnRPS6K 及多种卵巢发育关键基因（MnVtg、MnVtgr、MnCyclinB、MnCdc2）的表达；而多巴胺及 MnRPS6K-siRNA 则抑制其转录。MnRPS6K 沉默还引起滤泡细胞凋亡，并延缓卵母细胞发育。综上，MnRPS6K 通过调控卵子发生、卵黄生成及卵母细胞成熟，促进日本沼虾卵巢发育。

关键词：核糖体蛋白 S6 激酶，卵巢发育，重组蛋白，RNA 干扰，日本沼虾

Identification and ovarian developmental regulation of ribosomal protein S6 kinase in *Macrobrachium nipponense*

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Abstract： Ribosomal protein S6 kinase (RPS6K) is a Ser/Thr kinase. To elucidate its role in *Macrobrachium nipponense* ovarian development, we cloned the full-length MnRPS6K cDNA (2993 bp, encoding 932 amino acids) via RACE-PCR and analyzed its expression pattern using qRT-PCR. MnRPS6K contains two conserved S_TKc domains, and MnRPS6K shows highest expression in adult females, and peaks in the ovary at stage V. Immunohistochemistry revealed that MnRPS6K protein is mainly localized in the cytoplasm of oogonia, oocytes, and follicle cells. Recombinant MnRPS6K protein and 5-hydroxytryptamine treatment upregulated the expression of MnRPS6K and several key ovarian development-related genes (MnVtg, MnVtgr, MnCyclin B, and MnCdc2), whereas dopamine and MnRPS6K-siRNA downregulated these genes. Moreover, MnRPS6K silencing induced follicular cell apoptosis and resulted in delayed oocyte and ovarian development. These findings demonstrate that MnRPS6K can promote ovarian development by regulating oogenesis, vitellogenesis, and oocyte maturation in M. nipponense.

Key words: Ribosomal protein S6 kinase; Ovarian development; Recombinant protein; RNA interference; *Macrobrachium nipponense*

单细胞转录组分析揭示扇贝热应激下的心肌细胞异质性响应机制

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摘要：具有开放循环系统的水产动物在全球变暖背景下更易面临生存威胁，然而目前对其心脏响应高温的细胞异质性机制仍知之甚少。本研究以海湾扇贝为模型，整合形态学、代谢指标和单细胞转录组学，系统解析了心脏在热应激下的响应机制。结果表明，热胁迫加剧了心脏结构损伤，并诱发线粒体功能障碍与神经内分泌调节。我们鉴定出两个心肌细胞亚群——心室肌细胞（VM）和心房肌细胞（AM），它们表现出不同的热应答策略：AM 通过增强与免疫细胞及成纤维细胞的互作维持稳态；VM 则通过提升能量供应和再生潜力以应对胁迫。RNA 干扰实验表明，敲低热敏感候选基因 PLRP2-like 可显著降低扇贝的耐热性。本研究揭示了扇贝心脏细胞异质性热响应机制，并发现关键基因 AiPLRP2-like 具有独特的细胞定位模式，可能在水产动物耐热调控中起关键作用。该研究为理解海洋无脊椎动物的温度适应性进化提供了新理论依据，对水产抗逆品种选育具重要参考价值。

关键词：开放循环系统，软体动物，心脏，热应激，单细胞转录组，PLRP2

Single-cell transcriptome profiling reveals the heterogeneous response mechanisms of scallop cardiomyocytes to thermal stress

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Abstract： Aquatic animals with open circulatory systems are highly vulnerable to global warming, yet the cellular heterogeneity of their cardiac response remains unclear. Using the scallop Argopecten irradians, we integrated morphology, metabolism, and scRNA-seq to analyze cardiac response under heat stress. Results showed temperature-dependent cardiac structural damage, mitochondrial dysfunction, and neurohumoral activation. We identified two cardiomyocyte subpopulations—ventricular (VMs) and atrial myocytes (AMs)—each exhibiting distinct response strategies. AMs enhanced interactions with immune-like cells and fibroblasts to maintain homeostasis, while VMs upregulated energy supply and differentiation potential. RNAi knockdown of the thermosensitive gene PLRP2-like significantly reduced heat tolerance. This study reveals heterogeneous thermal responses in scallop hearts and identifies AiPLRP2-like as a key gene with unique localization and potential thermoregulatory roles. These findings offer valuable implications for breeding stress-resistant varieties in aquaculture.

Key words: Open circulatory systems, Mollusks, Heart, Heat stress, ScRNA-seq, PLRP2

利用基因编辑创制 YY 超雄与 XY 全雄罗非鱼及其育种应用

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摘要：罗非鱼是我国重要水产养殖品种，雄性生长较雌性快 30%以上，经济价值更高。全雄鱼主要依赖雄激素诱导，存在环境生态风险。项目团队最新研究发现，高温诱导表达的组蛋白去甲基化酶 kdm6bb 通过特异性去除 H3K27me3 修饰，激活雄性决定信号通路，进而驱动性别逆转过程。团队构建 kdm6bb 基因编辑模型，抑制 H3K27me3 去甲基化，使雄性关键基因（dmrt1/gsdf/amh）甲基化水平升高，成功诱导 XY 鱼性逆转成为伪雌鱼。通过 XY 伪雌鱼与野生 XY 雄鱼交配，筛选获得 YY 超雄鱼，再与 XX 雌鱼杂交创制 100%XY 全雄后代，建立"基因编辑 XY 伪雌鱼→YY 超雄鱼→XY 全雄鱼"三步法育种体系，为全雄单性育种提供了安全高效的技术方案。

关键词：罗非鱼；全雄单性育种；kdm6bb；表观调控

Generation of YY Supermales and XY All-Male Tilapia via Gene Editing and Their Breeding Applications

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Abstract： Tilapia is an important aquaculture species in China, with males growing over 30% faster than females. The production of all-male populations relies on androgen induction, which poses ecological risks. We recently found that the histone demethylase kdm6bb, whose expression is induced by high temperature, specifically removes the H3K27me3 modification, thereby activating the male-related genes and triggering sex reversal. We generated a kdm6bb gene-edited model. Suppressing kdm6bb expression blocked H3K27me3 demethylation, resulting in elevated methylation levels of key male-related genes (dmrt1, gsdf, amh) and inducing XY individuals to undergo sex reversal into pseudo-females. Mating these XY pseudo-females with wild-type XY males enabled the screening and acquisition of YY supermales, which were subsequently crossed with XX females to produce 100% XY all-male offspring. This work establishes an innovative three-step breeding strategy “gene-edited XY pseudo-female → YY supermale → XY all-male” providing a safe and efficient approach for all-male monosex breeding.

Key words: Tilapia; All-male moxosex breeding; kdm6bb; Epigentic regulation

厚壳贻贝（*Mytilus coruscus*）性腺发育周年变化及雌二醇（E2）对卵巢发育的影响

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摘要：厚壳贻贝是重要的经济养殖物种，具有较高的市场潜力，但在育种方面仍面临挑战。雌二醇（E2）在软体动物的生殖调控中发挥作用，但其在厚壳贻贝中的影响尚不明确。本研究从嵊泗海域采集四个时期的贻贝个体，结合性腺特征将发育时期鉴定为增殖期（9 月）、生长期（12 月）、产卵期（3 月）和休眠期（6 月）。E2 暴露实验（0–1000 μg/L）结果显示，100 μg/L E2 可显著增大卵母细胞直径，促进排卵，并降低 D 型幼虫畸形率（9.4%）。该处理下的转录组分析共鉴定出数千个差异表达基因，其中 2287 个被鉴定为雌性 E2 响应基因。KEGG 富集分析结果主要涉及“RNA 降解”和“自噬-动物”等通路。与卵巢发育相关的 Foxl2 基因在雌性中受 E2 调控显著上调，而在雄性睾丸中未检测到，表明 E2 可能对雄性具有抑制作用。本研究结果揭示了厚壳贻贝性腺发育的特征，并阐明了 E2 在卵巢发育的影响，为人工育种和分子机制研究提供了参考。

关键词：厚壳贻贝；性腺发育；周年变化；雌二醇

Annual variation in gonadal parameters and the effects of estradiol (E2) on ovarian development in the thick-shelled mussel, *Mytilus coruscus*

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Abstract： Mytilus coruscus is an important aquaculture species with market potential and breeding challenges. Although estradiol (E2) regulates reproduction in mollusks, its effects on M. coruscus remain unclear. Here, mussels were collected and identified from the Shengsi Sea across four gonadal stages: proliferation (September), growth (December), spawning (March), and resting (June) based on annual variation in gonadal parameters. In addition, E2 exposure experiments (0–1000 μg/L) showed that 100 μg/L E2 significantly increased oocyte diameter, promoted ovulation, and reduced D-larval malformation (9.4%). Transcriptomic analysis under 100 μg/L E2 identified thousands of differentially expressed genes, of which 2287 were identified as E2-responsive in females. KEGG enrichment highlighted “RNA degradation” and “Autophagy–animal”. Foxl2 was upregulated in ovarian by E2 but absent in testes, suggesting E2 suppression in males. These findings provide insights into gonadal development of M. coruscus and clarify E2’s role in ovarian regulation, supporting artificial breeding and molecular studies.

Key words: Mytilus coruscus; Gonadal development; Annual variation; Estradiol (E2)

小黄鱼基因组解析及其在抗内脏白点病育种中的应用研究

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摘要：小黄鱼是我国重要的经济鱼类，养殖受到变形假单胞菌引起的内脏白点病威胁，培育抗病品种迫在眉睫。本研究完成染色体级别高质量基因组（总长 677.35 Mb）；通过重测序筛选 SNP 位点，开发出小黄鱼 100K SNP 分型芯片。针对内脏白点病，分离出高致病菌株（96h 半数致死浓度 1×10^3 CFU/mL），建立靶向 gyrB 基因的 qPCR 检测法以动态追踪感染进程；首次在小黄鱼中鉴定出 Hepcidin 抗菌肽基因，其在肝脏中的表达与病原量呈显著负相关，有望成为抗病育种靶标。以感染后存活时间为抗病表型，结合芯片分型，构建包含 946 尾小黄鱼的参考群体。通过 GBLUP 模型预测候选群体，筛选高抗病性亲本，培育出养殖成活率提升 10%以上的抗病子代。经 GWAS 和转录组分析，锁定了 7 个抗病基因，其中 sting1 在抗病个体中显著上调表达，揭示其具有抗病功能。研究为小黄鱼种质保护、抗病育种及病害防控提供支撑。

关键词：小黄鱼；抗病；抗菌肽；基因组选择；功能基因

Genome analysis of *Larimichthys polyactis* and research on breeding application for resistance to Visceral White Spot Disease

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Abstract: The small yellow croaker (*Larimichthys polyactis*) is an important economic fish in China, but its aquaculture is threatened by visceral white spot disease caused by Pseudomonas plecoglossicida, urgently requiring disease-resistant varieties. In this study, we generated a chromosome-level high-quality genome of L. polyactis (total length: 677.35 Mb), with 97.90% of sequences anchored to 24 chromosomes. Using this reference genome, we screened SNPs via resequencing and developed a 100K SNP genotyping array for L. polyactis. For visceral white spot disease, we isolated a highly pathogenic P. plecoglossicida strain (96-h LC_{50}: 1×10^3 CFU/mL) and established an RT-qPCR method targeting the gyrB gene to dynamically track infection. Additionally, we first identified three antimicrobial peptide genes (Piscidin, Hepcidin, NK-lysin) in L. polyactis; Hepcidin expression in liver was significantly negatively correlated with pathogen load, indicating its potential as a disease-resistant breeding target. Using post-infection survival time as the disease resistance phenotype, we determined the phenotype and genotype of 946 L. polyactis individuals via array genotyping. GWAS and transcriptome analysis identified 7 disease-resistant genes, among which sting1 showed significantly higher gene and protein expression in resistant individuals, confirming its key disease-resistant function. With these 946 individuals as the reference population, we applied the GBLUP model to predict GEBVs of the candidate population, screened high-resistance parents, and successfully bred disease-resistant offspring with >10% higher cultivation survival rate. This study provides scientific support for L. polyactis germplasm conservation, disease-resistant breeding, and disease control, effectively promoting the sustainable development of mariculture.

Key words: Larimichthys polyactis; disease resistance; antimicrobial peptides; genomic selection; functional genes

中华鳖 HDACs 基因鉴定及性别分化中表达分析

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摘要：组蛋白去乙酰化酶(histone deacetylases, HDAC)介导的表观遗传调控在哺乳动物性腺发育中发挥重要作用。HDAC 是一类蛋白酶,通过维持与组蛋白乙酰转移酶(histone acetyl transferases, HAT)的动态平衡，在染色质重塑和基因的表达调控等方面发挥作用。然而，HDAC 在非哺乳动物性腺中的作用尚不清楚。本研究鉴定出中华鳖 HDAC 基因家族 10 个基因。qRT-PCR 结果显示，HDAC1 和 HDAC3 在卵巢中高表达，而 HDAC8 和 HDAC11 在睾丸中高表达，揭示其在不同组织中的功能存在差异。性腺分化过程中，HDACs 在胚胎第 16 期和第 17 期表达较高。HDACs 拮抗剂 Trichostatin A 处理后，雌鳖性腺皮质区退化，Foxl2、Cyp19a1、HSD17B1 和 Rspo1 表达下调（$p < 0.05$）。综上，HDACs 在中华鳖卵巢发育过程中起着重要的作用。

关键词：中华鳖；性腺分化；组蛋白去乙酰化酶；卵巢发育

Identification and Expression Analysis of HDACs genes in Sex Differentiation of the Chinese Soft-shelled Turtle (*Pelodiscus sinensis*)

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Abstract: Histone deacetylases (HDAC)-mediated epigenetic regulation plays a significant role in the development of mammalian gonads. HDAC are a class of proteases that play a crucial role in chromatin remodeling and gene expression regulation by maintaining a dynamic balance with histone acetyltransferases (HAT). However, the role of histone deacetylases in the gonads of non-mammalian animals remains unclear. This study identified 10 genes of HDAC family in Chinese Soft-shelled Turtle (Pelodiscus sinensis). qRT-PCR revealed Ps-HDAC1 and Ps-HDAC3 were highest expressed in ovary, whereas Ps-HDAC8 and Ps-HDAC11 were highest expressed in testis, and this result suggested diverse functions in different tissues. In the gonadal differentiation processes, HDACs showed higher expression at embryonic stage 16 and 17. Furthermore, HDACs antagonist (Trichostatin A) treatment resulted in degenerated cortex in female turtle gonad, and Foxl2, Cyp19a1, HSD17B1 and Rspo1 were down-regulated ($p < 0.05$). In summary, HDACs play a crucial role in the ovarian development process of P. sinensis.

Key words: Pelodiscus sinensis, gonadal differentiation, histone deacetylases, ovarian development

基于全基因组重测序分析中国蚬属的遗传结构和核质冲突

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摘要：在蚬属贝类中，无性雄核生殖和不同谱系之间的杂交导致核质冲突现象的产生，这使解析蚬属贝类的遗传关系存在挑战。本研究结合线粒体和核数据分析中国蚬属群体的遗传关系并揭示了核质冲突现象的存在。基于 17 个群体 73 个样本的重测序数据进行遗传分析，结果显示中国蚬属可划分为三个类群：CGA、CGB 和 CGC。基于基因组 SNP 和线粒体 COI 数据的系统发育分析结果表明，CGC 中的样本存在大量核质冲突。本研究结果表明中国蚬属贝类可划分为三个主要类群，并且存在广泛的核质冲突现象。

关键词：河蚬；核质冲突；系统发育基因组学；线粒体 COI

Integrative genomic analyses reveal genetic structuring and cyto-nuclear incongruences within the Corbicula species complex in China

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Abstract： Examining the genetic relationships within the Corbicula species complex is often challenging, primarily due to cyto-nuclear mismatches resulting from their unique asexual reproduction via androgenesis and hybridizations occur between distinct genetic lineages. In this study, we investigated the genetic relationships among Corbicula populations in the Chinese native range by cross-referencing mitochondrial and nuclear datasets for the first time, evaluating cyto-nuclear mismatches. Sequencing data obtained from 73 individuals across 17 Corbicula populations revealed substantial genetic structuring among the studied populations, delineating three major Corbicula groups: CGA, CGB and CGC. Phylogenetic analysis for genomic SNP and mitochondrial COI datasets revealed substantial topological conflicts within CGC. Our findings suggested that the Corbicula species complex can be designated into three major groups with substantial cyto-nuclear incongruences apparent within its native range.

Key words: Corbicula fluminea；cytonuclear mismatch；phylogenomics；mitochondrial COI

膨腹海马低氧适应机制及耐低氧新品系选育

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摘要：溶解氧是水生生物生存的关键环境因子。海马（*Hippocampus spp.*）经济和药用价值较高，是国家二级保护动物和海洋研究的旗舰物种。海马具有独特的“簇状鳃”结构且低氧适应机制尚未报道，同时缺乏耐低氧品系，极大限制了海马工厂化高密度养殖和产业化可持续发展。本研究以膨腹海马为研究对象，通过明确其低氧耐受阈值（LOEcrit）；构建涵盖行为响应、鳃组织形态、抗氧化及血液携氧能力的多维度评价体系；并探究“簇状鳃”海马低氧适应机制。此外，采用多代家系选育结合群体选育培育耐低氧海马新品系，并基于全基因组重测序挖掘其耐低氧 SNP 位点及候选基因。本研究为耐低氧海马新品种选育提供参考。

关键词：膨腹海马；簇状鳃；低氧

Mechanism of the hypoxia adaptation of big belly seahorses (*Hippocampus abdominalis*) and new hypoxia-tolerant strain breeding

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Abstract：Dissolved oxygen is a key environmental factor for the survival of aquatic organisms. As a flagship species for national second-class protected animals and marine research, seahorses (*Hippocampus spp*.) have high economic and medicinal value. Seahorses have a unique “tuft gills” structure and the mechanism of adaptation to hypoxia has not been reported, while the absence of hypoxia-tolerant seahorses greatly limits the industrial high-density breeding and sustainable development of seahorses. This study focuses on "tuft gills" big belly horses (Hippocampus abdominalis) and clarifies their hypoxia-tolerance threshold (LOEcrit). Meanwhile, a multidimensional evaluation system covering behavioral response, gill tissue morphology, antioxidant and blood oxygen carrying capacity was constructed. And the hypoxic adaptation mechanism of "tuft gills " seahorses was explored in our research. In addition, multi-generational family breeding combined with population breeding were used to cultivate hypoxia-tolerant seahorse strains. SNP sites and candidate genes for hypoxia-tolerant were mined base.

Key words: Hippocampus abdominalis; hypoxia; tuft gills

Scarb1 基因在中华锯齿米虾色素沉着中的作用分析

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摘要：体色是中华锯齿新米虾（Neocaridina denticulata sinensis）这一重要观赏虾类的关键经济性状。B 类I型清道夫受体基因（scarb1）可能是介导虾青素摄取、调控体色的关键因子。为探究 scarb1 与樱桃虾着色之间的关系，本研究通过基因表达谱分析、RNA 干扰和单核苷酸多态性（SNP）分型技术对该基因进行了系统研究。结果表明：scarb1 在四种体色品系及五个发育阶段中的表达量均存在显著差异（$p < 0.05$），其在红色品系和前无节幼体阶段表达水平最高。通过 dsRNA 干扰实验发现，在后无节幼体阶段干扰 scarb1 表达可显著促进色素细胞数量增加和发育分化，但在前溞状幼体阶段未观察到明显表型变化。此外，在黄色品系与其他品系间发现一个同义突变位点（G1593A）的基因型频率存在显著差异（$p < 0.05$）。上述结果说明，scarb1 通过影响色素细胞的发育进程参与体色形成调控。

关键词：清道夫受体 B 类 I 型；类胡萝卜素；RNAi；SNP 基因分型

Role Analysis of the Scarb1 Gene in the Pigmentation of *Neocaridina denticulata sinensis*

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Abstract： Body color is a key economic trait for *Neocaridina denticulata sinensis*, an important ornamental shrimp. Scarb1 may be an important mediator of astaxanthin uptake, changing the shrimp's body color. To discover the relationship between scarb1 and the pigmentation of cherry shrimp, the expression profiles, RNAi, and SNP genotyping of scarb1 were studied. There were significant differences in four color populations and five development stages ($p < 0.05$). The highest expression level of scarb1 appeared in the red population and the pre-nauplius stage. Exposure to scarb1 dsRNA increased the number and development of chromatophores at the metanauplius stage, but almost no phenotypic changes were observed at the pre-zoea stage. There was a synonymous SNP (G1593A) with a significantly different genotype frequency between the red and yellow populations ($p < 0.05$). The above results suggested that scarb1 is involved in pigmentation by affecting the development of chromatophores.

Key words: scavenger receptor class B type I; carotenoid; RNAi; SNP genotyping

美洲鳗鲡性早熟的神经内分泌机制的初步解析

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摘要：鳗鲡是降海洄游产卵鱼类，栖息于淡水及近岸水域的雌鳗卵巢发育停滞在 II 期（油球期，GSI<1.5），在降海洄游过程才逐步发育成熟。2024 年底，福建某近岸海水养殖网箱中发现约 40%的 2 龄美洲鳗鲡（*Anguilla rostrata*）的卵巢已发育至 III 期（卵黄生成期，GSI>4），属于典型的性早熟。这些鱼的血清雌二醇水平，脑-垂体-性腺-肝脏生殖调控轴相关基因 gnrh1，lh，lhr，cyp19a1 和 vtg 的表达量均显著高于未发育个体，表明这些雌鱼已性启动。为解析该现象的神经内分泌机制，通过分析卵黄生成期前后美洲鳗鲡脑转录组的差异，发现 14 个基因表达量提高，12 个基因表达量降低。其中介导营养能量摄入与生殖的甘丙肽样蛋白（galp），参与多巴胺合成的酪氨酸羟化酶(th)，催乳素（prl），及昼夜节律相关蛋白(rasd1)等基因的表达量显著提高，表明美洲鳗鲡可能受到内外环境的协同调控卵巢的发育。

关键词：性启动，生殖调控轴，类固醇激素，转录组，鳗鲡

Preliminary Analysis of the Neuroendocrine Mechanisms Underlying Precocious Puberty in American Eels

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Abstract：Anguilla eels, as catadromous fish, inhabiting rivers, estuaries, and coastal waters exhibit ovarian development arrested at oil droplet stage (GSI < 1.5), with maturation occurring only during seaward migration. By the end of 2024, approximately 40% of the second-year Anguilla rostrata reared in a nearshore marine cage were found to have developed vitellogenin stage (GSI > 4), indicating precocious puberty. The serum estradiol levels, key genes within the brain-pituitary-gonad-liver (BPGL) reproductive axis—gnrh1, lh, lhr, cyp19a1, and vtg— in these fish were significantly higher than those in undeveloped individuals, confirming sexual initiation. Furthermore, transcriptomic comparison of brains before and after vitellogenesis revealed 14 upregulated genes and 12 downregulated genes. Notably, pronounced upregulation was detected in galp (mediating energy intake and reproduction), th (dopamine synthesis); prl, and rasd1 (circadian rhythm). These finding suggests that the precocious puberty of American eels may be regulated by synergistic internal and external environment.

Key words: sexual initiation, brain-pituitary-gonadal axis, steroid hormone, transcriptome, eel

β-catenin 通过调控 cyp19a1a 表达参与淇河鲫卵巢分化

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摘要：淇河鲫鱼（*Carassius auratus*）作为银鲫（*Carassius gibelio*）的一个地方种群可以进行雌核发育殖产生全雌后代。虽然其繁殖策略已得到深入研究，但雌性性别决定的分子机制尚不明确。Wnt/β-catenin 通路在哺乳动物卵巢发育中有重要作用，为了探究其在淇河鲫雌性性腺发育中作用，我们通过组织学与分子分析进行研究。我们发现β-catenin 的表达与雌激素合成关键基因 cyp19a1a 在性腺分化过程中同步上调。β-catenin 与 cyp19a1a 在生殖细胞和体细胞中均存在共表达现象。采用β-catenin 药理抑制剂处理，可抑制 cyp19a1a 表达，启动子实验证实β-catenin-Lef1 复合物能直接激活 cyp19a1a 转录。这些结果表明β-catenin 是淇河鲫鱼卵巢分化的核心调控因子，首次为硬骨鱼类单性生殖中 Wnt/β-catenin 信号通路的功能提供了实验证据。

关键词： β-catenin ；调控；cyp19a1a；卵巢分化

The role of β-catenin in ovarian differentiation by upregulation cyp19a1a in a natural triploid teleost, Qi river crucian carp (*Carassius auratus*)

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Abstract: The Qi River crucian carp (Carassius auratus), a gynogenetic variant of Carassius gibelio, reproduces asexually to produce all-female offspring. While its reproductive strategy is well-studied, the molecular basis of its female sex determination remains unclear. This study investigates the role of the Wnt/β-catenin pathway—a key regulator of ovarian development in mammals—in this process. Through histological and molecular analyses, we found that β-catenin expression synchronizes with cyp19a1a, a critical gene for estrogen synthesis, during gonadal differentiation. β-catenin and cyp19a1a were co-expressed in both germ and somatic cells. Pharmacological inhibition of β-catenin suppressed cyp19a1a expression, and promoter assays confirmed that β-catenin-Lef1 complexes directly activate cyp19a1a transcription. These results identify β-catenin as a central regulator of ovarian differentiation in Qi River crucian carp, providing the first functional evidence for Wnt/β-catenin signaling in unisexual reproduction in teleosts.

Key words: β-catenin; regulate; cyp19a1a; ovarian differentiation

雌雄银鮈染色体核型比较分析

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摘要：为保护银鮈（*Squalidus argentatus*）的遗传资源，探索该物种的起源和进化状况，特对雌、雄银鮈的染色体核型差异进行分析。以银鮈头肾为材料，采用低渗和空气干燥的方法制备染色体标本，分别从雌雄银鮈的头肾中获得染色体核型。共统计50个雌性个体分裂相的染色体数目和50个雄性个体分裂相的染色体数目。结果表明：雌、雄银鮈染色体数目出现频率最高的均为50，分别占70％、74％。从中各选取5个染色体形态清晰、着丝粒可识别的中期分裂相进行核型分析，发现雌性银鮈染色体在核型分组上核型公式为2n=50=40m+6sm+4t，臂数NF=96，雄性银鮈染色体在核型分组上核型公式为2n=50=30m+20sm，臂数NF=100，均未发现异型染色体。独立样本t检验结果显示，雌、雄银鮈的染色体长度极显著差异（P＜0.01），染色体臂比则无显著差异（P＞0.05）。

关键词：银鮈；头肾；染色体；核型分析

Comparative Analysis of Chromosome Karyotypes in Female and Male Silver Gudgeon (*Squalidus argentatus*)

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Abstract： To protect the genetic resources of *Squalidus argentatus* and explore the origin and evolutionary status of this species, an analysis of karyotype differences between female and male S. argentatus was conducted. Using the head kidney tissue as material, chromosome specimens were prepared using hypotonic treatment and air-drying methods. Karyotypes were obtained from the head kidneys of both female and male individuals. Chromosome counts were performed on 50 metaphase spreads from female individuals and 50 from male individuals. The results showed that the most frequent chromosome number in both female and male S. argentatus was 50, accounting for 70% and 74% of spreads, respectively. Five clear metaphase spreads with identifiable centromeres were selected from each sex for karyotype analysis. The karyotype formula for female S. argentatus was determined as 2n=50=40m+6sm+4t, with the fundamental number of chromosome arms (NF)=96. The karyotype formula for male S. argentatus was 2n=50=30m+20sm, with NF=100. No heteromorphic sex chromosomes were found in either sex.

Key words: *Squalidus argentatus*; Head kidney; Chromosome; Karyotype analysis

不同波长的光谱对锦鲤红色体色的影响

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摘要：体色是决定锦鲤价值的关键性状之一，受多种环境因子的影响。现有研究证实光照可影响鱼类体色的形成，但光谱在红色体色中的作用尚不清晰。本研究将720尾纯红锦鲤置于5个单色光谱及对照条件下饲养95天，探究不同光谱对锦鲤红色体色的调控作用。结果显示，580nm和660nm下体色较红，色素细胞密度高且树状突较分散，而420nm、480nm和520nm下体色偏黄，色素细胞密度较低且收缩明显。色素含量和神经肽结果显示，随波长增加皮肤类胡萝卜素含量上升而蝶呤下降，血清中MSH升高、MCH降低。转录组分析发现480nm光谱显著上调免疫应答及Wnt信号通路基因，色素形成相关基因显著下调。综合以上结果推测480nm光谱可能通过光损伤加速细胞凋亡，使色素细胞数量减少，色素含量降低。综上研究表明580nm波长能促进神经肽及色素沉积相关基因表达，促进锦鲤红色体色形成。以上结果为提高锦鲤观赏价值和养殖效益提供了理论依据。

关键词：锦鲤；体色；光谱

Effects of different spectrum on the red body coloration of koi carp (*Cyprinus carpio*)

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Abstract： Body color is a key determinant of koi carp value and is influenced by environmental factors. Light is known to affect fish coloration, while the function of spectrum on red coloration remains unclear. This study investigated the effect of spectrum on coloration in 720 whole red koi under six spectra for 95 days. Koi under 580nm and 660nm exhibited redder coloration, with higher chromatophore density and dispersed dendrites. In contrast, koi under 420nm, 480nm, and 520nm showed yellowish body color, lower chromatophore density, and cell contraction. Pigment and serum analysis revealed that with wavelength increased, carotenoid content and MSH increased while pteridine and MCH decreased. Transcriptomic analysis indicated the 480nm group upregulated immune response and Wnt signaling pathway genes. We speculate 480nm light may accelerate cell cycle, reducing pigment content. Besides, the 580nm spectrum promotes neuropeptide and pigmentation-related genes, enhancing red coloration. These results provide a theoretical basis for improving koi ornamental value and aquaculture efficiency.

Key words: Koi carp; Body color; Light spectrum

斑马鱼 slc2a11b 基因在黄色素细胞形成中的调控机制研究

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摘要：黄色素细胞是决定鱼类黄色体色形成的关键细胞，但其分子调控机制尚不深入。本研究利用斑马鱼皮肤单细胞转录组数据筛选得到黄色素细胞标志基因，对其中 11 个候选基因进行敲除，发现 slc2a11b 等基因敲除可导致 F0 代幼鱼黄色素细胞缺失。进一步聚焦 slc2a11b 基因，结果显示其在 96hpf 胚胎及成鱼皮肤、鳍组织中高表达，其纯合突变体表现出明显的黄色素缺失。slc2a11b 缺失不仅影响蝶啶合成相关基因的表达，还导致黄色素细胞分化相关基因 csf1ra 显著下调，提示其在色素细胞命运调控中发挥作用。转录组分析显示，突变体相较于野生型个体皮肤中差异基因显著富集于 Wnt 等信号通路，并且与黄色素分化及蝶啶代谢相关基因表达出现显著改变，表明 slc2a11b 可能通过调控信号通路及蝶啶代谢共同影响黄色素细胞发育。本研究首次系统揭示了 slc2a11b 在斑马鱼体色形成中的重要功能，为水产经济鱼类的体色改良提供了理论基础。

关键词：斑马鱼；slc2a11b；黄色素细胞；CRISPR/Cas9；RNA-seq

Regulatory Role of slc2a11b in Xanthophore Development in Zebrafish

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Abstract：Body coloration affects fish survival, reproduction, and is an important aquaculture trait. Xanthophores are key to yellow pigmentation, but their molecular regulation remains unclear. Using zebrafish skin single-cell transcriptomes, we identified xanthophore marker genes and applied CRISPR/Cas9 multi-sgRNA screening of 11 candidates. Knockouts of slc2a11b, impdh1b, gmps, and paics caused xanthophore loss. Focusing on slc2a11b, we found high expression in embryos (96 hpf), skin, and fins, with homozygous mutants lacking xanthophores. slc2a11b loss altered expression of pteridine synthesis genes (gch1, xdh) and downregulated the differentiation factor csf1ra, implicating roles in pigment cell fate. Transcriptome analysis revealed differential enrichment of Wnt, TGF-β, MAPK, and Notch pathways, with marked changes in genes related to xanthophore differentiation and pteridine metabolism. These findings demonstrate slc2a11b as essential for zebrafish pigmentation and provide a basis for improving body coloration in aquaculture species.

Key words: Zebrafish; slc2a11b; xanthophores; CRISPR/Cas9; RNA-seq

高温诱导罗非鱼性逆转的分子机制研究

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摘要：破解温度依赖性性逆转（TSR）的核心分子事件颇具挑战，鱼类中将温度信号转导为性别决定信号的机制也尚不明确。本研究以尼罗罗非鱼为模型，通过多组学分析发现，H3K27 甲基化状态与性别分化相关基因的表达存在关联。进一步研究鉴定出 H3K27 去甲基化酶 Kdm6bb 是关键调控因子，其通过影响 H3K27 甲基化水平调控性别决定过程。具体而言，Kdm6bb 的 TSR 调控功能依赖于一个内含子的选择性剪接，该内含子的保留可促进 Kdm6bb 进入细胞核并发挥其调控作用。本研究强调了 mRNA 选择性剪接及亚细胞定位在温度诱导性逆转中的重要作用。

关键词：温度依赖型性逆转；kdm6bb；鱼类；组蛋白甲基化；核转位

The molecular mechanism of high - temperature - induced sex reversal in tilapia

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Abstract： Deciphering the core molecular events driving temperature-dependent sex reversal (TSR) remains challenging, and the mechanisms by which temperature signals are transduced into sex-determining cues in fish are still largely unclear. Using Nile tilapia (*Oreochromis niloticus*) as a model, our multi-omics analyses revealed an association between H3K27 methylation status and the expression of sex differentiation-related genes. Further studies identified the H3K27 demethylase Kdm6bb as a key regulator, which influences sex determination by modulating H3K27 methylation levels. Specifically, Kdm6bb’s TSR-regulating function depends on the alternative splicing of an intron—its retention facilitates Kdm6bb’s nuclear translocation and enables it to exert regulatory effects. Our findings highlight the critical role of mRNA alternative splicing and the demethylase’s subcellular localization in temperature-induced sex reversal.

Key words: temperature-dependent sex reversal; kdm6bb; fish; histone methylation; nuclear translocation

甲基法尼酯对罗氏沼虾生长和卵巢发育的影响及机制探究

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摘要：甲基法尼酯（Methyl farnesoate, MF）是一种倍半萜类激素，在甲壳动物的生殖发育中发挥重要调控作用。本研究以体重约 4.2 g 的罗氏沼虾为实验对象，在饲料中添加不同浓度的 MF（0、3、6、9 μg/g），连续投喂 56 天。结果显示，高剂量 MF（9 μg/g）显著促进卵巢发育，加速卵母细胞由 Oc2 向 Oc4 阶段转变，并显著增大卵母细胞直径，血淋巴中卵黄蛋白原含量在第 28–42 天显著升高。同时显著上调了 Met、Kr-h1 及 Vtg 基因的表达，提示 MF 可能通过 Met-Kr-h1-Vtg 信号通路促进卵黄发生。肠道菌群分析表明，MF 改变了微生物群落结构，高剂量组多样性指数最高，优势菌属转向肠杆菌属和梭菌属，可能与其增强免疫和营养代谢能力有关。相比之下，低剂量 MF（3 μg/g）表现出对生长和卵巢发育的抑制效应。综上，本研究首次系统揭示了 MF 对罗氏沼虾卵巢成熟的剂量效应及其可能的分子机制。

关键词：罗氏沼虾；甲基法尼酯；卵巢发育；肠道菌群；基因调控 1

Investigation on the Effects and Mechanisms of Methyl Farnesoate on the Growth and Ovarian Development of *Macrobrachium rosenbergii*

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Abstract：Methyl farnesoate (MF), a sesquiterpenoid hormone, exerts pivotal endocrine control over crustacean reproduction. To characterize its dose-dependent effects on ovarian maturation, female Macrobrachium rosenbergii (~4.2 g) were fed practical diets supplemented with 0, 3, 6 or 9 μg MF g^{-1} for 56 days. High-dose MF (9 μg g^{-1}) significantly accelerated ovarian development, evidenced by a faster transition of oocytes from stage Oc2 to Oc4 and a marked increase in oocyte diameter. Concomitantly, hemolymph vitellogenin peaked between days 28 and 42, while transcript levels of Met, Kr-h1 and Vtg were strongly up-regulated, indicating that MF stimulates vitellogenesis via the Met–Kr-h1–Vtg signalling axis. Gut-microbiome profiling revealed that MF restructured the microbial community; the 9 μg g^{-1} group exhibited the highest diversity, with dominant populations shifting toward Enterobacter and Clostridium, possibly enhancing immunity and nutrient metabolism. In contrast, the low dose (3 μg g^{-1}) suppressed both growth and ovarian development.

Key words:：*Macrobrachium rosenbergii*; methyl farnesoate; ovarian development; gut microbiota; gene regulation

Wnt4 通过 JNK/MAPK 信号通路促进中华鳖颗粒细胞增殖

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摘要：中华鳖（*Pelodiscus sinensis*）是我国传统水产养殖的重要品种之一，研究其卵泡发育对其育种有着重要的意义。卵泡发育是一个从卵母细胞被挑选出来逐步发育成小白卵泡、小黄卵泡直至成熟卵泡的过程，颗粒细胞作为卵泡的组成部分之一，在其中承担着调节卵泡发育的重要作用。本研究发现，Wnt4 在小白卵泡发育成小黄卵泡的过程中表达量急速上升，说明其在卵泡发育过程中发挥着重要的作用。Wnt4 主要在中华鳖卵泡颗粒细胞中表达，用添加了 Wnt4 抑制剂 IWP-2 的培养基对单独分离的颗粒细胞进行体外培养发现颗粒细胞的增殖受到了抑制，这是通过 RHOA 对 JNK/MAPK 信号通路进行抑制，JNK 无法受到正常的磷酸化激活，导致细胞无法顺利进入细胞周期。另外，抑制 Wnt4 还可能通过干扰能量代谢间接影响细胞的增殖。本研究揭示了 Wnt4 调控中华鳖颗粒细胞增殖的调控通路和作用机制，为研究中华鳖卵泡发育机制提供了理论基础。

关键词：中华鳖；Wnt4；颗粒细胞；JNK/MAPK 信号通路

Wnt4 Promotes the Proliferation of Granulosa Cells in *Pelodiscus sinensis* via the JNK/MAPK Signaling Pathway

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Abstract： Chinese soft-shelled turtle (*Pelodiscus sinensis*) is critical for China's traditional aquaculture. Studying its follicular development (selected oocytes differentiating into small white, small yellow, and mature follicles) is vital for breeding, with granulosa cells (follicle components) regulating this process.This study showed Wnt4 expression surged during small white-to-yellow follicle transition, indicating its role in follicular development. Wnt4 is mainly expressed in P. sinensis granulosa cells. In vitro, isolating these cells and culturing with Wnt4 inhibitor IWP-2 inhibited proliferation. Mechanistically, RHOA suppresses the JNK/MAPK pathway, impairing JNK phosphorylation/activation and blocking cell cycle progression. Wnt4 inhibition may also indirectly reduce proliferation by disrupting energy metabolism.This study clarifies Wnt4's regulatory pathway/mechanism in P. sinensis granulosa cell proliferation, laying a theoretical foundation for further follicular development research.

Key words: Chinese soft-shelled turtle; Wnt4; granulosa cells; JNK/MAPK signaling pathway

急性低氧胁迫对翘嘴鲌鳃组织损伤、血浆生化指标和相关基因表达的影响

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摘要：本研究针对翘嘴鲌养殖与运输中的低氧问题，设置低氧实验浓度为 0.60±0.05 mg·L⁻¹，采集胁迫 0h、2h、4h、6h、12h、24h 后的血液和鳃组织，深入解析低氧胁迫对翘嘴鲌生理机能和抗氧化-免疫相关基因表达的影响。结果显示：低氧胁迫前期鳃小片出现扭曲、缩短增厚，后期显著缩短并伴随血窦扩张与血细胞增多；各实验组鳃细胞凋亡率较对照组均显著升高。血浆生化分析表明，葡萄糖、脂代谢标志物及蛋白指标水平显著上调，提示糖脂代谢重构与蛋白质代谢紊乱。抗氧化相关基因 foxo1b、mapkapk2、irs2 和 ppargc1b 在胁迫 2h、4h、6h 及 24h 后表现为上调；tgfbr1、nfatc3 及 bcr 等免疫相关基因在 6H 组呈现显著上调，表明低氧胁迫可动态调控抗氧化及免疫应答相关基因的转录活性。综上所述，本研究系统解析翘嘴鲌对低氧胁迫的多层面响应，为解析鱼类低氧适应性机理提供了重要的理论依据。

关键词：翘嘴鲌；低氧胁迫；鳃组织；基因表达

Effects of acute hypoxia stress on gill tissue damage, plasma biochemical parameters and related gene expression in *Culter alburnus*

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Abstract： Low dissolved oxygen induces physiological and biochemical imbalances in fish. This study addressed hypoxic challenges during intensive farming and long-distance transport of Culter alburnus by setting a hypoxic concentration of 0.60±0.05 mg·L⁻¹. Blood and gill tissues were sampled at 0h, 2h, 4h, 6h, 12h, 24h post-stress to analyze the impacts on physiological functions and antioxidant-immune gene expression. Results showed that gill lamellae exhibited distortion, shortening, and thickening at the early hypoxic stage, followed by significant shortening with sinusoidal dilation and increased blood cells at the late stage. Gill cell apoptosis rates were significantly higher in all experimental groups than the control ($P<0.05$). Plasma biochemical analysis revealed elevated levels of glucose, lipid metabolic markers, and protein indices ($P<0.05$), indicating glycolipid metabolic reprogramming and protein metabolic disorders.Antioxidant-related genes foxo1b, mapkapk2, irs2, and ppargc1b were upregulated at 2h, 4h, 6h and 24h post-stress, suggesting a phased regulatory strategy in the antio

Key words: Culter alburnus; hypoxic stress; gill tissue; gene expression

通过 CUT&Tag 组蛋白修饰分析揭示南美白对虾（*Litopenaeus vannamei*）胚胎发育过程中动态的表观基因组景观和基因调控网络

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摘要：组蛋白修饰在模式生物的早期发育中通过精细调控基因表达发挥重要作用，但其在甲壳类动物中的作用尚不清楚。本研究首次利用 CUT&Tag 技术构建了南美白对虾胚胎发育的全面组蛋白修饰图谱，对四种关键组蛋白标记在囊胚至无节幼体七个发育阶段进行高分辨率分析，揭示了与发育进程相关的动态染色质状态转变。结合转录组数据分析，显示染色质状态与基因表达之间具有显著的时间相关性，尤其在合子基因组激活（ZGA）期间表现突出。此外，我们鉴定了与蜕皮、身体分节和神经发生等关键生物学过程相关的重要发育基因，并深入解析了潜在表观遗传调控机制。基于组蛋白修饰的顺式调控元件功能注释，进一步筛选出与关键发育基因密切相关的候选增强子和调控位点。本研究首次建立了南美白对虾胚胎表观基因组框架，揭示了早期发育中基于染色质的调控机制，为甲壳类功能基因组学研究及 ZGA 的保守性与物种特异性机制研究提供了重要资源和新的见解。

关键词：南美白对虾、CUT＆Tag 技术、组蛋白修饰、表观遗传调控、合子基因组激活

Dynamic epigenomic landscape and gene regulatory networks during embryonic development in Paciffc white shrimp (*Litopenaeus vannamei*) as revealed by histone modiffcation proffling using CUT&Tag

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Abstract： Histone modifications regulate gene expression during early development in model organisms, but their roles in crustaceans remain unclear. Here, we present the first comprehensive histone modification landscape of Litopenaeus vannamei embryogenesis using CUT&Tag. Profiling four histone marks across seven stages from blastula to nauplius revealed dynamic chromatin state transitions linked to developmental progression. Integration with transcriptome data showed strong temporal correlations with gene expression, especially during zygotic genome activation (ZGA). Key genes involved in molting, segmentation, and neurogenesis were identified, along with potential epigenetic regulatory mechanisms. Functional annotation highlighted candidate enhancers and regulatory loci linked to these genes. This study establishes the first epigenomic framework for L. vannamei embryogenesis, uncovering chromatin-based regulation and providing resources for crustacean functional genomics and insights into conserved and species-specific ZGA mechanisms.

Key words: *Litopenaeus vannamei*, CUT&Tag, Histone modiffcations, Epigenetic regulation, Zygotic genome activation

全基因组重测序揭示了四个尼罗罗非鱼群体的遗传差异和选择特征分析

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摘要：本研究旨在比较野生和中国养殖尼罗罗非鱼（*Oreochromis niloticus*）群体的遗传差异及选择特征，采集了来自埃及亚历山大港（AlT）、伊斯梅利亚省（IsT）、塞内加尔圣路易（SeT）的 3 个野生群体和中国无锡（QlT）的 60 个样本，利用全基因组重测序技术分析其遗传多样性和结构，以及选择性特征。结果表明，SeT 群体遗传多样性高，与 IsT 群体分化明显。主成分分析、系统进化树和遗传聚类分析揭示了其遗传结构，显示出显著的遗传分离。IsT 群体与 AlT 群体亲缘关系较近，但 AlT 群体与 SeT 群体间存在基因漂流。选择性扫描分析确定了六个比较组的受选择区域，发现 JAK-STAT 通路富集频率最高，与其免疫和生长调控相关。在该通路和代谢系统相关的嘌呤代谢通路内鉴定了 ifngr2, clcf1, cish, ak7, nme6, pde2a, pde4d 和 adcy8，8 个与抗病和繁殖相关基因。

关键词：全基因组重测序；尼罗罗非鱼；遗传多样性；遗传结构；选择特征

Genetic Differences and Selection Signatures of Four Nile Tilapia (*Oreochromis niloticus*) Populations as Determined by Whole-Genome Resequencing

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Abstract：Oreochromis niloticus, a key farmed fish in China's aquaculture, has seen reduced genetic diversity due to long-term inbreeding. To study genetic differences, we analyzed 60 samples from three wild populations and one domesticated population in China using whole-genome resequencing. The SeT population had the highest genetic diversity and differed significantly from IsT. Analyses showed clear genetic separation among the four populations. Close genetic ties were found between IsT and AlT, and gene flow between AlT and SeT. Selective sweep analyses revealed regions under selection in six comparisons, with the JAK-STAT signaling pathway showing the highest enrichment, linked to immune regulation and growth. Key genes in this pathway and purine metabolism were identified, indicating strong selection for disease resistance and reproductive traits in breeding programs. These findings will aid in genetic breeding strategies and germplasm characterization.

Key words: Whole-genome resequencing; *Oreochromis niloticus*; Genetic diversity; Genetic structure; Selection signatures

水流胁迫下黄河鲤肌肉发育的表观遗传调控：全基因组甲基化解析

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摘要：为阐明黄河鲤（*Cyprinus carpio haematopterus*）肌肉组织响应水流胁迫的表观遗传调控机制，本研究对水流胁迫组（EG，3 bl/s）和对照组（CG，0.30 cm/s）养殖12周后的肌肉组织进行了全基因组亚硫酸氢盐测序分析。结果显示，两组比较共鉴定出17955个差异甲基化区域，注释得到4824个差异甲基化基因。这些基因显著富集于MAPK信号通路、胰岛素信号通路以及肌动蛋白细胞骨架调控等通路。研究表明，水流胁迫可能通过降低肌肉生长相关基因的甲基化水平，激活其转录表达，从而增强黄河鲤的生理适应能力。本研究从表观遗传学角度揭示了黄河鲤肌肉组织适应水流胁迫的分子机制，为其生长性能的遗传改良提供了理论依据。

关键词：黄河鲤（*Cyprinus carpio haematopterus*）；水流胁迫；表观遗传；全基因组甲基化

Epigenetic Regulation of Muscle Development in Yellow River Carp (*Cyprinus carpio haematopterus*) under Water Flow Stress: A Genome-Wide DNA Methylation Analysis

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Abstract： To elucidate the epigenetic regulatory mechanisms underlying the response of muscle tissue to water flow stress in Yellow River carp (*Cyprinus carpio haematopterus*), this study conducted whole-genome bisulfite sequencing on muscle tissues from fish reared under water flow stress (EG, 3 bl/s) and control conditions (CG, 0.30 cm/s) for 12 weeks. The results revealed a total of 17,955 differentially methylated regions between the two groups, which were annotated to 4,824 differentially methylated genes. These genes were significantly enriched in key pathways including the MAPK signaling pathway, insulin signaling pathway, and regulation of actin cytoskeleton. The findings indicate that water flow stress may enhance physiological adaptability in Yellow River carp by reducing methylation levels of muscle growth-related genes and activating their transcriptional expression. This study provides epigenetic insights into the molecular mechanisms by which muscle tissue adapts to water flow stress, offering a theoretical foundation for genetic improvement of growth performance in this species.

Key words: Yellow River carp (*Cyprinus carpio haematopterus*); Water flow stress; Epigenetics; Whole-genome methylation

海带养殖群体的遗传同质化及其产业挑战

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摘要：海带（*Saccharina japonica*）是我国最重要的养殖藻类，其长期的大规模栽培促进了产业发展，但也导致了种质资源的遗传同质化风险。我们在山东荣成与福建两个核心产区，系统分析了主要养殖品系的遗传结构、农艺性状及化学成分。结果显示，不同品系在形态学指标上差异有限，遗传分化程度低，部分品系间存在明显同质化趋势。在十年的跟踪研究中，我们发现独立育苗场间普遍采用统一的亲本选择与育苗工艺，加之亲本共享与精子污染，显著加剧了群体间的遗传趋同。同时，杂交新品种（如 205×B013 后代）的引入能够有效增加群体的遗传复杂性，并在一定程度上改善产量与性状表现。然而，2021–2022 年荣成海带灾害也提示遗传单一性使养殖群体易受环境胁迫。整体上，海带养殖正面临“高产稳定”与“遗传多样性保持”的双重挑战。我们建议加强核心种质收集与利用，优化育种策略，并建立长期的遗传监测体系，以支撑海带产业的可持续发展。

关键词：海带；遗传同质化；种质资源；杂交育种；可持续养殖

Genetic Homogeneity in *Saccharina japonica* Aquaculture: Challenges and Implications for Sustainable Kelp Farming

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Abstract： *Saccharina japonica* is the most important cultivated macroalga in China. While large-scale aquaculture has boosted production, it has also raised concerns about genetic homogeneity in farmed stocks. We investigated principal cultivars in Rongcheng (Shandong) and Fujian, combining microsatellite genotyping, agronomic traits, and chemical composition analyses. Results revealed limited morphological variation among cultivars and low genetic differentiation, with clear signs of homogenization. Standardized parental selection, uniform hatchery practices, parental stock sharing, and sperm contamination have collectively accelerated convergence across hatcheries. Nevertheless, hybrid breeding provided new opportunities. The 205 × B013 hybrid lineage introduced distinct genetic components, increased diversity, and improved productivity. Yet, the 2021–2022 mass mortality in Rongcheng, where uniform stocks collapsed under prolonged high transparency, highlighted the vulnerability of homogeneous populations. Only genetically distinct hybrids such as Zhongbao No.1 showed stronger resilience.

Key words: *Saccharina japonica*; genetic homogeneity; germplasm resources; hybrid breeding; sustainable aquaculture

染色体水平的基因组揭示了黑斑蛙（*Pelophylax nigromaculatus*）中保守的性别决定区和 KANK1 的调控潜力

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摘要：黑斑侧褶蛙（*Pelophylax nigromaculatus*）具有明显的两性异形现象，其雌性个体显著大于雄性个体，因此雌性单性养殖具有更高的经济价值，但其性别决定机制长期不明。本研究利用长读长测序与 Hi-C 技术，获得首个染色体水平基因组，并在比较基因组学分析中发现第 1 号染色体存在保守性别决定区块，包含 DMRT 基因簇和 KANK1。对自然群体的全基因组重测序和 GWAS 进一步定位到 Chr1:460.0–460.4 Mb 的性别分化区，并开发出分子标记，实现超过 95%的性别判定准确率。转录组和 qPCR 结果表明 KANK1 在卵巢中显著上调，Hi-C 互作揭示该区域形成独立的拓扑结构域，提示其具有顺式调控潜力。综上，本研究首次解析黑斑蛙性别决定的基因组基础，提出 KANK1 为关键候选因子。本研究结果可为下一步开展黑斑蛙性别相关基因的功能研究以及性别相关分子标记的开发提供重要参考。

关键词：性别决定，黑斑侧褶蛙，染色体水平基因组组装，KANK1，Hi-C 染色质相互作用，比较基因组学

Chromosome-level genome assembly reveals a conserved sex-determining region and the regulatory potential of KANK1 in the black-spotted frog, *Pelophylax nigromaculatus*

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Abstract： The black-spotted pond frog (Pelophylax nigromaculatus) shows marked sexual dimorphism, with females much larger than males, making female monosex culture highly valuable. Yet its sex-determining mechanism remains unclear. Here we report the first chromosome-level genome assembly using long-read sequencing and Hi-C. Comparative genomics revealed a conserved sex-determining block on chromosome 1 containing the DMRT cluster and KANK1. Whole-genome resequencing and GWAS localized a sex-differentiated region (Chr1:460.0–460.4 Mb), from which molecular markers were developed with >95% accuracy for sex identification. Transcriptome and qPCR analyses showed strong ovary-biased expression of KANK1, and Hi-C maps indicated that this region forms a discrete topologically associating domain, suggesting cis-regulatory potential. Together, our study provides the first genomic basis of sex determination in P. nigromaculatus and identifies KANK1 as a candidate factor, offering valuable references for functional studies and marker development.

Key words: Sex determination, Pelophylax nigromaculatus, Chromosome-level genome assembly, KANK1, Hi-C chromatin interaction, Comparative genomics

基于性别分子标记探究刺参早期性别分化调控机制

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摘要：利用性别特异性分子标记实现了发育早期幼参的性别鉴定，并在此基础上开展性别分化机制研究。对 90 日龄幼参进行雌雄转录组比较分析，鉴定到大量差异选择性剪切事件，这些差异基因主要涉及转录相关蛋白、肌纤维蛋白形成及转运蛋白等功能。通过表达谱构建、差异基因筛选及功能富集分析，发现多个与早期性别分化相关的基因，其中类固醇合成与分泌通路具有重要作用。靶向代谢组学检测显示，9 种类固醇激素（包括几种性腺发育相关类固醇）在雌雄个体间无显著差异。通过 RNA 干扰技术敲降性类固醇合成通路中的 3 个下游关键基因，证实该通路在幼参早期性别分化过程中发挥重要调控作用。研究结果为阐明棘皮动物性别分化机制提供了分子基础。

关键词：刺参，性别分化，分子标记

Investigating the Regulatory Mechanisms of Early Sex Differentiation in *Apostichopus japonicus* Using Sex-Specific Molecular Markers

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Abstract：Utilizing sex-specific molecular markers, we achieved early sex identification in juvenile sea cucumbers and investigated their sex differentiation mechanisms. Transcriptomic analysis of 90-day-old individuals revealed numerous sex-specific alternative splicing events, primarily involving transcription-related, myofiber formation-related, and transport proteins. Integrated analysis identified multiple sex-differentially expressed genes, highlighting the significant role of steroid biosynthesis and secretion pathway. Targeted metabolomics showed no significant differences in nine steroid hormones (including gonadal development-related steroids) between sexes. RNAi-mediated knockdown of three key downstream genes in the steroidogenic pathway confirmed its crucial regulatory role in early sex differentiation. These findings provide important molecular insights into sex differentiation mechanisms in echinoderms.

Key words: *Apostichopus japonicus*；sex differentiation；molecular markers

香豆素联合传染性造血器官坏死病毒灭活疫苗对虹鳟的免疫效果

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甘肃农业大学

摘要：本研究成功研发了一种添加香豆素佐剂的 IHNV 灭活疫苗，提高了虹鳟的免疫力。实验分为三组：对照组、疫苗组和香豆素+疫苗组，每组注射 150μL。14 天后攻毒，香豆素+疫苗组存活率最高（66%），且脾脏损伤和炎症反应最小。该组血清抗氧化酶活性和免疫基因表达也最高，表明香豆素联合 IHNV 灭活疫苗能有效预防 IHNV 感染，对虹鳟养殖业中的 IHNV 控制具有重要意义。

关键词：香豆素; 疫苗; 虹鳟; 免疫效果; IHNV

Immune effects of coumarin combined with inactivated infectious hematopoietic necrosis virus vaccine on rainbow trout (*Oncorhynchus Mykiss*)

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Abstract： This study successfully developed an inactivated IHNV vaccine with coumarin adjuvant, which enhanced the immunity of rainbow trout. The experiment was divided into three groups: the control group, the vaccine group, and the coumarin + vaccine group, with each group receiving an injection of 150 μL. After 14 days, the fish were challenged with the virus. The survival rate of the coumarin + vaccine group was the highest (66%), and it had the least spleen damage and inflammatory response. The serum antioxidant enzyme activity and immune gene expression in this group were also the highest. This indicates that the combination of coumarin and inactivated IHNV vaccine can effectively prevent IHNV infection and is of great significance for the control of IHNV in rainbow trout aquaculture.

Key words: Coumarin; Vaccine; Rainbow trout; Immune effect; IHNV

肝脏转录组和代谢组联合解析大口黑鲈（*Micropterus salmoides*）剩余采食量差异的分子机制

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摘要：为探究大口黑鲈剩余采食量（RFI）差异的分子机制，本研究在单独饲养（15d 预实验+63d 正式实验）基础上，根据 RFI 值选取高（HRFI）、低（LRFI）组各 6 尾鱼，进行肝脏转录组与代谢组分析。共鉴定到 477 个差异表达基因（220 上/257 下）和 53 种差异代谢物（26 上/27 下）。KEGG 富集显示，LRFI 组显著富集于氨基酸代谢、能量代谢、类固醇激素代谢等通路。精氨酸生物合成与 mTOR 通路协同促进蛋白质合成；糖酵解/糖异生和丙酮酸代谢中关键基因上调，增强能量转化与葡萄糖利用；类固醇代谢中维生素 D 转和脱氢表雄酮含量降低，表明低 RFI 个体可能将更多能量用于生长；细胞色素 P450 通路中谷胱甘肽 S-转移酶及促炎因子表达升高，提示高 RFI 群体可能承受更高环境胁迫与免疫压力。本研究通过多组学分析揭示了大口黑鲈 RFI 差异的潜在机制，为其遗传育种提供依据。

关键词：剩余采食量；大口黑鲈；肝脏；转录组；代谢组

The molecular mechanism of the difference in residual feed intake of largemouth bass (*Micropterus salmoides*) was analyzed by liver transcriptome and metabolome

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Abstract: In order to explore the molecular mechanism of the difference in residual feed intake (RFI) of largemouth bass, on the basis of separate feeding (15 d pre-experiment + 63 d formal experiment), 6 fish in high (HRFI) and low (LRFI) groups were selected according to the RFI value for liver transcriptome and metabolomics analysis. A total of 477 differentially expressed genes (220 up / 257 down) and 53 differential metabolites (26 up / 27 down) were identified. KEGG enrichment showed that the LRFI group was significantly enriched in pathways such as amino acid metabolism, energy metabolism, and steroid hormone metabolism. Arginine biosynthesis and mTOR pathway synergistically promote protein synthesis ; key genes in glycolysis / gluconeogenesis and pyruvate metabolism were up-regulated to enhance energy conversion and glucose utilization. The contents of vitamin D and dehydroepiandrosterone in steroid metabolism decreased, indicating that individuals with low RFI may use more energy for growth.

Key words: Residual feed intake; *Micropterus salmoides*; Liver; Transcriptome; Metabolome

新型溴系阻燃剂十溴二苯乙烷 DBDPE 对鲤的毒性效应研究

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摘要：十溴二苯乙烷（Decabromodiphenyl ethane, DBDPE）作为一种新型溴代阻燃剂，使用量和产量逐年上升，已成为全球范围内广泛存在的新兴污染物, 在大气、水体、土壤、生物介质等中都有检出，其环境安全问题备受关注。本研究以鲤（*Cyprinus carpio*）作为实验对象，探究不同浓度（0.1μg/L，1μg/L，10μg/L）DBDPE 暴露对鲤各组织的影响。结果表明，DBDPE 暴露导致肠、鳃、肝、肾组织损伤, 随着浓度的增加，损伤加重。此外，对肠道进行微生物多样性测序分析，发现 DBDPE 暴露改变了鲤肠道菌群组成。有益菌丰度显著降低($P<0.05$)。综上所述，DBDPE 暴露会引起鲤各组织器官的不同程度损伤，改变肠道菌群组成。研究结果将为 DBDPE 对鱼类的毒性效应研究提供一定的理论依据。

关键词：十溴二苯乙烷；毒性效应；损伤；肠道菌群；鲤

Toxic Effects of a Novel Brominated Flame Retardant，Decabromodiphenyl Ethane (DBDPE) to Common Carp (*Cyprinus carpio*)

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Abstract：Decabromodiphenyl ethane (DBDPE), an emerging brominated flame retardant, has been increasingly produced and utilized in recent years. It is now ubiquitously detected across various environmental matrices, has been recognized as a widespread emerging contaminant on a global scale. In this study, juvenile common carp (Cyprinus carpio) were exposed to environmentally relevant concentrations of DBDPE (0.1, 1, and 10 μg/L) to evaluate its tissue-specific toxicity. The results demonstrated that DBDPE exposure induced concentration-dependent histopathological damage in multiple tissues, including the intestine, gill, liver, and kidney. Moreover, high-throughput 16S rRNA sequencing revealed significant disruptions in the composition of the gut microbiota following DBDPE exposure. Notably, the abundance of beneficial bacteria was markedly reduced ($P < 0.05$). In summary, these results demonstrate that DBDPE exposure induces multi-tissue toxicity and gut microbiota dysbiosis in common carp, providing important insights into the ecological risks of DBDPE in aquatic organisms.

Key words: Decabromodiphenyl ethane; Toxic effects; Damage; Gut microbiota; *Common carp*

碳酸碱暴露下大口黑鲈组织应答与肌肉营养品质的综合评价

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摘要：本研究综合考察了碳酸盐碱水环境下大口黑鲈的适应机制与养殖效果。通过急性碱胁迫实验，确定其 96 h-LC$_{50}$为 41.47 mmol/L。高碱组（CA45）出现鳃丝变形、肝细胞坏死等组织损伤，血清抗氧化能力先升后降，渗透调节相对稳定，而能量代谢和激素水平上升，但肝脏功能受损导致部分指标低于低碱组。转录组分析显示，鳃中固醇合成、萜类骨架合成及细胞黏附通路基因（如 hmgcs1、col1a 等）显著变化。在 80 天慢性碱水养殖实验中，随着碱度升高，肌纤维密度增加，肌肉质地未受显著影响。其中 CA20 组表现出较好的生长性能，出肉率和肥满度较高；CA15 组肌肉粗脂肪较低，氨基酸和脂肪酸组成更优，必须氨基酸评分最高，且多不饱和脂肪酸 EPA 和 DHA 含量提升。挥发性物质中壬醛和辛醛等刺激性风味含量减少，并鉴定出 16 种特征风味物。以上结果表明，适度碱水养殖可改善大口黑鲈肌肉品质和风味，但过高碱度会引发组织损伤和代谢抑制。

关键词：碳酸盐碱；大口黑鲈；组织应答；肌肉品质

Comprehensive Evaluation of Tissue Response and Muscle Nutritional Quality in Largemouth Bass (*Micropterus salmoides*) under Carbonate Alkalinity Exposure

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Abstract： This study comprehensively investigates the adaptive responses and aquaculture performance of largemouth bass (*Micropterus salmoides*) under carbonate alkaline water conditions. Acute alkaline stress tests determined a 96 h-LC$_{50}$ value of 41.47 mmol/L. High alkalinity exposure (CA45 group) resulted in tissue damage including gill filament deformation and hepatocellular necrosis. Serum antioxidant capacity initially increased but was subsequently suppressed, osmoregulation remained relatively stable, and energy metabolism and hormone levels were elevated; however, impaired liver function led to certain physiological indicators being lower than those in the low alkalinity group. Transcriptome analysis revealed significant alterations in the expression of genes involved in steroid biosynthesis, terpenoid backbone biosynthesis, and cell adhesion pathways (e.g., hmgcs1, col1a) in gill tissue. In an 80-day chronic aquaculture trial, muscle fiber density increased with rising alkalinity, while muscle texture parameters remained largely unaffected.

Key words: Carbonate alkalinity; Largemouth bass; Tissue response; Muscle quality

克氏原螯虾体色的全基因组遗传解剖及彩色品种的潜在育种应用

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摘要：克氏原螯虾（*Procambarus clarki*i），俗称小龙虾，在水产养殖和观赏领域均具有重要价值，但其产量与营养品质的提升仍面临挑战。本研究分析了野生型（WT）、黑魂（BK）、白虾（W）、红虾（R）、蓝幽灵（BG）、三色（T）、橙幽灵（OG）和中国蓝（CB）8个种质群体，通过核基因组与线粒体基因组比较证实它们均属于克氏原螯虾变种。BK、OG和R/W群体与WT存在明显的遗传分化，而CB、BG和T则表现出来自其它5个变种的混合遗传背景。与WT相比，BK品系以螯足细长为特征，表现出更高的腹部出肉率、更低的攻击性以及更高的高密度养殖存活率。SCARB1基因被确定为白-红色变异的重要候选基因。这些发现为螯虾体色研究提供了基础遗传学与分子生物学见解，并筛选出具有提升产量、观赏价值与品质性状潜力的优良种质。

关键词：克氏原螯虾（*Procambarus clarkii*）；种质资源；体色；全基因组重测序；遗传特征；育种潜力

Genome-wide genetic dissection of body color and potential breeding application of the colourful varieties of red swamp crayfish (*Procambarus clarkii*)

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Abstract： The red swamp crayfish (*Procambarus clarkii*) is valued in both aquaculture and ornamental contexts, yet enhancing its production and nutritional quality remains challenging. We analyzed eight germplasm populations—wild-type (WT), Black King (BK), White (W), Red (R), Blue Ghost (BG), Tricolor (T), Orange Ghost (OG), and China Blue (CB)—and confirmed their classification as P. clarkii varieties through nuclear and mitochondrial genome comparisons. BK, OG, and R/W populations showed clear genetic differentiation from WT, while CB, BG, and T exhibited mixed ancestry from the other five varieties. BK crayfish, characterized by slimchelae, displayed a higher abdominal meat yield, reduced aggression, and improved survival in high-density aquaculture compared to WT. The scavenger receptor B1 (SCARB1) gene was identified as a candidate for white-red color variation, while color differences between BK and BG were attributed to two genetic factors. These findings provide foundational genetic and molecular insights into crayfish body color and identify promising germplasms for enhancing product.

Key words: Red swamp crayfish (*Procambarus clarkii*); Germplasm resources; Body colour; Whole-genome sequence; Genetic characteristics; Potential breeding application

H2O2 调控坛紫菜自由丝状体成熟分子机制的初步解析

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摘要：丝状体发育不同步是限制紫菜良种规模化推广应用的关键因素之一。过氧化氢（H_2O_2）作为一种信号分子，广泛参与植物生长发育全过程。然而，H_2O_2是否及如何调控坛紫菜自由丝状体的成熟尚不明确。本研究拟通过藻体生长形态、生理指标测定和转录组学来探究清除 H_2O_2 对丝状体成熟过程的影响。实验结果表明，与正常促熟的丝状体相比，在添加 DMTU（H_2O_2清除剂）后丝状体的生长与成熟均受到明显的抑制，且该抑制现象可逆。进一步分析转录组数据发现，在清除 H_2O_2 的条件下，丝状体的光合效率和氮代谢途径均受到明显抑制，与此同时，丝状体的碳代谢、抗氧化系统以及 MAPK 信号通路发生了动态调整，并且藻体通过增强机体的硫代谢、上调热激蛋白表达以及进一步激活 PI 信号通路等方式来积极应对基础代谢受到的抑制，这些调控最终导致清除 H_2O_2 处理促熟条件下丝状体的成熟速度受到抑制。

关键词：坛紫菜；自由丝状体；H_2O_2；成熟

Preliminary analysis of the molecular mechanism of H_2O_2 regulating the maturation of free conchocelis in *Pyropia haitanensis*

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Abstract：The asynchrony in the development of conchocelis is one of the critical factors limiting the large-scale application and promotion of high-quality Pyropia varieties.H2O2 as a signaling molecule, is widely involved in the entire process of plant development.However, whether and how H2O2 regulates the maturation of free conchocelis in *Pyropia haitanensis* remains unclear.The experimental results showed that compared with conchocelis under normal ripening conditions, the growth and maturation of conchocelis were significantly inhibited after the addition of DMTU, and this inhibitory effect proved to be reversible. Further analysis revealed that under H2O2-scavenging conditions, both the photosynthetic efficiency and nitrogen metabolism pathway of conchocelis were significantly inhibited. Moreover, the algae actively responded to the inhibition of basic metabolism by enhancing sulfur metabolism in their cells. These regulatory responses ultimately led to the inhibition of the maturation rate of conchocelis under the ripening condition with H2O2-scavenging treatment.

Key words: *Pyropia haitanensis*；free conchocelis；H_2O_2；maturation

转座元件介导的顺式调控驱动青鱼 dmrt1 进化为候选主性别决定基因

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摘要：脊椎动物的性别决定机制具有高度进化可塑性，其中剂量敏感基因 dmrt1 多次通过基因重复或等位基因多样化演化为主性别决定（MSD）基因，但其分子基础仍知之甚少。本研究基于青鱼（Mylopharyngodon piceus）雌雄单倍型基因组，在第 4 号染色体上鉴定出仅包含 dmrt1 的约 40 kb 区域，作为候选性别决定位点。进一步分析发现，该区域启动子上存在两个 Y 特异性插入：13.4 kb 高重复元件和 11 bp 基序。功能验证表明，这些插入分别作为增强子和启动子元件，在性腺分化前驱动 dmrt1 的早期特异性上调。其中，13.4 kb 插入包含的转座元件可作为顺式调控模块，介导 Y 特异性激活。本研究揭示了转座元件介导的调控创新在 dmrt1 雄性决定功能形成中的作用，并为深入理解脊椎动物性别决定系统的起源与多样化提供了新的理论依据。

关键词：青鱼、性别决定、dmrt1 基因、转座元件、等位基因多样化

Transposable element-mediated cis-regulation drives the evolution of dmrt1 as a candidate master sex-determining gene in black carp

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Abstract： Sex determination in vertebrates shows remarkable evolutionary plasticity, with diverse mechanisms and master sex-determining (MSD) genes evolving independently. The dosage-sensitive gene dmrt1 has repeatedly been recruited as an MSD gene through gene duplication or allelic diversification, but the molecular basis remains unclear. Here, we assembled haplotype-resolved genomes of XX and XY black carp (*Mylopharyngodon piceus*) and identified a ~40 kb region on chromosome 4 containing only dmrt1 as the candidate sex-determining locus. We detected two Y-specific insertions in its promoter: a 13.4 kb repetitive element and an 11 bp motif. Functional analyses showed that they act as enhancer and promoter elements, driving early allele-specific upregulation of dmrt1 before gonadal differentiation. Notably, the 13.4 kb insertion harbors transposable elements functioning as cis-regulatory modules that mediate Y-specific activation. These results highlight a transposable element–mediated regulatory innovation underlying the evolution of dmrt1 in sex determination.

Key words: Black carp, sex determination, dmrt1, transposable elements, allelic diversification

组学分析揭示急性盐度应激下草鱼组织的特异性反应

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摘要：盐度是影响硬骨鱼生存的一个关键环境因素。本研究评估了草鱼（*Ctenopharyngodon idella*）在急性盐度压力下的反应机制，重点关注鳃、肾脏和皮肤，采用组织学评估、生理和生化评估以及转录组分析。结果表明，盐度压力引起了组织的病理变化和氧化损伤。在暴露于 9 ppt 盐度压力 24 小时后，在鳃、肾脏和皮肤中分别鉴定出 306、1241 和 259 个差异表达基因（DEGs），其中重叠基因与次级主动转膜转运活性显著相关。此外，鳃主要激活与脂质代谢相关的机制，如糖鞘脂生物合成和类固醇激素生物合成，而肾脏则主要激活与细胞命运调控相关的通路，包括 Notch 和 ErbB 信号通路。相反，在盐度压力下，皮肤主要启动细胞内降解通路，如蛋白酶体和自噬通路。这表明鱼类在盐度环境中的耐盐性是多脏器协调功能的结果。总之，这项研究结果为草鱼应对盐度压力的组织特异性反应提供了见解，为培育耐盐草鱼种提供了理论基础。

关键词：草鱼，盐度，转录组，组织特异性反应

Transcriptome and serum metabolites analysis revealed tissue-specific response pathways to acute salinity stress in grass carp

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Abstract： Salinity is a key environmental factor affecting the survival of teleost fish. This study evaluated the tolerance mechanisms of grass carp (*Ctenopharyngodon idella*) under acute salinity stress, with a focus on the gills, kidneys, and skin, using histological evaluation, physiological and biochemical assessments, and transcriptomic profiling. The results indicated salinity stress induced pathological changes and oxidative damage in the tissues. Transcriptomic analysis revealed that the overlapping genes among three tissues were significantly associated with secondary active transmembrane transporter activity. Furthermore, enrichment analysis revealed that while the gills primarily activated mechanisms related to lipid metabolism, the kidneys, in contrast, mainly activated pathways associated with cell fate regulation.Conversely, the skin mostly initiated intracellular degradation pathways under salinity stress, such as the proteasome and autophagy pathways.In conclusion, the findings of this study provide insights into the tissue-specific responses of grass carp to salinity stress.

Key words: Grass carp; Salinity stress; Transcriptome; Tissue-specific response

水流刺激后的遗留效应对黄河鲤肌肉品质和风味特征的影响

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摘要：为探究停止水流刺激后的遗留效应对黄河鲤（*Cyprinus carpio haematopterus*）肌肉品质和风味特征的影响。对持续水流速组（3 bl/s，24 h/d）停止水流速后和对照组（0 bl/s）进行 12 周的养殖实验。养殖结束后，对其肌肉品质和风味特征进行分析。结果表明，肌肉品质方面，0 bl/s 组硬度和羟脯氨酸含量显著高于 3 bl/s 组（P＜0.05）；0 bl/s 组精氨酸含量显著高于 3 bl/s 组，但 C18:3n6 含量显著低于 3 bl/s 组（P＜0.05）。风味特征方面，3 bl/s 组游离氨基酸中的精氨酸、丙氨酸及异亮氨酸显著低于 0 bl/s 组（P＜0.05）；0 bl/s 组醇类和醛类含量显著高于 3 bl/s 组（P＜0.05）。这表明，水流速停止后的遗留效应对肌肉品质和风味特征的影响较大，0 bl/s 组在风味方面更为丰富，为今后通过停止水流速调控黄河鲤肌肉品质提供了参考。

关键词：水流速；遗留效应；黄河鲤；肌肉品质；风味特征

Impact of legacy effects after water flow stimulation on muscle quality and flavor characteristics of Yellow River carp (*Cyprinus carpio haematopterus*)

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Abstract： To investigate legacy effects of water flow cessation on muscle quality and flavor of Yellow River carp (*Cyprinus carpio haematopterus*), a 12-week experiment compared a group after flow cessation (3 bl/s, 24 h/d) with a static control (0 bl/s). Post-rearing analyses revealed significantly higher hardness, hydroxyproline, and arginine in the 0 bl/s group, but lower C18:3n6 ($P < 0.05$). For flavor, the 0 bl/s group had higher levels of arginine, alanine, isoleucine, alcohols, and aldehydes ($P < 0.05$), indicating greater flavor complexity. These results demonstrate that water flow cessation legacy effects enhance muscle quality and flavor richness, supporting flow management for quality improvement in Yellow River carp.

Key words: water flow cessation; *Cyprinus carpio haematopterus;*

皮肤 miRNA 转录组鉴定揭示了 novel-m0065-3p 通过调控 IRF7 介导虹鳟抗 IHNV 免疫应答

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摘要：miRNA 是调控宿主先天性免疫应答的关键因子，但其在虹鳟抗病毒免疫调控中的功能研究仍然较少。本研究分析了虹鳟感染 IHNV 后 48 h 与对照组的 miRNA 图谱、novel-m0065-3p 与干扰素调节因子 7（IRF7）的时空表达，以及 novel-m0065-3p-IRF7 的免疫调控机制。miRNA-seq 鉴定了 23 个上调和 25 个下调的差异表达 miRNAs（DEMs）。表达模式表明 novel-m0065-3p 与 IRF7 可能是虹鳟免疫应答的潜在调控因子。功能分析显示 novel-m0065-3p 的过表达显著降低了肝细胞中 IRF7 的表达，而 IRF7 的引入则减弱了这种效应。过表达 novel-m0065-3p 可以促进肝细胞增殖并抑制凋亡。此外，IRF7 的过表达显著降低了 IHNV 的病毒拷贝数。体内注射 novel-m0065-3p 显著改变了 IRF7 的表达。本研究为靶向药物研发和定向育种提供了宝贵的信息。

关键词：虹鳟；RNA-seq；Novel-m0065-3p-IRF7

Skin microRNA transcriptomic and functional analysis revealed novel-m0065-3p regulating antiviral immune responses via targeting IRF7 in rainbow trout (*Oncorhynchus mykiss*) infected with IHNV

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Abstract： Studies on the involvement of miRNAs in rainbow trout (*Oncorhynchus mykiss*) antiviral response are still lacking. In this study, miRNA profiles of 48 hpi compared to control, novel-m0065-3p and IRF7 expression, and novel-m0065-3p-IRF7 functions were examined in rainbow trout skin following IHNV challenge. Transcriptome analysis identified 23 up-regulated and 25 down-regulated DEMs. Expression patterns suggested that novel-m0065-3p and IRF7 were potential regulators in antiviral immune responses of rainbow trout. Functional analysis revealed that the overexpression of novel-m0065-3p reduced significantly IRF7 expression in liver cells, which was attenuated by the introduction of IRF7, whereas the opposite result was obtained by silencing novel-m0065-3p. Overexpressed novel-m0065-3p promoted liver cell proliferation and inhibited apoptosis. Furthermore, IRF7 overexpression inhibited significantly IHNV replication. In vivo, the injection of novel-m0065-3p changed significantly the expression of IRF7. This study provided valuable information for drug-targeted diseases research.

Key words: Rainbow trout; RNA-seq; Novel-m0065-3p-IRF7

微塑料对鲫鱼生长、抗氧化以及能量代谢的影响

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摘要：微塑料（MPs）作为新兴污染物，可通过食物链威胁鱼类健康。本研究以鲫（*Carassius auratus*）为对象（5.05±1.49g），通过投喂含不同浓度 500 μm 聚苯乙烯微塑料（PE-MPs）的饲料（0、5、50 和 100 μg/g）28 天，探究其对肌肉生长、肝脏抗氧化及肠道能量代谢的影响。结果发现，存活率无变化，但体重和生长率随浓度增加下降；肠道、肝脏和肌肉出现剂量依赖性损伤，如肠绒毛缩短、肝细胞空泡化和肌纤维排列紊乱；高浓度 MPs 使肝脏抗氧化酶（T-SOD、GSH-Px）和乳酸脱氢酶（LDH）活性显著降低，提示氧化应激与代谢功能受损；肠道潜在致病菌（如 Chlamydiota 和 Cyanobacteria）丰度上升，有益菌（如 Bacillus）减少。研究表明，微塑料经食物摄入后，首先破坏肠道结构与菌群，进而经体内循环加剧肝脏氧化应激和代谢紊乱，为评估 MPs 系统毒性及健康养殖提供了依据。

关键词：微塑料；鲫；肌肉生长；抗氧化；能量代谢

Effects of Microplastics on Growth, Antioxidant Capacity, and Energy Metabolism in Crucian Carp (*Carassius auratus*)

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Abstract：Microplastics (MPs), as an emerging pollutant, can threaten fish health through the food chain. This study examined the effects of dietary exposure to 500 μm polystyrene MPs (0, 5, 50, and 100 μg/g) for 28 days on crucian carp (Carassius auratus; 5.05±1.49g). Investigating its effects on muscle growth, hepatic antioxidant capacity, and intestinal energy metabolism. Results showed reduced growth and dose-dependent tissue damage, including intestinal villi shortening, hepatic vacuolation, and muscle disorganization. High MP levels decreased liver antioxidant enzyme (T-SOD, GSH-Px) and lactate dehydrogenase (LDH) activities, indicating oxidative stress and metabolic dysfunction. Gut microbiota shifts showed increased potential pathogens (Chlamydiota and Cyanobacteria) and decreased beneficial bacteria (Bacillus). These findings suggest that ingested MPs cause intestinal damage and dysbiosis, subsequently inducing systemic oxidative stress and metabolic disruption. This study provides critical insights into MPs systemic toxicity in aquatic species.

Key words: Microplastics; *Crucian carp*; Muscle growth; Antioxidant capacity; Energy metabolism

基于磷酸化蛋白质组学探究坛紫菜耐盐机制

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摘要：盐胁迫是制约全球农业生产的最严重的非生物胁迫之一。潮间带红藻坛紫菜（*Pyropia haitanensis*）因其极强的耐盐性，成为研究植物耐盐机制的理想模型。本研究整合定量蛋白质组与磷酸化修饰组学技术，系统分析了坛紫菜在 110‰高盐胁迫下不同时间点（0、15 min、1 h、12 h）的磷酸化修饰动态变化。结果显示，共鉴定到 2,904 个蛋白质的 16,404 个磷酸化位点。利用趋势分析进一步揭示了应答盐胁迫的时序特征：早期胁迫（15 min-1 h）以广泛的蛋白质去磷酸化为主，旨在快速抑制碳代谢、光合作用等耗能过程以节省能量；而长期胁迫（12 h）则转变为以磷酸化为主导，激活囊泡运输、RNA 降解、剪接体及核苷酸切除修复等通路，以重建细胞稳态。值得注意的是，绝大多数（1,959 个）差异磷酸化蛋白的丰度并未发生改变，表明磷酸化修饰是坛紫菜快速应对盐胁迫的核心调控策略。

关键词：坛紫菜；盐胁迫；磷酸化蛋白质组学

Investigation into the Mechanisms of Salt Tolerance in *Pyropia haitanensis* Based on Phosphoproteomic Analysis

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Abstract： Salinity stress is a major abiotic constraint on global agriculture. The intertidal red alga *Pyropia haitanensis*, renowned for its extreme salt tolerance, is an ideal model for studying salt tolerance mechanisms. This study employed quantitative proteomics and phosphoproteomics to analyze dynamic phosphorylation changes in *P. haitanensis* under 110‰ salinity at 0, 15 min, 1 h, and 12 h. We identified 16,404 phosphorylation sites on 2,904 proteins. Trend analysis revealed a time-dependent response: early stress (15 min–1 h) involved widespread dephosphorylation to rapidly inhibit energy-consuming processes like carbon metabolism and photosynthesis. In contrast, long-term stress (12 h) shifted to phosphorylation-mediated activation of pathways such as vesicle transport, RNA degradation, and DNA repair to restore cellular homeostasis. Notably, most (1,959) differentially phosphorylated proteins showed no abundance change, highlighting phosphorylation as a key rapid regulatory strategy in salt adaptation.

Key words: *Pyropia haitanensis*; Salt stress; Phosphoproteomics

运输胁迫条件下虹鳟脾脏免疫响应规律研究

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摘要：虹鳟鱼是一种冷水鱼类，在活体运输过程中容易受到环境压力。本研究使用全同胞成年个体，设置 18°C 下的运输组：0 小时（对照组）、2 小时、6 小时运输以及 24 小时恢复期。测试了脾脏抗氧化/免疫指标，并进行了转录组和蛋白质组分析。结果显示，运输压力损害了鱼的抗氧化和免疫功能。转录组分析揭示了在运输和恢复期间通过炎症和免疫稳态进行的动态免疫调节；蛋白质组分析表明，压力触发了炎症并破坏了细胞膜稳态，而恢复期激活了免疫补偿。综合分析显示，压力直接通过细胞外基质重塑和炎症起作用，而恢复期增强了免疫力，抑制了异常获得性免疫激活并修复了损伤。这为优化虹鳟鱼运输策略和促进可持续水产养殖提供了基础。

关键词：运输胁迫；脾脏；免疫；转录组；蛋白质组

Study on the immune response of rainbow trout spleen under transport stress

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Abstract: Rainbow trout, a cold-water fish, is prone to environmental stress during live transportation. This study used full-sibling adult individuals, setting groups at 18°C: 0h (control), 2h, 6h of transportation, and 24h of recovery. Spleen antioxidant/immune indicators were tested, with transcriptome and proteome analyses conducted.Results showed transportation stress impaired the fish’s antioxidant and immune functions. Transcriptome analysis revealed dynamic immune regulation via inflammation and immune homeostasis during transportation and recovery; proteome analysis indicated stress triggered inflammation and disrupted cell membrane homeostasis, while recovery activated immune compensation. Combined analysis showed stress acted directly via extracellular matrix remodeling and inflammation, and recovery enhanced immunity, inhibited abnormal acquired immune activation, and repaired damage.This provides a basis for optimizing rainbow trout transportation strategies and promoting sustainable aquaculture.

Key words: transportation stress; spleen; immunity; transcriptome; proteome

瓦氏雅罗鱼鳃组织 miRNA 与 mRNA 整合分析揭示碱性环境适应的分子调控新机制

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摘要：瓦氏雅罗鱼（*Leuciscus waleckii*）作为具有重要经济价值的鲤科鱼类，展现出对极端碱性和盐碱环境等恶劣条件的卓越适应能力，使其成为研究盐碱适应和渗透调节机制的重要模型。面对全球土地盐碱化的挑战及盐碱水域水产养殖日益增长的趋势，解析瓦氏雅罗鱼等鱼类的适应机制对盐碱环境水产养殖的成功至关重要。本研究采集了碱胁迫 1、5、10 天（AW1、AW5、AW10）及转回淡水 1、5、10 天（FW1、FW5、FW10）的鳃组织样本，以 AW10 组作为对照。RNA 测序分析发现在胁迫阶段和恢复阶段分别存在 444 和 856 个差异表达基因。KEGG 富集分析表明：碱胁迫主要激活 ECM-受体相互作用、黏着斑和类固醇激素生物合成通路，而恢复过程则涉及细胞因子-细胞因子受体相互作用及 Toll 样受体/FoxO 信号通路。小 RNA 测序与差异表达分析联合揭示了 miRNA 与初级胆汁酸生物合成及免疫调控间的关联。

关键词：瓦氏雅罗鱼；碱度适应；转录组；miRNA-mRNA 调控网络

Integrated miRNA and mRNA analysis in gills of Amur Ide (*Leuciscus waleckii*) reveals novel insights into the molecular regulatory mechanism of alkaline acclimation

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Abstract： *Leuciscus waleckii*, a cyprinid fish of significant commercial value, demonstrates remarkable adaptability to a range of environmental conditions, including extreme alkaline and saline environments. This adaptability makes it an important model for investigating the mechanisms underlying saline-alkali adaptation and osmoregulation. Given the global challenge of land salinization and the increasing trend of aquaculture in saline-alkali environments, understanding the adaptation mechanisms of fish species such as L. waleckii is crucial for the success of aquaculture in these areas. In this study, gill tissue samples were collected from fish at 1, 5, and 10 days during alkali stress (AW1, AW5, AW10) and after transfer to freshwater (FW1, FW5, FW10), with AW10 serving as the control group. RNA sequencing identified a range of 444 and 856 differentially expressed genes (DEGs) during the stress and recovery phases. KEGG enrichment analysis highlighted key pathways: alkali stress activated ECM-receptor interaction, focal adhesion, and steroid hormone biosynthesis.

Key words: Keywords: *Leuciscus waleckii*; alkaline acclimation; Transcriptome; miRNA-mRNA regulatory network

pnp4a 和 pnp4b 在锦鲤体色中的功能研究

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摘要：锦鲤作为全球水产养殖业的重要组成部分，在观赏鱼类养殖领域占据显著地位。但目前研究多集中于红、黄色素细胞和黑色素细胞，有关虹彩细胞的体色调控研究相对较少。pnp4a 是虹彩细胞的标志基因，调控鸟嘌呤代谢和嘌呤小板形成。由于硬骨鱼的全基因组复制事件，pnp4a 存在一个旁系同源基因 pnp4b，但 pnp4b 的功能尚不明确。本研究通过基因克隆和系统进化分析发现，pnp4a 和 pnp4b 分别编码 291 和 304 个氨基酸，与斑马鱼直系同源基因高度保守。免疫双荧光发现，Pnp4a 在表皮和真皮基底层中均高表达，Pnp4b 仅分布在表皮且表达量较低。抑制剂处理实验证实，pnp4a 受 sox10 等基因调控参与嘌呤合成影响体色光泽度；而 Pnp4b 更多参与免疫应答，与 il-6 等免疫基因表达呈正相关。本研究揭示了 pnp4a 和 pnp4b 在锦鲤体色形成中的功能，为虹彩细胞的体色调控机制提供了新的思路。

关键词：pnp4a,pnp4b,锦鲤,体色,虹彩细胞

The functions of pnp4a and pnp4b in body color of koi carp

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Abstract：The koi carp, a globally significant component of aquaculture, occupy a prominent position in ornamental fish farming. However, the studies of body coloration primarily focus on melanophores and erythrophores/xanthophores, while researches associated with iridophore-mediated pigmentation are still limited. pnp4a, a marker gene of iridophores, regulates the metabolic conversion of guanosine to guanine and is implicated in purine platelet formation. Due to teleost-specific whole-genome duplication, pnp4a retains a paralogous gene, pnp4b. In this study, gene cloning revealed that pnp4a and pnp4b encode 291 and 304 amino acid protein. Immunofluorescence revealed that pnp4a was highly expressed in both the epidermal and dermal basal layers, while pnp4b was restricted to the epidermis and showed lower expression. Inhibitor treatment assays confirmed that pnp4a was regulated by sox10 and other genes to participate in purine synthesis, while pnp4b was predominantly engaged in immune response. This study elucidates the distinct roles of pnp4a and pnp4b in color pattern formation of koi carp.

Key words: pnp4a,pnp4b,koi carp ,body coloration, iridophores

大口黑鲈 MsAFP-IV基因克隆、系统进化及表达分析

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摘要：为阐明大口黑鲈（*Micropterus salmoides*）MsAFP-IV基因的分子特征、进化地位及低温应答规律，为其在胚胎玻璃化冷冻保存中的应用提供理论依据。本研究克隆并分析了抗冻蛋白基因 MsAFP-IV，探究其序列结构、系统进化及表达模式。结果显示，MsAFP-IV基因 ORF 全长 387 bp，编码 128 个氨基酸，系统进化分析表明其与太阳鱼科小口黑鲈 AFP-IV相似性最高，形成独立进化分支。实时荧光定量 PCR（qRT-PCR）检测显示，MsAFP-IV在肠组织中表达量最高，脾中表达最低；进一步探究常温（22℃）、16℃与 10℃低温胁迫下各组织表达变化，结果显示低温（16 ℃和 10 ℃）处理显著上调其在肝、血液、肌肉等组织中的表达水平，且呈温度梯度依赖性；表明 MsAFP-IV为低温诱导型抗冻基因，可作为优化玻璃化冷冻、减轻冰晶损伤的候选分子，助力大口黑鲈种质资源保护。

关键词：大口黑鲈；MsAFP-IV；抗冻蛋白；低温适应

Cloning, Phylogenetic Analysis and Expression Profiling of MsAFP-IV in *Micropterussalmoides*

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Abstract: To elucidate the molecular characteristics, evolutionary status, and low-temperature responsiveness of the antifreeze protein gene MsAFP-IV in Micropterus salmoides, and to provide a theoretical basis for its application in embryonic vitrification cryopreservation, this study cloned and characterized the MsAFP-IV gene. Sequence analysis revealed that the open reading frame (ORF) of MsAFP-IV is 387 bp in length, encoding a protein of 128 amino acids. Phylogenetic analysis demonstrated that MsAFP-IV shares the highest similarity with AFP-IV from Micropterus dolomieu, forming a distinct evolutionary clade within the Centrarchidae family. Quantitative real-time PCR (qRT-PCR) analysis showed that MsAFP-IV was expressed in the intestine, with the lowest expression in the spleen. Under low-temperature stress (16 °C and 10 °C), the expression of MsAFP-IV was upregulated in tissues such as liver, blood, and muscle in a temperature-dependent manner. These results indicate that MsAFP-IV is a cold-inducible antifreeze gene with potential applications in fish embryonic cryopreservation.

Key words: *Micropterus salmoides*; MsAFP-IV; antifreeze protein; low-temperature adaptation

斑点叉尾鮰（Ictalurus punctatus）应对禁食与复投喂的分子响应机制研究

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摘要：为阐明斑点叉尾鮰应对禁食与复投喂的分子响应机制，通过分析其在三周禁食及三周复投喂期间的生长性能、肝脏和肠道组织学特征及肝脏基因表达模式，结合转录组及 qPCR 等方法开展研究。结果显示，禁食显著抑制鮰鱼生长，复投喂后呈现生长补偿效应；禁食导致肝肠组织发生凋亡损伤，复投喂后肝脏仍存在少量凋亡细胞。三周对照组与禁食-复投喂组肝脏存在 787 个差异表达基因，而六周对照组与禁食-复投喂组仅 35 个；禁食可影响细胞周期、代谢及免疫相关基因的表达，其中代谢与细胞过程响应基因显著下调。本研究揭示了鮰鱼应对禁食与复投喂的生理机制，为理解鱼类适应营养缺乏压力的分子调控规律提供了重要参考。

关键词：斑点叉尾鮰； 禁食；复投喂；细胞凋亡；分子机制

Insights into the molecular response mechanisms of fasting stress and refeeding in channel catfish (*Ictalurus punctatus*)

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Abstract：To clarify the molecular response mechanisms of channel catfish to fasting and refeeding, this study analyzed their growth performance, liver and intestinal histological characteristics, and liver gene expression patterns during three weeks of fasting and three weeks of refeeding, combined with transcriptome and qPCR. The results showed that fasting significantly inhibited the growth of catfish, with a growth compensation effect observed after refeeding. Fasting caused apoptotic damage to liver and intestinal tissues, and a small number of apoptotic cells remained in the liver after refeeding. Transcriptome analysis revealed 787 significantly differentially expressed genes between the three-week control group and the fasting-refeeding group, while only 35 were found between the six-week control group and the fasting-refeeding group. Fasting affected gene expression related to the cell cycle, metabolism, and immune responses, among which genes involved in metabolism and cellular process responses were significantly downregulated.

Key words: Channel catfish; Fasting; Refeeding; Apoptosis; Molecular mechanisms

温度对鲇性别分化、性别相关基因表达及生长的影响

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摘要：为探究温度对鲇（Silurus asotus）性别分化、性别相关基因表达及生长的影响，对刚孵化出膜的鲇卵黄囊期仔鱼至40日龄幼鱼分别进行22℃、26℃（对照组）和30℃养殖试验，接着将各组鱼转入自然水温下培育至60日龄，对各组性比、性腺组织发育、性别相关基因表达与生长情况进行测定。结果显示，30℃组鲇的雄性率为60.9%，显著高于26℃组（42.1%）和22℃组（31.4%）（$p<0.05$）；同时，该组鲇的性腺发育速度快于26℃组和22℃组，其生殖细胞直径较大；组内雄性性别相关基因sox9a在性腺分化完成的40日龄表达量最高，而22℃组雌性性别相关基因foxl2和cyp19a1a在40日龄表达量最高（$p<0.05$）。此外，随着温度的升高，各组鱼的体长、全长、体重均逐渐增加，30℃组鲇的生长指标均显著高于26℃组和22℃组，成活率也最高（$p<0.05$）。

关键词：鲇；温度；性别分化；性比；生长

Effects of Temperature on Sex Differentiation, Sex-Related Gene Expression, and Growth in *Silurus asotus*

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Abstract：To investigate the effects of temperature on sex differentiation, sex-related gene expression, and growth in *Silurus asotus*, newly hatched yolk sac stage fry were reared at 22℃, 26℃(control group), and 30℃ until 40 days post-hatch. Subsequently, all groups were transferred to natural water temperatures for rearing until 60 days old. Sex ratios, gonadal tissue development, sex-related gene expression, and growth parameters were then measured across groups. Results showed that the male ratio in the 30℃ group was 60.9%, significantly higher than in the 26℃group (42.1%) and 22℃group (31.4%) ($p<0.05$). Additionally, gonadal development in the 30℃group progressed faster than in the 26℃ and 22℃groups, with larger germ cell diameters. Within this group, the male-associated gene sox9a exhibited peak expression at 40 days post-hatch when gonadal differentiation was complete. Conversely, the female-associated genes foxl2 and cyp19a1a in the 22℃group showed highest expression at 40 days ($p<0.05$). Furthermore, as temperature increased, body length, total length, and body weight gradually increase.

Key words: *Silurus asotus*；Temperature；Sex Differentiation；Sex Ratio;；Growth

转录组学揭示 LPS 与 poly(I:C)感染下鳜皮肤免疫防御机制

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摘要：本研究通过 LPS 和 poly(I:C)刺激鳜（Siniperca chuatsi）皮肤组织，在 0 h、3 h、6 h 和 12 h 时间点检测基因表达谱。结果显示：LPS 处理组发现 648 个共同差异表达基因（DEG）spoly(I:C)处理组发现 484 个共同 DEGs，其中 288 个 DEGs 呈现一致性调控。分析表明，MAPK 信号通路和细胞因子-细胞因子受体相互作用通路分别是显著富集和最显著受抑制的通路。信号通路中的 DEGs 分别为（dusp1、dusp2、dusp5、dusp8a、jun、jund-a、jund-b、jun-l、fosab、epha2a、nr4a1、nr4a1l、hras、il1b、fgf1、nfatc1 和 prkacab）及（tnfrsf9、tnfrsf10b、tnfrsf12a、il10ra、il21r、il1bpf2）且所有实验组中均发显著变化。

关键词：鳜；皮肤；LPS；poly (I:C)；免疫应答

Transcriptome to reveal the immunological defenses in mandarin fish (*Siniperca chuatsi*) skin with LPS and poly (I:C) infection

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Abstract：This study explored gene expression profiles and potential immune signaling path ways in the skin of mandarin fish (Siniperca chuatsi) following stimulation with LPS or poly (I:C) at 0 h, 3 h, 6 h, and 12 h. Results revealed 648 shared differentially expressed genes (DEGs) across LPS treatment groups and 484 shared DEGs under poly (I:C) treatment. Among these, 288 DEGs were consistently regulated across all condi tions. Functional analysis identified the MAPK signaling pathway and cytokine–cytokine receptor interaction as the most significantly enriched and suppressed pathways. The DEGs within the MAPK signaling pathway (dusp1, dusp2, dusp5, dusp8a, jun, jund-a, jund-b, jun-l, fosab, epha2a, nr4a1, nr4a1l, hras, il1b, fgf1, nfatc1, and prkacab) and cytokine-cytokine receptor interaction (tnfrsf9, tnfrsf10b, tnfrsf12a, il10ra, il21r, il1b, pf2) were significantly changes in all compared groups. The protein-protein interactions analysis suggested that jun was the hub gene.

Key words: *Siniperca chuatsi;* skin; LPS; poly (I:C); immune response

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

Effects of thyroxine on embryonic and larval growth and development of Fujian oyster (*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 of 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 TH levels and T4 concentration in larvae after direct T4 treatment ($P < 0.05$), with no significant difference between TU and control groups. In the 1.29×10^{-8} mol/L T4 group, the T3/T4 ratio increased from the cleavage to the blastula stage but decreased in other groups. Low to moderate T4 levels promote larval growth, with T3/T4 ratio changes from the cleavage to blastula stage that may regulate development. Broodstock exposure is better for studying THs' impact on embryonic development.

Key words: *Crassostrea angulata*; thyroxine (T4); embryonic developme

黄条鰤 GAL/GALR 系统鉴定及信号转导机制研究

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摘要：Galanin (GAL)是一种由 29 个 aa 组成的神经肽，由其受体 GALR 介导参与多种生理过程。为探究 GAL/GALR 信号转导通路，本研究以黄条鰤为模型克隆并鉴定出了 gal 基因和六种 galr 基因。配体/受体互作实验表明，GAL 能增强转染了 GALR2a/2b 的 COS-7 细胞中的 CRE-luc 活性且此效应能被 PKA 通路的两种抑制剂阻断。同样，用 GAL 刺激转染 GALR1a、GALR1b、GALR2a 或 GALR2b 的细胞后，胞中的 SRE-luc 活性增强且可被 PKC 通路的两种阻断剂抑制该作用。此外，GAL 还可增强表达 GALR1a、GALR2a 或 GALR2b 的细胞中 NFAT-RE-luc 活性且该作用能被两种 Ca2+途径拮抗剂抑制。而用 GAL 刺激转染 GALR1b 的细胞后，抑制了细胞中 NFAT-RE-luc 活性。综上，黄条鰤 GAL 与特定 GALR 结合后激活或抑制下游多种信号通路，进而发挥其生理功能的多样性。

关键词：甘丙肽；甘丙肽受体；信号转导；黄条鰤

Identification and signal transduction mechanisms of the GAL/GALR system in yellowtail kingfish (*Seriola lalandi*)

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Abstract: Galanin (GAL) is a 29-amino acid neuropeptide, mediating various physiological processes through its receptors (GALRs). To explore the GAL/GALR signaling pathway, this study cloned the gal gene and identified six galanin receptor genes using yellowtail kingfish as a model. Ligand-receptor interaction assays demonstrated that GAL significantly increased CRE-luc activity in COS-7 cells expressing its cognate receptors GALR2a/2b, and this stimulatory effect was attenuated by two inhibitors of the PKA pathway. Similarly, an evident induction of SRE-luc activity was observed when COS-7 cells transfected with GALR1a, GALR1b, GALR2a, or GALR2b were challenged with GAL, and two blockers of the PKC pathway suppressed this action. In addition, GAL also elevated NFAT-RE-luc activity in COS-7 cells expressing GALR1a, GALR2a, or GALR2b, and this promotion was inhibited by two antagonists of the Ca2+ route. However, GAL inhibited NFAT-RE-luc activity in COS-7 cells expressing GALR1b. Overall, GAL activates and inhibits multiple signaling pathways, contributing to diverse physiological functions.

Keywords: GAL; Galanin receptor; Signaling pathway; Yellowtail kingfish

半滑舌鳎 TAC3/TACR3 系统鉴定及信号转导机制研究

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摘要：NKB 和 NKBRP 是由 tac3 基因编码的下丘脑神经肽，通过结合其受体 tacr3 参与了脊椎动物生殖和摄食等多种生理过程。为了深入探究 TAC3/TACR3 信号转导机制，首先从半滑舌鳎的脑组织中鉴定出 NKB/NKBRP 的编码基因 tac3a 及两个受体基因 tacr3a 和 tacr3b。荧光定量结果显示 tac3、tacr3a 和 tacr3b 在各个组织中广泛表达，其中 tac3 在脑和肠中高表达，tacr3a 在肠中显著表达，而 tacr3b 在卵巢中表达量最高。配体/受体互作实验结果表明，NKB/NKBRP 与受体 TACR3a 和 TACR3b 结合后均能显著增加 COS-7 细胞中 CRE-luc、SRE-luc 和 NFAT-RE-luc 活性；相关信号通路抑制剂均降低了 NKB/NKBRP 的诱导作用。综上所述，半滑舌鳎中存在 TAC3/TACR3 系统，并且 AC/PKA、PLC/PKC 和 Ca2+三条信号通路均介导了其生理功能。

关键词：NKB; NKBRP; TACR3;信号转导；半滑舌鳎

Identification and signal transduction mechanism of the TAC3/TACR3 system in the half-smooth tongue sole (*Cynoglossus semilaevis*)

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Abstract: Neurokinin B (NKB) and neurokinin B related peptide (NKBRP) are hypothalamic neuropeptides encoded by the gene *tac3*, which participate in various physiological processes such as reproduction and feeding in vertebrates by binding to TACR3. To explore the signal transduction of the TAC3/TACR3 system, *tac3a* and two *tacr3* genes were identified in the half-smooth tongue sole. Quantitative real-time PCR analysis showed that *tac3a* highly expressed in the brain and intestine, *tacr3a* is predominantly expressed in the intestine, and *tacr3b* is mainly expressed in the ovary. The stimulatory effects of NKB and NKBRP were found to be mediated by inhibitors and coupled to the AC/PKA, PLC/PKC and Ca^{2+} signal pathways. Overall, our results have revealed that activation of TACR3s by NKB and NKBRP may occur with same downstream signaling events.

Keywords: NKB; NKBRP; Signaling pathway; Tongue sole

端粒到端粒基因组组装揭示大黄鱼着丝粒及环境适应性进化特征

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摘要：大黄鱼（*Larimichthys crocea*）是中国最重要的海水经济鱼类，目前养殖量最多的为闽-粤东族和岱衢族。它们在遗传背景、生长环境等方面存在差异，亟需解析其遗传信息。本研究结合 PacBio HiFi、 ONT 和 Hi-C 三种测序技术，构建了闽-粤东族与岱衢族 XY 大黄鱼端粒到端粒基因组。结果显示 24 条染色体均达 T2T 水平，基因组大小分别为 708.23 和 706.62 Mb，注释到 26,144 和 26,949 个蛋白编码基因。进一步分析发现，两族着丝粒非编码序列主要由 42 bp 的串联重复序列（命名为 Cen-42） 和 LTR/ERV1 转座元件构成，但编码基因数量和种类差异显著；系统发育分析推测两族在约 418 万年前分化，且在低温适应、花生四烯酸代谢、化学感知功能等方面存在适应性差异，这些差异在基因组结构和基因表达水平上均得到验证。本研究为大黄鱼基因组特征、生态适应与进化研究提供了重要资源和见解。

关键字：大黄鱼；着丝粒；T2T；适应性进化

T2T Genomes Unveil Centromere Architecture and Adaptive Divergence in Large Yellow Croaker (*Larimichthys crocea*)

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Abstract: The large yellow croaker (*Larimichthys crocea*) is a crucial marine economic fish in China, currently, aquaculture mainly involves the MYD and DQ populations, which differ in genetic background, growth environment, emphasizing the need to explore their complete genetic backgrounds. This study utilized PacBio HiFi, ONT, and Hi-C sequencing technologies to construct T2T genomes of XY male individual from the MYD and DQ populations. The 24 chromosomes of both populations reached T2T level, with genome sizes of 708.23 and 706.62 Mb, and 26,144 and 26,949 protein-coding genes, respectively. The centromeric regions were mainly composed of Cen-42 and LTR/ERV1 elements, with significant differences in coding genes between the populations. Phylogenetic analysis indicated divergence around 4.18 million years ago, with adaptive differences in cold tolerance, arachidonic acid metabolism, sensory functions, and circadian rhythm regulation. This study provides valuable genetic resources and insights into the ecological adaptation and evolution of the species.

Key words: *Larimichthys crocea*, T2T-genome, centromeric, adaptive evolution

Differential activation of six galanin receptors by the spexin peptide in yellowtail kingfish (Seriola lalandi)

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Abstract： Spexin (SPX1) is a novel neuropeptide composed of 14 amino acids and well conserved across vertebrates, and it has been implicated in various physiological functions via galanin receptor 2 (GALR2) and GALR3. However, the detailed signaling pathways mediating its actions in target cells are still largely unknown. Accordingly, we addressed this issue in the present study using yellowtail kingfish as a model. SPX1 significantly increased CRE-luc activity in COS-7 expressing its cognate receptors GALR2a and GALR2b, and this stimulatory effect was attenuated by two inhibitors of the PKA pathway. Similarly, an evident induction of SRE-luc activity was observed when COS-7 cells transfected with GALR1b, GALR2a, GALR2b, GALR type 1, or GALR type 2 were challenged with SPX1, and two blockers of the PKC pathway suppressed this stimulatory action. Moreover, SPX1 markedly elevated NFAT-RE-luc activity in COS-7 cells expressing GALR1a, GALR2a, or GALR2b, and this promotion was inhibited by two antagonists of the Ca^{2+} route.

Key words: spexin; galanin receptor; signaling pathway; PKA; PKC; Ca^2

中国海水鱼养殖生产的空间演变规律研究

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摘要：伴随全球海洋经济蓬勃发展，中国海水鱼养殖业已崛起为沿海地区重要的经济支柱产业。本研究聚焦中国海水鱼养殖生产，基于 2003~2023 年省级面板数据，运用空间计量分析方法，系统解析其时空动态演变特征及空间分异规律。结果表明：（1）规模维度：中国海水鱼产量持续增长，区域差异显著，形成以华南为核心、多极协同的“一核多极”空间格局。（2）时空模式：呈现显著的“集聚-扩散”双模态特征，早期高度集聚于华南沿海，2015 年后显现向江浙沿海扩散的新态势。（3）驱动机制：自然资源禀赋、流通设施完善度与市场潜力构成核心驱动要素，共同推动养殖区域的扩张与空间转移。基于此，从产业集群发展、区域优势资源规划、科技人才投入等方向提出建议，以期优化产业空间布局、应对演变中的挑战与机遇，为实现中国海水鱼养殖业可持续发展提供科学决策支持。

关键词：中国海水鱼；空间演变；影响因素；渔业可持续发展

A Study on the Spatial Evolution Pattern of Marine Fish Aquaculture Production in China

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Abstract：Amid the global blue economy boom, China’s marine fish aquaculture has become a key economic pillar in coastal regions. Using provincial panel data (2003–2023) and spatial econometric methods, this study analyzes the spatiotemporal evolution and spatial differentiation of the industry. Key findings include:(1) Production has grown steadily with marked regional disparities, forming a “core-multipolar” pattern centered in South China.(2) Spatiotemporal dynamics show clear agglomeration-diffusion: early concentration in South China, with post-2015 diffusion toward Jiangsu and Zhejiang.(3) Key drivers are natural resources, logistics infrastructure, and market potential, which jointly shape aquaculture zonation and relocation.Recommendations cover industrial clustering, regional resource planning, and tech-talent investment to optimize spatial layout and support sustainable development.

Key words: Chinese marine fish; spatial evolution; influencing factors; sustainable fisheries development

共同富裕视域下浙江省渔民收入差距缩小路径研究

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摘要：浙江省作为全国共同富裕示范区，渔民收入问题具有典型性。本研究聚焦浙江省渔民收入现状，采用浙江省渔业统计年鉴数据，系统分析了2019-2023年浙江省渔民收入动态变化和家庭收支结构特征，深入剖析影响渔民收入的主要因素，探索新形势下缩小渔民差距的路径，为乡村振兴战略下实现渔民共同富裕提供政策参考。

关键词：共同富裕；渔民；浙江省；增收路径

Research on the Path of Narrowing the Income Gap of Fishermen in Zhejiang Province from the Perspective of Common Prosperity

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Abstract： As a national demonstration zone for common prosperity, Zhejiang Province presents a typical case of fisher income issues. This study focuses on the current status of fisher income in Zhejiang, using data from the Zhejiang Fishery Statistical Yearbook to systematically analyze the dynamic changes in fisher income and the characteristics of household income and expenditure structures in Zhejiang from 2019 to 2023. In-depth analysis the key factors influencing fisher income .and then explores pathways to narrow the fishery income gap an the new context, providing policy references for achieving fisher common prosperity under the rural revitalization strategy.

Key words: Common prosperity; fisherman; Zhejiang Province; Path to increasing income

出罪入拘：非法捕捞轻罪治理新路径证成

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摘要：随着非法捕捞水产品案件的激增，大量有悖普通民众法感和朴素认知的案件频发，该现象凸显了刑事治理背后理论与司法实践的困顿。在生态环境保护大背景下，非法捕捞轻罪的入罪不仅是由司法解释肆意扩张造成，其犯罪标准也严重依赖行政违法化，违反宽严相济的刑事政策的同时，也带来一系列严重的犯罪附随后果，引发社会矛盾。因此，应引入“出罪入拘”，这一非法捕捞轻罪治理新路径，即对该类案件严格按照刑法谦抑性要求和法益保护原则需要，用“行政拘留”的方式替代“刑事处罚”。行政拘留处理非法捕捞轻罪不仅符合二元制处罚模式逻辑和比例原则要求，也具有一定的制度基础和现实优势，能够实际解决刑事治理中的诸多难题。与其他治理路径相比，行政拘留能够达到较好的社会治理效果。

关键词：非法捕捞水产品罪；出罪；行政拘留；情节轻微

Justification of the New Path for the Governance of Minor Illegal Fishing Offenses: From Conviction to Detention

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Abstract： Against the backdrop of ecological and environmental protection, the criminalization of minor illegal fishing offenses is not only caused by the arbitrary expansion of judicial interpretations, but also heavily relies on administrative violations. This not only violates the criminal policy of leniency and severity, but also brings a series of serious criminal consequences and social conflicts. Therefore, a new approach to the governance of minor illegal fishing offenses, namely "exemption from criminal punishment and administrative detention", should be introduced. Such cases, the requirements of criminal law's restraint and the principle of protection of legal interests should be strictly followed, and "administrative detention" should be used to replace "criminal punishment". The handling of minor illegal fishing offenses through administrative detention not only conforms to the logic of the dual-penalty model and the principle of proportionality, but also has certain institutional foundations and practical advantages, and can effectively solve many problems in criminal governance.

Key words: The crime of illegally catching aquatic products; exemption from criminal liability; administrative detention; minor circumstances

全球水产品出口贸易网络韧性的季节周期识别和形成机制

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摘要：贸易网络韧性对保障供应链稳定愈加重要，但已有研究大多局限在趋势分析。本文从周期视角，基于2021-2023年期间全球水产品出口贸易月度数据，通过构建有向加权的网络韧性指标进行测度，并采用STL分解和非线性MS模型，识别其季节周期。研究发现：（1）水产品出口贸易网络韧性存在较为明显的季节周期。（2）层级性的季节周期与主产区的生产周期有关。（3）匹配性的季节周期与市场竞争态势有关。（4）传输性的季节周期与贸易的驱动因素有关。（5）聚集性的季节周期与供应中断风险有关。研究结果不仅补充了贸易网络韧性的季节周期形成机制，对提升贸易韧性也有一定的启示。

关键词：复杂网络；网络韧性；韧性周期；水产品出口

Seasonal Cycle Identification and Formation Mechanism of Resilience in Global Aquatic Product Export Trade Network

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Abstract： The resilience of trade networks is becoming increasingly important for ensuring supply chain stability, but most existing research has been limited to trend analysis. This article takes a cyclical perspective, based on monthly data of global aquatic product export trade from 2021 to 2023, and measures it by constructing a directed weighted network resilience index. STL decomposition and nonlinear MS model are used to identify its seasonal cycle. Research has found that: (1) There is a significant seasonal cycle in the resilience of aquatic product export trade networks. (2) The hierarchical seasonal cycle is related to the production cycle of the main production areas. (3) The seasonal cycle of matching is related to the market competition situation. (4) The seasonal cycle of transmission is related to the driving factors of trade. (5) The clustered seasonal cycle is related to the risk of supply disruption. The research results not only supplement the seasonal cycle formation mechanism of trade network resilience, but also provide some insights for enhancing trade resilience.

Key words: complex network, network resilience, resilience cycle, aquatic products export

中西太平洋南部海域金枪鱼延绳钓渔业海鸟兼捕物种组成及时空分布特征

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摘要：金枪鱼延绳钓渔业在部分海域存在严重的海鸟兼捕问题，已成为全球渔业管理与生态保护的重要议题。本文基于 2013—2019 年中西太平洋渔业委员会观察员数据，分析中西太平洋南部海域海鸟兼捕的物种组成、年际变化与空间分布特征。采用单位捕捞努力量兼捕量（BPUE）和兼捕死亡率等指标，结合年际热力图与空间可视化方法，揭示兼捕格局及高风险区域。结果显示，该海域海鸟兼捕存在明显的物种差异、年际波动和空间不均。新西兰信天翁（Thalassarche bulleri）与白颏风鹱（Procellaria aequinoctialis）为主要兼捕种，数量在 2015—2016 年和 2019 年达到高峰，且 BPUE 与死亡率均高于其他年份。兼捕与死亡呈纬度梯度分布，随纬度升高而增加，高风险区域集中于 35°S 以南，为海鸟管理和养护措施的制定提供科学依据。

关键词：中西太平洋；延绳钓渔业；海鸟兼捕；物种易感性；时空分布特征

Species Composition and Spatiotemporal Distribution of Seabird Bycatch in the Tuna Longline Fishery of the Southern Western and Central Pacific Ocean

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Abstract：Serious seabird bycatch occurs in parts of the tuna longline fishery, posing a major concern for global fisheries management and ecosystem conservation. Using observer data from the Western and Central Pacific Fisheries Commission (WCPFC) during 2013–2019, this study examines species composition, interannual variation, and spatial distribution of seabird bycatch in the southern Western and Central Pacific Ocean (WCPO). Bycatch per unit effort (BPUE) and mortality rate were applied, combined with interannual heatmaps and spatial visualization, to reveal patterns and high-risk areas. Results show marked species differences, annual fluctuations, and spatial heterogeneity. Thalassarche bulleri and Procellaria aequinoctialis were dominant, peaking in 2015–2016 and 2019, with higher BPUE and mortality. Both bycatch and mortality increased with latitude, with high-risk areas mainly south of 35°S. These findings provide a scientific basis for targeted seabird management and conservation.

Key words: Western and Central Pacific Ocean; longline fishery; seabird bycatch; species susceptibility; spatiotemporal distribution pattern

中国海水鱼养殖生产的空间演变规律研究

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摘要：伴随全球海洋经济蓬勃发展，中国海水鱼养殖业已崛起为沿海地区重要的经济支柱产业。本研究聚焦中国海水鱼养殖生产，基于 2003~2023 年省级面板数据，运用空间计量分析方法，系统解析其时空动态演变特征及空间分异规律。结果表明：（1）规模维度：中国海水鱼产量持续增长，区域差异显著，形成以华南为核心、多极协同的“一核多极”空间格局。（2）时空模式：呈现显著的“集聚-扩散”双模态特征，早期高度集聚于华南沿海，2015 年后显现向江浙沿海扩散的新态势。（3）驱动机制：自然资源禀赋、流通设施完善度与市场潜力构成核心驱动要素，共同推动养殖区域的扩张与空间转移。基于此，从产业集群发展、区域优势资源规划、科技人才投入等方向提出建议，以期优化产业空间布局、应对演变中的挑战与机遇，为实现中国海水鱼养殖业可持续发展提供科学决策支持。

关键词：中国海水鱼；空间演变；影响因素；渔业可持续发展

A Study on the Spatial Evolution Pattern of Marine Fish Aquaculture Production in China

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Abstract： Amid the global blue economy boom, China’s marine fish aquaculture has become a key economic pillar in coastal regions. Using provincial panel data (2003–2023) and spatial econometric methods, this study analyzes the spatiotemporal evolution and spatial differentiation of the industry. Key findings include:(1) Production has grown steadily with marked regional disparities, forming a “core-multipolar” pattern centered in South China.(2) Spatiotemporal dynamics show clear agglomeration-diffusion: early concentration in South China, with post-2015 diffusion toward Jiangsu and Zhejiang.(3) Key drivers are natural resources, logistics infrastructure, and market potential, which jointly shape aquaculture zonation and relocation.Recommendations cover industrial clustering, regional resource planning, and tech-talent investment to optimize spatial layout and support sustainable development.

Key words: Chinese marine fish; spatial evolution; influencing factors; sustainable fisheries development

我国北方河口渔业区潜在病原体和抗生素耐药基因的风险评估

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摘要：病原体及抗生素抗性基因（ARGs）是河口生物污染的常见类型，也是渔业生产中重要威胁之一。然而，我们对病原菌和 ARGs 在河口渔业区不同生境下分布理解有限，这不利于我国蓝色粮仓和渔业经济的可持续发展。本研究以辽河河口渔业区为例，基于 118 个样本，结合高通量测序与自建病原菌数据库和结构化的 ARGs 数据库，对潜在病原菌和 ARGs 进行鉴别，使用多元统计法、结构方程建模以及共线性网络分析等方法，分析水体、土壤和沉积物中细菌群落、潜在病原体及 ARGs 的分布特征。结果表明，细菌群落结构及多样性受生境类型、pH 和温度显著影响，且不同生境下潜在病原菌（如弧菌属、假交替单胞菌属、嗜酸寡养单胞菌属）和 ARGs（如氨基糖苷类、四环素类）呈显著差异分布。网络分析揭示微生物间复杂互作关系。研究强调生境特异性对微生物生态安全的影响，为我国河口渔业区生态安全评估提供科学依据，为维护渔业生态系统和公共健康提供关键数据支撑。

关键词：河口渔业区；微生物群落多样性；潜在病原体；抗生素抗性基因；风险评估

Assessing the Risks of Potential Pathogens and Antibiotic Resistance Genes among Heterogeneous Habitats in a Fishery Area of Liaohe Estuary

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Abstract： Pathogens and antibiotic resistance genes (ARGs) are common biological pollutants in estuaries that threaten fishery production. However, our understanding of these pollutants' distribution across different habitats in estuarine fishery zones remains limited, hindering the sustainable development of China's blue economy. This research identified pathogens and ARGs in 118 samples using high-throughput sequencing and a proprietary database. Multivariate statistical methods examined the distribution of bacterial communities, potential pathogens, and ARGs in water, soil, and sediments. The results show that habitat type, pH, and temperature influence bacterial community structure and diversity. Potential pathogens and ARGs exhibit different distribution patterns across different habitats and interact complexly with each other. This network analysis highlights habitat specificity's impact on microbial ecology, providing scientific basis for ecological safety assessments in China's estuaries and critical data support for safeguarding ecosystems and public health.

Key words: Estuarine fishery area; microbial community diversity; potential pathogens; antibiotic resistance genes; risk assessment

生活史策略塑造微生物特征:刀鲚肠道微生物群的比较研究

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摘要：刀鲚(*Coilia nasus*)作为典型的洄游-定居多态性物种，其不同生态型间因摄食习性及栖息环境(如水温、盐度等)差异，表现出不同的肠道菌群特征。本研究构建了涵盖洄游型(海水群体与淡水群体)、定居型和养殖型三种生态型刀鲚的肠道菌群数据库，探讨环境选择、营养代谢需求与宿主生活史策略驱动菌群分化的生态机制。结果显示，刀鲚核心菌群由厚壁菌门复合类群、变形菌门及放线菌门组成。高盐生境通过环境过滤效应抑制洄游型海水群体刀鲚部分微生物类群，并促进 Proteobacteria 和 Psychrobacter 等海水优势菌的富集。定居型刀鲚中 Plesiomonas 的富集与其浮游动物摄食习性相关，而养殖型刀鲚中 Actinobacteriota 的高丰度则与人工饲料中蛋白质/脂类添加相关。本研究为刀鲚种质资源溯源和生态型鉴别提供潜在分子标记，提供宿主-微生物共进化机制及基于菌群调控的野生种群保护策略理论。

关键词：刀鲚；肠道微生物；16S rDNA 高通量测序；生态型

Life history strategies shape microbial signatures: a comparative study on the gut microbiome of *Coilia nasus*

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Abstract：This study constructed a database of intestinal microbiota for three ecological types of C. nasus, namely migratory type (comprising marine populations and freshwater populations), sedentary type and aquaculture-reared type. The research aimed to explore the ecological mechanisms by which microbiota differentiation is driven by environmental selection, nutritional metabolism requirements, and the host's life history strategies. The results showed that the core flora of *C. nasus* consisted of Firmicutes_A/D, Proteobacteria and Actinomycetota. The high salinity habitat inhibited some microbial groups in the migratory marine population of *C. nasus* through environmental filtering effect, and promoted the enrichment of seawater dominant bacteria such as Proteobacteria and Psychrobacter. The enrichment of Plesiomonas in sedentary population *C. nasus* is significantly positively correlated with its zooplanktonic feeding habit, while the high abundance of Actinobacteriota in aquaculture-reared population *C. nasus* is related to the addition of protein/lipid in artificial feed.

Key words: *Coilia nasus*; intestinal microbiota; 16S rDNA sequencing; ecotype

巢湖中存在洄游型刀鲚及其出生溯源的耳石微化学证据

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摘要：为了解巢湖中刀鲚(*Coilia nasus*)的生境履历及出生起源。利用 EMPA 分析 2022/7/25 采集的 9 尾刀鲚成鱼矢耳石的 Sr/Ca。并进一步利用 LA-MC-ICP-MS 分析其中 5 尾成鱼矢耳石的 87Sr/86Sr。结果显示，7 尾个体耳石锶钙比值自核心至边缘均低于 3，呈现淡水生活史特征。22CH03 个体锶钙比值虽短暂高于 3，但锶同位素值稳定在 0.71053 附近，显示为淡水生活史个体。22CH07 个体耳石 Sr/Ca 值存在显著波动，由核心附近的低 Sr/Ca 值升至 5.37±0.57，最终降至 3 以下，反映出其生于淡水、长于河口近海、后又上溯到淡水的洄游生活史。其锶同位素值从初始 0.71451 降至 0.70945，边缘为 0.71079，该变化表明该个体可能源自鄱阳湖，后迁移到河口等半咸水生境生活，最终抵达巢湖。提示巢湖仍具有一定的江湖连通性。受样本量所限，需进一步研究确认是否存在本地繁殖洄游种群。

关键词：刀鲚；耳石；巢湖；溯河洄游；微化学；Sr/Ca; 87Sr/86Sr

Otolith microchemistry provides evidence for the existence of migratory *Coilia nasus* in the Chaohu Lake and traces their natal origins

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Abstract：To investigate the habitat history and origin of *Coilia nasus* in Chaohu Lake, otolith Sr/Ca ratios from nine specimens collected on 25 July 2022 were analyzed via electron probe microanalysis, with ^{87}Sr/^{86}Sr ratios examined in five individuals using laser ablation multi-collector ICP-MS. Seven specimens showed Sr/Ca ratios consistently below 3, indicating freshwater residency. Individual 22CH03 exhibited a temporary Sr/Ca increase above 3 but maintained a stable ^{87}Sr/^{86}Sr ratio near 0.71053, supporting freshwater residence. Specimen 22CH07 displayed notable Sr/Ca fluctuations, reaching 5.37±0.57 before declining below 3. Its ^{87}Sr/^{86}Sr ratios began at 0.71451, suggesting Poyang Lake origin, decreased to 0.70945 indicating brackish habitat use, and ended at 0.71079, matching Chaohu Lake. These results confirm an anadromous individual in Chaohu Lake, suggesting river-lake connectivity persists. Further research is needed to determine if a local anadromous population exists.

Key words: *Coilia nasus*; otolith; the Chaohu Lake; anadromy; microchemistry; Sr/Ca; 87Sr/86Sr

基于物种分布模型的长江口中华绒螯蟹空间分布特征初步研究

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摘要：中华绒螯蟹（*Eriocheir sinensis*）是长江水系的典型洄游性甲壳类物种，当前对于该物种在长江口的空间分布特征及其生态适宜性区间尚缺乏定量化研究。本研究基于 2023 年冬季至 2024 年初在长江口海域开展的资源调查及水文环境监测数据，然后构建了物种分布模型。结果显示，中华绒螯蟹在长江口呈现显著的上游积聚，下游分散格局。模型分析表明，中华绒螯蟹资源密度与盐度（SA）呈持续下降趋势，在低盐区（<5）最为集中；与浊度（NTU）的关系则呈复杂非线性响应，在约 50 NTU 时密度达到峰值，过高则显著下降。GAM 模型整体解释率为 42.6%，其中盐度的偏差解释率最高（29.3%）。本研究初步厘清了中华绒螯蟹在长江口的空间分布特征，为后续的资源动态监测与生态管理提供了理论支撑。

关键词：中华绒螯蟹；物种分布模型；空间分布特征

Preliminary Study on the Spatial Distribution Pattern of *Eriocheir sinensis* in the Yangtze River Estuary Based on Species Distribution Modeling

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Abstract：*Eriocheir sinensis* is a typical migratory crustacean species of the Yangtze River system. At present, there is a lack of quantitative research on the spatial distribution characteristics and ecological suitability range of this species in the Yangtze River Estuary. Based on resource surveys and hydrological monitoring conducted in the estuarine waters from winter 2023 to early 2024, this study constructed a species distribution model. The results showed that E. sinensis exhibited a distinct pattern of upstream aggregation and downstream dispersion in the estuary. Model analysis indicated that the resource density of E. sinensis showed a continuous decline with increasing salinity (SA), with the highest density concentrated in low-salinity areas (<5). Its relationship with turbidity (NTU) exhibited a complex nonlinear response, with a peak density at around 50 NTU, followed by a significant decline at higher turbidity levels. The Generalized Additive Model (GAM) had an overall explanatory power of 42.6%, with salinity contributing the highest deviance explained (29.3%). This study preliminarily clarified the spatial distribution characteristics of E. sinensis in the Yangtze River Estuary, providing theoretical support for future resource monitoring and ecological management.

Key words: *Eriocheir sinensis*; Species distribution model; Spatial distribution pattern

基于环境 DNA 技术的元江鱼类生物多样性研究

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摘要：元江是云南地区最主要的河流之一，本研究通过利用环境 DNA 技术对元江鱼类进行调查，2023 年 10 月在元江设置了 16 个站位采集水样，共检出鱼类 47 种。Alpha 多样性分析显示，各站位 Shannon 指数 0.92~2.41，Simpson 指数为 0.44~0.88，Pielou 指数为 0.35~0.60，Margalef 指数为 0.30~1.16。采用层次聚类 Cluster 和非度量多维尺度分析 NMDS 方法对鱼类群落空间分布特征进行分析，结果显示鱼类群落在空间分布上存在差异，各站位从下游至上游分为三组，表现为在地理空间上相近的站位聚在一起。采用冗余分析方法(RDA)分析了鱼类多样性与环境因子的关系，发现元江鱼类群落主要受海拔、盐度、电导率、总溶解固体、氧化还原电位和总磷等环境因子影响。本研究表明环境 DNA 技术可以用于元江鱼类种类组成和分布的分析，该方法可作为元江鱼类生物多样性监测和保护的重要手段。

关键词：环境 DNA(eDNA)；鱼类多样性；元江

Assessment of fish diversity in the Yuanjiang River using environmental DNA (eDNA) metabarcoding

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Abstract：This study employed environmental DNA (eDNA) technology to survey fish species in the Yuanjiang River. In October 2023, 16 sampling stations were established, and fish diversity was analyzed using eDNA techniques. A total of 47 fish species were detected. Alpha diversity analysis revealed: Shannon-Wiener index (0.92~2.41), Simpson index (0.44~0.88), Pielou evenness index (0.35~0.60), and Margalef index (0.30~1.16). Hierarchical cluster analysis and NMDS analysis showing distinct differences among stations that grouped into three clusters from downstream to upstream, with geographically proximate stations clustering together. RDA assessed relationships between fish diversity and environmental factors, indicating that the Yuanjiang River fish community is primarily influenced by altitude, salinity, conductivity, total dissolved solids, redox potential, and total phosphorus. This study demonstrates that eDNA technology is effective for analyzing fish species composition and distribution in the Yuanjiang River and can serve as a crucial tool for biodiversity monitoring and conservation.

Key words: Yuanjiang River; Environmental DNA (eDNA); Fish diversity

氨氮胁迫对橄榄蛏蚌鳃组织生理、转录组和代谢组的影响

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摘要：氨是水生系统中常见的有毒物质，是影响水产养殖的关键因素之一。然而，关于软体动物，特别是淡水软体动物对氨氮的毒性反应和应对机制的数据仍然缺乏。本研究评估了淡水软体动物橄榄蛏蚌对氨的耐受性，并通过生理学、代谢组和转录组分析来探究其应对机制。结果表明，橄榄蛏蚌的 96 h 半致死氨氮浓度为 63.29 mg/L。氨胁迫增加了抗氧化、免疫和氨解毒相关酶的活性，并导致鳃的氧化损伤和细胞凋亡。氨胁迫后，共鉴定出 97 种差异代谢（DMs）和 3431 个差异表达基因（DEGs）。大多数 DMs 和 DEGs 参与免疫反应、抗氧化、细胞凋亡、碳水化合物代谢、氨基酸代谢和脂质代谢。糖酵解和脂质代谢的增强可能为免疫反应和氨解毒提供能量。谷氨酰胺合成、丙氨酸合成和尿素循环参与氨解毒。这些发现将为评估环境氨对淡水软体动物的潜在生态风险提供有价值的信息，并为橄榄蛏蚌的健康养殖提供理论指导。

关键词：软体动物；氨氮；转录组；代谢组；免疫

Integrated analysis of physiological, transcriptome, and metabolome analyses of the gills in *Solenaia oleivora* under ammonia exposure

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Abstract：This study evaluated the tolerance of a freshwater mollusk Solenaia oleivora to ammonia and investigated its coping mechanisms by combining physiological, metabolic, and transcriptomic analyses in gills. Our results showed that the LC50–96 h of ammonia in S. oleivora was 63.29 mg/L. Ammonia stress increased the activities of antioxidant, immune and ammonia detoxiffcation-related enzymes and caused oxidative damage and cell apoptosis of gills. A total of 97 differential metabolites (DMs) and 3431 differential expressed genes (DEGs) were identiffed after ammonia stress. Most DMs and DEGs were involved in immune response, antioxidant, cell apoptosis, metabolisms. The enhancement of glycolysis and lipid metabolisms may provide energy for immune response and ammonia detoxiffcation. Glutamine synthesis, alanine synthesis and urea cycle were involved in ammonia detoxiffcation. These findings will provide valuable information for assessing the potential ecological risks of environmental ammonia to freshwater mollusks and theoretical guidance for the healthy aquaculture of S. oleivora.

Key words: Mollusk; Ammonia; Transcriptome; Metabolome; Immune

半封闭海湾牡蛎增殖对环境以及菌落结构功能的扰动研究

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摘要：牡蛎养殖是一种重要的水产养殖活动。本研究旨在探讨牡蛎养殖对半封闭海湾微生物群落结构与功能的扰动效应及其潜在环境意义。研究通过对牡蛎养殖区和非养殖区的表层水体和沉积物进行多时间尺度的采样分析，运用 16S rRNA 基因测序以及环境理化参数测定等方法，评估了微生物群落的组成、多样性、功能潜力和环境因子间的关联。研究结果表明，牡蛎养殖显著改变了海湾沉积物微生物群落的结构和多样性。长期养殖导致特定细菌类群（如固氮菌和反硝化细菌）的富集，这些微生物在营养循环中扮演关键角色。牡蛎的生物沉积作用增加了沉积物有机质的输入，进而影响了微生物的代谢活动和功能潜力。牡蛎养殖区沉积物中总有机碳（TOC）总金属等含量显著高于对照区，牡蛎养殖增加了沉积物有机质的积累。同时，养殖活动也可能诱导微生物群落对特定环境压力产生适应性响应，微生物群落结构对牡蛎健康状况具有响应。

关键词：牡蛎；半封闭海湾；微生态；功能；群落结构

Disturbance of oyster aquaculture on environment and bacteria community structure and function in semi-enclosed bay

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Abstract: Oyster culture significantly impacts microbial communities in semi-enclosed bays' biogeochemical cycles. This study evaluated microbial composition, diversity, functional potential, and environmental correlations through multi-time scale sampling of water/sediments in oyster-culture and control areas, combined with 16S rRNA sequencing and physicochemical analysis. Aquaculture altered sediment microbial diversity and enriched specific bacterial groups (e.g., nitrogen-fixing and denitrifying bacteria), crucial for nutrient cycling. Oyster biodeposition increased sediment organic matter (OM), elevating total organic carbon (TOC) and total metal content in culture zones. Microbial communities exhibited adaptive responses to environmental pressures (e.g., OM accumulation), linking community structure to oyster health. Ecological Implications： These changes affect microbial metabolic activity and functional potential, highlighting oyster farming’s environmental footprint. This work provides a scientific basis for assessing aquaculture’s ecological effects in semi-enclosed ecosystems.

Key words: Oyster; semi-enclosed bay; microecology; function; community structure

中国蚌超科（双壳纲：蚌目）系统分类及物种分布格局

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摘要：蚌类是淡水生态系统中主要组成部分，具有重要的生态功能。中国是世界上蚌类（蚌超科）的重要分布地, 也是东亚蚌类的分布中心，特有种极为丰富。传统上，蚌类分类主要依据贝壳形态特征，但贝壳形态可塑性极高，导致物种界定困难、分类系统存在争议。本研究基于系统发育组学线粒体全基因组和核基因数据，重建目前最为全面的蚌目系统发育框架，确立了中国蚌超科 31 属的分类地位，提出了中国蚌超科 2 科 5 亚科 13 族 42 属的分类系统。整理和复核我国蚌超科物种多样性、分布信息，确定了中国蚌超科共 123 种，长江流域、黄河流域和淮河流域是集中分布区。通过对比分析不同级别的濒危等级评估结果，发现我国蚌类物种普遍面临严峻的生存威胁，且存在显著的评估数据缺失现象。本研究强调亟需开展全国性调查，深化科学研究并促进可持续利用。

关键词：蚌超科； 系统分类；物种多样性；保护；中国

Taxonomic System and species distribution patterns of chinese freshwater mussels (*Bivalvia: Unionida*)

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Abstract： Freshwater mussels (Unionoidea) are ecologically vital in aquatic ecosystems. China is a global hotspot for Unionoidea diversity, especially in East Asia, with remarkable endemism. Traditional shell-based taxonomy faces challenges due to morphological plasticity, causing species delimitation disputes. In this study, we conducted a comprehensive phylogenomic analysis utilizing complete mitochondrial genomes and multiple nuclear markers, establishing the most robust phylogenetic framework for Unionoidea to date. Our results clarify the systematic positions of 31 Chinese genera and propose an updated taxonomic classification system consisting of 2 families, 5 subfamilies, 13 tribes, and 42 genera. Through compilation and verification of species diversity and distribution data, we identified 123 Unionoidea species in China, concentrated in the Yangtze, Yellow, and Huai River basins. Conservation assessments reveal severe threats and critical data gaps, urging nationwide surveys and science-based management.

Key words: Unionoidea; systematic taxonomy; species diversity; conservation; China

梯级大坝影响下鱼类栖息地连通性时空动态演变及修复阈值研究

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摘要：为阐明梯级大坝对鱼类栖息地连通性的扰动机制及修复阈值，本研究以珠江流域东江为例，基于连通性指数 DCI 定量建模，解析 1970-2020 年梯级开发驱动下连通性的时空演变特征，通过非线性耦合模型揭示大坝通行性 p 与 DCI 的响应关系，并结合鱼类群落调查数据识别连通性关键修复节点。结果显示 1970-2020 年大坝数量增至 16 座，天然 DCI 衰减 90.99% 至 9.01，2000-2010 年损失贡献率达 78.14%；非线性分析：$p<0.6$ 时 DCI 增幅≤10.41，响应平缓；$p>0.8$ 时呈指数增长，p 由 0.8 至 0.9 时 DCI 提升 16.53，明确 0.8 为临界阈值。空间异质性建模表明，$p=0.8$ 基准下，剑潭大坝通行性提升使 DCI 增加 4.68，显著高于苏雷坝 0.58。本研究通过多模型耦合的量化分析方法，为梯级大坝干扰下的鱼类栖息地连通性修复提供定量化科学支撑。

关键词：梯级大坝；栖息地破碎化；河流连通性；时空动态；关键修复阈值；东江流域

Habitat Connectivity Dynamics and Restoration Thresholds of Cascade Dams in the Mainstream of Dongjiang River: Based on DCI and Fish Community Characteristics

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Abstract：This study measured the habitat connectivity (quantified via the Habitat Connectivity Index, DCI) and dam passability (p) in the mainstream of the Dongjiang River . It identified a non-linear relationship between p and DCI: specifically, DCI increased slowly when $p < 0.6$, whereas an exponential growth pattern emerged when $p > 0.8$. From 1970–2020, dams increased from 3 to 16, cutting natural DCI by 90.99% (78.14% lost 2000–2010). Key dams like Jiantan Dam mattered more—improving its passability lifted DCI by 4.68 (at $p=0.8$), while 0.58 for Sulei Dam. A 2024 survey showed 84.2% native fish, 18.8% migratory, with generalist residents dominant. This study identifies $p = 0.8$ as a critical threshold for habitat connectivity restoration and provides a scientific basis for prioritizing the restoration of key dams.

Key words: Dendritic Connectivity Index (DCI); Fish diversity; Habitat fragmentation; Dongjiang river

海洋牧场典型渔业种类呼吸代谢研究

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摘要：呼吸代谢可以反映水生生物自身的生理生态状况，其变化趋势和自身因素及环境因子之间紧密相关。呼吸代谢是生物能量学研究的重要内容之一，是能量收支研究的重要组分，它既反映出生物的生理状态，也反映了环境条件对其生理活动的影响。为获知不同鱼类呼吸代谢与温度及体重的关系，以鲻鱼、青石斑鱼和黑鲷为研究对象，采用室内封闭流水式呼吸代谢实验装置，开展不同水温梯度、不同体重的南海野生经济鱼类的呼吸代谢实验。结果表明，在适宜水温范围内，耗氧率和排氨率随温度的升高而上升。生物耗氧率和排氨率随着体重的增大而不断降低，这与生物体内维持生命代谢的器官组织所占生物体总重量的比例有关。鱼类代谢的能源物质均由蛋白质和脂肪混合供给，蛋白质和脂肪的比例因水温的不同而具有此消彼长的趋势。希冀通过对野生渔业资源生物基础生理的研究，从个体生理生态扩展到群体生理生态面，从而为海洋牧场增殖放流及增殖容量评估提供数据支撑。

关键词：渔业资源生物；呼吸代谢；耗氧率；排氨率

The research of respiratory metabolism for natural waters of fishery resources in marine ranching

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Abstract：Respiratory metabolism can reflect the physiological condition of aquatic life. It trends to own factors and the environment. Respiratory metabolism is one of the most important aspects in bioenergetics and the important components of energy budget. It can reflect not only biological physiological condition, but also the environmental conditions on the effect of physical activity. Discussed the relationship of different fishes like Mugil cephalus, Epinephelus awoara and Sparus macrocephlus in South China Sea between oxygen consumption rate, ammonia excretion rate and different water temperature, different weight and the respiratory metabolism substrate by breather apparatus in closed static seawater type equipment. The experimental results show that oxygen consumption rate and ammonia excretion rate increased as the temperature increased and the body weight decreased. The oxygen consumption rate and ammonia excretion rate increased as the body weight decreased. The result may cause by proportion of tissues and organs.

Key words: fishery resources organism; respiratory metabolism; oxygen consumption rate; ammonia excretion rate

基于环境 DNA 技术的黄河调水调沙期间鱼类多样性初探

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摘要：黄河流域调水调沙活动对水生生态系统造成显著扰动。鱼类群落作为水域生态系统的关键组成部分，可有效指示系统结构与功能的稳定性。环境 DNA（eDNA）技术作为一种高效的鱼类资源调查方法，较传统手段具有明显优势，尤其适用于禁渔区等敏感水域。为探究调水调沙期间黄河河南段鱼类资源及多样性的变化，本研究采用 eDNA 技术对该时段鱼类多样性进行分析。结果显示，eDNA 方法共检出淡水鱼类 50 种，隶属 8 目 16 科 44 属，以鲤形目为主，物种数显著多于传统网捕方法（31 种，6 目 10 科 28 属），但未进行资源量定量分析。多样性指数分析表明，调水调沙期间鱼类多样性高于前期，原因可能包括小浪底水库上游鱼类随水流下移，或水体搅动及泥沙含量增加使底层鱼类上浮而易被检出。本研究证实 eDNA 技术在黄河等特殊水体鱼类多样性监测中具有良好的适用性和优势。

关键词：环境 DNA；调水调沙；鱼类；多样性

Preliminary study on fish diversity during water and sediment regulation in the Yellow River based on environmental DNA technology

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Abstract： The water-sediment regulation in the Yellow River significantly disturbs aquatic ecosystems. Fish communities are key ecological indicators, and environmental DNA (eDNA) technology is more efficient than traditional methods for surveys, especially in protected areas. This study used eDNA to assess fish diversity in the Henan section during the regulation period. Results revealed 50 fish species (8 orders, 16 families, 44 genera), predominantly Cypriniformes, surpassing traditional netting (31 species, 6 orders, 10 families, 28 genera). Although biomass was not quantified, diversity indices were higher during regulation than before, likely due to downstream transport of fish from the Xiaolangdi Reservoir and sediment-induced upward movement of benthic species. The study confirms the effectiveness and utility of eDNA for monitoring fish diversity in turbid, dynamic systems like the Yellow River.

Key words: Environmental DNA; Water and sediment regulation; Fish; Biodiversity

基于基因组学的 *Acinetobacter soil* G33 分离及其异养硝化-好氧反硝化与除磷功能表征与机制研究

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摘要：集约化养殖废水氨氮负荷高，传统处理方法效率低且成本高。异养硝化-好氧反硝化（HN-AD）技术能在单一好氧条件下同步脱氮，高效去除氨氮和亚硝酸盐，是可持续污水处理的有力方案。本研究采用纯培养法，从养殖尾水中分离出 141 株细菌，经功能筛选，鉴定出 32 株具备 HN-AD 能力的菌株。其中，菌株 Acinetobacter soil G33 脱氮除磷性能突出。在 30℃、pH 7 条件下，其对 NO_2^-、NO_3^-、NH_4^+、TN 和 PO_4^{3-}的去除率分别高达 99.80%、98.26%、92.45%、78.48%和 56.32%。该菌在 20–35°C、pH 6–10 范围内，氮去除率仍能维持在 80%以上。单因素碳源试验表明，琥珀酸钠、乙酸钠和柠檬酸钠是其生长与脱氮的最适底物。全基因组分析发现，G33 携带多种氮代谢及聚磷酶基因，但缺乏某些典型 HNAD 基因（如 amo 和 HAO），暗示其氮代谢途径可能有别于常规 HNAD 菌株。

关键词：不动杆菌；脱氮除磷；尾水处理

Based on genomic analysis, this study involved the isolation of *Acinetobacter soil* G33 and investigated its functional characterization and mechanisms in heterotrophic nitrification-aerobic denitrification and phosphorus removal.

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Abstract: Wastewater from intensive aquaculture operations exhibits high ammonia nitrogen concentrations, with conventional treatment methods often being inefficient and costly. Heterotrophic nitrification-aerobic denitrification (HN-AD) technology enables simultaneous nitrogen removal under aerobic conditions, demonstrating high efficacy in eliminating ammonium and nitrite, thereby representing a promising sustainable wastewater treatment solution.This study employed pure culture techniques to isolate 141 bacterial strains from aquaculture effluent. Through functional screening, 32 strains exhibiting HN-AD capability were identified. Among these, Acinetobacter soil G33 demonstrated remarkable nitrogen and phosphorus removal performance. Under optimal conditions (30°C, pH 7), its removal rates for NO_2^-, NO_3^-, NH_4^+, TN, and PO_4^{3-} reached 99.80%, 98.26%, 92.45%, 78.48%, and 56.32%, respectively. The strain maintained nitrogen removal efficiency above 80% within temperature and pH ranges of 20-35°C and 6-10, respectively.

Key words: Acinetobacter;Nitrogen and Phosphorus Removal;Effluent Treatment

海洋褐藻胶降解菌的分离、鉴定与降解机制研究

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摘要：褐藻胶是褐藻细胞壁的主要成分，也是海洋重要的有机碳源，解析其微生物降解机制对理解海洋碳循环至关重要。本研究从浙江舟山近海沉积物中分离获得一株高效褐藻胶降解菌H02，属于 Qipengyuania 属的一个新种，基因组大小为 2.95Mbp。在以褐藻酸钠为唯一碳源的条件下，H02 中三种褐藻胶裂解酶基因 Aly2048（PL7_6 家族）、Aly2050（PL6_1 家族）和 Aly2051（PL17_2 家族）显著上调。经异源表达与纯化分析，三者在最适温度、pH 及对 polyM/polyG 区段的降解偏好上存在显著差异。降解产物分析表明，不同酶能够生成单糖至六糖长度不等的褐藻寡糖。分子对接与分子动力学模拟进一步揭示，三类酶在底物结合口袋构象及关键催化残基分布上的差异，构成其功能互补的结构基础。综上，菌株 H02 通过多家族裂解酶的协同作用高效降解褐藻胶，促进有机物的矿化与再循环，为近海碳循环提供了新的微生物学视角。

关键词：Qipengyuania；褐藻胶裂解酶；酶学性质；异源表达；协同降解

Isolation, characterization, and mechanistic insights into marine alginate-degrading bacteria

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Abstract: Alginate, a major brown algae cell wall component and marine organic carbon source, is crucial for marine carbon cycling. We isolated efficient alginate-degrading bacterium H02 from Zhoushan coastal sediments, a new Qipengyuania species. With sodium alginate as sole carbon source, three lyase genes—Aly2048 (PL7_6), Aly2050 (PL6_1), Aly2051 (PL17_2)—were upregulated. Heterologous expression revealed differences in optimal temperature, pH, and polyM/polyG preferences. Enzymes generated oligosaccharides from mono- to hexasaccharides. Molecular docking and dynamics simulations showed distinct substrate-binding conformations and catalytic residue distributions, explaining functional complementarity. Strain H02 efficiently degrades alginate via synergistic multi-family lyases, promoting organic matter recycling and providing microbiological insights into coastal carbon cycling.

Key words: Qipengyuania;alginate lyase；enzyme characteristics；heterologous expression；synergistic degradation

微纤维对月形四链藻种群增殖、光合活性、营养成分和氧化应激的影响

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摘要：微纤维是一种新兴污染物，主要由纺织品磨损与洗涤释放。研究显示，全球淡水环境中微纤维丰度达 1000–5000 个/m³。因粒径小、难降解，在水体流动或机械搅动下易与水生生物发生相对运动。亟待开展在流动与静止水体条件下微纤维对水生生物的毒性效应。以月形四链藻为受试生物，分别在摇床和静置条件下培养，设对照组与各浓度微纤维（1、10、100 mg/L）暴露组，于 25℃、3000 lux 及 12 h:12 h 光暗周期下处理 15 天，每组 3 个平行。通过测定藻密度、色素及蛋白含量等指标，探究微纤维在不同培养条件下对月形四链藻的影响。结果表明，高浓度暴露下，藻密度与色素含量显著下降，ROS 大量积累。摇床组 Fv/Fm、光合色素、蛋白含量显著高于静置组；静置条件下，胞内多糖含量显著升高。研究表明，微纤维对月形四链藻的毒性效应具有浓度依赖性，且受培养条件影响。本研究为评估微纤维的环境行为与生态风险提供了理论依据。

关键词：微纤维；月形四链藻；毒性效应

Effects of microfibers on the growth, photosynthetic activity, nutrient composition, and oxidative stress in *Tetradesmus lagerheimii*

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Abstract: Microfibers (MFs), an emerging contaminant mainly from textile abrasion and laundering, are ubiquitous in freshwater systems at concentrations of 1000–5000 particles/m³. Given their small size and persistence, MFs easily interact with aquatic organisms under flow or agitation. Assessing MF toxicity under both flow and static conditions is therefore critical.To evaluate the physiological impacts of microfibers, Tetradesmus lagerheimii was cultured for 15 days under static and agitated conditions at concentrations of 0, 1, 10, and 100 mg/L (n=3). Cultivation occurred at 25°C under 3000 lux illumination with a 12 h:12 h photoperiod, and responses were measured via algal density, pigment, protein content, and other physiological metricsHigh-concentration MFs inhibited algal growth and pigments while elevating ROS.Agitated cultures exhibited elevated Fv/Fm, photosynthetic pigments, and protein, but lower polysaccharides than static cultures.These results demonstrate hydrodynamic-condition-dependent toxicity in Tetradesmus lagerheimii, critical for ecological risk assessment.

Key words: Microfibers; *Tetradesmus lagerheimii*; Toxicological effect

GenX 对鲤氧化应激毒性的影响

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摘要：六氟环氧丙烷二聚酸（GenX）作为新兴 PFAS，被广泛应用于制造业，导致其在土壤、地表水和河流沉积物等环境介质中被频繁检出。然而，其对水生生物的潜在危害研究却十分有限，因此亟需评估其环境风险。本研究选取鲤作为受试生物，设置对照组和不同浓度 GenX（2，20，200 μg/L）暴露组，对鲤进行六个月的暴露。通过测定鲤大脑和肝脏组织内抗氧化系统相关酶的活性以及氧化损伤指标，评估 GenX 对鲤的潜在危害。结果显示，高浓度 GenX 抑制鲤大脑内 T-AOC、SOD 和 CAT 等酶的活性，导致 MDA 含量显著高于对照组，表明 GenX 对鲤大脑产生了氧化损伤。在肝脏组织中，高浓度 GenX 抑制了 CAT 活性，降低组织内 GSH 的含量，并引起 MDA 含量的显著性升高。与大脑组织相比，肝脏显示出更显著的氧化损伤，本研究丰富了 GenX 对鱼类的毒理学危害数据，并揭示 GenX 毒性效应在不同组织之间的差异性，为后续研究提供了重要参考。

关键词：GenX；鲤；氧化应激

The effect of GenX on oxidative stress toxicity in common carp

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Abstract: Hexafluoropropylene oxide dimer acid (GenX), an emerging PFAS, is widely used in manufacturing, leading to its frequent detection in environmental media such as soil, surface water, and river sediments.However, research on its potential hazards to aquatic organisms remains limited, making it imperative to assess its environmental risks. This study selected carp as the test organism, establishing a control group and exposure groups at different GenX concentrations (2, 20, 200 μg/L) for a six-month exposure period. The results showed that high concentrations of GenX significantly inhibited T-AOC, SOD, and CAT activities in the brain while increasing MDA levels.In liver tissue, high-concentration GenX inhibited CAT activity, reduced GSH content, and caused a significant increase in MDA levels. Compared to brain tissue, the liver exhibited more pronounced oxidative damage. This study enriches the toxicological hazard data on GenX for fish and reveals the differential toxicity effects of GenX across different tissues, providing important reference for subsequent research.

Key words: GenX; common carp; oxidative stress.

基于 Ecopath 模型的丹江口水库生态系统功能研究

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摘要：为全面了解丹江口水库生态系统的结构和功能，本研究基于 2023 年调查数据，应用 Ecopath with Ecosim 6.6 软件构建了丹库的 Ecopath 模型，对其营养级特征、能量流动效率、系统规模和成熟度等进行评价。结果显示，丹江口水库 Ecopath 模型由 18 个功能组组成，各组分营养级为 1-3.50；主要经济鱼类的 EE 值为 0.67-0.87，浮游植物和碎屑的 EE 值<0.5；食物网能量传递包括碎屑食物链和牧食食物链两条路径，能量占比分别为 39.1%和 60.9%；系统总流量 12988.45 t·km-2 ·a-1，渔获物平均营养级为 2.61，总的能量传输效率为 6.02%。结果表明，该生态系统规模相对较小，发育不成熟，渔业结构不合理，食物网间联结程度简单，营养级间能量传递阻塞的现象明显，能量再循环效率低。建议通过增加滤食性鱼类增殖放流力度等调节食物网结构，提升能量利用效率，促进生态系统平衡稳定。

关键词：丹江口水库；Ecopath 模型；食物网，生态系统；功能评价

Ecosystem Functions of the Water Source in the Middle Route of China’s South-to-North Water Diversion Project

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Abstract: Based on a survey conducted in 2023 in the Dan Reservoir, a mass balance model was constructed using Ecopath with Ecosim 6.6software to characterize its food web structure and ecosystem properties. The model consisted of 18 functional groups. The fractional trophic level of functional groups ranged from 1.00 to 3.50. The ecotrophic efficiencies of the main economic fish species were all less than 0.9, and the ecotrophic efficiencies of phytoplankton and detritus were less than 0.5. There were two main food chains: the detritus food chain (39%) and the grazing food chain (61%). The total energy transfer efficiency between trophic levels was only 6.02%。Our results suggest that it is necessary to scientifically adjust the structure of the fish community,enhance the proportion of filter-feeding and omnivorous fish to improve the energy flow efficiency,and promote the maturity and stability of the Dan Reservoir.

Key words: Danjiangkou Reservoir;Ecopath model; Food web; Ecosystem; Function Evaluation

半叶马尾藻中国变种对海洋酸化和氮富集的生理及转录组响应

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摘要：半叶马尾藻中国变种是一种重要的大型褐藻，在生态和经济上具有重要意义。海洋酸化和氮富集是海洋生态系统面临的严重威胁，主要通过改变生物的生理机能发挥作用。然而，半叶马尾藻中国变种对海洋酸化与氮水平升高复合作用的响应仍尚不清楚。本研究开展了一项为期 7 天的双因素实验，探究了半叶马尾藻中国变种在两种 CO_2浓度和硝酸盐浓度条件下的生理和转录响应。结果表明，高 CO_2和 NO_3^-浓度促进了包括 qN 和 NPQ 在内的光合色素合成。生理结果显示，高 CO_2处理以及高 NO_3^-与高 CO_2联合处理均提高了生长速率和硝酸盐吸收速率，但硝酸还原酶（NR）活性显著降低。转录组分析鉴定出参与氧化磷酸化、碳代谢、三羧酸循环（TCA 循环）和氮代谢途径的差异表达基因。这些发现阐明了半叶马尾藻中国变种适应海洋酸化和氮富集的分子机制，为其应对外界变化海洋环境的能力研究提供了重要见解。

关键词：半叶马尾藻中国变种；海洋酸化；硝酸氮；生理作用；转录组

Physiological and Transcriptomic Responses of Sargassum hemiphyllum var chinense to Ocean Acidification and Nitrogen Enrichment

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Abstract： Sargassum hemiphyllum var. chinense is a major brown macroalga and has important ecological and economic significance. Ocean acidification and nitrogen enrichment are serious threats to marine ecosystems primarily by altering the physiology of organisms. However, the response of S. hemiphyllum var. chinense to the combined effects of ocean acidification and elevated nitrogen levels remains unclear. This study conducted a 7-day dual-factor experiment to investigate the physiological and transcriptional responses of S. hemiphyllum var. chinense under two CO2 levels and $NO3^-$ levels. The results showed that high CO2 and NO3- concentrations promoted the synthesis of photosynthetic pigments including qN and NPQ. Physiological results showed that high CO2 and the combined high NO3- and CO2 treatments enhanced growth rate and NO3- uptake rate, but NR activity was significantly decreased. These findings elucidate the molecular mechanisms by which S. hemiphyllum var. chinense adapts to ocean acidification and nitrogen enrichment.

Key words: Sargassum hemiphyllum var. chinense; acidification; nitrate nitrogen; physiology; transcriptome

小浪底水库“调水调沙”前渔业资源声学调查

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摘要：小浪底水库是黄河干流上具有防洪、减淤、供水、发电等多重功能的大型水利枢纽工程，也是实施“调水调沙”工程的核心，在防洪安全和泥沙调控方面发挥了重要作用。同时，小浪底水库也是黄河河南段的重要水生态系并具有丰富的渔业资源，其状态的长期监测对促进水库周边地区的高质量经济发展具有重要意义。2025 年 6 月 5 日至 6 月 7 日，在库区实施“调水调沙”之前，使用搭载国产声呐的 AI 智能无人艇与 Simrad E80 协同作业，对库尾至坝下河道开展了系统性的渔业资源声学调查。将回波积分和回波计数相结合，对库区不同区域的渔业资源密度，特别是银鱼(*Hemisalanx prognathus*)资源，进行了定量评估。调查结果为掌握小浪底水库“调水调沙”前的渔业资源状况、了解银鱼分布特征以及制定后续生态调控与渔业管理措施提供了重要的科学依据。

关键词：小浪底水库；渔业资源；渔业声学；银鱼；回波积分；回波计数

Acoustic Survey of Fishery Resources Before the Water and Sediment Regulation at Xiaolangdi Reservoir

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Abstract：Xiaolangdi Reservoir is an important aquatic ecosystem in the Henan reach of the Yellow River and supports abundant fishery resources. Monitoring its status is important for promoting economic development in surrounding areas. From 5 to 7 June 2025, before the Water and Sediment Regulation was implemented, we conducted a systematic acoustic survey of fishery resources from the reservoir tail to the river reach below the dam. An unmanned vessel equipped with a domestically manufactured sonar operated in coordination with a Simrad EK80. The survey covered the reach from the reservoir tail to the river channel below the dam. Echo integration and echo counting were combined to quantify fishery resource densities across different zones of the reservoir. Particular emphasis was placed on assessing the Hemisalanx prognathus. The results provide an essential baseline for the status of fishery resources prior to regulation. They clarify the distribution characteristics of H. prognathus and offer a scientific basis for subsequent ecological regulation and fisheries management.

Key words: Xiaolangdi Reservoir; fishery resource; fishery acoustic; Hemisalanx prognathus; echo integration; echo counting

布兰斯菲尔德海峡和南设得兰群岛南极磷虾种群结构与动态

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摘要：南极磷虾是南极海洋生态系统关键物种，兼具生态与经济价值。本研究基于 6 年中层拖网数据（含超 16 万条体长测量数据），分析其时空动态和种群组成，为渔业管理提供参考。研究显示，磷虾渔场向南迁移，较小个体多分布于冰层丰富的南部纬度区；商业捕捞优先选择高密度区域，捕获物中 1+龄组占比最高（42.80%），2+龄组次之（39.42%），≥3+龄组占 17.44%。2017 年磷虾平均体长下降，随后持续恢复，2022 年达峰值，且该年≥4 年龄组占比最高（12.6%），表明近年捕捞努力增加未导致个体体型缩小。磷虾平均体长与群落深度、温度呈显著正相关，与资源密度、年份、纬度呈显著负相关。体长呈 U 型时间趋势，在纬度和经度上呈非线性关系。体型与深度正相关；随温度升高，体型先增后稳定；随密度增加，平均长度先增后缓减。近期变暖加剧种群迁移，可能对生态系统结构和碳封存产生连锁影响。

关键词：南极磷虾；年龄；密度；GAM；CCAMLR；气候变暖；磷虾渔业管理

Population dynamics and body size structure of the Antartic krill *Euphausia superba* in the Bransfield Strait and South Shetland Islands

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Abstract: Antarctic krill (*Euphausia superba*), a keystone species in the Antarctic marine ecosystem, has significant ecological and economic value. This study analyzed 6-year midwater trawl data to clarify spatio-temporal dynamics and population composition, aiding fishery management. Krill fishing grounds shift south; smaller individuals favor ice-rich southern latitudes. Commercial fishing targets high-density areas, not larger individuals. Catches: 1+ (42.80%), 2+ (39.42%), ≥3+ (17.44%). Mean length declined in 2017, recovered, peaking in 2022, with increased fishing effort not reducing individual size. Mean length correlates positively with cluster depth/temperature, negatively with resource density/year/latitude, showing U-shaped temporal trends and latitudinal/longitudinal nonlinearity. Body size links positively with depth. With rising temperature, size first increases then stabilizes; with density, mean length first rises then declines slowly. Recent warming intensifies population shifts, potentially cascading effects on ecosystem structure and carbon sequestration.

Key words: Antarctic krill; age, density; GAM; CCAMLR; climate change; krill fishery management

多频声学方法在狭鳕幼鱼、浮游动物与高眼鲽分布研究中的应用

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摘要：在日本北海道喷火湾，狭鳕幼鱼与其捕食者高眼鲽常混合分布。以往针对狭鳕幼鱼的声学调查难以区分二者。本研究开发了基于 38 kHz 与 200 kHz 回声强度差异的辨识方法，成功区分两者。随后，我们开展春季喷火湾多频（38/120/200 kHz）声学测量并结合生物采样，根据回声频率响应和强度特征提取浮游动物、狭鳕幼鱼和高眼鲽的分布信息，分析其时空变化及相互关系。结果显示，该方法可同时识别多类海洋生物并估算其分布。浮游动物春季在喷火湾各处均有分布，随时间变化小；狭鳕幼鱼集中于湾内并逐渐向湾外迁移；高眼鲽分布广泛，春末产卵下沉致使探测减少。狭鳕幼鱼与高眼鲽的空间分布显著正相关，胃含物分析亦证实高眼鲽摄食狭鳕幼鱼。本研究证明多频声学技术可有效同时识别多种海洋生物并估算其分布，为解析海洋捕食-猎物关系提供了有力工具。

关键词：多频声学；狭鳕幼鱼；高眼鲽；浮游动物

Application of Multi-Frequency Acoustics to Study the Spring Distributions of Juvenile Walleye Pollock, Zooplankton, and Pointhead Flounder in Funka Bay

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Abstract: In Funka Bay, Japan, conventional acoustic surveys have been unable to distinguish juvenile walleye pollock (Gadus chalcogrammus) from their predator, the pointhead flounder (Cleisthenes pinetorum). This has potentially led to overestimation of pollock abundance due to overlapping distributions. To address this issue, we developed an acoustic identification method based on the difference in relative frequency response at 38 kHz and 200 kHz, which successfully discriminated juvenile pollock from pointhead flounder. We applied this method in an acoustic survey of juvenile pollock around Funka Bay. Building on this approach, we conducted multi-frequency (38, 120, 200 kHz) acoustic surveys combined with net sampling, to simultaneously estimate the distributions of zooplankton, juvenile walleye pollock, and pointhead flounder. Using differences in echo frequency responses and volume backscattering strength characteristics, we classified the echoes for each organism and analyzed their spatiotemporal distribution patterns and interactions.

Key words:multi-frequency acoustics; juvenile walleye pollock; pointhead flounder; zooplankton

山药多糖缓解嗜水气单胞菌诱导鲤细胞铁死亡作用机制

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摘要：嗜水气单胞菌引起的细菌性败血症会引起鲤脾脏坏死和体表出血，死亡率较高。针对鱼类细菌性疾病防治，山药多糖是天然的中草药活性成分，具有抗菌和抗氧化活性，不产生耐药性。本研究采用细胞生物学、生物信息学等方法检测了鲤脾脏组织和 EPC 细胞中铁死亡相关因子的变化，研究了铁死亡标志基因的表达量，并分析了鲤组织中嗜水气单胞菌的含量和鱼体存活率。结果显示，与对照组相比，嗜水气单胞菌刺激后鲤脾脏组织 Fe3+聚集，MDA、SOD 和总铁含量上升，GSH 含量下降，铁死亡标志基因表达量上升。与对照组相比，嗜水气单胞菌诱导线粒体损伤并降低膜电位，促进 ROS 和 lipid ROS 产生，引起 Fe2+含量升高，促进铁死亡标志基因的表达量升高。此外，山药多糖可抑制嗜水气单胞菌诱导的脾脏组织损伤，以剂量依赖性逆转嗜水气单胞菌对 EPC 细胞活性的抑制。综上所述，山药多糖可有效抑制嗜水气单胞菌感染诱导的鲤细胞铁死亡，减轻炎症反应。

关键词：鲤；铁死亡；炎症反应；嗜水气单胞菌；山药多糖

Mechanism of Yam Polysaccharide in Alleviating Aeromonas hydrophila-Induced Ferroptosis in *Common Carp*

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Abstract: Bacterial septicemia caused by Aeromonas hydrophila leads to spleen necrosis and surface hemorrhage in common carp, with a high mortality rate. For the prevention and treatment of bacterial diseases in fish, yam polysaccharides (YP) are natural active components of Chinese herbal medicine. The results showed that, compared to the control group, stimulation by Aeromonas hydrophila led to Fe3+ accumulation in common carp spleen tissues, increased levels of MDA, SOD, and total iron, decreased GSH content, and elevated expression levels of ferroptosis marker genes. Aeromonas hydrophila induced mitochondrial damage and decreased membrane potential, promoted the production of lipid ROS, caused an increase in Fe2+ content, and enhanced the expression of ferroptosis marker genes. In addition, YP inhibited Aeromonas hydrophila-induced spleen tissue damage and reversed the inhibition of EPC cell activity by Aeromonas hydrophila in a dose-dependent manner. In summary, YP effectively suppressed Aeromonas hydrophila infection-induced ferroptosis in common carp cells and alleviated inflammatory.

Key words: Common carp; Ferroptosis; Inflammatory response; Aeromonas hydrophila; Yam polysaccharide.

巴氏灭活 *Akkermansia muciniphila* 缓解奥氮平致斑马鱼代谢紊乱的机制研究

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摘要：奥氮平（Olanzapine, OLZ）广泛用于精神分裂症治，因持续释放至水环境而备受关注。为此，本研究通过建立斑马鱼（*Danio rerio*）OLZ 暴露模型（35.5、177.5 和 355.5 μg/L）。OLZ 暴露导致斑马鱼体重显著增加，并伴随 TC、LDL 和 TG 水平升高。肝脏出现脂肪蓄积，且 srebp、acc、fas 表达上调，lpl、hsl、cpt1b 表达下调。运动能力、社交行为减少及焦虑样行为增加。Plesiomonas 丰度显著增加，而 Cetobacterium 丰度降低，且这些变化呈现剂量依赖性。本研究在高浓度 OLZ 组中补充 P-Akk 进行干预 P-Akk 处理显著降低了肝体比、脏体比及血脂水平，减轻了肝脏脂质蓄积，并逆转了脂质代谢相关基因的表达异常和行为学异常。这些发现不仅阐明了 OLZ 对水生生物的潜在危害，也为开发基于微生物干预的环境污染物毒性缓解策略提供了理论依据。

关键词：奥氮平；脂质代谢；行为学；P-Akk

Mechanism of heat-inactivated Akkermansia muciniphila in alleviating olanzapine-induced metabolic disorders in zebrafish (*Danio rerio*)

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Abstract: Olanzapine (OLZ) is widely used in the treatment of schizophrenia and has garnered significant attention due to its continuous release into aquatic environments. To investigate its ecological impact, this study established an OLZ exposure model in zebrafish (*Danio rerio*) at concentrations of 35.5, 177.5, and 355.5 μg/L. OLZ exposure led to a significant increase in body weight in zebrafish, accompanied by elevated levels of TC, LDL, and TG. Hepatic lipid accumulation was observed, along with upregulation of *srebp*, *acc*, and *fas* expression, and downregulation of *lpl*, *hsl*, and *cpt1b* expression. Additionally, OLZ reduced motor capacity and social behavior while increasing anxiety-like behaviors. A significant dose-dependent increase in the abundance of *Plesiomonas* and a decrease in *Cetobacterium* were detected.In the high-concentration OLZ group, intervention with *P-Akk* was implemented. *P-Akk* supplementation significantly reduced the hepatosomatic index, viscerosomatic index, and blood lipid levels, alleviated hepatic lipid accumulation, and reversed the dysregulated expression of lipid metabolism-related genes as well as behavioral abnormalities. These findings not only elucidate the potential hazards of OLZ to aquatic organisms but also provide a theoretical basis for developing microbiome-based intervention strategies to mitigate the toxicity of environmental pollutants.

Keywords: Olanzapine; lipid metabolism; behavioral analysis; P-Akk

类芽孢杆菌 GD3 胞外多糖对大口黑鲈抗 LMBV 的影响

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摘要：大口黑鲈虹彩病毒（*Largemouth bass iridovirus*, LMBV）严重危害着我国重要淡水渔业资源本文的养殖，且无有效法治手段。本文以一株强壮类芽孢杆菌（Paenibacillus kribbensis）GD3 菌株产生的粗胞外多糖为研究对象，注重于探究 GD3 胞外多糖对 LMBV 的抵抗作用。采用鱼体内外两种方式进行双重研究，在体外通过研究 LMBV 感染 GD3 胞外多糖溶液预处理过的细胞，发现其能够抑制 LMBV 感染细胞中的病毒基因转录以及蛋白表达。针对鱼体内研究，通过对大口黑鲈持续投喂拌有 GD3 胞外多糖溶液的饲料 28 日后，注射 LMBV 制作疾病感染模型，发现 GD3 胞外多糖不仅能够延缓疾病发生，降低疾病导致的死亡率，且能够抑制 LMBV 对大口黑鲈肝脾的损伤作用。此研究表明 GD3 胞外多糖作为饲料添加剂在防控大口黑鲈虹彩病毒中具有一定的应用前景。

关键词：大口黑鲈；LMBV；细菌胞外多糖；抗病毒；饲料添加剂

Effect of Exopolysaccharides from *Paenibacillus* GD3 on Resistance of Largemouth Bass to LMBV

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Abstract: Largemouth bass iridovirus (LMBV) severely threatens the aquaculture of this important freshwater fish resource in China, and there are currently no effective control measures. In this study, the crude exopolysaccharides produced by a strain of Paenibacillus kribbensis GD3 were used as the research subject, focusing on exploring the resistance effect of GD3 exopolysaccharides against LMBV. Dual studies were conducted both in vitro and in vivo. In vitro, by examining LMBV infection in cells pretreated with GD3 exopolysaccharide solution, it was found that the exopolysaccharides could inhibit viral gene transcription and protein expression in infected cells. In vivo, largemouth bass were continuously fed for 28 days with feed supplemented with GD3 exopolysaccharide solution, followed by injection with LMBV to establish an infection model. The results showed that GD3 exopolysaccharides not only delayed disease onset and reduced mortality caused by the virus but also alleviated LMBV-induced damage to the liver and spleen.

Key words:*Largemouth bass*; LMBV; Bacterial exopolysaccharides; Antiviral; Feed additive

苦参碱通过抑制炎症和氧化应激反应以抑制 SGIV 体外感染

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摘要：新加坡石斑鱼虹彩病毒（SGIV）是石斑鱼养殖中引发高死亡率的主要病原体。目前针对SGIV的有效疫苗或治疗方法有限，亟需开发新型抗病毒制剂以预防潜伏感染并降低其致病性。苦参碱是一种从苦参中提取的四环喹诺里西啶类生物碱，对多种病毒具有广谱抗病毒活性，包括SARS-CoV-2、乙型肝炎病毒、猪繁殖与呼吸综合征病毒。然而，其对SGIV的抗病毒功效及作用机制尚不明确。本研究以新加坡石斑鱼脾脏（GS）细胞为体外模型，通过qPCR、蛋白质免疫印迹、间接免疫荧光、活性氧（ROS）检测及荧光素酶报告基因实验评估苦参碱的抗SGIV活性。结果表明，苦参碱以浓度依赖方式抑制SGIV复制，其主要在病毒感染早期阶段发挥抗病毒作用。机制上，苦参碱通过调控NF-κB介导的免疫与炎症反应、增强细胞抗氧化能力以抑制SGIV诱导的ROS生成，并促进干扰素相关基因表达。这些发现表明苦参碱是一种具有潜力的抗SGIV候选药物。

关键词：石斑鱼；SGIV；苦参碱；炎症；氧化应激

Matrine Suppresses Inflammatory and Oxidative Stress Responses to Inhibit SGIV Infection In *Vitro*

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Abstract: Singapore grouper iridovirus (SGIV) is a major pathogen causing high mortality in grouper aquaculture. Given the limited availability of effective vaccines or therapeutics against SGIV, novel antiviral agents are needed to prevent latent infection and reduce viral pathogenicity. Matrine, a tetracyclic quinolizidine alkaloid derived from Sophora flavescens, exhibits broad-spectrum antiviral activity against diverse viruses, including SARS-CoV-2, hepatitis B virus, and porcine epidemic diarrhea virus. However, its efficacy and mechanism of action against SGIV remain uncharacterized. Using Singapore grouper spleen (GS) cells as an in vitro model, we evaluated matrine's anti-SGIV.Results demonstrate that matrine inhibits SGIV replication in a concentration-dependent manner, exerting antiviral effects primarily during early infection stages. Mechanistically, matrine modulates NF-κB-mediated immune and inflammatory responses, enhances cellular antioxidant capacity to suppress SGIV-induced ROS production, and promotes interferon-related gene expression.

Key words: Grouper; SGIV; Matrine; Inflammation; Oxidative stress

牛蒡苷佐剂通过促进免疫应答与调控代谢适应性增强虹鳟（*Oncorhynchus mykiss*）IHNV 疫苗效力

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摘要：传染性造血器官坏死病毒（IHNV）严重威胁我国虹鳟（*Oncorhynchus mykiss*）养殖。本研究首次将牛蒡苷（arctiin, ARC）作为 IHNV 疫苗佐剂，并系统评估其免疫增强作用。经色谱与光谱分析确认，提取 ARC 纯度超过 95%，理化性质符合标准。免疫试验表明，ARC 联合疫苗将虹鳟病毒攻毒存活率提高至 70.0%（对照组 24.0%），血清中和抗体效价升高 2.3 倍，并显著促进肝脏非特异性免疫酶（ACP、AKP）和抗氧化酶（T-SOD、CAT）活性。组织学观察显示，ARC 联合疫苗有效抑制病毒诱导的肝细胞空泡化和凋亡。多组学分析揭示，该联合疫苗激活 MHC I/II 介导的抗原递呈通路，上调抗原加工基因（TAP2、PA28）和 T 细胞标志物（CD8、CD4），并调节核苷酸代谢通路、胆汁酸-ABC 转运等提高宿主免疫代谢适应性。本研究为水产疫苗生态友好与高效设计提供了理论依据和实践框架。

关键词：疫苗；牛蒡苷；传染性造血器官坏死病毒；虹鳟

Arctiin adjuvant enhances IHNV vaccine efficacy in rainbow trout (*Oncorhynchus mykiss*) through immune response promotion and metabolic adaptation modulation

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Abstract: Infectious hematopoietic necrosis virus (IHNV) severely threatens rainbow trout (*Oncorhynchus mykiss*) aquaculture in China. This study, for the first time, employed arctiin (ARC) as an IHNV vaccine adjuvant and systematically evaluated its immunopotentiating effects. Chromatographic and spectroscopic analyses confirmed that the extracted ARC had >95% purity and met physicochemical standards. Immunization trials showed that ARC combined with the vaccine increased fish survival after viral challenge to 70.0% (vs. 24.0% in controls), enhanced serum neutralizing antibody titers by 2.3-fold, and significantly elevated hepatic non-specific immune enzymes (ACP, AKP) and antioxidant enzymes (T-SOD, CAT). Histological observations indicated that the ARC + vaccine treatment effectively suppressed virus-induced hepatocyte vacuolization and apoptosis. Multi-omics analyses revealed that this combined vaccine activated MHC I/II-mediated antigen presentation pathways, upregulated antigen-processing genes (TAP2, PA28) ,and regulated nucleotide metabolism to improve host immunometabolic adaptability.

Key words: Vaccine; Arctiin; Infectious hematopoietic necrosis virus; Oncorhynchus mykiss

PI3K 磷酸化中华绒螯蟹 14-3-3ζ，调控活性氧抵御螺原体侵染

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摘要：本研究首先通过磷酸化蛋白组学发现螺原体感染后 Es14-3-3ζ磷酸化水平显著上升，并经 IP 与 qRT-PCR 验证。同时，筛选出靶向 Es14-3-3ζ的 miR-2309，其转染可抑制该蛋白磷酸化。GST pull-down 及质谱鉴定出 Es14-3-3ζ与 PI3K、Trx1、Catalase 互作，Co-IP 证实磷酸化促进互作，且共定位于细胞质。点突变模拟磷酸化后，细胞 ROS 与活力上升，凋亡与螺原体拷贝数下降。最后，沉默 Es14-3-3ζ后感染螺原体，血淋巴中病原拷贝数增加，存活率下降。综上 PI3K 磷酸化 Es14-3-3ζ，促进 Es14-3-3ζ与抗氧化蛋白相互作用调控 ROS 水平，进而影响细胞活力及细胞凋亡，最终帮助宿主抵御螺原体侵染。

关键词：中华绒螯蟹；中华绒螯蟹螺原体；Es14-3-3ζ；磷酸化

PI3K-mediated 14-3-3ζ phosphorylation enhances reactive oxygen species production to defend against *Spiroplasma eriocheiris* infection

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Abstract: This study first employed phosphoproteomics and identified a significant upregulation of Es14-3-3ζ phosphorylation following S.eriocheiris infection, which was confirmed by IP and qRT-PCR. Meanwhile, miR-2309, which targeted Es14-3-3ζ, was identified, and its transfection suppressed the phosphorylation of this protein. GST pull-down coupled with mass spectrometry revealed that Es14-3-3ζ interacted with PI3K, Trx1, and Catalase. Co-IP experiments demonstrated that phosphorylation enhanced these interactions, and the proteins co-localized in the cytoplasm. Point mutation to mimic phosphorylation led to increased ROS levels and cell viability, alongside decreased apoptosis and the copy number of S. eriocheiris. Finally, silencing Es14-3-3ζ before infection resulted in an elevated pathogen load in hemolymph and a reduced survival rate. In conclusion, PI3K-mediated phosphorylation of Es14-3-3ζ promoted its interaction with antioxidant proteins, modulated ROS levels, which in turn influenced cell viability and apoptosis, ultimately aiding the host in resisting S. eriocheiris infection.

Key words: Eriocheir sinensis; Spiroplasma eriocheiris; Es14-3-3ζ; ,phosphorylation

罗氏沼虾野田村病毒诱导下的罗氏沼虾 miRNA 筛选与功能分析

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摘要：作为极具代表性的具有卫星病毒的罗氏沼虾野田村病毒，因其引起的白尾病是罗氏沼虾养殖产业的重要病原之一，爆发高峰期几乎在全球各地的所有罗氏沼虾繁育和养殖场中都有发生。本研究选取 MrNV 中国株感染的罗氏沼虾淡化后幼苗为试验材料，利用 llumina HiSeq 2500 测序平台和生物信息学分析，通过 miRNA 的靶基因功能注释结合 RT-qPCR 实验结果，挑选出表达极显著的两个 miRNAs（MIR-4 和 MIR-19），并筛选预测与 MIR-4 和 MIR-19 作用相关的靶基因。功能分析表明 MIR-4 的靶基因 cuticle protein 和 MIR-19 的靶基因β1 laminin 的相对表达量与对应 miRNA 的表达量呈正相关；MIR-4 和 MIR19 的过表达和沉默在成虾中 MrNV 拷贝数变化趋势基本一致，表明其可能参与了 MrNV 的侵染，MIR-4 和 MIR19 在 MrNV 感染中发挥的是正向和负向作用。

关键词：罗氏沼虾；罗氏沼虾野田村病毒；miRNAs；靶基因

Screening and Functional Analysis of *Macrobrachium rosenbergii* miRNAs Mediated by *Macrobrachium rosenbergii* Nodavirus Infection

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Abstract: As a highly representative satellite virus, Macrobrachium rosenbergii Nodamura virus (MrNV) is one of the significant pathogens in the giant river prawn aquaculture industry due to the white tail disease it causes. During outbreak peaks, the disease occurs in almost all breeding and farming facilities of Macrobrachium rosenbergii worldwide. In this study, post-larval juveniles of Macrobrachium rosenbergii infected with the Chinese strain of MrNV were selected as experimental materials. Using the Illumina HiSeq 2500 sequencing platform and bioinformatics analysis, combined with functional annotation of miRNA target genes and RT-qPCR experimental results, two highly significantly expressed miRNAs (MIR-4 and MIR-19) were identified, and their potential target genes were predicted. Functional analysis revealed that the relative expression levels of the target gene cuticle protein for MIR-4 and β1 laminin for MIR-19 were positively correlated with the expression levels of their corresponding miRNAs.

Key words:*Macrobrachium rosenbergii*, *Macrobrachium rosenbergii* Nodamura virus, miRNAs, target genes

中华绒螯蟹热休克同源蛋白 71 乙酰化修饰响应螺原体感染的机制研究

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摘要：HSP70 已被证实参与调控抗病毒天然免疫，然而 HSP70 翻译后修饰在病原感染过程中的调控机制尚不清楚。我们发现中华绒螯蟹 HSC71 在螺原体感染后乙酰化水平显著降低；敲低 HSC71 会促进血淋巴细胞凋亡并减弱中华绒螯蟹对螺原体的抵抗力；过表达乙酰化模拟突变体 HSC71 K579Q 可以抑制细胞凋亡并增强 ROS 生成来限制螺原体对果蝇 S2 细胞的侵染。机制上，Crat 介导 HSC71 第 579 位赖氨酸的乙酰化，并减弱其泛素化降解促进 HSC71 蛋白稳定。HSC71 K579 位点的乙酰化会减弱其与 SOD 的结合，进而导致细胞内 ROS 生成增多。使用 SIRT1 特异性抑制剂 EX-527 可以提高中华绒螯蟹血淋巴细胞和果蝇 S2 细胞中 HSC71 的乙酰化水平，导致 ROS 水平升高和螺原体胞内增殖减少，表明该调控机制在节肢动物中可能具有保守性。我们的研究结果凸显了靶向 HSC71 乙酰化修饰在开发甲壳类病原性疾病治疗策略方面的潜力。

关键词：乙酰化；泛素化；热休克同源蛋白 71；中华绒螯蟹；螺原体

HSC71 acetylation confers protection against *Spiroplasma eriocheiris* infection by inhibiting apoptosis and promoting ROS production in crustaceans

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Abstract: HSP70 has been implicated in regulating antiviral innate immunity, yet the role of its post-translational modifications during pathogenic infection remains unclear. Here, we demonstrated that crab HSC71 undergoes deacetylation upon spiroplasma infection. HSC71 depletion enhanced hemocyte apoptosis and increased crab susceptibility to spiroplasma. Ectopic expression of acetylation-mimetic HSC71 K579Q protects S2 cells from spiroplasma infection by attenuating apoptosis and enhancing ROS generation. Mechanistically, Crat acetylated HSC71 at K579 and stabilized HSC71 by impairing its ubiquitination. Acetylation at K579 weaken the interaction between HSC71 and SOD, leading to accumulation of ROS. Treatment with SIRT1 inhibitor EX-527 promoted HSC71 acetylation in both hemocytes and S2 cells, resulting in increased ROS and decreased spiroplasma proliferation, suggesting evolutionary conservation of this regulatory mechanism among arthropods. Our results underscore the therapeutic potential of targeting HSC71 acetylation in controlling pathogenic diseases in crustaceans.

Key words:acetylation; ubiquitination; HSC71; crab; spiroplasma

核酸纳米材料介导的水产病原精准检测与基因靶向干扰

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摘要：针对海洋弧菌病害防控缺乏靶向性、低效的问题，借助核酸纳米材料对毒力基因的靶向识别，进行鳗弧菌毒力基因 empA 的精准检测和靶向干扰。设计和合成了对鳗弧菌 empA 基因具有特异识别性的核酸纳米金探针，结合 LAMP 等温扩增，对 empA 的扩增子进行可视化检测。设计反义寡核苷酸序列并由碳点高效负载和递送至鳗弧菌。通过荧光显微镜、流式细胞术和 RT-qPCR 评估 ASO 的胞内递送效率和基因沉默效果。结果显示，核酸纳米探针可介导实现海洋弧菌精准快检(20 分钟)，假阳性率降至 4%。利用反义寡核苷酸-碳点对 empA 的 mRNA 特异性结合，现了对鳗弧菌 empA 毒力基因的靶向干扰，金属蛋白酶 EmpA 表达下调 70%以上。本研究将核酸纳米材料引入并贯穿弧菌病害防控链条，为构建靶向、高效的水产病害防控体系提供了新思路。

关键词：鳗弧菌；empA 基因；核酸纳米材料；基因干扰；大菱鲆

Accurate detection and targeted gene regulation of aquacultural pathogen mediated by nucleici acid nanomaterials

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Abstract：To address the issues of lack of targeting and low efficiency in control of Vibrio diseases, this study leverages the targeted recognition of virulence genes by nucleic acid nanomaterials to achieve accurate detection and targeted interference of the empA virulence gene in *Vibrio anguillarum*. Nucleic acid-gold nanoprobes with specific recognition capability for the empA gene of *Vibrio anguillarum* were designed and synthesized. Combined with LAMP (Loop-Mediated Isothermal Amplification), visual detection of empA amplicons was realized. Antisense oligonucleotide (ASO) sequences were designed, and efficiently loaded onto carbon dots for delivery into Vibrio anguillarum. The intracellular delivery efficiency of ASOs and their gene silencing effects were evaluated using fluorescence microscopy, flow cytometry, and RT-qPCR. The results showed that nucleic acid nanoprobes enabled accurate and rapid detection of marine Vibrio (20 min), reducing the false positive rate to 4%. Targeted interference with the empA gene was achieved, leading to a more than 70% downregulation in empA expression.

Key words: Vibrio anguillarum; empA gene; nucleic acid nanomaterials; gene interference; Scophthalmus maximus

石斑鱼 DHCR24 介导 STING-TBK1 通路蛋白的降解促进新加坡石斑鱼虹彩病毒的感染

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摘要：24-脱氢胆固醇还原酶（DHCR24）作为胆固醇合成中的关键酶，已有研究表明其在多种病毒感染中发挥重要作用，但在鱼类病毒感染中的功能仍未知。本研究中，我们成功克隆了来自斜带石斑鱼的同源物 EcDHCR24，新加坡石斑鱼虹彩病毒（SGIV）感染后，EcDHCR24 的转录水平显著增加。亚细胞定位结果显示，EcDHCR24 分布于细胞质中，且与内质网和高尔基体存在共定位。EcDHCR24 的过表达能够促进 SGIV 的复制，且抑制干扰素相关基因和促炎因子的转录水平。过表达 EcDHCR24 会显著下调 EcSTING、EcTBK1、EcIRF3 和 EcIRF7 诱发的 IFN1、ISRE 和 NF-κB 启动子的荧光素酶活性。此外，EcDHCR24 与 EcSTING 和 EcTBK1 存在相互作用和共定位，且 EcDHCR24 通过自噬-溶酶体途径降解 EcSTING 和 EcTBK1。这些发现为石斑鱼抵抗病毒感染的先天免疫机制提供新思路。

关键词：石斑鱼；DHCR24；SGIV；STING；TBK1

Grouper DHCR24 mediates the degradation of STING-TBK1 pathway protein to promote the infection of Singapore grouper iridovirus

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Abstract： 24-dehydrocholesterol reductase (DHCR24), a key enzyme in cholesterol synthesis, has been shown to play an important role in viral infections, but its function in fish viral infections is still unknown. In this study, we cloned the homolog EcDHCR24 from orange-spotted grouper, and the transcriptional level of EcDHCR24 was increased after infection with Singapore grouper iridovirus (SGIV). Subcellular localization results showed that EcDHCR24 was distributed in the cytoplasm and co-localized with the endoplasmic reticulum and Golgi apparatus. Overexpression of EcDHCR24 promoted SGIV replication and inhibited the transcription levels of interferon-related genes and pro-inflammatory factors. Overexpression of EcDHCR24 down-regulated the luciferase activities of IFN1, ISRE, and NF-κB promoters induced by EcSTING, EcTBK1, EcIRF3, and EcIRF7. In addition, EcDHCR24 interacted with EcSTING and EcTBK1, and EcDHCR24 degraded EcSTING and EcTBK1 through the autophagy-lysosome pathway. These findings provide new ideas for the innate immune mechanism of grouper to resist viral infections.

Key words:*Epinephelus coioides*; DHCR24; SGIV; STING; TBK1

无乳链球菌 VII 型分泌系统（T7SS）通过调控镁离子的转运促进荚膜的完整性

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摘要：VII 型分泌系统（T7SS）目前已经在无乳链球菌中被鉴定，但其发挥功能的具体机制目前还不清楚。本研究构建了无乳链球菌 HN016 T7SS 核心组分 essC 的缺失株（ΔessC）以及回补株（CΔessC），发现ΔessC 胞内镁离子浓度显著下降。根据转录组数据分析，essC 缺失后细菌荚膜相关蛋白表达量显著下调，并通过 WB、流式和透射电镜发现 T7SS 缺失后荚膜不稳定。为了进一步推断胞内镁离子的减少影响链球菌荚膜的稳定性，构建了经典镁离子转运蛋白 corA2 的缺失株（ΔcorA2）和镁离子通道结合位点突变株，发现荚膜都减少了，表明胞内镁离子是调控荚膜合成的关键。在细胞水平和罗非鱼感染模型中，发现ΔessC 的毒力显著降低，且突破血脑屏障的能力也显著下降。本研究揭示无乳链球菌 T7SS 调控胞内镁离子的转运促进荚膜的完整性，进而发挥毒力的机制，为进一步开发抗细菌药物提供新靶标。

关键词：VII 型分泌系统；B 族链球菌；镁离子；荚膜；毒力

The type VII secretion system of Group B Streptococcus mediate magnesium transport contribute to capsule integrity

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Abstract：The Type VII Secretion System (T7SS) has been identified in Streptococcus agalactiae, but its functional mechanism remains unclear. This study constructed essC deletion (ΔessC) and complementation (CΔessC) mutants in S. agalactiae HN016. The ΔessC strain showed a significant decrease in intracellular magnesium levels. Transcriptomic analysis indicated downregulation of capsule-related proteins, and Western blot, flow cytometry, and TEM confirmed capsule instability in the T7SS mutant. Further experiments with a corA2 deletion mutant (ΔcorA2) and a magnesium channel binding site mutant demonstrated that reduced intracellular magnesium led to decreased capsule synthesis, indicating magnesium’s key role in capsule regulation. Both in vitro and in a tilapia infection model, the ΔessC mutant exhibited reduced virulence and a diminished ability to cross the blood-brain barrier. This study reveals that T7SS promotes capsule integrity and virulence by regulating magnesium transport, offering a new target for antibacterial drug development.

Key words:type VII secretion system; Group B Streptococcus (GBS); magnesium; capsule; virulence

石斑鱼 TRIM47 蛋白通过靶向 STING 蛋白负调控干扰素应答

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摘要：越来越多的证据表明，TRIM 家族成员在宿主病原体感染后发挥关键作用。然而，石斑鱼 EcTRIM47 在鱼类虹膜病毒感染过程中的作用仍未知。在此，我们通过 qPCR 分析显示石斑鱼 TRIM47 针对 SGIV 感染诱导 TRIM47 的表达呈时间依赖性。TRIM47 的过表达显著促进了 CPE 的严重程度以及病毒基因的转录和蛋白表达。此外，体外过表达 TRIM47 降低了 IFN 相关免疫信号分子的转录水平，提示 TRIM47 的抗病毒作用是由于对 IFN 反应的负调控所致。随后，我们利用免疫共沉淀实验发现 TRIM47 与 STING、TBK1、IRF3 和 IRF7 相互作用，而且 TRIM47 的过表达可以剂量依赖性方式降解 STING，从而抑制 STING 诱导的抗病毒作用。综上，表明 TRIM47 作为促病毒宿主因子发挥作用，通过降解 STING 蛋白来抑制的 STING 介导的抗病毒免疫反应从而促进 SGIV 复制。

关键词：TRIM47；干扰素反应；STING；SGIV

The grouper TRIM47 protein negatively regulates the interferon response by targeting STING

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Abstract: Members of the TRIM family play crucial roles following host-pathogen infections. However, the function of grouper EcTRIM47 during infection with the fish iridovirus remains unknown. Here, we demonstrate via qPCR analysis that grouper TRIM47 exhibits time-dependent expression induction in response to SGIV infection. Overexpression of TRIM47 significantly enhanced the severity of cytopathic effects (CPE), transcription of viral genes, protein expression, and transcriptional levels of IFN-related immune signaling molecules, suggesting that the antiviral action of TRIM47 results from negative regulation of the IFN response. Subsequently, immunoprecipitation experiments revealed TRIM47 interacts with STING, TBK1, IRF3, and IRF7. Moreover, TRIM47 overexpression dose-dependently degraded STING, thereby suppressing STING-mediated antiviral responses. Collectively, these findings demonstrate that TRIM47 functions as a pro-viral host factor by degrading STING protein, thereby suppressing STING-mediated antiviral immunity and promoting SGIV replication.

Key words:TRIM47; IFN response; STING; SGIV

枯草芽孢杆菌传递的鱼用传染性脾肾坏死病毒口服抗体的制备及应用

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摘要：大口黑鲈（*Micropterus salmoides*）是中国重要的水产养殖物种，但高密度养殖导致病害频发，其中传染性脾肾坏死病毒（ISKNV）造成严重经济损失。该病毒侵袭脾肾组织，引发肿大、坏死及功能衰竭，具有高传染性和快速传播特点，目前尚无商业化治疗药物。本研究旨在利用枯草芽孢杆菌表达 ISKNV 口服抗体，并评估其免疫效果。通过噬菌体展示技术筛选特异性单链抗体，将抗体基因克隆至 pHT43 质粒并转化至枯草芽孢杆菌 WB600 中。PCR、测序和 Western blot 验证了重组蛋白的表达。口服免疫实验显示，病毒感染后存活率达 95.0%，对照组为 33.3%，病毒载量显著降低。综上所述，本研究开发的枯草芽孢杆菌 WB600/PHT43 口服抗体能够通过中和病毒提供被动免疫保护，显著降低大口黑鲈感染 ISKNV 后的死亡率，具有一定的预防 ISKNV 感染的潜力，为该病毒的防控提供了新策略。

关键词：大口黑鲈；传染性脾肾坏死病毒；芽孢分泌表达；口服抗体

Preparation and Application of Orally Administered Antibodies Against Infectious Spleen and Kidney Necrosis Virus in Fish Using Bacillus subtilis as a Delivery System

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Abstract: The largemouth bass (*Micropterus salmoides*) represents an economically significant aquaculture species in China. However, intensive cultivation practices have led to frequent disease outbreaks, with infectious spleen and kidney necrosis virus (ISKNV) imposing substantial economic losses on the industry. This pathogen primarily targets splenic and renal tissues, eliciting tissue enlargement, necrosis, and subsequent functional impairment. Characterized by high infectivity and rapid transmission dynamics, ISKNV currently lacks commercially available therapeutic interventions. This study developed an orally delivered antibody against ISKNV using Bacillus subtilis as an expression platform and evaluated its immunoprotective efficacy. Through phage display technology, a specific single-chain variable fragment (scFv) was isolated. The corresponding antibody gene was successfully cloned into the pHT43 plasmid and transformed into Bacillus subtilis WB600. Recombinant protein expression was verified via PCR amplification, DNA sequencing, and Western blot analysis.

Key words: Largemouth bass; Infectious spleen and kidney necrosis virus; Spore-secreted expression; Oral antibody

基于 CRISPR-Cas12a 系统的肿大细胞虹彩病毒检测方法的建立与应用

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摘要：本研究旨在建立一种高效、灵敏且特异的 ERA-CRISPR 分子检测方法，用于肿大细胞病毒属的快速诊断，该病毒属包括传染性脾肾坏死病毒（ISKNV）、真鲷虹彩病毒（RSIV）和大菱鲆红体病虹彩病毒（TRBIV）。研究基于 MCP 基因设计 ERA 引物及 crRNA，优化反应条件并构建通用检测体系；同时针对 RSIV 的 ORF098 基因开发特异性检测方法，实现 ISKNV 与 RSIV 的区分。结果表明，该方法在恒温条件下可快速扩增并结合 Cas12a 实现特异识别，具有高灵敏度、强特异性和操作简便等优势，适用于现场检测和大规模应用。本研究成果为鱼类虹彩病毒的早期诊断与精准防控提供了有效技术支撑，对降低养殖损失和促进水产养殖业可持续发展具有重要意义。

关键词：ERA-CRISPR-Cas12a；肿大细胞；快速检测；灵敏特异；虹彩病毒

Establishment and Application of a CRISPR-Cas12a-Based Detection Method for Megalocytivirus

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Abstract：This study aimed to establish an efficient, sensitive, and specific ERA-CRISPR molecular detection method for the rapid diagnosis of Megalocytivirus, including Infectious Spleen and Kidney Necrosis Virus (ISKNV), Red Sea Bream Iridovirus (RSIV), and Turbot Reddish Body Iridovirus (TRBIV). ERA primers and crRNAs were designed based on the MCP gene, and reaction conditions were optimized to construct a universal detection system. In addition, primers and crRNAs targeting the RSIV ORF098 gene were developed to distinguish ISKNV from RSIV. The results demonstrated that this method enables rapid amplification under isothermal conditions, coupled with Cas12a-mediated specific recognition, exhibiting high sensitivity, strong specificity, and operational simplicity. It is suitable for on-site detection and large-scale application. The findings provide effective technical support for the early diagnosis and precise prevention of fish iridoviruses, contributing to the reduction of aquaculture losses and the sustainable development of the aquaculture industry.

Key words:ERA-CRISPR-Cas12a; Megalocytivirus; Rapid detection; Sensitivity and specificity; Iridovirus

无乳链球菌 VII 型分泌系统（T7SS）通过调控镁离子的转运促进荚膜的完整性

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摘要：VII 型分泌系统（T7SS）目前已经在无乳链球菌中被鉴定，但其发挥功能的具体机制目前还不清楚。本研究构建了无乳链球菌 HN016 T7SS 核心组分 essC 的缺失株（ΔessC）以及回补株（CΔessC），发现ΔessC 胞内镁离子浓度显著下降。根据转录组数据分析，essC 缺失后细菌荚膜相关蛋白表达量显著下调，并通过 WB、流式和透射电镜发现 T7SS 缺失后荚膜不稳定。为了进一步推断胞内镁离子的减少影响链球菌荚膜的稳定性，构建了经典镁离子转运蛋白 corA2 的缺失株（ΔcorA2）和镁离子通道结合位点突变株，发现荚膜都减少了，表明胞内镁离子是调控荚膜合成的关键。在细胞水平和罗非鱼感染模型中，发现ΔessC 的毒力显著降低，且突破血脑屏障的能力也显著下降。本研究揭示无乳链球菌 T7SS 调控胞内镁离子的转运促进荚膜的完整性，进而发挥毒力的机制，为进一步开发抗细菌药物提供新靶标。

关键词：VII 型分泌系统；B 族链球菌；镁离子；荚膜；毒力

The type VII secretion system of Group B Streptococcus mediate magnesium transport contribute to capsule integrity

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Abstract: The Type VII Secretion System (T7SS) has been identified in Streptococcus agalactiae, but its functional mechanism remains unclear. This study constructed essC deletion (ΔessC) and complementation (CΔessC) mutants in S. agalactiae HN016. The ΔessC strain showed a significant decrease in intracellular magnesium levels. Transcriptomic analysis indicated downregulation of capsule-related proteins, and Western blot, flow cytometry, and TEM confirmed capsule instability in the T7SS mutant. Further experiments with a corA2 deletion mutant (ΔcorA2) and a magnesium channel binding site mutant demonstrated that reduced intracellular magnesium led to decreased capsule synthesis, indicating magnesium’s key role in capsule regulation. Both in vitro and in a tilapia infection model, the ΔessC mutant exhibited reduced virulence and a diminished ability to cross the blood-brain barrier. This study reveals that T7SS promotes capsule integrity and virulence by regulating magnesium transport, offering a new target for antibacterial drug development.

Key words:type VII secretion system; Group B Streptococcus (GBS); magnesium; capsule; virulence

鱼类 T 细胞抗感染免疫的机制

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摘要：鱼类 T 细胞的免疫功能和调控机制尚未被充分阐明。我们发现，罗非鱼 CD4+T 细胞分化为 Th1 和 Th17 亚群，分别抵御胞内和胞外细菌感染；CD8+T 细胞则依赖 FasL 执行细胞毒性功能。在肠道中，T 细胞还通过鲸杆菌维持微生物群落和免疫稳态，增强抗感染免疫。机制方面，罗非鱼 T 细胞活化后发生显著的代谢重编程，其利用脂联素受体、ERK1/2、 GSK3-β调控的糖酵解途径，以及 mTORC1-c-Myc 轴介导的谷氨酰胺代谢途径，共同促进 T 细胞免疫。有趣的是，罗非鱼还通过短期禁食、行为发烧等主动行为，增强 T 细胞免疫，抵御病原感染。此外，我们发现 PRMT2 通过甲基化 KEAP1，阻碍 NRF2 入核，从而抑制 ROS 清除、损伤 T 细胞免疫；而敲除 PRMT2 能够增强 T 细胞的功能和存活，赋予罗非鱼更强的抗感染免疫能力。在此基础上构建了基于行为发烧、短期禁食、PRMT2 敲除等的病害防控策略，显著提高了鱼类抵御细菌感染的能力。

关键词：罗非鱼；适应性免疫；T 细胞；抗感染免疫；调控机制

Mechanisms of Fish T Cell–Mediated Antimicrobial Immunity

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Abstract： The immunological functions and regulatory mechanisms of fish T cells remain poorly defined. Using Nile tilapia, we demonstrate that CD4$^+$ T cells differentiate into Th1 and Th17 subsets to combat intracellular and extracellular bacteria, while CD8$^+$ T cells mediate FasL-dependent cytotoxicity. T cells also interact with intestinal Cetobacterium to sustain microbial and immune homeostasis. Mechanistically, tilapia T cells undergo metabolic reprogramming, relying on glycolysis (adiponectin receptor–ERK1/2–GSK3β) and glutamine metabolism (mTORC1–c-Myc) to support immune function. We further show that PRMT2 suppresses T-cell immunity by methylating KEAP1 and blocking NRF2-dependent ROS clearance, whereas PRMT2 deficiency enhances T-cell survival and antimicrobial activity. Strikingly, tilapia employ adaptive behaviors, including short-term fasting and behavioral fever, to boost T-cell responses against pathogens. These findings uncover evolutionarily conserved regulatory pathways and behavioral strategies that optimize fish T-cell immunity and provide new avenues for disease control.

Key words: Nile tilapia; Adaptive immunity; T cells; Antimicrobial immunity; Mechanism

克氏原螯虾不同类型抗脂多糖因子的抗菌作用研究

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摘要：抗脂多糖因子（ALF）是甲壳动物中重要的天然免疫效应分子，具有广谱抗菌活性。本研究以克氏原螯虾（*Procambarus clarkii*）为对象，探究其不同 ALF 亚型的功能机制。通过原核表达及体外抑菌实验发现，重组蛋白 rPcALF1 对革兰氏阴性菌和阳性菌均表现出显著抑菌活性，效果优于其他亚型。体内实验表明，干扰 PcALF1 表达显著降低了宿主对嗜水气单胞菌（Aeromonas hydrophila）的抗性；而回补 rPcALF1 蛋白或其脂多糖结合域（LBD）多肽可提高感染个体存活率 20%–30%，并修复肠道组织损伤，逆转菌群失调。转录组分析表明，rPcALF1 通过结合细菌 LPS 破坏细胞膜结构，进而引起代谢障碍与过度应激，最终导致细菌死亡。该多靶点作用机制表明其不易诱发耐药性。综上，rPcALF1 在防治克氏原螯虾细菌感染方面具有良好的应用潜力。

关键词：克氏原螯虾；抗脂多糖因子；抗菌肽；嗜水气单胞菌；抗菌活性；肠道微生物群

Study on the Antibacterial Effects of Different Types of Anti-Lipopolysaccharide Factors in *Procambarus clarkii*

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Abstract： Antilipopolysaccharide factors (ALFs) are crucial innate immune effectors in crustaceans with broad-spectrum antimicrobial activity. This study investigates ALF subtypes in Procambarus clarkii, focusing on their conserved disulfide-stabilized lipopolysaccharide-binding domain (LBD). Recombinant proteins rPcALF1 and rPcALF2 demonstrated superior antibacterial activity against Gram-negative and Gram-positive bacteria versus other ALFs. PcALF1knockdown via RNAi reduced host resistance to Aeromonas hydrophila; functionality was partially restored by rPcALF1 or its LBD peptide, improving survival by 30% and 20%, respectively. Treatment repaired intestinal damage and reverted dysbiosis. Transcriptomics revealed that rPcALF1/2 induces bacterial gene reprogramming: disrupting membrane integrity, suppressing central metabolism, and upregulating stress responses, culminating in a multi-target bactericidal mechanism with low resistance potential. These findings position rPcALF1/2 as promising antimicrobial agents for aquaculture disease control.

Key words:*Procambarus clarki*i; Anti-lipopolysaccharide factor; Antimicrobial peptides; *Aeromonas hydrophila*; Antimicrobial activity; Intestinal microbiota

miRNA-7565 通过靶向 IL-13Ra1，负调控大黄鱼 IL-4/13 介导的 Th2 型免疫应答

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摘要：白细胞介素-4(IL-4)和 IL-13 是结构相关的细胞因子，通过激活受体复合物并诱导 MAPK 和 mTOR 信号通路，在 Th2 免疫应答中起关键作用。微小 RNA(miRNAs)通过抑制 mRNA 翻译或促进其降解调控基因表达。尽管 miR-7565 与鱼类胚胎发育相关，但其免疫功能尚不明确。本研究在大黄鱼(*Larimichthys crocea*)中鉴定出 miR-7565 成熟序列，该序列在脊椎动物中高度保守。RNA pul-down 实验表明，miR-7565 可直接结合 LcIL-13Ra1 的 3'-UTR。在原代头肾白细胞(PKLs)中过表达 miR-7565 显著降低 LcIL-13Ra1 mRNA 水平，并在 LcIL-4/13AB 刺激下明显抑制 MEK1/2 和 4E-BP 的磷酸化，从而减弱 MAPK 和 mTOR 通路活性。同时，miR-7565 还抑制了 LcIL-4/13A/B 诱导的 T 细胞增殖、分化及 B 细胞增殖。

关键词：大黄鱼；miR7565；mTOR 信号通路

MicroRNA-7565 negatively regulates the lL-4/13-mediated Th2 immune response by targeting lL-13Ra1 in large yelow croaker (*Larimichthys crocea*)

Jiamei Liu
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Abstract：Interleukin-4 and lL-13 are structurallv related cvtokines that plav key roles in the Th2 immune response bv activating thellreceptor complexes and inducing the MAPK and mTOR signaling pathways. MicroRNAs regulate gene expression by suppressing mRNA translation or promoting degradation. While miR-7565 has been linked to fish embryonic development, its role in immunity remains unclear. in this study, we identiied the mature sequence of miR-7565 in large yellow croaker, whichis highly conserved among vertebrates. RNA pull-down assavs showed that miR-7565 directly binds the 3'-UTR of LclL-13Ra1. Overexpression of miR-7565 in primary head kidney leukocytes (PKLs) significantly reduced LclL-13Ra1 mRNA levels. Upon stimulation with LclL-4/13A and LclL-4/138,miR-7565 overexpression markedlv decreased the phosphorvlation oiMEK1/2 and 4E-BP_-two critical components of the MAPK and mTOR pathways in PKLs. Moreover, miR-7565 attenuated LclL-4/13A/B-induced T cell proliferation, differentiation, and B cell proliferation. These results demonstrate that miRNA-mediated requlation in fish immunity

Key words:miR-7565; 1L-13Ra1; Th2 immune response; mTOR pathway; large yellow croaker (*Larimichthys crocea*)

罗氏沼虾响应低温胁迫下肝胰腺组织全转录组综合表征分析

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摘要：本研究通过全转录组测序技术，系统分析了罗氏沼虾（*Macrobrachium rosenbergii*）在急性低温胁迫下肝胰腺组织中 mRNA、lncRNA、circRNA 和 miRNA 的表达特征。实验设置低温组（13.5°C）和对照组（26°C），每组 3 个生物学重复。结果显示，共鉴定出 80 个 lncRNA、2250 个 mRNA、2 个 circRNA 和 23 个 miRNA 存在显著差异表达。功能富集分析表明，差异基因显著富集于 TNF 信号通路、细胞凋亡、内吞作用和免疫相关通路。通过构建 ceRNA 调控网络，发现 lncRNA 与 mRNA 之间存在 8729 个靶向关系对，并筛选出 26 个可能与低温响应密切相关的关键基因。RT-qPCR 验证结果与测序数据一致。本研究初步揭示了罗氏沼虾响应低温胁迫的分子调控机制，为解析其耐寒性遗传基础提供了理论依据和数据支持。

关键词：罗氏沼虾；低温胁迫；全转录组；肝胰腺

Comprehensive Transcriptome-wide Characterisation of hepatopancreatic tissues in response to low-temperature stress in the *Macrobrachium rosenbergii*

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Abstract：This study comprehensively characterized the transcriptomic profiles of mRNA, lncRNA, circRNA, and miRNA in the hepatopancreas of *Macrobrachium rosenbergii* under acute low-temperature stress using whole-transcriptome sequencing. The experiment included a low-temperature group (13.5°C) and a control group (26°C), each with three biological replicates. A total of 80 lncRNAs, 2,250 mRNAs, 2 circRNAs, and 23 miRNAs were identified as significantly differentially expressed. Functional enrichment analysis revealed significant involvement in TNF signaling, apoptosis, endocytosis, and immune-related pathways. A ceRNA regulatory network was constructed, identifying 8729 lncRNA–mRNA targeting pairs and 26 key genes potentially critical for cold stress response. RT-qPCR validation confirmed the reliability of the sequencing data. These findings provide insights into the molecular mechanisms underlying low-temperature adaptation in M. rosenbergii and offer valuable genetic resources for further research on cold tolerance in crustaceans.

Key words:*Macrobrachium rosenbergii*; low-temperature stress; whole transcriptome; hepatopancreas

CTRP9 通过 AdipoR1 增强罗非鱼 T 细胞抗菌免疫

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摘要：脂联素受体（AdipoR）对 T 细胞免疫的调控效应仍存争议，这种功能差异可能源于其配体的多样性。为此，本研究采用罗非鱼（编码 AdipoR1 但不产生脂联素）及小鼠为模型进行研究。在罗非鱼中，替代性脂肪因子 CTRP9 与 AdipoR1 结合，诱发 Ca^{2+} 内流并激活 CaM–CaMKKβ–AMPK 轴，通过与 TCR 信号发生串扰，促进糖酵解，从而增强 T 细胞活化、增殖及抗菌免疫。类似地，小鼠中 CTRP9 也促进 T 细胞活化、增殖与细胞因子产生，并提升抗 CD19-CAR-T 细胞在体外清除 B 细胞淋巴瘤的效果。CTRP9 对 T 细胞免疫的促进作用与脂联素的抑制效应截然相反，这源于机制上二者对 T 细胞糖酵解代谢的异质性调控：CTRP9 增强而脂联素抑制该代谢途径。本研究揭示了 AdipoR1 通过选择性识别不同配体（CTRP9 与脂联素）以差异调控 T 细胞免疫应答的新机制，该发现也为发展鱼类免疫调节策略提供了重要的理论依据。

关键词：罗非鱼；T 细胞；CTRP9；脂联素受体；糖酵解

CTRP9 enhances the antibacterial immunity of tilapia T cells by binding AdipoR1

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Abstract： Adiponectin receptor (AdipoR) signaling in T cell immunity remains controversial, potentially due to ligand diversity. Using tilapia (which expresses AdipoR1 but lacks adiponectin) and mouse models, this study demonstrates that the adipokine CTRP9 binds AdipoR1, triggering Ca^{2+} influx and activating the CaM–CaMKKβ–AMPK axis. This pathway crosstalks with TCR signaling to promote glycolysis, enhancing T cell activation, proliferation, and antibacterial immunity in tilapia. Similarly, in mice, CTRP9 augments T cell activation, proliferation, cytokine production, and improves the in vitro efficacy of anti-CD19-CAR-T cells against B cell lymphoma. Importantly, CTRP9 enhances—while adiponectin suppresses—T cell glycolysis, resulting in opposing immunomodulatory effects. These findings reveal a ligand-specific mechanism whereby AdipoR1 differentially regulates T cell responses via CTRP9 or adiponectin, providing a theoretical basis for immune modulation strategies in fish.

Key words: Tilapia; T cells; CTRP9; AdipoR; glycolysis

hnRNPM 调控乌鳢水泡病毒复制的机制研究

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摘要：确定对病毒复制至关重要的宿主蛋白并揭示调控机制对于阐明病毒发病机制非常关键。我们筛选了影响乌鳢水泡病毒（SHVV）复制的异质核核糖核蛋白（hnRNPs）。8 个 hnRNP 促进 SHVV 复制，其中 hnRNPM 促进效果最强。SHVV 感染促进了 hnRNPM 的表达，但对其亚细胞定位没有影响。此外，我们发现 hnRNPM 与病毒核蛋白（N）相互作用。HnRNPM 促进 N mRNA 和 N 蛋白的表达，以及病毒 N-N 相互作用。且 hnRNPM 与病毒 RNA 结合并促进 N-RNA 相互作用，并抑制 RIG-I-RNA 相互作用。hnRNPM 还与 IRF7 相互作用，通过抑制 IRF7 磷酸化、二聚化及入核来降低 IRF7 诱导的 IFN 表达。本研究有助于了解 hnRNPM 在单股负链 RNA 病毒复制中的功能。

关键词：hnRNPM；乌鳢水泡病毒；核蛋白；病毒 RNA；IRF7

The mechanism of hnrnpM regulating SHVV replication

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Abstract： Determination of host proteins critical for viral replication and revealing the regulatory mechanisms is essential for understading viral pathogenesis. Here, we screened the effects of heterogeneous nuclear ribonucleoproteins (hnRNPs) on the replication of snakehead vesiculovirus (SHVV). Eight hnRNPs promote SHVV replication, in which hnRNPM was identified as the most significant pro-SHVV factor. SHVV infection facilitated the expression of hnRNPM but had no effect on its subcellular localization. Besides, we found that hnRNPM interacted with the viral nucleoprotein (N). HnRNPM facilitated the expression of N mRNA and N protein and promoted viral N-N interaction. Additionally, we found that hnRNPM bound to viral RNA and promoted N-RNA interaction, and inhibited RIG-I-RNA interaction. Moreover, hnRNPM interacted with IRF7 and reduced IRF7-induced IFN expression through inhibiting its phosphorylation, dimerization, and cytoplasm-nuclear transpot. This study will help understanding the function of hnRNPM in the replication of single-stranded negative-sense RNA viruses.

Key words:hnRNPM; SHVV; N protein; vRNA; IRF7

大口黑鲈蛙虹彩病毒 basic-RPA、 RPA-LFD 快速检测方法的建立与应用

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摘要：大口黑鲈虹彩病毒病毒（LMBRaV）病导致大口鲈鱼养殖业高死亡率。建立快速灵敏的病毒检测方法是预防病毒传播和疾病爆发的当务之急。本研究针对 LMBRaV 建立了基本重组酶聚合酶扩增（basic-RPA）和 RPA 结合侧流层析试纸条（RPA -LFD）检测方法，以检测低病毒载量下的病毒。对 basic-RPA 和 RPA-LFD 检测的引物浓度、反应温度和时间进行了优化。basic-RPA 在 38℃下扩增 25 分钟 RPA-LFD 检测需要在 45°C 下进行 15 分钟的现场目测。检测方法的特异性表明，无法检测到其他水生病毒。两种检测方法的检测限均为 1 copy/μL DNA 样品。此外，与 PCR 检测法相比，basic-RPA 和 RPA-LFD 检测法均能多检测出 9 个临床样本。因此，basic-RPA 和 RPA-LFD 检测方法为现场诊断 LMBRaV 提供了更灵敏、快速和简便的方法。

关键词：大口黑鲈；LMBRaV；basic-RPA；RPA -LFD

Establishment of basic-RPA and RPA-LFD rapid detection methods for ranavirus in largemouth bass (*Microterus salmoides*)

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Abstract：Largemouth bass ranavirus (LMBRaV) disease causes a high mortality rate in largemouth bass aquaculture industry. Establishment of rapid and sensitive virus detection assays is an urgency for prevention of virus transmission and disease outbreak. In this study, basic recombinase polymerase amplification (basic-RPA) and RPA combined with lateral flow dipstick (RPA -LFD) assays for LMBRaV were established to detect virus at low viral loads. The mcp gene of LMBRaV was the target sequence for primers and probes design. Then the primer concentrations, reaction temperature and time of basic-RPA and RPA-LFD assays were optimized. The basic-RPA was amplified under 38°C for 25 minutes. The RPA-LFD assay required 15 minutes at 45°C for on-site visual results. The specificity of two assays showed that other aquatic viruses could not be detected. The detection limit was 1 copy/μL DNA sample for both basic-RPA and RPA-LFD assays. Therefore, the basic-RPA as well as RPA-LFD assays provided more sensitive, rapid and simple operation methods for the on-site diagnosis of LMBRaV.

Key words: Largemouth Bass; LMBRaV; basic-RPA; RPA-LFD

阳澄湖原产及“洗澡”中华绒螯蟹形态及微化学动态特征研究

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摘要：为采取科学的手段对阳澄湖原产蟹和“洗澡蟹”进行鉴别以确保其生产者和消费者的利益。本研究基于几何形态测量学、电感耦合等离子质谱和稳定同位素质谱等技术对“洗澡”式养殖第 0、7、14、30 天时昆山池塘和阳澄湖湖区的原产蟹与“洗澡蟹”的背甲形态、第三步足微化学“指纹”进行分析。结果显示，“洗澡”式养殖不同阶段的中华绒螯蟹的背甲形态、第三步足微化学“指纹”均存在差异，“洗澡蟹”会逐渐缩小与原产蟹的产地差异，但在“洗澡”一个月后原产蟹与“洗澡蟹”仍存在形态及微化学“指纹”差异，判别分析、聚类分析等多元统计方法均可将其准确鉴别。本研究首次研究探索池塘及湖区养殖中华绒螯蟹在“洗澡”这一过程中的产地特征的动态变化，证实“洗澡蟹”不会具有原产蟹的形态及微化学特征，为阳澄湖大闸蟹和其他地理标志产品的保护提供更详实的理论支撑。

关键词：中华绒螯蟹；“洗澡蟹”；阳澄湖；几何形态测量学；矿质元素；稳定同位素

Study on Dynamical Characteristics of Morphology and Microchemistry for Genuine and “Bathed” *Eriocheir sinensis* from the Yangcheng Lake of China

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Abstract： To accurately distinguishing between genuine Yangcheng Lake Eriocheir sinensis and "bathed crabs", this study employed geometric morphometrics, ICP-MS, and IRMS to analyze the carapace morphology and microchemical "fingerprints" of the third pereiopod of crabs from both Kunshan ponds and Yangcheng Lake. The analysis covered genuine crabs and "bathed crabs" at different stages of "bathing" (0, 7, 14, and 30 days). The results show that the carapace morphology and microchemical "fingerprints" of the third pereiopod in "bathed crabs" gradually converge with those of genuine crabs over different stages. However, even after 30 days of "bathing", persistent differences in both morphology and microchemical "fingerprints" remain between genuine crabs and "bathed crabs." Multivariate statistical methods such as discriminant analysis and cluster analysis accurately differentiated between the two groups. This study confirms that "bathed crabs" do not acquire the morphological or microchemical traits of genuine crabs, providing theoretical support for the protection of Yangcheng Lake crabs.

Key words:*Eriocheir sinensis*; “bathed crabs”; Yangcheng Lake; geometric morphometrics; mineral elements; stable isotopes

I 型鮰疱疹病毒（*Ictalurid herpesvirus 1*）中国株分离鉴定及其特征分析

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摘要：鮰疱疹病毒对全球鮰鱼养殖业构成重大威胁。本研究从中国患病斑点叉尾鮰（*Ictalurus punctatus*）中成功分离鉴定出一株高致病性 I 型鮰疱疹病毒，并阐明其生物学特性及遗传进化特征。首先，通过 PCR 检测结合透射电镜观察，在病鱼组织中检出鮰疱疹病毒基因片段及特征性病毒粒子。利用 CCO/BB 细胞分离获得病毒株 IcHV1-JS01，该病毒可诱导细胞产生典型病变（CPE）及合胞体形成。感染实验证实该毒株对鮰幼体具有强致病性（死亡率≥50%），死亡鱼体呈现腹水、出血和眼球突出等症状，且肾脏组织病毒载量高。测序获得其 133.53 kb 的完整基因组序列，与已知 IcHV1 毒株具有高度相似性，但存在大量核苷酸变异，提示其特有的遗传特征。系统发育分析将其明确归类为 Ictavirus 属成员，确证 IcHV1-JS01 为具有地域特征的中国本土分离株。本研究为我国鮰产业流行病学监测及病害防控奠定了重要基础。

关键词：斑点叉尾鮰；鮰疱疹病毒；病毒分离株；基因组

Identification and characterization of a new strain of *Ictalurid herpesvirus 1* isolated from channel catfish in China

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Abstract： Ictalurid herpesvirus poses a significant threat to global catfish aquaculture. Here, an Ictalurid herpesvirus 1 (IcHV1) strain, isolated from diseased channel catfish in China, was investigated. PCR assays using IcHV1 gene primers detected viral gene fragments in the tissues of diseased catfish. Transmission electron microscopy (TEM) confirmed the presence of herpesvirus-like virions. This virus, designated IcHV1-JS01, was isolated through incubation with CCO/BB cells, which was verified via PCR and immunoblotting; and infections with this virus triggered cytopathic effects and syncytial formation in CCO/BB cells. Subsequently, a catfish-challenge experiment proved its high virulence, with extremely high viral loads in dead fish. High-throughput sequencing of IcHV1-JS01 revealed a 133,530-bp genome, which shared high similarity with known viral genome, but harboured numerous variations. Phylogenetic analysis classified IcHV1-JS01 as a member of the genus Ictavirus, representing a unique Chinese isolate.

Key words:channel catfish, virus disease, fish herpesvirus, *Ictalurid herpesvirus*, IcHV1 isolate

鲤 IKKα和 IKKβ基因克隆与生物信息学分析

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摘要：NF-κB 通路是生物中普遍存在的核因子转录激活通路。NF-κB 信号通路由 IKK、IκB 和 NF-κB 家族蛋白组成。当细胞受到肿瘤坏死因子-α（TNF - α）、LPS 等刺激时，IKKγ会被招募到细胞膜上，通过与上游信号分子的相互作用，促进 IKKα与 IKKβ组装并实现 IKK 功能激活。IKK 复合体进一步激活 IκB，使之泛素化失活，从而释放κB 二聚体入核，激活转录。本研究克隆得到鲤 IKKα和 IKKβ同源序列，分别命名为 CcIKKα和 CcIKKβ。CcIKKα的开放阅读框为 2274 bp，编码 757 个氨基酸，预测其相对分子质量为 87.78 kDa，等电点为 6.85。CcIKKβ的开放阅读框为 2319 bp，编码 772 个氨基酸，预测其相对分子质量为 89.16 kDa，等电点为 6.28。CcIKKα含有 N 端激酶结构域（20aa-309aa），SDD 结构域（386aa-663aa）和 IKKγ结合结构域（710aa-745aa），由 431 个α螺旋构成。CcIKKβ同样含有 N 端激酶结构域（20aa-338aa）和 SDD 结构域（418aa-690aa），由 415 个α螺旋构成。基因同源性比对分析显示在鲤鱼（*Cyprinus carpio*）、人(*Homasapiens*)、小鼠(*Musmusculus*)中 IKKα与 IKKβ高度同源。以上研究结果为进一步研究 IKK 在转录激活中的作用奠定理论基础。

关键词：鲤；IKKα；IKKβ；转录激活

Cloning and Bioinformatics Analysis of IKKα and IKKβ Genes from *Cyprinus carpio*

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Abstract：NF-κB pathway is a ubiquitously existing nuclear factor transcriptional activation pathway in organisms. The NF-κB signaling pathway consists of IKK, IκB, and NF-κB family proteins. When cells are stimulated by tumor necrosis factor-α (TNF-α), LPS, IKKγ is recruited to the cell membrane. Through interaction with upstream signaling molecules, it promotes the assembly of IKKα and IKKβ and activates IKK function. The IKK complex further activates IκB, leading to its ubiquitination and inactivation, thereby releasing the κB dimer into the nucleus to activate transcription. In this study, the homologous sequences of carp IKKα and IKKβ were cloned and named *Cc*IKKα and *Cc*IKKβ, respectively. The open reading frame of *Cc*IKKα is 2274 bp, encoding 757 amino acids, with a predicted relative molecular mass of 87.78 kDa and an isoelectric point of 6.85. The open reading frame of *Cc*IKKβ is 2319 bp, encoding 772 amino acids, with a predicted relative molecular mass of 89.16 kDa and an isoelectric point of 6.28. *Cc*IKKα contains an N-terminal kinase domain (20aa-309aa), an SDD domain (386aa-663aa), and an IKKγ-binding domain (710aa-745aa), consisting of 431 α-helices. *Cc*IKKβ also contains an N-terminal kinase domain (20aa-338aa) and an SDD domain (418aa-690aa), consisting of 415 α-helices. Gene homology alignment analysis shows that IKKα and IKKβ are highly homologous among *Cyprinus carpio*, *Homasapiens*, and *Mus musculus*. The above research results lay a theoretical foundation for further studying the role of IKK in transcriptional activation.

Key words: *Cyprinus carpio*; IKKα; IKKβ; transcriptional activation

鲤 NF-κB 基因克隆与生物信息学分析

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摘要：NF-κB 1 和 NF-κB 2 是 NF-κB（Nuclear Factor kappa-B，核因子κB）转录因子家族的核心成员，在免疫调节、炎症反应和细胞存活中起关键作用。本研究在鲤中克隆获得 NF-κB 1 与 NF-κB 2 的同源基因，分别命名为 *Cc*NF-κB 1 和 *Cc*NF-κB 2。其开放阅读框（ORF）长度分别为 2805 bp 和 2742 bp，编码 934 和 913 个氨基酸，预测分子量分别为 101.20 kDa 和 100.58 kDa。两者均包含 1 个 IPT 结构域、6 个 ANK 结构域和 1 个 DEATH 结构域；*Cc*NF-κB 1 具有 34 个α螺旋与 34 个β折叠，*Cc*NF-κB 2 则含 29 个α螺旋与 29 个β折叠，且各具 2 个磷酸化位点。共线性分析显示，鲤 *Cc*NF-κB 1 和 *Cc*NF-κB 2 基因在基因组中的位置、转录方向及邻近基因排列与斑马鱼和人类高度保守。序列比对表明 *Cc*NF-κB 1 和 *Cc*NF-κB 2 的氨基酸一致性为 40.43%。系统进化分析显示，两者均首先与鲫及斑马鱼聚为一支，再与其它硬骨鱼类汇合。以上研究结果为进一步研究鲤 NF-κB 基因的免疫功能提供了理论基础。

关键词：鲤；*Cc*NF-κB 1；*Cc*NF-κB 2；炎症反应

Cloning and Bioinformatic Analysis of NF-κB Genes in Common Carp (*Cyprinus carpio*)

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Abstract： NF-κB 1 and NF-κB 2 are core members of the NF-κB (Nuclear Factor kappa-B) transcription factor family and play critical roles in immune regulation, inflammatory response, and cell survival. In this study, homologous genes of NF-κB 1 and NF-κB 2 were cloned from common carp (*Cyprinus carpio*) and designated as *Cc*NF-κB 1 and *Cc*NF-κB 2, respectively. Their open reading frames (ORFs) are 2805 bp and 2742 bp in length, encoding 934 and 913 amino acids, with predicted molecular weights of 101.20 kDa and 100.58 kDa, respectively. Both proteins contain one IPT domain, six ANK repeats, and one DEATH domain. *Cc*NF-κB 1 consists of 34 α-helices and 34 β-sheets, while *Cc*NF-κB 2 contains 29 α-helices and 29 β-sheets; each possesses two phosphorylation sites. Synteny analysis revealed that the genomic location, transcriptional orientation, and flanking gene arrangement of common carp NF-κB genes are highly conserved with those of zebrafish and humans. Sequence alignment showed that the amino acid identity between *Cc*NF-κB 1and *Cc*NF-κB 2 is 40.43%. Phylogenetic analysis indicated that both genes first cluster with crucian carp and zebrafish, then with other teleost fishes. These findings provide a theoretical foundation for further investigation into the immune functions of NF-κB genes in common carp.

Key words: Common carp; *Cc*NF-κB 1; *Cc*NF-κB 2; inflammatory response

嗜水气单胞菌感染通过诱导氧化应激破坏中华鳖肠道紧密连接屏障

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摘要：肠道屏障完整性对维持动物生理稳态至关重要，而紧密连接是其功能基础。本研究以中华鳖为对象，探究嗜水气单胞菌感染对肠道屏障的损伤机制。结果显示，与对照组相比，嗜水气单胞菌感染 72 小时后显著破坏了中华鳖前肠组织形态：导致微绒毛萎缩，其宽度、长度及隐窝深度显著降低；并损伤紧密连接超微结构，显著下调了紧密连接蛋白（Zo-1 和 Occludin）的 mRNA 和蛋白表达水平。感染还诱发了显著的细胞凋亡和氧化应激，表现为晚期凋亡细胞数量极显著增加， ROS 水平上升而抗氧化酶活性下降。为进一步探究机制，研究通过过氧化氢构建了氧化应激模型，并发现过氧化氢同样能引发炎症、抑制紧密连接蛋白表达及破坏肠道结构。反之，在嗜水气单胞菌感染模型中注射抗氧化剂 N-乙酰半胱氨酸（NAC）则有效缓解了紧密连接损伤。综上所述，嗜水气单胞菌感染主要通过诱发氧化应激，进而导致中华鳖肠道紧密连接功能障碍和屏障完整性破坏。

关键词：嗜水气单胞菌；中华鳖；肠道；紧密连接

Aeromonas hydrophila infection impairs the intestinal tight junction barrier in soft-shelled turtle (*Pelodiscus sinensis*) by inducing oxidative stress

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Abstract： Aeromonas hydrophila infection significantly compromised intestinal barrier function in Pelodiscus sinensis, manifesting as villus atrophy, reduced crypt depth, and impaired tight junction ultrastructure. Key tight junction proteins (Zo-1 and Occludin) were downregulated at both mRNA and protein levels. Infection induced severe oxidative stress, characterized by elevated ROS and suppressed antioxidant enzyme activity, alongside increased apoptosis. To elucidate the mechanism, hydrogen peroxide (H_2O_2) was used to establish an oxidative stress model, which recapitulated the damage patterns observed with bacterial infection, including inflammation and tight junction disruption. Conversely, administration of the antioxidant N-acetylcysteine (NAC) attenuated A. hydrophila-induced tight junction damage. These findings demonstrate that A. hydrophila impairs intestinal barrier integrity primarily through oxidative stress, providing insights into potential therapeutic strategies for mitigating infection-related pathologies.

Key words: *Aeromonas hydrophila*; Pelodiscus sinensis; Intestine; Tight junction;

冷应激对中华鳖抗氧化能力及肠道健康的影响

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摘要：为了评估冷应激对中华鳖抗氧化能力及肠道健康的影响，本研究将幼鳖置于 28 ℃、14 ℃和 7 ℃温度下分别处理 1、2、4、8 和 16 天。结果表明，超氧化物歧化酶、过氧化氢酶和谷胱甘肽过氧化物酶的活性随冷应激时间的变化而变化。14 ℃和 7 ℃冷应激导致肠道组织发生形态学改变和病理学损伤，该变化和损伤呈现应激时间依赖性。16S rDNA 测序结果表明 7 ℃组的肠道微生物群落发生了显著改变。转录组分析发现多个与冷应激相关的差异表达基因（DEGs），主要富集在 Toll 样受体信号通路、NOD 样受体信号通路、细胞凋亡和 p53 信号通路等。比较代谢组学揭示响应冷应激的关键代谢物（DEMs），包括有机酸类和氨基酸类。DEGs 与 DEMs 的联合分析揭示了响应冷应激的三个关键信号通路：亚油酸代谢、神经活性配体-受体相互作用和 FoxO 信号通路。

关键词：冷应激；肠道；组织学；微生物群落；多组学；中华鳖

The influence of cold stress on anti-oxidative capacity and intestinal health of the Chinese soft-shelled turtle (*Pelodiscus sinensis*)

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Abstract： To evaluate the impact of cold stress on anti-oxidative capacity and intestinal health in Chinese soft-shelled turtle, the turtles were challenged with 28 ℃, 14 ℃, and 7 ℃, for duration of 1, 2, 4, 8, and 16 days. The results showed that cold stress changed the activities of superoxide dismutase, catalase, and glutathione peroxidase. The 14 ℃ and 7 ℃ induced morphological and histopathological damage in intestine. The 16S rDNA sequencing demonstrated 7 ℃ significantly altered the structure and abundance of intestinal microbiota. Transcriptome discovered differentially expressed genes (DEGs) responding to cold stress, involved in Toll-like receptor signaling pathway, NOD-like receptor signaling pathway, apoptosis, and p53 signaling pathway. Metabolome revealed differentially expressed metabolites (DEMs) coping with cold stress, such as organic acids and amino acids. Joint analysis of DEGs and DEMs highlighted three critical pathways by cold stress, including linoleic acid metabolism, neuroactive ligand-receptor interaction, and FoxO signaling pathway.

Key words: Cold stress; Intestine; Histology; Microbial communities; Multi-omics; Chinese soft-shelled turtle

鲤 OPTN 通过损害自噬和先天免疫应答促进嗜水气单胞菌的定植

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摘要：O*PTN (Optineurin)* 是一种多功能蛋白，参与多种细胞功能，在细胞自噬和先天免疫中均发挥重要作用。本研究从鲤 *(Cypr*inus carpio) 中克隆了两个 OPTN 基因。嗜水气单胞菌为条件致病菌，可感染多种鱼类，使其爆发细菌性败血症，导致养殖鱼类大量死亡，已严重制约水产养殖业可持续发展。对其与宿主相互作用的全面分析可为鱼类疾病预防和治疗提供重要见解。因此，我们建立了嗜水气单胞菌感染模型，经嗜水气单胞菌刺激后，CcOPTNs 的表达水平总体呈现上调趋势，提示 CcOPTNs 可能参与嗜水气单胞菌刺激的免疫响应。此外，CcOPTNs 通过抑制细胞自噬和损害先天免疫反应来促进嗜水气单胞菌定植，从而降低鲤存活率。综上所述，我们的研究结果表明，CcOPTNs 是细胞自噬和先天免疫的关键调节因子，在对嗜水气单胞菌感染的免疫反应中发挥着关键作用，这一结果为鱼病细菌性疾病的防治提供了新的理论参考。

关键词：细胞自噬；选择性自噬受体；炎症反应；先天免疫

OPTN facilitates Aeromonas hydrophila colonization by impairing autophagy and innate immune responses in *Cyprinus carpio*

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Abstract： OPTN (Optineurin) is a multifunctional protein involved in various cellular processes, including autophagy and innate immunity. In this study, two OPTN genes were cloned from Cyprinus carpio. Aeromonas hydrophila, an opportunistic pathogen, can infect diverse fish species, leading to bacterial septicemia and mass mortality, which severely impacts sustainable aquaculture. Analysis of host–pathogen interactions may provide critical insights for disease control. Here, we established an A. hydrophila infection model. Following challenge, CcOPTN expression was up-regulated, suggesting its involvement in the immune response. Moreover, CcOPTNs facilitated A. hydrophila colonization by suppressing autophagy and impairing innate immunity, thereby reducing host survival. In summary, CcOPTNs are key regulators of autophagy and innate immunity and play an essential role in the immune response to A. hydrophila, offering new theoretical insights for controlling bacterial diseases in fish.

Key words: Autophagy; Selective autophagy receptor; Inflammatory reaction; Innate immune response

低氧胁迫下细点石斑鱼(*Epinephelus cyanopodus*)缺氧诱导因子-1α的分子特征及表达分析

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摘要：细点石斑鱼是一种生活在珊瑚礁的石斑鱼，具有很高的市场价值和生态价值。在集约化养殖和活鱼运输过程中，鱼类经常面临急性缺氧应激。我们克隆并鉴定了细点石斑鱼 HIF-1α (EcHIF-1α)。缺氧后 EcHIF-1α表达显著上调，同时，哈维氏弧菌显著诱导头肾和肝脏中 EcHIF-1α的上调表达，表明 EcHIF-1α参与了免疫应答。缺氧处理后，提前了哈维氏弧菌诱导的 EcHIF-1α显著性表达，表明低氧会提前激活免疫反应。这些结果不仅证实了 HIF-1α在鱼类病原体感染中的关键作用，而且首次通过实验证明了低氧胁迫可以预先激活细点石斑鱼对致病菌的免疫反应。总的来说，这项工作不仅有助于深入了解硬骨鱼的耐缺氧机制，而且为进一步探索缺氧和水生病原体疾病的爆发提供了新的视角。

关键词：细点石斑鱼；低氧；低氧诱导因子-1α；哈维氏弧菌；免疫反应

Molecular characterization and expression analysis of hypoxia inducible factor-1α during hypoxic stress in speckled blue grouper (*Epinephelus cyanopodus*)

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Abstract： The Epinephelus cyanopodus is a coral reef-dwelling grouper with high market and ecological value. During intensive aquaculture and the transportation of live fish, fish often expose acute hypoxic stress. E. cyanopodus HIF-1α (EcHIF-1α) was cloned and characterized, and the expression of EcHIF-1α was significant after hypoxia. Meanwhile, EcHIF-1α was significantly induced by Vibrio harveyi in the head kidney and liver, indicating that EcHIF-1α was involved in the immune response. After hypoxia treatment, the significant expression of EcHIF-1α induced by Vibrio harveyi was further advanced and enhanced. These results not only confirmed the key role of HIF-1α in fish pathogen infection, but also demonstrated experimentally for the first time that oxygen stress can pre-activate the immune response of speckled blue grouper against pathogenic bacteria. Overall, the work not only contributes to a thorough understanding of the hypoxia tolerance mechanism of teleost, but also provides a new perspective for further exploration of hypoxia and the outbreak of aquatic pathogen disease.

Key words:*Epinephelus cyanopodus*, Hypoxia, HIF-1α, Vibrio harveyi, Immune response

聚维酮碘对罗氏沼虾的毒性效应：氧化应激、免疫抑制与修复能力的梯度响应

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摘要：以罗氏沼虾为对象，急性毒性测定聚维酮碘 24h-96hLC50，基于 96hLC50 设 1.14mg/L、1.89mg/L、2.84mg/L 三个浓度，探究 4d 暴露和 7d 清水恢复对鳃超微结构、细胞凋亡、抗氧化及免疫基因的影响。结果：聚维酮碘毒性呈浓度-时间依赖性，其 24h、48h、72h 和 96hLC50 为 8.49mg/L、6.90mg/L、6.08mg/L 和 5.67mg/L，安全浓度为 1.37mg/L。暴露显示，1.89mg/L 和 2.84mg/L 诱导鳃组织线粒体空泡化，上调凋亡基因表达，抑制肝胰腺抗氧化基因表达；高浓度组免疫基因 Toll 持续高表达，而 ACP 显著降低。清水恢复 7d 后，抗氧化基因转录水平完全恢复，但酶活性及鳃组织凋亡信号仍有残留损伤。表明，高浓度聚维酮碘通过线粒体依赖性凋亡通路和氧化应激引发不可逆鳃损伤，而低浓度暴露后修复能力较强。为罗氏沼虾养殖中聚维酮碘安全剂量及毒性风险评估提供数据

关键词：聚维酮碘；罗氏沼虾；免疫抑制；氧化应激

Toxic effects of povidone-iodine on *Macrobrachium rosenbergii*: Concentration-dependent responses in oxidative stress, immunosuppression, and recovery potential

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Abstract：This study employed *M. rosenbergii* as the model organism to evaluate the acute toxicity and sublethal effects of PVP-I through 4day exposure experiment followed by 7day depuration period.Acute toxicity tests enabled the determination of 24–96h LC50,with the 96h LC50 being 5.67mg/L and the SC being 1.37mg/L.Based on this,three sublethal concentrations (1.14,1.89,2.84mg/L) were tested over 4-day exposure followed by 7-day depuration period.Subacute exposure at 1.89 and 2.84mg/L induced mitochondrial vacuolization,upregulated apoptosis-related genes,and downregulated antioxidant gene expression.The high-concentration group also showed sustained Toll gene overexpression and ACP gene suppression.After depuration, antioxidant gene expression normalized;however,apoptotic markers in gill tissue remained impaired.Overall,high concentrations cause irreversible gill damage via mitochondrial mediated apoptosis whereas lower concentrations allow for greater recovery.These results offer crucial toxicodynamic insights for safer PVP-I use and risk assessment in M. rosenbergii aquaculture.

Key words:povidone-iodine; *Macrobrachium rosenbergii;* immunosuppression; oxidative stress

八角茴香（*Illicium verum*）水提物抗鲤疱疹病毒Ⅱ型活性评价

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摘要：鲤疱疹病毒II型（Cyprinid Herpesvirus 2, CyHV-2）是一种具有囊膜的双链 DNA 病毒，可引起鲫和金鱼的病毒性造血器官坏死病。槲皮素（Quercetin）是一种广泛分布于各类植物中的黄酮类化合物，前期研究发现槲皮素可以通过抑制 PI3K/AKT 信号通路核心蛋白 AKT 的磷酸化来抑制 CyHV-2 复制，本研究发现槲皮素在鱼体水平也具有抗 CyHV-2 作用。槲皮素是八角茴香的主要成分之一，检测了八角中除槲皮素外的 14 种活性成分，并评估它们在体外抗 CyHV-2 作用，其中 9 种成分具有抗 CyHV-2 作用。为了验证八角茴香抗 CyHV-2 的潜能，本研究建立了标准化的八角茴香水提工艺，八角水提物在体内和体外均表现出抗 CyHV-2 作用。此外，还研究了槲皮素在肝脏、肾脏和血液中的药代动力学。本研究为槲皮素和八角茴香水提物的实践应用提供了理论支撑，为水产养殖绿色抗 CyHV-2 药物的开发提供了前景。

关键词：抗 CyHV-2；八角茴香水提物；槲皮素；体内；体外

Evaluation of anti-CyHV-2 effects of star anise (*Illicium verum*) aqueous extract

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Abstract： Cyprinid herpesvirus 2 (CyHV-2), a virus that triggers Herpesvirus Hematopoietic Necrosis Disease. Previous studies have reported that quercetin inhibits viral replication by suppressing phosphorylation of AKT, the core protein of the PI3K/AKT signaling pathway. This study further found that quercetin also has anti-CyHV-2 effects in vivo. Quercetin was found to be a one of major component of star anise. We further examined 14 key compounds in star anise other than quercetin and evaluated their anti-CyHV-2 effects in vitro. Nine active ingredients had antiviral effects. To verify the anti-CyHV-2 potential of star anise, a standardized water extraction process for star anise was established, and its aqueous extracts exhibited significant anti-CyHV-2 effects both in vivo and in vitro. Additionally, quercetin pharmacokinetics in the liver, kidney, and blood were investigated. The present study provides valuable theoretical support for the practical application of quercetin and star anise aqueous extracts, offering prospects for the development of green anti-CyHV-2 drugs for aquaculture.

Key words: Anti-CyHV-2; Anise aqueous extract; Quercetin; In vitro; In vitro

一种与海参腐皮综合征相关的新病原体（*Photobacterium damselae* SCXP）的鉴定和转录组分析

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摘要：海参腐皮综合征（SUS）与多种细菌和寄生虫病原体有关。然而，关于新型病原体鉴定和预防策略的研究仍然有限。我们从 *Apostichopus japonicus* 上分离、鉴定出了一种命名为 *P. damselae* SCXP 的腐皮综合征新病原体。开发了一种基于 TaqMan 探针的 qPCR 检测方法，用于快速检测。并在人工感染实验中证实，P. damselae SCXP 对 SUS 的促进作用。药物敏感性试验显示对 16 种抗生素高度敏感。KEGG 富集分析确定了不同的信号通路，这些通路在感染后 6、12 和 24 小时在 P.damselae SCXP 感染组中差异表达。Venn 分析表明，包括 DNase I 和 ASIC1 在内的基因受到抑制，并通过 qRT-PCR 进行了验证。这是首次对 *A. japonicus* 体腔细胞对 *P. damselae* SCXP 的反应进行转录组学研究，为预防 P. damsela 诱导的海参 SUS 提供了理论依据。

关键词：仿刺参；腐皮综合征；美人鱼发光杆菌；转录组学

Identification and transcriptomic analysis of a new pathogen, *Photobacterium damselae* SCXP, associated with sea cucumber skin ulceration syndrome

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Abstract： Sea cucumber skin ulceration syndrome (SUS) is associated with diverse bacterial and parasitic pathogens. However, research on novel pathogen identification and prevention strategies remains limited. Here, we identified a Photobacterium damselae strain, designated *P. damselae* SCXP, as a novel SUS pathogen in Apostichopus japonicus. A TaqMan probe-based qPCR assay was developed for rapid detection. Artificial infection experiments confirmed that *P. damselae* SCXP promotes SUS progression. Drug sensitivity testing of *P. damselae* SCXP showed high susceptibility to 16 antibiotics. The KEGG enrichment analysis identified distinct signaling pathways that were differentially expressed in the *P. damselae* SCXP-infected groups at 6, 12, and 24 h post-infection. Venn analysis indicated suppression of genes including DNase I and ASIC1, validated by qRT-PCR. This is the first transcriptomic study of A. japonicus coelomocytes respond to P. damselae SCXP, and provides a theoretical basis for preventing P. damselae-induced SUS in sea cucumbers.

Key words: Sea cucumber Apostichopus japonicus; Skin ulceration syndrome; Photobacterium damselae; Transcriptomic

嗜水气单胞菌通过激活 SOCS3 抑制鲤鱼 JAK2/STAT3 通路

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摘要：细胞因子信号转导抑制因子通过影响包括 JAK/STAT 在内的多种信号通路在调节炎症反应中发挥重要作用。尽管在硬骨动物中已经发现了大量的 SOCS 蛋白家族成员，但它们在非哺乳动物脊椎动物中的功能特征尚未被广泛研究。为了进一步了解 SOCS3 在硬骨鱼类中的功能，我们鉴定了黄河鲤鱼的 SOCS3a 和 SOCS3b。发现在哺乳动物和其他硬骨动物中具有较高的序列和域保守性，并在鲤鱼黄河的多个组织中表达，尤其是在鳃、脾和头肾中表达量较高。我们发现它们可以被嗜水气单胞菌在组织中上调，并且它们在黄河鲤鱼中的过表达增加了组织中的载菌量并降低了存活率。此外，我们发现 SOCS3a 和 SOCS3b 抑制了 JAK2，并抑制了由嗜水气单胞菌诱导的 STAT3 的入核表达和磷酸化。我们首次在鲤鱼黄河中发现了 SOCS3a 和 SOCS3b，并发现嗜水气单胞菌通过上调 SOCS3a 和 SOCS3b 抑制 JAK2/STAT3 通路，从而破坏机体的免疫平衡。

关键词：SOCS3；JAK/STAT 信号；黄河鲤

Aeromonas hydrophila inhibits the JAK2/STAT3 pathway by activating SOCS3s in common carp（*Cyprinus carpio*）

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Abstract：The SOCS plays a crucial role in the regulation of inflammatory responses by influencing various signaling pathways, including the JAK/STAT. Although numerous members of the SOCS protein family have been identified in teleosts, their functional characteristics in non-mammalian vertebrates have not been extensively studied. To further understand the function of SOCS3 in teleosts, we identified and characterized the SOCS3a and SOCS3b of the Common carp huanghe. They exhibit high sequence and domain conservation with mammals and other teleosts, and are expressed in multiple tissues of the Common carp huanghe, with particularly high expression in the gills, spleen, and head kidney.We found that they could be upregulated by Aeromonas hydrophila in the tissues examined, and their overexpression in Common carp huanghe increased the bacterial load in tissues and reduced the survival rate.Furthermore, we discovered that SOCS3a and SOCS3b inhibit JAK2 and suppress the nuclear expression and phosphorylation of STAT3 induced by *A. hydrophila*.

Key words:SOCS3; JAK/STAT signaling; *Cyprinus carpio*

当年春繁小规格草鱼种夏季免疫接种试验与应用

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摘要：鱼类疫苗接种多选择在春季进行，本研究探索了夏季草鱼免疫接种技术。自 2008 年 8 月以来，在江西省南昌县向塘镇与武阳镇交界地带约 5000 亩的草鱼苗种培育基地，持续开展了针对当年春繁小规格草鱼种的“夏季免疫接种”技术试验与示范推广工作。经过长达十余年的跟踪监测与数据分析，结果显示，采用夏季免疫接种技术的草鱼，其成活率、养殖产量和经济效益均实现了显著提升，寸片苗种转塘至冬片鱼种阶段的回捕率由试验前的 50%提高至目前的 90%；草鱼冬片鱼种的平均亩产量由 450kg 提升至 1000kg，试验组的平均亩利润达到了对照组的 1.92 倍。目前，该项技术已纳入江西省地方标准“草鱼疫苗免疫技术规程”，并被推广为全省及周边渔区水产养殖户广泛采纳的技术规范。针对当前技术推广中面临的疫苗稳定性、水质管理以及免疫程序优化等问题，本文提出了具体的技术改进建议。

关键词：夏季；草鱼种；免疫接种

Experimental Study and Field Application of Summer Immunization for Spring-Bred Fingerlings of *Grass Carp*

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Abstract：Vaccination of fish is mostly conducted in spring, while this study explored the technology for grass carp vaccination in summer. Since August 2008, at a grass carp seedling cultivation base covering 5,000 acres located at the junction of Xiangtang town and Wuyang town in Nanchang county, Jiangxi Province, continuous trials, demonstrations, and promotion of the "summer immunization" technology have been carried out on small-sized grass carp seedlings bred in spring . After more than a decade of tracking, monitoring, and data analysis, the results showed that grass carp subjected to the summer immunization technology have witnessed significant improvements in survival rate, aquaculture yield, and economic benefits. The recapture rate of fingerling seedlings transferred from nursery ponds to overwintering seedling ponds has increased from 50% to 90%. The average yield per acre of grass carp overwintering seedlings has risen from 450 kg to 1,000 kg, and the average profit of the experimental group has reached 1.92 times that of the control group.

Key words: Summer; *Grass carp* fingerlings; Immunization

2 种不同海拔裂腹鱼头肾转录组分析

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摘要：裂腹鱼类是适应青藏高原极端环境的重要类群，为探究其适应辐射过程中免疫适应的分子遗传学机制，对 2 种不同海拔高度裂腹鱼极边扁咽齿鱼（*Platypharodon extremus*，PE）（海拔 3750～4750 m）和重口裂腹鱼（*Schizothorax davidi*，SD）（海拔 1250～2500 m）的头肾进行转录组比较分析。筛选出 11407 个差异表达基因，GO(Gene Ontology)和 KEGG（Kyoto Encyclopedia of Genes and Genomes)富集分析发现，差异表达基因主要显著富集在细胞凋亡、RIG 样受体、白细胞介导免疫等生物过程、抗原加工与呈递等免疫相关通路上。推测高海拔鱼类因长期受到高寒低氧强紫外线等环境因素影响发生细胞凋亡，并处于免疫抑制状态。本研究为全面理解脊椎动物先天性免疫系统对不同海拔梯度环境的适应性进化过程和机制提供重要资料和科学依据。

关键词：转录组；海拔；裂腹鱼；头肾

Transcriptome Analysis of Head Kidney of two Schizothoracine Fish at Different Altitudes

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Abstract： The schizothoracine fish is a group adapted to the extreme environment of the Qinghai-Tibet Plateau. To study the molecular genetic mechanisms of immune adaptation during their adaptive radiation, a transcriptomic analysis was conducted on the head kidneys of two schizothoracine species from different altitudes: Platypharodon extremus(altitude 3750–4750 m) and Schizothorax davidi(altitude 1250–2500 m). A total of 11,407 differentially expressed genes(DEGs)were identified. Gene Ontology and Kyoto Encyclopedia of Genes and Genomes enrichment analyses show that these DEGs were mainly enriched in Apoptosis,RIG-I-like receptor signaling pathway and leukocyte-mediated immunity.We hypothesize that high-altitude fish, due to long-term exposure to harsh environmental factors such as cold, hypoxia, and intense ultraviolet radiation, undergo increased apoptosis and exist in an immunosuppressed state.This study provides valuable data and new insights for a comprehensive understanding of the adaptive evolution of the innate immune system in vertebrates across different altitudinal gradients.

Key words: Transcriptome; Altitude; Schizothoracine fish; Head kidney

几种鲤灭活疫苗的免疫效果评价及另一种疫苗策略的初步研究

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摘要：本研究针对鲤养殖中频发的细菌性疾病，从病鲤体内分离鉴定出维氏气单胞菌、嗜水气单胞菌、弗氏柠檬酸杆菌和类志贺邻单胞菌四种病原菌，并研制了四联灭活疫苗。该疫苗免疫健康鲤后可显著诱导血清 IgM 抗体水平上升，促进脾、肾等组织中 IL-1β、TNF-α等免疫相关基因表达，增强非特异性免疫酶活性。攻毒实验表明，该灭活疫苗对四种病原菌及混合感染均具有一定免疫保护率（RPS 40%–83%）。在此基础上，进一步针对维氏气单胞菌构建了两种重组蛋白亚单位疫苗及其二联疫苗。初步结果显示，该类亚单位疫苗可激发更高效的特异性体液免疫应答，其针对维氏气单胞菌感染的相对保护率较灭活疫苗有进一步提高。研究表明，四联灭活疫苗对多种病原具有广谱保护效果，而针对维氏气单胞菌的亚单位疫苗则展现出更高特异性免疫潜力，为鲤细菌性疾病特别是维氏气单胞菌感染的防控提供了新策略。

关键词：鲤；维氏气单胞菌；分离鉴定；灭活疫苗；亚单位疫苗；免疫保护率

Evaluation of the Immunogenic Effect of an Inactivated Vaccine against Several Bacterial Pathogens in Common Carp (*Cyprinus carpio*) and a Preliminary Study on an Alternative Vaccine Strategy

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Abstract： This study developed a quadrivalent inactivated vaccine against Aeromonas veronii, A. hydrophila, Citrobacter freundii, and Plesiomonas shigelloides isolated from diseased common carp. The vaccine significantly induced serum IgM antibody production, up-regulated immune-related genes (IL-1β, TNF-α) in spleen and kidney tissues, and enhanced non-specific immune enzyme activities. Challenge experiments demonstrated relative percent survival (RPS) rates of 40%–83% against single or mixed infections. Furthermore, two recombinant subunit vaccines and a bivalent formulation targeting A. veronii were developed. Preliminary results indicated that the subunit vaccines, especially the bivalent vaccine, elicited stronger specific humoral immune responses and higher RPS against A. veronii compared to the inactivated vaccine. The study suggests that the inactivated vaccine provides broad protection, while the subunit vaccine exhibits higher specificity and efficacy, offering a promising strategy for controlling bacterial diseases in carp.

Key words: Common carp; Aeromonas veronii; Isolation and identification; Inactivated vaccine; Subunit vaccine; Immunoprotection rate

基于 miRNA-mRNA 转录组分析探索 IL-17B 在黄河鲤免疫反应中的功能

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摘要：MicroRNA（miRNA）是一类在转录后水平调控基因表达的非编码 RNA，广泛参与免疫反应等生命过程。哺乳动物中，IL-17B 可调控炎症反应，但其在硬骨鱼中的免疫功能尚不明确。为探究 IL-17B 在黄河鲤 miRNA–mRNA 调控网络中的作用，本研究使用 IL-17B 重组蛋白孵育鲤头肾原代细胞，并进行转录组测序。共鉴定出 23 个 DE miRNA 和 1100 个 DE mRNA。经靶基因预测与负相关分析，发现 19 个 DE miRNA 与 297 个靶基因存在负调控关系。进一步聚焦免疫通路，识别出 4 个 DE miRNA 与 31 个靶基因显著关联，其中 SRC、DNM11、SOS1、STRN3 和 TRAF5 个免疫基因表达上调，参与细胞自噬、抗病毒及炎症调控等免疫过程。结果表明，IL-17B 可能通过 miRNA–mRNA 互作网络调控黄河鲤的免疫应答，为低等脊椎动物 IL-17B 的功能机制研究提供了新依据。

关键词：IL-17B；miRNA；mRNA;免疫

Exploring the Function of IL-17B in the Immune Response of Yellow River Carp Based on miRNA–mRNA Transcriptome Analysis

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Abstract: MicroRNAs (miRNAs) are non-coding RNAs that regulate gene expression post-transcriptionally and play key roles in immune responses. In mammals, IL-17B modulates inflammation, but its function in teleost fish is poorly understood. To explore the role of IL-17B in common carp, primary head kidney cells were treated with recombinant IL-17B and transcriptome-sequenced. We identified 23 differentially expressed (DE) miRNAs and 1,100 DE mRNAs. Through target prediction and negative correlation analysis, 19 DE miRNAs were found to interact with 297 target genes. Further immune-related pathway analysis highlighted 4 DE miRNAs linked to 31 target genes. Among these, five immune-related genes (SRC, DNM11, SOS1, STRN3, and TRAF2) were up-regulated and involved in autophagy, antiviral immunity, and inflammation. These findings indicate that IL-17B may regulate immune responses in common carp via a miRNA–mRNA network, offering new insights into its function in lower vertebrates.

Key words:IL-17B; novel-m0270-5p; TRAF2; Immunity

基于转录组学研究 lncRNA SARL/miR-205-z/SOCS3 轴参与虹鳟感染 IHNV 的负调控免疫机制

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摘要：LncRNA 是参与各种生物学过程的新型调控因子，但 lncRNA 对虹鳟抗病毒免疫反应的调控作用仍不清楚。本研究测定了虹鳟皮肤感染 IHNV 后 48 h 与对照组的 lncRNA 图谱、lncRNA、miRNA 和基因的表达水平以及 lncRNA SARL/miR-205-z/SOCS3 轴的功能。转录组分析鉴定了 16 个 DElncRNAs 和 12 个关键的 ceRNA 网络。表达模式表明 lncRNA SARL、miR-205-z 和 SOCS3 的表达呈现 ceRNA 调控关系。功能研究发现，lncRNA SARL 在体外通过海绵吸附 miR-205-z 竞争性结合 SOCS3，在虹鳟免疫反应中发挥负调控作用。此外，miR-205-z 是虹鳟肝细胞增殖的正向调节因子。SOCS3 的过表达促进了 IHNV 的复制。在体内，注射 antagomiR-205-z 显著了增加 SOCS3 的表达。本研究为深入探究虹鳟抗病育种和靶向药物治疗提供了基础数据。

关键词：虹鳟；RNA-seq；lncRNA SARL/miR-205-z/SOCS3

LncRNA transcriptome analysis of rainbow trout (*Oncorhynchus mykiss*) skin infected with IHNV reveals that lncRNA SARL/miR-205-z/SOCS3 axis negatively regulates antiviral immunity mechanisms

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Abstract：LncRNA are new gene regulators involved in various biological processes. However, the regulatory effect of lncRNA on the rainbow trout (*Oncorhynchus mykiss*) antiviral response has not been reported. Here, we measured lncRNA profiles at 48 hpi compared to the control group, expression levels of lncRNA, miRNA, and gene, and lncRNA SARL/miR-205-z/SOCS3 functions after rainbow trout skin infected with IHNV. Transcriptome identified 16 DElncRNAs and 12 immune-related ceRNA networks. Expression patterns suggested that changes in lncRNA SARL, miR-205-z, and SOCS3 expression presented a ceRNA regulatory relationship. The lncRNA SARL was a ceRNA of SOCS3 by sponging miR-205-z in vitro, thereby playing a negative regulatory role in immune response. We also found that miR-205-z was a positive regulator of rainbow trout liver cell proliferation. In vivo, SOCS3 expression were significantly increased after antagomiR-205-z injection. Furthermore, SOCS3 promoted the replication of IHNV. This study provides fundamental data for disease resistance breeding and targeted drug therapy in rainbow trout.

Key words: Rainbow trout; RNA-seq; LncRNA SARL/miR-205-z/SOCS3

草鱼干扰素 IFIT5L 基因克隆及功能研究

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摘要：干扰素诱导的四肽重复蛋白（IFIT）在哺乳动物中具有广谱抗病毒功能，然而其在鱼类中的免疫机制尚不明确。草鱼（Ctenopharyngodon idella）呼肠孤病毒（GCRV）感染引起的草鱼出血病严重阻碍草鱼养殖业的发展，因此，明确草鱼 IFIT 在 GCRV 感染中的作用及其调控机制对出血病的防控具有重要意义。本研究成功克隆草鱼 IFIT5L 基因，其开放阅读框为 1015 bp，编码 488 个氨基酸，预测分子量为 55.86 kDa。系统进化分析显示该基因与硬骨鱼类 IFIT 聚为一支，亲缘关系最近。组织表达谱显示，IFIT5L 在肝脏、心脏、皮肤、脾脏等多种组织中均有表达，其中在肝脏中表达最高。GCRV 感染可显著上调脾、肾、鳃和肠组织中 IFIT5L 转录水平，呈现先升后降的应答模式。体内过表达 IFIT5L，可显著诱导 IRF-3、IFN-1、MDA5 和 MAVS 等免疫相关基因表达，提高其存活率，并有效抑制病毒。

关键词：草鱼；呼肠孤病毒；干扰素诱导的四肽重复蛋白；抗病毒

Cloning and Functional Study of the Interferon-Induced Tetratricopeptide Repeat Protein 5-like (IFIT5L) Gene in *Grass Carp*

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Abstract： Interferon-induced tetratricopeptide repeat protein (IFIT) exhibits broad-spectrum antiviral activity in mammals, yet its immune mechanism in fish remains poorly understood. Grass carp reovirus infection, which causes hemorrhagic disease, severely hinders the development of grass carp aquaculture. Therefore, clarifying the role and regulatory mechanism of grass carp IFIT in GCRV infection is of great significance for disease prevention and control.This study successfully cloned the grass carp IFIT5L gene, which contains an open reading frame of 1015 bp, encoding 488 amino acids with a predicted molecular weight of 55.86 kDa. Tissue expression profiling showed that IFIT5L is expressed in various tissues including the liver, heart, skin, and spleen, with the highest expression in the liver. GCRV infection significantly up-regulated IFIT5L transcription in the spleen, kidney, gill, and intestine, showing an initial increase followed by a decrease.In vivo overexpression of IFIT5L significantly induced the expression of immune-related genes such as IRF-3, IFN-1,improved survival rates.

Key words:*Grass carp;* Reovirus; Interferon-induced tetratricopeptide repeat protein; Antiviral; Survival rate

嗜水气单胞菌感染黄河鲤细胞免疫应答的单细胞转录组分析

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摘要：本研究通过单细胞转录组分析技术，研究了嗜水气单胞菌感染黄河鲤后头肾组织中巨噬细胞的免疫响应机制。结合病理学、血清免疫酶活性检测、免疫因子分析、组织病理观察、免疫组化及蛋白质组学等多维度方法，解析了感染过程中巨噬细胞的异质性、功能分化及其分子调控网络。鉴定出 10 类巨噬细胞亚群，其中 Macro_cxcl19 亚群在感染后比例显著变化；通过 hdWGCNA 分析筛选出 5 个关键基因模块，富集于 T 细胞毒性、B 细胞信号调控等免疫通路；拟时序分析揭示巨噬细胞从 Naive 状态（Macro_cxcl19_NEW2）向 M2 极化状态（Macro_cxcl19_NEW1）的分化轨迹，并鉴定出 cfbl 等关键调控基因；蛋白质组学验证了差异表达蛋白，进一步支持转录组结果。本研究在单细胞水平揭示黄河鲤应对嗜水气单胞菌感染的巨噬细胞免疫应答机制，为鱼类免疫调控及疾病防控提供了重要理论依据。

关键词：单细胞转录组；免疫应答；鲤鱼；嗜水气单胞菌

Single-cell transcriptome analysis reveals a cellular immune response in Yellow River carp infected with *Aeromonas hydrophila*

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Abstract： The Yellow River carp represents a freshwater species of significant economic value in China, yet it is frequently threatened by infections from A. hydrophila. This investigation utilized scRNA-seq to analyze the immune response of head kidney macrophages post-infection, identifying ten distinct macrophage subtypes. Among these, the Macro_cxcl19 subset demonstrated the most substantial alterations following infection. The hdWGCNA identified key modules enriched in immune-related pathways, such as T cell-mediated cytotoxicity and B cell receptor signaling. Pseudotime trajectory analysis elucidated the differentiation process from naive (Macro_cxcl19_NEW2) to M2-polarized (Macro_cxcl19_NEW1) macrophages, with cfbl emerging as a pivotal regulator. Proteomic profiling supported the transcriptomic data, revealing differential expression of proteins associated with immune and metabolic processes. These findings offer a detailed cellular atlas of the immune response in carp macrophages and elucidate the molecular mechanisms underpinning host defense against A. hydrophila.

Key words: Single-cell transcriptome; Immune response; *Cyprinus carpio*; Aeromonas hydrophila

齐口裂腹鱼 TLR11 亚家族成员的基因克隆及对无乳链球菌和维氏气单胞菌的表达响应

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摘要：Toll 样受体（TLRs）是先天免疫系统中的关键模式识别受体，在鱼类抵御病原体侵染的过程中发挥重要作用。鱼类 TLR11 亚家族包含 TLR13、TLR19-23 和 TLR26 多个成员，但其免疫功能及其作用机制尚不十分明晰。本研究克隆鉴定了齐口裂腹鱼（*Schizothorax prenanti*）的 3 个 TLR11 亚家族成员——spTLR19、spTLR20 和 spTLR21 的开放阅读框全长序列，分别为 2868 bp、2835 bp 和 2946 bp。三种 TLRs 在健康鱼不同组织器官中组成型表达，但 mRNA 表达水平具有明显的组织特异性。无乳链球菌和维氏气单胞菌分别感染后，这些 TLRs 在齐口裂腹鱼鳃、脾脏、肝脏中的表达出现不同程度的显著上调，这表明它们可能参与了抗菌免疫反应。本研究可为解析 TLR11 亚家族成员在鱼类免疫中的功能提供重要资料，并为进一步研究齐口裂腹鱼的抗病能力和免疫调节奠定理论基础。

关键词：Toll 样受体；齐口裂腹鱼；无乳链球菌；维氏气单胞菌

Molecular Cloning and expression responses to *Streptococcus agalactiae* and *Aeromonas veronii* of TLR11 Subfamily Genes in *Schizothorax prenanti*

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Abstract： Toll-like receptors (TLRs) are key pattern recognition receptors of the innate immune system and play important roles in pathogen defense in teleosts. The teleost TLR11 subfamily includes TLR13, TLR19–23, and TLR26, but their immune functions and mechanisms remain incompletely understood. In this study, we cloned and identified three TLR11 subfamily members from Schizothorax prenanti: spTLR19, spTLR20, and spTLR21, with full-length open reading frames of 2868 bp, 2835 bp, and 2946 bp, respectively. All three TLRs were constitutively expressed in healthy fish tissues, but their mRNA levels showed distinct tissue specificity. Following infection with Streptococcus agalactiae and Aeromonas veronii, these TLRs were significantly upregulated in the gill, spleen, and liver, suggesting their involvement in antibacterial immune responses. These findings provide important data for elucidating the functional roles of TLR11 subfamily members in teleost immunity and lay a theoretical basis for further studies on disease resistance and immune regulation in *S. prenanti*.

Key words: Toll-like receptors; *Schizothorax prenanti*; *Streptococcus agalactiae*; *Aeromonas veronii*

黄河鲤含 Jacalin 结构域蛋白的基因克隆与表达分析

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摘要：Jacalin 类凝集素（Jacalin-related lectins,JRLs）是植物凝集素的一个家族，在其宿主防御中发挥作用。近年在七鳃鳗、大西洋鳕鱼和斑马鱼中发现含 JRL 的蛋白，而功能研究鲜有报道。本研究通过 RT-PCR 得到黄河鲤 2 个含 JRL 结构域蛋白（Cc-JRLs）的 cDNA 序列，Cc-JRL1 ORF 为 1041bp，编码 346aa，Cc-JRL2 ORF 为 948bp，编码 315aa，均包含 JRL 和 Aerolysin 结构域。QRT-PCR 显示两基因在被检组织均呈组成型分布，注射 A.hydrophila 和 SVCV 后，两基因在鳃、头肾、皮肤和脾脏中上调表达，呈先升后降的趋势，在表达响应时间上，A.hydrophila 组在 6~24h 达最高，而 SVCV 组在 12~48h 达到峰值。对 JRL 结构域进行原核表达，得到 33kDa 的重组蛋白，纯化后的重组蛋白以 Ca^{2+}依赖的方式与细菌发生凝集。

关键词：黄河鲤；Jacalin；结构特征；组织表达；凝集活性

Gene cloning and expression analysis of jacalin domain-containing protein in *Cyprinus carpio*

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Abstract：Jacalin-related lectins are a family of plant lectins that play roles in host defense. In recent years, JRL-containing proteins were discovered in Lampreys, Gadus morhua and Danio rerio, but functional studies remain scarce. In this study, the cDNA sequences of two JRL domain-containing proteins from Cyprinus carpio were obtained via RT-PCR.The ORF of Cc-JRL1 is 1041 bp, encoding 346 amino acids, and the ORF of Cc-JRL2 is 948 bp, encoding 315 amino acids, both containing JRL and Aerolysin domains. QRT-PCR revealed both genes exhibited constitutive expression in all examined tissues. After injection with Aeromonas hydrophila and SVCV, both genes showed upregulated expression in gills, head kidney, skin, and spleen, displaying an initial increase followed by a decrease. Regarding the expression response time, the A. hydrophila group peaked at 6-24 h, while the SVCV group reached peak expression at 12-48 h. Prokaryotic expression of the JRL domain yielded a 33 kDa recombinant protein， and the purified recombinant protein demonstrated bacterial agglutination in a Ca^{2+}-dependent manner.

Key words:*Cyprinus carpio*; Jacalin; Structural characteristics; Tissue expression; Agglutination activity

DNA 甲基化调控大黄鱼 B 细胞活化功能研究及 IgH 基因座注释

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摘要：DNA 甲基化是一种经典的表观遗传修饰，在多种生物学过程中发挥重要功能。然而，DNA 甲基化在鱼类 B 细胞免疫应答中的功能及作用机制尚不明确。本研究以大黄鱼为研究对象，通过脂多糖（LPS）和壳寡糖（COS）诱导大黄鱼 IgM+ B 细胞活化，发现 LPS/COS 处理可促进 B 细胞活化相关基因表达、吞噬能力和抗体分泌能力。有意思的是，B 细胞活化过程伴随着 Pax5 表达下调。进一步研究发现 Pax5 启动子区域存在两个 CpG 岛，其中 CpG 岛 1 在初始 B 细胞中呈现低甲基化，而在 B 细胞活化后转变为高甲基化。DNA 甲基化抑制剂 AZA 处理可抑制 CpG 岛 1 的高甲基化，同时阻碍 Pax5 的下调和 B 细胞活化。以上结果表明 DNA 甲基化可通过抑制 Pax5 的表达来调控大黄鱼 B 细胞活化过程。进一步地，本研究注释了大黄鱼免疫球蛋白重链编码基因（IgH），为理解鱼类抗体产生和 B 细胞免疫应答过程奠定了基础。

关键词：DNA 甲基化；大黄鱼；B 细胞；IgH

The role of DNA methylation in teleost B cell activation and identification of IgH locus in large yellow croaker

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Abstract：DNA methylation is a classic epigenetic modification, and plays essential roles in various biological processes. However, its function and underlying mechanisms in teleost B cell activation remain elusive. In this study, we used large yellow croaker as a model. LPS/COS treatment significantly enhanced the expression of activation-related genes, antibody secreting ability and phagocytic capacity of IgM+ B cells in large yellow croaker, and downregulated Pax5 expression. Interestingly, two CpG islands were identified within the promoter region of Pax5. Both CpG islands exhibited hypomethylation in naive B cells, while CpG island1 was specifically transited into hypermethylation upon B cell activation. Treatment with DNA methylation inhibitor AZA prevented the hypermethylation of CpG island1, and concomitantly impaired the downregulation of Pax5 and activation of B cells. Furthermore, we identified the immunoglobulin heavy chain (IgH) coding gene of large yellow croaker. Our results would provide insight into the immunoglobulin production and B cell activation process in teleosts.

Key words:DNA methylation; Large yellow croaker; B cells; IgH locus

白斑综合症病毒入侵及胞内感染机制研究

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摘要：白斑综合征病毒（WSSV）是目前已知最大的动物病毒之一，其发病机制尚未完全阐明。本研究发现，WSSV 可利用肌动蛋白细胞骨架以及网格蛋白介导的内吞途径入侵虾类细胞。入侵后的病毒粒子通过内吞囊泡和内体在胞内运输；在内体中，病毒囊膜与内体膜融合并完成脱囊膜，随后脱囊膜的病毒核衣壳沿微管运输至核孔外周；核衣壳则进一步通过 CqImportin α1/β1-CqRan 介导的细胞核转运途径靶向核孔，并在核孔处释放病毒基因组入核转录。此外，WSSV 亦利用 CqImportin α1/β1-CqRan 途径将新合成的含核定位信号（NLS）的病毒结构蛋白转运入核组装。上述发现为 WSSV 发病机制提供了新见解，即 WSSV 通过劫持宿主因子实现感染，并提示通过 Ivermectin 靶向阻断 CqImportin α1/β1 可能成为潜在的抗 WSSV 策略。

关键词：白斑综合征病毒；胞内运输；核转运蛋白；核定位信号；抗病毒靶点

Mechanisms of White Spot Syndrome Virus Entry and Intracellular Infection

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Abstract： White spot syndrome virus (WSSV) is recognized as one of the largest animal viruses, yet its pathogenic mechanism remains incompletely understood. In this study, we found that actin nucleation and clathrin-mediated endocytosis were recruited for the internalization of WSSV into shrimp cells. This was followed by intracellular transport of invading virions via endocytic vesicles and endosomes. After envelope fusion within endosomes, penetrated nucleocapsids were transported along microtubules toward nuclear pore periphery. Furthermore, the nuclear transporters CqImportin α1/β1 together with CqRan were recruited, via binding of CqImportin β1 to nucleoporins CqNup35/62, for both the nuclear pore targeting of the incoming nucleocapsids and the nuclear import of expressed viral structural proteins containing the nuclear localization sequences (NLSs). Our findings provide a novel explanation for WSSV pathogenesis involving systemic hijacking of host factors, which can be exploited for antiviral targeting against WSSV disease, such as blockade of CqImportin α1/β1 with ivermectin.

Key words:white spot syndrome virus; intracellular trafficking; importin; nuclear localization sequence; antiviral targeting

鉴定偷死野田村病毒（CMNV）为双壳贝类新病原

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摘要：2020–2021 年，中国北方沿海养殖双壳贝类持续死亡，同期山东暴发了对虾 CMNV 疫情。鉴于 CMNV 跨种传播风险，本研究系统评估其对太平洋牡蛎、魁蚶、文蛤的易感性与致病性。RT-PCR 显示，2020–2022 年采集的太平洋牡蛎、魁蚶、文蛤样本中 CMNV 阳性率依次为 62.50%（15/24）、33.33%（2/6）和 50%（12/24）；2022–2023 年青岛市场采集的双壳贝类样本阳性率达 82.86%（58/70）。基于 CMNV 部分 RdRp 构建的系统发育树显示贝类中 CMNV 与山东对虾疫情及对虾饵料中的毒株高度同源。组织病理学结果显示，CMNV 阳性样本发生外套膜与消化腺上皮坏死、肌溶解、巨包涵体及巢状聚集体；ISH 证实包涵体内 CMNV 阳性信号明显；TEM 于牡蛎、魁蚶外套膜和性腺观察到约 30 nm 病毒样颗粒。研究首次确证 CMNV 可感染并致双壳贝类病变，提示对野生种群具潜在生态威胁。

关键词：偷死野田村病毒；双壳贝类；病理损伤；生态风险；病毒溢出

Covert mortality nodavirus identified as a new causative agent in bivalves

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Abstract: During 2020–2021, mass mortalities of farmed bivalves along northern China coincided with a CMNV outbreak in shrimp in Shandong. To investigate cross-species risk of CMNV, samples of bivalves including Pacific oyster Crassostrea gigas, ark shell Scapharca broughtonii, and clam Meretrix meretrix were collected and analyzed from coastal areas of northern China in 2020-2022. The RT-PCR results showed that the CMNV positive rates in the collected samples of oysters, ark shells, and clams were 62.50% (15/24), 33.33% (2/6), and 50% (12/24), respectively. RdRp-based phylogeny showed that CMNV isolates from bivalves were clustered tightly with the isolates of the CMNV outbreak from Penaeus vannamei and their bait in Shandong. Histopathology revealed mantle and digestive-gland epithelial necrosis, myonecrosis, vacuolation, giant inclusions and nest-like aggregates. ISH localized viral RNA within inclusions; TEM showed 30 nm virions and inclusion bodies in mantle and gonad. The study highlighted CMNV as a pathogen of bivalves with potential threat to the wild population in the same habitat.

Key words: Covert mortality nodavirus (CMNV); bivalves; pathological lesion; ecological risk; spillover infectio

鲤 IκBα同源基因的鉴定与分子特征分析

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摘要：核因子κB 抑制蛋白α（Inhibitor of Nuclear Factor κB Alpha，IκBα）是 IκB 家族的核心成员，通过抑制 NF-κB 信号通路在炎症、免疫及细胞凋亡中起关键作用。本研究以鲤为对象，克隆获得三个 IκBα同源基因，分别命名为 IκBα-A、IκBα-B 和 IκBα-C。其开放阅读框长度分别为 969 bp、1029 bp 和 1077 bp，编码 323、342 和 358 个氨基酸，预测分子量分别为 35.88 kDa、38.49 kDa 和 41.98 kDa。结构域分析显示，IκBα-A 和 IκBα-B 均含 5 个 ANK 结构域，而 IκBα-C 仅含 2 个；IκBα-A 与 IκBα-B 均由 19 个α螺旋构成，IκBα-C 则由 21 个α螺旋和 4 个β折叠组成。三者均具有 2 个关键磷酸化位点。共线性分析表明，鲤 IκBα基因在基因组中的位置及邻近基因排列与斑马鱼和人类高度保守。序列一致性分析显示，三个 IκBα间氨基酸一致性仅为 37.37%，其中 IκBα-B 与斑马鱼 IκBα同源性最高（73.26%）。系统进化分析提示 IκBα-B 与金鱼及斑马鱼 IκBα亲缘最近，表明三个同源基因可能存在进化分歧。本研究为深入探讨 IκBα基因的免疫功能提供了理论基础。

关键词：鲤；IκBα；炎症反应

Identification and Molecular Characterization of IκBα Homologs in Common Carp (*Cyprinus carpio*)

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Abstract： Inhibitor of Nuclear Factor κB Alpha (IκBα), a core member of the IκB family, plays a critical role in inflammation, immunity, and apoptosis by inhibiting the NF-κB signaling pathway. In this study, three IκBα homologous genes were cloned from common carp (*Cyprinus carpio*), designated as IκBα-A, IκBα-B, and IκBα-C. Their open reading frames measure 969 bp, 1029 bp, and 1077 bp, encoding 323, 342, and 358 amino acids, with predicted molecular weights of 35.88 kDa, 38.49 kDa, and 41.98 kDa, respectively. Domain analysis revealed that both IκBα-A and IκBα-B contain five ANK domains, while IκBα-C contains only two. IκBα-A and IκBα-B each comprise 19 α-helices, whereas IκBα-C consists of 21 α-helices and 4 β-sheets. All three isoforms possess two key phosphorylation sites. Synteny analysis indicated that the genomic location and transcriptional orientation of IκBα genes, as well as their adjacent genes, are highly conserved among common carp, zebrafish, and humans. Sequence alignment showed low amino acid identity among the three IκBα homologs (37.37%), with IκBα-B exhibiting the highest homology to zebrafish IκBα (73.26%). Phylogenetic analysis revealed that IκBα-B clusters closely with IκBα from goldfish and zebrafish, suggesting potential evolutionary divergence among the three homologs. These findings provide a theoretical foundation for further investigation into the immune functions of IκBα genes.

Key words: Common carp; IκBα; inflammatory response

鱼源宋氏鲸杆菌的分离鉴定及其对大口黑鲈脂质代谢和肌肉品质的影响

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摘要：益生菌作为一种低成本、高安全性的功能性食品，已发展成为预防或改善饮食引起的脂质代谢紊乱的创新策略。宋氏鲸杆菌作为淡水鱼肠道的优势菌，已被报道与鱼类健康有关。然而，鱼源宋氏鲸杆菌能否影响宿主本身的脂代谢尚不清楚。本研究从不同鱼源分离得到 5 株宋氏鲸杆菌并进行体外益生评价，筛选得到一株产 SCFAs 含量较多的菌株，以大口黑鲈为对象，采用对照饲料（CFD）、高脂饲料（HFD）、低、中、高浓度宋氏鲸杆菌饲料进行试验。结果表明，高浓度组显著降低了血清中 TG、TC、LDL-C、ALT、AST 含量，提高了 HDL-C 含量，降低了肝脏中粗脂肪含量，减轻了肝脏脂滴蓄积。基因表达分析表明，高浓度组上调了肝脏 acc-β、hsl 基因，抑制了 acc、acc-α、fas 表达。此外，高浓度组还改善了肌肉质构特性、理化性质。综上所述，高浓度宋氏鲸杆菌能够影响宿主本身的脂质代谢，并对肌肉品质有一定的改善作用。

关键词：高脂饲料；大口黑鲈；宋氏鲸杆菌；脂质代谢；肌肉品质

Isolation and Identification of *Cetobacterium somerae* from Fish and Its Effects on Lipid Metabolism and Muscle Quality of Largemouth Bass (*Micropterus salmoides*)

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Abstract：Probiotics, as low-cost and safe functional foods, offer a innovative strategy to prevent or ameliorate diet-induced dyslipidemia. Cetobacterium somerae, a dominant gut bacterium in freshwater fish, is associated with host health, yet its direct role in lipid metabolism remains unclear. This study isolated five C. somerae strains from fish and selected a high SCFA-producing strain for feeding trials in largemouth bass. Fish were fed control (CFD), high-fat (HFD), or HFD supplemented with low/medium/high-dose C. somerae. Results showed the high-dose group significantly reduced serum TG, TC, LDL-C, ALT, and AST levels, increased HDL-C, decreased hepatic crude fat, and alleviated lipid accumulation. Gene expression analysis revealed upregulation of acc-β and hsl, and downregulation of acc, acc-α, and fas. Muscle texture and physicochemical properties were also improved. In conclusion, high-dose C. somerae modulates host lipid metabolism and enhances muscle quality.

Key words: High-fat diet; Largemouth bass; Cetobacterium somerae; Lipid metabolism; Muscle quality

Lactococcus lactis Z-2 对高脂饲料饲喂鲤脂代谢的调节作用

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摘要: 本研究通过在高脂饲料（HFD）中添加不同剂量的乳酸乳球菌 *Z-2*（*Lactococcus lactis Z-2*），探究其对鲤（Cyprinus carpio）脂代谢的调节作用。将 300 尾幼鲤随机分为五组，即对照组、高脂组及在 HFD 中添加低、中、高剂量（$5×10^7$、$5×10^8$、$5×10^9$ CFU/g）*L. lactis Z-2* 组，每组 3 个重复，饲喂 8 周。结果显示，高脂组鲤肠道脂肪酶、肝胰腺脂代谢酶活性及血脂水平均显著升高，组织脂肪沉积增加，免疫与抗氧化能力受损，并出现组织病理损伤。添加 *L. lactis Z-2* 后可有效恢复肠道和肝胰腺的完整性，增强机体抗氧化和免疫功能，促进脂分解基因（lpl、hsl 等）及抑制脂合成基因（fas、acc 等）的表达，并改善血脂水平。综上，*L. lactis Z-2* 具有缓解 HFD 诱导鲤脂代谢紊乱的潜力，为水产养殖中高能饲料的安全应用提供策略。

关键词: 乳酸乳球菌 Z-2；高脂饲料；脂质代谢；鲤

Impact of *Lactococcus lactis Z-2* on lipid metabolism regulation in common carp (*Cyprinus carpio*) fed high-fat diets

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Abstract: This study investigated the regulatory effects of *Lactococcus lactis Z-2* at different dosages, incorporated into a high-fat diet (HFD), on lipid metabolism in common carp (*Cyprinus carpio*). Three hundred juvenile carp were divided into five groups: control, HFD, and HFD supplemented with low, medium, and high doses ($5×10^7$, $5×10^8$, $5×10^9$ CFU/g) of *L. lactis Z-2*, with three replicates each, over an eight-week feeding trial. The HFD group showed elevated intestinal lipase and hepatopancreatic lipid enzyme activity, increased blood lipids, tissue fat deposition, impaired immunity and antioxidant capacity, and histopathological damage. Supplementation with *L. lactis Z-2* effectively restored intestinal and hepatopancreatic integrity, enhanced antioxidant and immune functions, promoted expression of lipolytic genes (lpl, hsl, etc.) and inhibited lipogenic genes (fas, acc, etc.), while improving blood lipid levels. Overall, *L. lactis Z-2* shows promise in mitigating HFD-induced lipid disorders in carp, supporting safe high-energy feed use in aquaculture.

Key words: *Lactococcus lactis Z-2*; High-fat diets; Lipid metabolism; Common carp

裂壶藻油对草鱼肝脏代谢功能的影响

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摘要：裂壶藻富含多不饱和脂肪酸 DHA 以及维生素 E、类胡萝卜素，能够促进鱼类生长，提升免疫能力。尽管如此，裂壶藻在调节鱼类肝脏代谢的具体机制中仍有待深入探索。因此，本研究基于非靶向代谢组学探究裂壶藻油对草鱼肝脏代谢方面的具体机制，试验以初始体重（103.83±1.17）g 草鱼为研究对象，随机分为空白对照组和实验组（藻油添加比例为 1.6%），持续 58 天的循环水养殖试验。结果显示， POS 模式下共检测出 193 个差异代谢物（DEMs）变化。NEG 模式下共检测出 120 个 DEMs 变化。进一步通过 KEGG 显著性气泡图显示 POS 模式下 DEMs 主要富集于 D-氨基酸代谢，甘油磷脂代谢，醚脂代谢。NEG 模式下 DEMs 主要富集在不饱和脂肪酸的生物合成。其中棕榈酸，油酸和顺式-4,7,10,13,16,19 -二十二碳六烯酸（DHA）脂肪酸代谢物上调。综上，藻油的添加能够提升脂肪酸在草鱼肝脏中的含量，改善草鱼肝脏代谢。

关键词：裂壶藻油；代谢功能；草鱼

The Effect of *Schizochytrium* Oil on Hepatic Metabolic Function in Grass Carp（*Ctenopharyngodon idella*）

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Abstract: *Schizochytrium* is rich in docosahexaenoic acid (DHA, a polyunsaturated fatty acid), which can promote fish growth and enhance immune capacity. Nevertheless, the role of *Schizochytrium* in regulating fish hepatic metabolism remains to be explored. Therefore, this study investigated the effect of Schizochytrium oil on the hepatic metabolism of grass carp based on untargeted metabolomics. For the experiment, grass carp with an initial body weight of (103.83±1.17) g were used as research subjects, randomly divided into a blank control group and an experimental group (with 1.6% algae oil added), and a recirculating aquaculture experiment was conducted for 58 consecutive days. The results showed that in the POS mode, differential metabolites (DEMs) were mainly enriched in D-amino acid metabolism, glycerophospholipid metabolism, and ether lipid metabolism. In the NEG mode, DEMs were mainly enriched in the biosynthesis of unsaturated fatty acids. In summary, algae oil can increase the content of fatty acids in the liver of grass carp and improve the hepatic metabolism of grass carp.

Key words: *Schizochytrium* Oil, metabolic function, Grass Carp

Akk 介导“ALDH5A1—少突细胞—乳酸”途径改善斑马鱼脂质代谢的肠脑轴作用研究

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摘要：巴氏灭活 Akkermansia muciniphila（P-Akk）已被证明在改善斑马鱼脂质代谢方面有益，其机制可能与肠脑轴的神经内分泌途径相关。本研究对高脂饮食（HFD）斑马鱼外源补充 1×10^9 CFU/g P-Akk 后发现， P-Akk 显著抑制 HFD 组斑马鱼摄食行为，并改善脑部氧化应激与 γ-氨基丁酸（GABA）异常蓄积，该效应与线粒体酶 ALDH5A1 表达变化相关。脑转录组 WGCNA 分析表明，ALDH5A1 所在模块的功能显著富集于少突胶质细胞分化过程。进一步通过 CNPASE IF 染色发现，P-Akk 可改善 HFD 诱导的少突胶质细胞发育异常。鉴于少突胶质细胞发育过程中的乳酸分泌与大脑能量代谢密切相关，而脑内乳酸水平在 HFD 组显著下降。因此，推测 P-Akk 可能通过减少 HFD 斑马鱼脑部氧化应激与 GABA 蓄积，促进少突胶质细胞发育，提升脑内乳酸水平，恢复大脑能量稳态，进而改善斑马鱼脂质代谢紊乱。

关键词：斑马鱼；脂质代谢；γ-氨基丁酸；氧化应激；少突胶质细胞

The gut-brain axis mechanism of P-Akk in improving lipid metabolism in zebrafish by mediating the ALDH5A1–Oligodendrocyte–Lactate pathway

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Abstract: Pasteurized Akkermansia muciniphila (P-Akk) has demonstrated benefits in metabolic regulation. In this study, zebrafish were fed a high-fat diet (HFD) and supplemented with lyophilized P-Akk at 1×10^9 CFU/g. The results indicate that P-Akk significantly inhibited feeding behavior in HFD-fed zebrafish, decreased oxidative stress in the brain, and restored normal levels of GABA. These effects were associated with altered expression of the mitochondrial enzyme ALDH5A1. WGCNA analysis of brain transcriptomes revealed that the module containing ALDH5A1 was significantly enriched in functions related to oligodendrocyte differentiation. Furthermore, immunofluorescence staining of CNPASE demonstrated that P-Akk ameliorated HFD-induced impairments in oligodendrocyte development. Given the reduction in cerebral lactate levels induced by HFD and the critical role of lactate in oligodendrocyte maturation, we propose that P-Akk enhances oligodendrocyte development, increases lactate availability, and restore the energy homeostasis of the brain, thereby ameliorating lipid metabolism.

Key words: Zebrafish; Lipid metabolism; Gamma-aminobutyric acid; Oxidative stress; Oligodendrocyte

牛蛙蝌蚪生长与变态发育的最适蛋白质和脂肪比

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摘要：为了探究饲料蛋白质和脂肪比例对牛蛙蝌蚪生长性能、饲料利用、抗氧化能力和变态率的影响，本试验配制了 9 种饲料，蛋白水平分别为 37%、42%、47%，脂肪水平分别为 7%、11%、15%。每个处理设置 3 个重复，每个重复 34 只蝌蚪（初始均重 0.005g），试验为期 77 天。结果表明：增重率、血浆甲状腺素水平、干物质和总能表观消化率以及 41 期变态率均分别随蛋白和脂肪水平的升高而升高。37P 和 7L 组生长性能和变态率较低。与 11L 组相比，15L 组显著降低了存活率和肝脏抗氧化能力。47P/11L 和 42P/11L 两组蝌蚪均表现出较好的生长性能和较高的变态率。因此，基于对牛蛙蝌蚪存活率、生长和肝脏健康的综合评估，42P/11L 为牛蛙蝌蚪饲料的最适蛋白质和脂肪比，而 47P/15L 对促进牛蛙蝌蚪的变态率最为有效。

关键词：牛蛙蝌蚪；生长；蛋白；脂肪；变态

Optimal dietary protein-to-lipid ratio for the growth and metamorphosis of bullfrog (*Aquarana catesbeianus*) tadpoles

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Abstract: This study aimed to evaluate the effects of dietary protein-to-lipid ratio on growth performance, feed utilization, antioxidant, and metamorphosis of bullfrog tadpoles. Nine diets were formulated to contain three crude protein levels (37, 42, and 47%) and three crude lipid levels (7, 11, and 15%). Triplicate replicates of 34 tadpoles (0.005g) were fed for 77 days. The results showed significant enhancement of WG, T4 in serum, apparent digestibility of dry matter and gross energy, and metamorphosis rate at stage 41 with increasing protein and lipid levels, respectively. Compared to the 11L groups, the 15L groups significantly reduced the survival rate and liver antioxidant capacity. Both 47P/11L and 42P/11L groups demonstrated favorable growth performance and metamorphosis outcomes. Consequently, based on a comprehensive evaluation of survival rate, growth, and liver health of bullfrog tadpoles, 42P/11L has been identified as the optimum protein-to-lipid ratio in diets for bullfrog tadpoles. Whereas a diet with 47P/15L was most effective in promoting metamorphosis rate.

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

Lactococcus lactis Z-2 胞外多糖对鲤脂代谢的调控作用及机制

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摘要：本研究以乳酸乳球菌 *Z-2*（*Lactococcus lactis Z-2*）胞外多糖（EPS）在鱼类体内的免疫调节、抗氧化和抗病特性为基础，探究其对鲤（Cyprinus carpio）脂代谢的调节机制。通过油酸（OA）诱导构建体外高脂模型发现，胞外产物（ECP）和 EPS 在有效剂量范围内可显著降低 OA 诱导的肝细胞 TG、TC 和 LDL-C 水平，提高 HDL-C，并下调脂合成基因（fas、srebp 等）、上调脂分解基因（lpl、hsl 等）表达。进一步机制研究表明，ECP/EPS 通过激活 PKA 信号通路发挥调节作用，该通路被抑制后其脂代谢调节效应被完全逆转。此外，体内灌喂实验证实，EPS 可改善 HFD 引起的肠道绒毛萎缩、肝胰腺脂肪沉积和血脂异常，并调控多组织中脂代谢相关基因的表达。上述结果表明，EPS 可通过激活 PKA 信号通路有效调节鲤的脂质代谢，为其作为水产饲料添加剂防治代谢性疾病提供了理论依据和应用前景。

关键词：胞外多糖；脂质代谢；鲤

Regulatory effects and mechanisms of exopolysaccharides from *Lactococcus lactis Z-2* on lipid metabolism in common carp (*Cyprinus carpio*) fed a high-fat diet

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Abstract: This study investigates the regulatory mechanism of *Lactococcus lactis Z-2* extracellular polysaccharide (EPS) on lipid metabolism in Cyprinus carpio, based on its immunomodulatory, antioxidant and disease-resistant properties in fish. An in vitro high-fat model induced by oleic acid revealed that both extracellular products (ECP) and EPS reduced TG, TC, and LDL-C levels, increased HDL-C, down-regulated lipogenic genes (fas, srebp, etc.), and up-regulated lipolytic genes (lpl, hsl, etc.). Mechanistic studies showed that PKA signaling mediates these lipid-modulating effects, as pathway inhibition nullified the benefits. In vivo, EPS mitigated HFD-induced intestinal villus atrophy, hepatopancreatic fat deposition, and dyslipidemia, while regulating lipid metabolism genes across tissues. These results suggest EPS modulates carp lipid metabolism via PKA signaling, offering theoretical and practical support for its use as an aquatic feed additive to prevent metabolic disorders.

Key words: extracellular polysaccharides; lipid metabolism; *Cyprinus carpio*

GIP 及其受体在大口黑鲈中的分子鉴定与功能探析

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摘要：鱼类饲料使用碳水化合物可节约蛋白质并降低成本，但过量可致鱼类肝脏代谢紊乱。GIP 及其受体 GIPR 在糖脂代谢调控中作用重大。本研究克隆了大口黑鲈 gip、gipr cDNA 序列，分析组织表达，利用原代肝细胞培养和腹腔注射实验评估功能。gip、gipr cDNA 全长分别为 318 bp、1614 bp，分别编码 105、537 个氨基酸。Gip mRNA 在胃高表达，gipr mRNA 在大脑及前、中、后肠高表达。高糖脂摄入上调胃 gip mRNA，下调前肠 gipr mRNA。 GIP 处理原代肝细胞后，上调 g6pase、acc1、fas、pi3k、akt 表达，下调 gk、pfk、hsl、lpl 表达。腹腔注射 gip siRNA 后，血清葡萄糖和甘油三酯降低，肝脏 g6pase、fbp1、hsl 及 PI3K/Akt 通路相关基因表达升高，acc1、fas 表达降低。综上，GIP 及 GIPR 在大口黑鲈糖脂代谢调控中起重要作用。

关键词：gip；gipr；大口黑鲈；鉴定；代谢

Molecular identification and functional analysis of GIP and its receptor in *Micropterus salmoides*

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Abstract: Carbohydrates in fish feed conserve protein and cut costs but cause liver metabolic disorders when excessive. Glucose-dependent insulinotropic peptide (GIP) and its receptor (GIPR) are key for glucose and lipid metabolism regulation. This study cloned gip and gipr cDNA from largemouth bass, analyzed their tissue expression, assessed functions via primary hepatocyte culture and intraperitoneal injection. gip cDNA is 318 bp (encodes 105 amino acids), gipr cDNA 1614 bp (encodes 537 amino acids). gip mRNA is highly expressed in the stomach; gipr mRNA in the brain, foregut, midgut, and hindgut. High glucose and lipid intake upregulates gastric gip mRNA but downregulates foregut gipr mRNA. GIP treatment on primary hepatocytes upregulates g6pase, acc1, fas, pi3k, akt, and downregulates gk, pfk, hsl, lpl. Intraperitoneal injection of gip siRNA reduces serum glucose and triglycerides, upregulates liver g6pase, fbp1, hsl and PI3K/Akt pathway-related genes, downregulates acc1, fas. In conclusion, GIP and GIPR play important roles in regulating largemouth bass glucose and lipid metabolism.

Key words: gip; gipr; largemouth bass; identification; metabolism

亮氨酸通过 *Sar1b/Sestrin2/Ampk1* 通路减轻高脂饮食诱导的刺鱼内质网应激介导的脂毒性损伤

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摘要：随着高脂饲料投喂增多，养殖鱼类中脂肪肝疾病日益普遍。本研究探讨了亮氨酸对高脂饲料诱导的黑鲷肝损伤的保护作用。通过体内实验（在高脂饲料中添加 0.50%–2.00%亮氨酸）和体外油酸诱导肝细胞模型，发现亮氨酸可通过激活 Sar1b/Sestrin2 和 Ampkα1/Sirt1 通路，增强脂解、抑制脂生成，从而显著减轻肝脏脂质沉积。同时，亮氨酸下调内质网应激标志物表达，抑制 Nf-κb P65/Jnk 磷酸化，进而缓解炎症及细胞凋亡。过表达 Ampkα1、Sar1b 或 Sestrin2 能够模拟亮氨酸的保护效应。该研究不仅揭示了亮氨酸缓解肝脏脂毒性的作用机制，也为制定可持续水产养殖中的营养干预策略提供了科学依据。

关键词：Ire1a；Ampka1/Sar1b/Sestrin2；炎症；凋亡；亮氨酸

Leucine alleviates ER-stress mediated lipotoxic injury induced by high-fat diet via *Sar1b/Sestrin2/Ampk1* pathways in *Acanthopagrus schlegelii*

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Abstract: With the rising prevalence of high-fat diet (HFD)-induced fatty liver disease in farmed fish, this study investigated leucine's protective role against HFD-induced liver injury in black seabream. In vivo, HFD (18% lipid) supplemented with varying leucine levels (0.50%–2.00%) and in vitro OA-induced hepatocyte models were used. Leucine significantly reduced hepatic lipid deposition by activating Sar1b/Sestrin2 and Ampkα1/Sirt1 pathways, enhancing lipolysis and inhibiting lipogenesis. It also downregulated ER stress and suppressed Nf-κb P65/Jnk phosphorylation, alleviating inflammation and apoptosis. Overexpression of Ampkα1, Sar1b, or Sestrin2 replicated leucine's protective effects. These findings reveal leucine's role in mitigating lipotoxic injury and provide insights into nutritional strategies for sustainable aquaculture.

Key words: Ire1a; *Ampka1/Sar1b/Sestrin2*; inflammation; apoptosis; leucine

基于乌鳢模型的肌肉 -肠道轴探究沙葱黄酮缓解脱氧雪腐镰刀菌烯醇诱导的肠道炎症及改善肉质的作用

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摘要：脱氧雪腐镰刀菌烯醇（DON）在植物源饲料中广泛存在，威胁着动物健康和食品安全。沙葱黄酮（AMRF）是一种具有多种生物学功能的天然植物提取物，但它能否减轻 DON 诱导的生物毒性尚不明确。因此，研究了 AMRF 对 DON 诱导的乌鳢肠道炎症和肉质的影响。在基础饲料中添加 DON（2mg/kg）和 AMRF（40mg/kg），形成三个饲料组，对乌鳢进行为期 8 周的投喂。结果表明，饲料中添加 AMRF 显著缓解 DON 诱导的生长抑制，提高消化酶活性，增强肠道对 DON 的解毒能力，鱼体内毒素残留量显著降低。同时，炎症反应（nf-κb、i-κb、tnf-α、il-1β、il-2、il-6、il-8、ifn-γ）也得到缓解，AMRF 可能通过 TRAF6/Sufu/p-p65 相关途径缓解 DON 诱导的炎症。此外，炎症反应还导致肠道微生物群发生变化。另外，AMRF 增加了肌肉蛋白质含量和抗氧化能力，改善肉质的质地特性，并减少腥味物质。

关键词：沙葱黄酮；脱氧雪腐镰刀菌烯醇；乌鳢肌肉-肠道轴；炎症；肉质

Exploring *Allium mongolicum* Regel flavonoids alleviation of deoxynivalenol-induced gut inflammation and flesh-quality improvement based on muscle-intestinal axis in a *Channa argus* model

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Abstract: Deoxynivalenol exists in plant-based feed,endangering animal health and food safety.*Allium mongolicum* Regel flavonoids,a substance with various biological functions,has an unknown effect on mitigating DON-induced biotoxicity Hence,the effect of DON-induced gut inflammation and flesh-quality in *Channa argus* by AMRF were examined.DON(2mg/kg)and AMRF(40mg/kg)were supplemented to the basic formula feed to develop three dietary groups and C.argus were fed for 8 weeks.Results showed that dietary AMRF significantly alleviated DON-induced growth inhibition,increased digestive enzyme activity,and enhanced intestinal DON detoxification,directly reducing toxin residues in fish.Meanwhile,the inflammatory response(nf-κb, i-κb, tnf-α, il-1β, il-2, il-6, il-8, ifn-γ)was also alleviated,and AMRF alleviated DON-induced inflammation possibly through the TRAF6/Sufu/p-p65-related pathway.Furthermore,inflammatory response also induced changes in gut microbiota,Additionally,AMRF increased muscle protein content and antioxidant capacity,improved textural properties,and reduced fishy substances.

Key words: AMRF; DON; *Channa argus;* Muscle-intestinal; axis Inflammation; Flesh quality

艾叶副产物促进高脂日粮饲喂下鲤生长并改善其脂质代谢

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摘要：为探讨艾叶副产物-艾叶粉（MLP）在高脂日粮中对鲤生长性能及脂质代谢的影响。本实验选取鲤幼鱼，分别饲喂基础日粮（CT，5%脂肪）、高脂日粮（HF，10%脂肪）及添加 0.6%（MLP1）、1.2%（MLP2）、1.8%（MLP3）、2.4%（MLP4）艾叶粉的高脂日粮共 8 周。结果表明，相较于 HF 组，MLP1、MLP2 组鲤的终末体重和饲料利用率显著升高，MLP2、MLP3 和 MLP4 组的肠道绒毛高度和消化酶活性均显著增加（$P < 0.05$）。MLP2 组肠道抗炎基因表达上调。此外，添加超 1.2%的 MLP 显著降低了肝胰腺中的粗脂、甘油三酯、胆固醇和游离脂肪酸含量，同时下调肝胰腺中脂质合成基因 fas 的表达，并上调脂肪分解基因 cpt1 的表达。此外，脂肪组织中脂合成相关基因表达也呈现下调趋势，MLP 显著减轻肝细胞空泡化程度并缩小脂肪细胞体积。综上所述，鲤高脂日粮中添加艾叶粉可改善生性能、调节脂质代谢。

关键词：鲤；艾叶副产物；生长；脂质代谢

Artemisia argyi coproducts promote carp growth and improve lipid metabolism under high-fat diet feeding

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Abstrac: To investigate the effects of Artemisia coproducts(MLP) on growth performance and lipid metabolism of common carp fed high-fat diets, juvenile common carp were fed basal diets (CT,), high-fat diest (HF), and HF supplemented with 0.6% (MLP1), 1.2% (MLP2), 1.8% (MLP3), and 2.4% (MLP4) MLP for 8 weeks. The growth performance and feed utilization in MLP1 and MLP2 groups were significantly enhanced compared to HF group. Intestinal villus height and digestive enzyme activity increased in MLP2 and MLP3 groups. Furthermore, intestinal anti-inflammatory gene expression was up-regulated in MLP2 group. Supplementation with more than 1.2% MLP significantly decreased the crude lipid, triglyceride, cholesterol, and free fatty acid content in the hepatopancreas, as well as down-regulated the expression of the lipid synthesis gene fas and up-regulated the lipolysis gene expression of cpt1 in hepatopancreas. Moreover, gene expressions related to lipid synthesis in adipose tissue also exhibited a down-regulated tendency.In conclusion, MLP improves growth and regulates lipid metabolism in common carp.

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

单宁酸对中华鳖幼鳖生长性能、抗细菌感染能力及肠道健康的影响

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摘要：对 12.54 g 中华鳖投喂含 0 (CG)、0.5、1、2 和 4 g/kg 单宁酸（TA）饲料 98 d 发现，0.5–4 g/kg TA 能提高生长性能和饲料利用率，增加小肠绒毛高度和黏膜下层厚度，降低嗜水气单胞菌感染后的死亡率，且 2 g/kg TA 效果最明显。小肠 16SrDNA 分析发现 2 g/kg TA 提高微生物丰富度和多样性，增加放线菌门并抑制厚壁菌门丰度。转录组数据表明，2 g/kg TA 显著影响 PPAR 信号通路，氨基酸代谢通路和类固醇合成通路中的基因表达。代谢组发现 2 g/kg TA 改变胆碱基组氨酸、钙泊三醇、13-O-十四烷酰法波醋酸酯、12-醋酸盐和六聚高甲硫氨酸等代谢物含量。联合分析揭示 2 g/kg TA 可通过激活 PPAR 通路缓解炎性反应，通过调控类固醇生物合成和α-亚麻酸代谢等脂质代谢途径提高生长性能。综上，2 g/kg 单宁酸可改善中华鳖肠道健康、提高生长性能和抗细菌感染能力。

关键词：单宁酸；中华鳖；生长性能；细菌感染；肠道健康；信号通路

Effect of dietary tannic acid on growth performance, bacterial resistance, and intestinal health in the juvenile Chinese soft-shelled turtles (*Pelodiscus sinensis*)

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Abstract: The Chinese soft-shelled turtles with 12.54 g body weight were fed with 0 (CG), 0.5, 1, 2, and 4 g/kg TA diets for 98 days. The results showed 0.5–4 g/kg TA increased the growth performance, feed utilization, villus height, and submucosa thickness of small intestine. The 0.5–2 g/kg TA reduced the cumulative mortality induced by Aeromonas hydrophila, with the 2 g/kg dosage leading to the lowest mortality. The 16SrDNA found 2 g/kg TA enhanced the richness and diversity of the microbiota by increasing Actinobacteria but inhibiting Firmicutes. The transcriptome demonstrated the differentially expressed genes in TA2 were mainly enriched in the PPAR signaling pathway and steroid biosynthesis. The differentially expressed metabolites discovered by metabolome included cholylhistidine, calcipotriol, and hexahomomethionine in CG vs. TA2. Integration of two omics revealed TA mitigated inflammation by activating the PPAR signaling pathway and promoted the growth performance via regulating the lipid metabolism. In general, 2 g/kg of TA can optimally promote growth and bacterial resistance.

Key words: tannic acid; Chinese soft-shelled turtle; growth performance; bacterial infection; intestinal health; signaling pathways

鱼源 *Bacillus velezensis* FLU-1 肠道定植及拮抗嗜水气单胞菌感染的分子机制研究

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摘要：近年来，高密度集约化养殖模式导致细菌性疾病频发，抗生素使用增加。随着国家“禁抗减抗”政策的实施，寻找抗生素替代品已成为研究热点。本实验室前期从鱼肠道中分离出一株 *Bacillus velezensis* FLU-1，该菌株在体外对 Aeromonas hydrophila 具有显著拮抗作用。投喂 FLU-1 可显著降低鲤脾脏和肝脏中的 A. hydrophila 载菌量（$P<0.05$），并提高鲤的存活率。同时，与对照组相比实验组鲤的促炎因子（IL-8、IL-15、TNF-α）表达量呈明显降低趋势。FITC 标记实验表明，FLU-1 能够稳定定植在鲤肠道。细胞实验显示，FLU-1 能够黏附于鲤多种类型的原代肠细胞。基于全基因组测序结果，我们注释到一个与黏附相关的基因（bslA）。综上，FLU-1 可能通过 BslA 蛋白黏附并定植于鲤肠道，进而通过生态位竞争与免疫调节功能促宿主肠道内 A. hydrophila 的清除。

关键词：*Bacillus velezensis*；鲤；嗜水气单胞菌；定植；bslA

Molecular Mechanisms of Intestinal Colonization by Fish-Derived *Bacillus velezensis* FLU-1 and Its Antagonism against *Aeromonas hydrophila* Infection

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Abstract: Intensive aquaculture has increased bacterial diseases and antibiotic use. National "antibiotic reduction" policies have spurred research into alternatives. We isolated a strain of Bacillus velezensis FLU-1 from fish intestines, which exhibited significant antagonistic effects against *Aeromonas hydrophila* in vitro. Feeding FLU-1 significantly reduced the bacterial load of A. hydrophila in the spleen and liver of carp ($P<0.05$) and improved their survival rate. Meanwhile, compared to the control group, the expression levels of pro-inflammatory factors (IL-8, IL-15, TNF-α) in carp showed a significant decreasing trend. FITC labeling experiments demonstrated that FLU-1 could stably colonize the carp intestine. Cell experiments revealed that FLU-1 could adhere to various types of primary intestinal cells in carp.We identified an adhesion-related gene (bslA).*FLU-1* likely adheres to and colonizes the carp intestine via the BslA protein, thereby promoting the clearance of A. hydrophila in the host intestine through niche competition and immune regulation functions.

Key words: *Bacillus velezensis*; Cyprinus carpio; *Aeromonas hydrophila*; Colonization; bslA

支链氨基酸对饥饿诱导的鲤大自噬和分子伴侣介导自噬的影响

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摘要：研究以鲤为对象，探究其在越冬饥饿期间的肌肉变化及支链氨基酸（BCAAs）的调节作用。实验设对照组、饥饿组和 4 个氨基酸补充组（Leu、Val、Ile 和 BCAAs），每组 3 个重复，每个重复 20 尾。饥饿组在饥饿 3、7、14 天后采样。氨基酸补充组，一个亚组饥饿 7 天，另一个亚组饥饿 14 天，两个亚组补充 14 天氨基酸后再采样。结果表明，饥饿使肌纤维总横截面积减少，饥饿 14 天后自噬体和溶酶体更明显被观察到，而补充 BCAAs 有助于恢复肌肉形态。饥饿条件下，巨自噬相关基因（atg4b、atg12 和 lc3）和伴侣介导的自噬相关基因（hsp70 和 lamp2a）表达上调，补充 BCAAs 后下调；p62 和 gfap 则相反。蛋白水平上，LC3-II、溶酶体相关膜蛋白 2A 和热休克蛋白 70 饥饿后上调，补充 BCAAs 后下调，P62 相反。以上结果为减少鱼类因越冬引起的肌肉萎缩提供营养策略。

关键词：支链氨基酸；饥饿；大自噬；分子伴侣介导自噬；鲤

Effects of branched-chain amino acids on starvation-induced macroautophagy and chaperone-mediated autophagy in common carp (*Cyprinus carpio*)

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Abstract: This study examined how branched-chain amino acids (BCAAs) affect muscle in common carp(*Cyprinus carpio*) during winter starvation. Carp were divided into control, starvation, and four amino acid supplement groups (Leu, Val, Ile, and BCAAs), each with three replicates of 20 fish. Results indicated that starvation reduced muscle fiber size and increased autophagosomes and lysosomes after 14 days, while BCAAs supplementation improved these results.Under starvation conditions, macroautophagy-related (atg4b, atg12, lc3) and CMA-related (hsp70,lamp2a) genes were upregulated. After BCAAs supplementation, these genes were downregulated, while p62 and gfap showed the opposite trend. At the protein level after starvation, LC3-II, LAMP2A, and HSP70 levels increased, while BCAAs supplementation caused these proteins to decrease. Conversely, P62 levels rose with the addition. These nutritional strategies may combat muscle atrophy in overwintering fish.

Key words: BCAAs; Starvation;Macroautophagy; Chaperone-mediated autophagy; Common carp (*Cyprinus carpio*)

鼠李糖乳杆菌改善 TBT 暴露诱发的斑马鱼神经和心血管系统损伤

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摘要：本研究以斑马鱼为模型，探究饲料中添加鼠李糖乳杆菌（*Lactobacillus rhamnosus*）对三丁基锡（TBT）毒性的改善作用。270 尾实验鱼分为对照组（DMSO）、TBT 暴露组及 TBT 暴露添加鼠李糖乳杆菌组（TBT+PRO），采集肠、脑、心脏组织及血液样本进行组织病理学、RT-qPCR、ELISA 及 16S rRNA 测序等分析。结果表明，补充鼠李糖乳杆菌显著提高了厚壁菌门和乳杆菌属丰度，减轻脑室肿大和心脏炎症浸润。显著下调肠道、脑和心脏中 tnf-α、il-1β的表达，上调 il-10 和紧密连接蛋白基因 *claudin-2*、*zo-1*。脑、血清和肠道中脂多糖（LPS）水平下降，基因 crhr2、pomc 等表达受抑，神经元基因 bdnf、shha 等恢复正常，基因 *caspase-3*、*bax* 等表达下调。研究表明鼠李糖乳杆菌可通过肠-心血管-脑轴有效改善 TBT 的跨系统毒性。

关键词：鼠李糖乳杆菌（*Lactobacillus rhamnosus*）；斑马鱼；三丁基锡（TBT）；神经系统；肠道；心血管；脑

Lactobacillus murinus improves TBT exposure-induced neurovascular and cardiovascular damage in zebrafish

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Abstract: This study used zebrafish to investigate the ameliorative effect of dietary supplementation with *Lactobacillus rhamnosus* on tributyltin (TBT)-induced toxicity. A total of 270 fish were divided into control (DMSO), TBT-exposed, and TBT+PRO (TBT + *L. rhamnosus*) groups. Tissues, including intestine, brain, heart, and blood, were collected for histopathological, RT-qPCR, ELISA, and 16S rRNA sequencing analyses. Results showed that *L. rhamnosus* increased the abundance of Firmicutes and *Lactobacillus*, alleviated cerebral ventricular enlargement, and cardiac inflammatory infiltration. It downregulated the expression of tnf-α and il-1β, while upregulating il-10 and tight junction genes claudin-2 and zo-1 in the intestine, brain, and heart. lipopolysaccharide (LPS) levels decreased in the brain, serum, and intestine; gene expression of crhr2 and pomc was suppressed; neuronal genes bdnf and shha normalized; and expression of caspase-3 and bax was downregulated. The study demonstrates that *L. rhamnosus* effectively mitigates TBT-induced trans-systemic toxicity via the gut–cardio–brain axis.

Key words: *Lactobacillus rhamnosus*; zebrafish; TBT; nervous system; gut; cardiovascular; brain

色氨酸对大口黑鲈生长、抗氧化能力和肠道健康的影响

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摘要：本研究将初始体重为 16.19±0.06g 的大口黑鲈分为 5 组，设置对照组（C，0%）、0.1%、0.2%、0.4%和 0.8%Trp 组，养殖 9 周。结果表明，添加 Trp 后大口黑鲈终末体重、增重率和特定生长率均显著高于 C 组，其中 0.4Trp 组显著高于其他补充 Trp 组；同时，补充 Trp 后血清和肠道中抗氧化酶 CAT、GSH-Px、SOD 和 T-AOC 活性显著高于 C 组，血清 MDA 含量显著低于 C 组；与 C 组相比，0.4%Trp 组 Nrf2 基因表达上调，添加 Trp 组 Keap1 和 HSP70 表达下调；此外，相较于 C 组，0.4%Trp 组前肠消化酶胰蛋白酶、脂肪酶活性显著升高，同时补充 Trp 组中肠绒毛高度、肌层厚度显著增加，并下调促炎基因表达，上调抑炎基因表达。综上所述，饲料中添加 0.4%Trp 可以提高大口黑鲈肠道抗氧化酶及消化酶活性，改善肠道健康，促进生长，为可以高效配制大口黑鲈养殖饲料提供理论依据。

关键词：关键词：色氨酸；大口黑鲈；生长；抗氧化能力；肠道健康

Effects of Tryptophan on Growth, Antioxidant Capacity and Intestinal Health of Largemouth Bass (*Micropterus salmoides*)

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Abstract: In a 9-week study, largemouth bass (16.19 ± 0.06 g) were fed diets supplemented with 0、0.1 、 0.2 、 0.4 and 0.8% tryptophan (Trp). The 0.4% Trp group showed the most significant improvement final body weight, weight gain rate, and specific growth rate. Trp supplementation significantly increased serum and intestinal antioxidant enzyme activities (CAT, GSH-Px, SOD, T-AOC) and reduced serum MDA. The 0.4% Trp group upregulated Nrf2 and downregulated Keap1 and HSP70 expression. It also enhanced foregut trypsin and lipase activity, improved villus height and muscle thickness, downregulated pro-inflammatory genes, and upregulated anti-inflammatory genes. Thus, 0.4% dietary Trp improves antioxidant capacity, digestive function, and intestinal health, promoting growth and supporting efficient feed formulation for largemouth bass.

Key words: tryptophan; largemouth bass; growth; antioxidant capacity; intestinal health

宿主来源的 Bacillus velezensis T20 提高了大菱鲆的抗病力并改善了大菱鲆的肠道健康

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摘要：本研究对一株从健康大菱鲆肠道中分离出的 *Bacillus velezensis* T20（T20）的益生潜力进行了评估。试验设置了两组饲料，即对照组及在对照组饲料中添加 1 × 108 CFU/g T20 的实验组，进行为期 8 周的养殖实验。实验结果显示，饲料添加 T20 显著降低了大菱鲆 Edwardsiella tarda 攻毒后的死亡率，并且提高了大菱鲆肠道的抗氧化能力及消化酶活性，增强了肠道物理屏障功能。此外，T20 的添加显著改变了大菱鲆的肠道菌群结构，提高了肠道黏膜和肠道内容物中 Bacillus 和 B. velezensis 的相对丰度，降低了肠道内容物中潜在致病菌如，Mycoplasma、Staphylococcus 和 Weissella 等的相对丰度。综上所述，本研究表明，饲料中添加宿主来源的 Bacillus velezensis T20 可增强大菱鲆的抗病性，改善肠道菌群结构，促进肠道健康。

关键词：益生菌；抗病力；肠道健康；肠道菌群；大菱鲆

Host-associated *Bacillus velezensis* T20 improved disease resistance and intestinal health of juvenile turbot (*Scophthalmus maximus*)

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Abstract: The present study evaluates the probiotic potential of *Bacillus velezensis* T20 (T20) isolated from the intestine of turbot. In the experiment, turbots were fed with two diets: the control diet (CON) and CON supplemented with 1×10^8 CFU/g T20 for 8 weeks. Results showed that the addition of T20 significantly decreased the mortality of turbot challenged by *Edwardsiella tarda*. Moreover, T20 improved intestinal antioxidant capacity, physical barrier and digestive enzymes activities of turbot. In terms of intestinal microbiota, T20 modulated intestinal microbiota communities. Specifically, T20 increased the relative abundances of *Bacillus* and *B. velezensis* in both intestinal mucosa and digesta, and decreased potential pathogen such as *Mycoplasma*, *Staphylococcus* and *Weissella* in intestinal digesta. In conclusion, the present study showed that dietary *B. velezensis* T20 could enhance the disease resistance, improve the communities of intestinal microbiota and promote the intestinal health of turbot.

Key words: Probiotics; Disease resistance; Intestinal health; Intestinal microbiota; Turbot.

月桂酸单甘油酯对鲤肝细胞脂质代谢的影响

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摘要：为探究 GML 对鲤肝细胞脂质代谢的影响。实验以鲤原代肝细胞为研究对象，用油酸孵育 24 h 构建鲤离体高脂模型。设置 C 组（对照组）、HF 组（0.4 mmol/L OA, 24 h）、DMSO 组、HF 组含 0.1、0.2、0.4 mmol/L GML 组，并连续处理 3 h、6 h、12 h。结果表明，GML 对鲤脂肪肝细胞没有毒性， GML 处理 3 h 后，GML1 组显著降低脂肪肝细胞的 TG 含量。处理 12 h 后，GML 显著降低脂肪肝细胞的 AST 含量。GML 处理 3 h 后，GML1 组和 GML3 组脂肪肝细胞脂合成关键基因显著下调；GML 处理 6 h 和 12h 后，GML1 组和 GML3 组脂肪肝细胞脂分解关键基因显著上调。细胞油红 O 染色结果表明，GML 处理 3 h 后，可减轻脂肪肝细胞的脂质蓄积，且随着 GML 浓度的升高，脂质蓄积程度逐渐降低。综上，GML 的添加可以通过调节脂代谢相关基因的表达进而改善鲤肝细胞脂质代谢。

关键词：单月桂酸甘油酯；脂质代谢；鲤。

The effect of glycerol monolaurate on lipid metabolism of common carp hepatocytes

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Abstract: To investigate the effects of GML on lipid metabolism in common carp hepatocytes, this study utilized hepatocytes as the experimental model and induced an in vitro high-lipid condition using oleic acid. The experiment had a control (C), an OA group (HF, 0.4 mM, 24 h), a DMSO group, and HF groups with 0.1, 0.2, and 0.4 mM GML for 3 h, 6 h, and 12 h. The results indicated that GML was not toxic to fatty hepatocytes. Treatment for 3 h, the GML1 group could reduce the TG content. Treatment for 12 h, GML could reduce the AST content. Treatment for 3 h, the GML1 and GML3 groups downregulated the expression of key genes involved in lipid synthesis in fatty hepatocytes. Treatment for 6 h and 12 h, the GML1 and GML3 groups upregulated the expression of key genes involved in lipid degradation. Oil Red O staining indicated that after 3 h of GML treatment, lipid accumulation in fatty hepatocytes could be reduced. In summary, the addition of GML could enhance lipid metabolism in common carp hepatocytes by regulating the expression of genes related to lipid metabolism.

Key words: Glycerol monolaurate; lipid metabolism; Common carp.

肌酸通过促进 Mfn2 介导的线粒体融合来改善高脂对草鱼肝脏脂代谢的不良影响

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摘要：随着高脂饲料在水产饲料应用中日益增加，其对养殖动物的不利影响值得关注。肌酸是一种富有前景的绿色饲料添加剂，但关于其是否具有减轻高脂饲料负面影响的功能仍知之甚少。本研究旨在研究肌酸对高脂诱导的肝脂代谢紊乱和肌肉质量降低的缓解作用。采用三种实验饮食;对照组（5.20％脂质）,高脂组（8.11％脂质），肌酸组（8.11％脂质，2％肌酸）喂养草鱼 8 周。结果表明（1）肌酸能缓解高脂对草鱼生长性能和饲料利用效率的不良影响。（2）肌酸能改善高脂饲料喂养下的肌肉质量（3）肌酸通过增强肝脏 mfn2 介导的线粒体融合和β氧化缓解脂质沉积。此外本研究还发现肌酸通过 PPARα转录因子与 mfn2 基因启动子结合促进线粒体融合。本实验从多器官/组织角度结合线粒体动力学分析了肌酸在水产养殖中的营养价值。研究结果表明肌酸具有够缓解饲料中高脂对鱼类的不良影响的作用。

关键词：肌酸；草鱼；肝脂代谢；高脂饮食；线粒体融合

Creatine Ameliorates the Adverse Effects of High-Fat Diet on Hepatic Lipid Metabolism via Activating Mfn2-Mediated Mitochondrial Fusion in Juvenile Grass Carp

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Abstract: With the increasing prevalence of high-fat diets (HFD) in aquaculture practices, the detrimental effects of HFD on farmed fish have garnered significant attention. Creatine has emerged as a promising green feed additive for aquaculture species; however, its potential role in mitigating the negative impacts of HFD remains poorly understood. The present study was designed to investigate the protective effects of dietary creatine supplementation on HFD-induced hepatic lipid metabolism disorders and muscle quality deterioration in juvenile grass carp. The key findings of this study revealed that (1) Dietary creatine supplementation significantly ameliorated the adverse effects of HFD on growth performance and feed utilization efficiency in juvenile grass carp. (2) Creatine supplementation improved muscle quality parameters in juvenile grass carp. (3) Creatine attenuated hepatic lipid accumulation by enhancing β oxidation and mfn2-dependent mitochondrial fusion. Creatine also activates mitochondrial fusion through the binding of pparα transcription factor of Mfn2 gene promoter.

Key words: creatine, grass carp, hepatic lipid metabolism, high-fat diet, mitochondrial fusion

山茱萸提取物减轻盐碱胁迫对大口黑鲈氧化应激和脂质代谢的影响

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摘要：为缓解盐碱胁迫对大口黑鲈的不利影响，本研究在饲料中添加 0.5%山茱萸提取物（COE），设置 C、COE、S（8.5 ppt 盐度）、CA（15 mmol/L $NaHCO_3$）、SCOE 及 CAC 六组，养殖 60 d。结果显示：S 组血清 ALT、MDA 显著升高，T-AOC、SOD 显著降低（$P < 0.05$）；CA 组 SOD、T-AOC 下降（$P < 0.05$）。相比之下，SCOE 组血清 ALT、MDA 显著低于 S 组（$P < 0.05$），血清和鳃 SOD、肾 T-AOC 显著上调；CAC 组血清和肾 T-AOC、血清和肝 SOD、鳃 CAT 均显著高于 CA 组（$P < 0.05$）。脂代谢方面，S、CA 组血清 TG 显著低于 C 组（$P < 0.05$），CA 组肝 TG、TC 也降低；SCOE 组血清 TG 显著低于 S 组（$P < 0.05$）。综上，添加 0.5%COE 可提高盐碱胁迫下大口黑鲈的抗氧化能力，改善脂质代谢提供能量，缓解大口黑鲈的盐碱胁迫损伤。

关键词：大口黑鲈；山茱萸提取物；盐碱胁迫；氧化应激；脂质代谢

Cornus officinalis extract alleviated the effects of saline-alkali stress on oxidative stress and lipid metabolism in largemouth bass (*Micropterus salmoides*)

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Abstract: To mitigate the adverse effects of saline–alkaline stress on largemouth bass (*Micropterus salmoides*), six dietary groups were designed: basal diet (C), 0.5 % cornus officinalis extract (COE), 8.5 ppt salinity (S), 15 mmol L^{-1} $NaHCO_3$ (CA), salinity + COE (SCOE) and $NaHCO_3$ + COE (CAC). Fish were fed for 60 d. Compared with C, S and CA markedly elevated serum ALT and MDA, and reduced T-AOC and SOD activities ($P < 0.05$). COE supplementation reversed these trends: SCOE displayed lower ALT and MDA, and higher serum & gill SOD and kidney T-AOC than S ($P < 0.05$); CAC showed higher serum & kidney T-AOC, serum & liver SOD and gill CAT than CA ($P < 0.05$). Saline–alkaline stress decreased serum TG ($P < 0.05$), and CA also lowered hepatic TG and TC; SCOE further reduced serum TG versus S ($P < 0.05$). Dietary 0.5 % COE thus enhances antioxidant capacity, modulates lipid metabolism and alleviates saline–alkaline injury in largemouth bass.

Key words: *Micropterus salmoides*; Cornus Officinalis extract; saline-alkali stress; oxidative stress; lipid metabolism

Ism-1 与草鱼脂质代谢和蛋白质合成相关基因的关联分析

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摘要：为分析高脂饲喂下，脂肪细胞因子 *Isthmin-1*（Ism-1）对草鱼脂质代谢和蛋白质合成相关基因的影响，本研究通过 56 d 高脂饲料饲喂草鱼后采集肝胰脏、脂肪以及肌肉组织，检测三种组织中 *Ism-1* 以及脂质代谢和蛋白质合成相关基因的转录水平变化。结果发现，在脂质代谢方面，*Ism-1* 与肝胰脏、肌肉和脂肪组织的脂合成基因（*fas*、*pparγ*）表达水平呈负相关（$P < 0.05$），与肝胰脏和肌肉组织脂分解基因 lpl 表达水平呈负相关（$P < 0.05$），但与脂肪组织中 lpl 基因表达水平呈正相关（$P < 0.05$）。在蛋白质代谢方面，*Ism-1* 与肝胰脏和肌肉组织的蛋白质合成基因（pi3k、akt、mtor）表达水平呈正相关（$P < 0.05$），与蛋白质分解基因 foxo1a 表达水平呈负相关（$P < 0.05$）。综上，在高脂饲喂条件下，*Ism-1* 可能是调控草鱼脂质代谢和蛋白质合成的关键因子之一。

关键词：*Ism-1*；高脂饲喂；脂代谢；蛋白质代谢；相关性分析；草鱼

Correlation analysis between Ism-1 and lipid metabolism and protein metabolism genes in *Ctenopharyngodon idellus*

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Abstract: To investigate the effects of *Isthmin-1* (Ism-1) on lipid metabolism and protein synthesis-related genes in grass carp under high-fat feeding conditions, this study conducted a 56-day high-fat diet feeding trial. Following the experimental period, hepatopancreas(HP), adipose tissue, and muscle samples were collected, and analysis key genes involved in lipid metabolism and protein synthesis. The results showed that in terms of lipid metabolism, Ism-1 was negatively correlated with lipogenic genes (*fas*, *pparγ* in HP, muscle and adipose tissue ($P < 0.05$), and negatively correlated with lipolytic gene lpl in HP and muscle tissue ($P < 0.05$), but positively correlated with lpl in adipose tissue ($P < 0.05$). In terms of protein metabolism, Ism-1 was positively correlated with protein synthesis genes (*pi3k*, *akt*, *mtor)* in HP and muscle tissues ($P < 0.05$), and negatively correlated with protein decomposition gene foxo1a ($P < 0.05$). In summary, Ism-1 may be one of the key factors involved in the regulation of fat and protein metabolism in grass carp under high-fat feeding conditions.

Key words: I*sm-1*; High-fat diet; Metabolism; Synthesis; Correlation analysis; *Ctenopharyngodon idellus*

刺参肠道菌群组成特征及其与生长变化的关系

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摘要：刺参是中国重要的水产养殖物种之一，具有较高的营养和药用价值。然而，在其生长发育过程中普遍存在明显的个体生长差异。本研究从肠道微生物的角度出发，通过分析刺参肠道菌群组成、消化能力及代谢通路的差异，旨在揭示导致生长速率差异的内在机制。研究选取相同遗传背景和生长环境、但生长表现显著差异的个体，采集肠道组织进行16S rRNA测序分析。通过LEfSe分析发现，快速生长和慢速生长刺参的肠道微生物组成存在显著区别。快速生长组表现出更高的整体代谢活性，且体重与多个代谢通路呈显著正相关。快速生长刺参的消化能力明显增强。快速生长个体展现出更为复杂的代谢网络，涉及多种生物分子的合成与代谢途径。这些结果表明，刺参生长速率的差异主要与肠道菌群的功能活性有关，其可能在促进宿主生长中起到关键作用。了解微生物对生长的影响机制，不仅为解析生长变异的生物学基础提供了新视角，也为优化海参养殖策略提供了有益参考。

关键词：海参；肠道微生物群；增长变化；消化酶活性；代谢途径

Characterizing gut microbiota composition and its correlation with growth variation in sea cucumber *Apostichopus japonicus*

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Abstract: *Apostichopus japonicus* is one of the key aquaculture species in China, possessing high nutritional and medicinal value. Significant variations in growth are commonly observed among individuals during their development. This study investigates the differences in gut microbiota composition, digestive capacity, and metabolic pathways in A. japonicus, aiming to elucidate the underlying relations contributing to growth rate discrepancies from the perspective of gut microbiota. Intestinal tissues of the same family were collected for 16S rRNA sequencing analysis.Significant differences in gut microbiota were observed between fast- and slow-growing A. japonicus. The fast-growing group exhibited enhanced digestive capacity, a more complex microbial network structure, and higher overall metabolic activity, with body weight showing significant positive correlations with multiple metabolic pathways. These findings indicate that growth rate variation in sea cucumbers is primarily associated with functional activity of the gut microbiota, which likely plays a key role in promoting host growth.

Key words: Sea cucumber; Gut microbiota; Growth variation; Digestive enzyme activity; Metabolic pathways

PI3K-AKT 通路在低磷导致的花鲈肝脏脂肪沉积中的作用机制探究

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摘要：本研究旨在探究低磷通过 PI3K-AKT 信号通路调控花鲈肝脏脂代谢的分子机制。以磷酸二氢钠和磷酸氢二钾为磷源，分别配制低磷（0.38%，LP）和正常磷（0.75%，NP）饲料，养殖花鲈 63 天。结果表明，LP 组花鲈末均重、增重率显著低于 NP 组，肝体比、脏体比和腹脂率显著高于 NP 组。与 NP 组相比，LP 组花鲈血清总胆固醇、低密度脂蛋白含量和谷丙转氨酶和谷草转氨酶活性显著增加，空腹血糖和胰岛素水平显著升高，肝脏甘油三酯和总胆固醇显著增加，糖原含量及糖原合成酶活性显著降低。通过糖耐量和胰岛素耐量试验发现低磷饲料会诱导花鲈产生胰岛素抵抗。LP 组花鲈肝脏 PI3K-AKT 通路相关基因（*insr*、*pi3k*、*akt*）和蛋白（PI3K）表达均显著下调。综上，低磷饲料显著抑制花鲈生长，可能通过抑制 PI3K-AKT 通路表达，诱发肝脏胰岛素抵抗，并干扰多条脂肪代谢途径，最终导致肝脏脂肪异常沉积。

关键词：花鲈；磷；脂代谢；PI3K；肝脏

Study of the Mechanism of the PI3K-AKT Pathway in Liver Fat Deposition in *Lateolabrax maculatus* Induced by Low Phosphorus Diets

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Abstract: This study aims to investigate the molecular mechanism by which low phosphorus regulates lipid metabolism in the liver of spotted seabass (*Lateolabrax maculatus*) through the PI3K-AKT signaling pathway. Low-phosphorus (0.38%, LP) and normal-phosphorus (0.75%, NP) diets were formulated, and the fish were cultured for 63 days. The WGR of the LP group were significantly lower than those of the NP group, while the HSI, VSI, and AFR were significantly higher. Compared with the NP group, the LP group exhibited significantly increased serum TC, LDL, as well as elevated ALT and AST activities. The LP diet induced insulin resistance in spotted seabass. The expression of PI3K-AKT pathway-related genes (*insr*, *pi3k*, *akt*) and protein (PI3K) in the liver of the LP group was significantly downregulated. In conclusion, the LP diet significantly inhibited the growth of spotted seabass, likely by suppressing the PI3K-AKT pathway expression, inducing hepatic insulin resistance, and disrupting multiple lipid metabolism pathways, ultimately leading to abnormal lipid deposition in the liver.

Key words: *Lateolabrax maculatus*; phosphorus; lipid metabolism; PI3K; liver

烟酰胺通过 SIRT1 /PGC-1α改善高淀粉饲喂鲤的肝胰脏损伤和糖脂代谢紊乱

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摘要：本研究旨在探究烟酰胺（NAM）对高淀粉日粮诱导的鲤肝胰损伤和糖脂代谢紊乱的改善及其机制。选用 270 尾鲤，随机分为 3 组，分别饲喂正常日粮（NSD）、高淀粉日粮（HSD）和添加 30mg/kg 烟酰胺的高淀粉（HSD+NAM），持续 8 周。结果显示，烟酰胺显著降低血清及肝胰脏中的总胆固醇（TC）和甘油三酯（TG）含量，降低血清丙氨酸氨基转移酶（ALT）活性，改善肝脏损伤。此外。还提高血清中谷胱甘肽（GSH）活性并降低了丙二醛（MDA）含量，从而增强机体的抗氧化能力。此外，烟酰胺还提高了 NAD^+含量，促进了线粒体生物发生（pgc-1α、nrf-1、tfam、cox-1 和 cox-2）、糖酵解（gk）和脂肪分解（hsl、pparα、acaa1、acaa2 和 cpt-1）相关基因的表达，从而改善糖脂代谢过程。通过促进 SIRT1/PGC-1α通路的表达，改善高淀粉日粮引起的肝胰脏损伤和糖脂代谢紊乱。

关键词：烟酰胺；高淀粉日粮；糖脂代谢；肝胰脏损伤；鲤

Nicotinamide ameliorates hepatopancreatic injury and dysregulation of glucose and lipid metabolism in high-starch-fed carp via SIRT1/PGC-1α

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Abstract: This experiment investigates the effects of nicotinamide (NAM) on lipid metabolism disorders and liver damage in carp caused by high-starch diets. A total of 270 carp were divided into three groups: a normal starch diet (NSD), a high-starch diet (HSD), and a high-starch diet supplemented with 30 mg/kg of NAM (HSD+NAM) for 8 weeks. Results showed that NAM significantly reduced total cholesterol (TC) and triglycerides (TG) levels in serum and liver, lowered serum alanine aminotransferase (ALT) activity, and improved liver damage. It increased glutathione (GSH) activity while decreasing malondialdehyde (MDA) levels, enhancing antioxidant capacity. Additionally, NAM raised NAD^+ levels and promoted the expression of genes related to mitochondrial biogenesis (pgc-1α, nrf-1, tfam, cox-1, and cox-2), glycolysis (gk), and lipolysis(hsl, pparα, acaa1, acaa2, and cpt-1), improving energy metabolism and ameliorating liver cell injury and lipid disorders from high-starch diets.

Key words: Nicotinamide; High-starch diet; Glycolipid metabolism; Hepatopancreatic injury; Common carp (*Cyprinus carpio*)

白鲫、禾花乌鲤及杂交 F1 的肌肉营养成分分析及品质评价

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摘要：通过对白鲫、禾花乌鲤及杂交 F1 背部肌肉的营养成分进行分析和品质评价，结果显示，杂交 F1 肌肉蛋白质含量、脂肪酸总量、饱和脂肪酸（SFA）中的 C16：0（棕榈酸）含量及多不饱和脂肪酸（PUFA）中的 C18：1n-9c（油酸）含量均高于白鲫而低于禾花乌鲤，杂交 F1 肌肉中氨基酸总量、8 种人体必需氨基酸总量及多不饱和脂肪酸（PUFA）中的 C18：2n-6c（亚油酸）含量明显高于白鲫和禾花乌鲤，鲜味氨基酸总量低于白鲫而高于禾花乌鲤，DHA 的含量却低于白鲫和禾花乌鲤。可见，杂交 F1 肌肉营养成分相比白鲫得到了明显的提升和改良，而禾花乌鲤在该杂交 F1 品质改良方面具有明显效应，显著提高了其肌肉的营养品质。

关键词：白鲫；禾花乌鲤；杂交 F1；肌肉营养成分；品质评价

Analysis of Nutritional Composition and Quality Evaluation of Muscle Tissue in White Crucian Carp, Black Carp, and Their F1 Hybrid

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Abstract: The nutritional composition of dorsal muscle tissues from white crucian carp, Hehua black carp, and their F1 hybrid was analyzed and evaluated. The results revealed that the protein content, total fatty acid content, and the levels of palmitic acid (C16:0) among saturated fatty acids, as well as oleic acid (C18:1n-9c), in the F1 hybrid were higher than those in white crucian carp but lower than those in Hehua black carp. Notably, the total amino acid content, the cumulative amount of eight essential amino acids, and the linoleic acid (C18:2n-6c) content in the hybrid F1 muscle were significantly elevated compared to both parent species. The total umami amino acid content in the hybrid was lower than that of white crucian carp yet surpassed that of Hehua black carp. However, the DHA content in the hybrid was inferior to that of both parent species. These findings suggest that the nutritional profile of hybrid F1 muscle has been markedly enhanced relative to white crucian carp, with Hehua black carp contributing significantly to the quality improvement of the hybrid, thereby elevating

Key words: white crucian carp; Hehua black carp; F1 hybrid; muscle nutrition; quality assessment

基于 KEGG 通路富集与胆汁酸谱解析揭示金雀异黄素对黄河鲤胆汁酸代谢的调控作用

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摘要：胆汁酸代谢谱变化与多种代谢性疾病的发生密切相关。为探究金雀异黄素对鲤肝胰脏胆汁酸代谢谱的影响，本研究以 85.50 ± 0.67 g 黄河鲤为实验对象，设置高脂组（HF）及药物添加组（HG， HF + 500 mg/kg 金雀异黄素），进行 9 周养殖实验。多变量统计分析显示，与 HF 组相比，HG 组胆汁酸代谢谱发生明显重塑。鉴定出 16 种具有显著差异的胆汁酸代谢物，其中 βGCA 和 ILCA 在 HG 组中含量显著上升，而 TCA、Ta-MCA、CDCA-3Gln、TCDCA、LCA、CA、CDCA-3S、coproCA、TLCA-3S 及 Tω-MCA 含量均显著降低。KEGG 通路富集分析表明，HG 组中胆汁酸及相关有机酸代谢水平发生显著变化，尤其是牛磺胆酸盐结合型胆汁酸含量明显下降。综上所述，金雀异黄素能够重塑高脂饲料诱导的黄河鲤肝胰脏胆汁酸代谢谱，并影响胆汁酸代谢相关代谢通路。

关键词：黄河鲤；KEGG 通路富集；胆汁酸谱；金雀异黄素

Integration of KEGG pathway enrichment and bile acid profiling reveals the regulatory effect of genistein on bile acid metabolism in *Cyprinus carpio*

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Abstract: Alterations in bile acid metabolism are closely linked to the development of various metabolic disorders. A 9-week study on Yellow River carp (85.50 ± 0.67 g) fed a high-fat diet (HF) or HF plus 500 mg/kg genistein (HG) showed that genistein significantly reshaped the hepatopancreatic BA profile. Multivariate analysis revealed a significant restructuring of the bile acid metabolism profile in the HG group compared to the HF group. Sixteen bile acid metabolites were identified, with notable increases in βGCA and ILCA in the HG group, and significant decreases in TCA, Ta-MCA, CDCA-3Gln, TCDCA, LCA, CA, CDCA-3S, coproCA, TLCA-3S, and Tω-MCA. KEGG pathway enrichment analysis demonstrated substantial alterations in bile acid and related organic acid metabolism in the HG group, particularly a marked reduction in taurocholate-conjugated bile acids. In summary, genistein was found to reshape the bile acid metabolism profile in the hepatopancreas of Cyprinus carpio exposed to a high-fat diet, impacting pathways associated with bile acid metabolism.

Key words: Yellow River carp; KEGG pathway enrichment analysis; Bile acid profile; Genistein

饲料来源对养殖拟穴青蟹营养组成的影响研究

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摘要：取体重相近的蟹，分成两组，分别饲喂配合饲料和冰鲜鱼，试验周期42d，试验期后分离其肌肉和性腺，测定肌肉和性腺营养成份。结果表明：饲料组和冰鲜鱼组的肌肉和性腺的基本营养成分之间有不同程度的差异。饲料组肌肉中总氨基酸（TAA）、必需氨基酸(EAA)和呈味氨基酸（FAA）总量、异亮氨酸和缬氨酸的氨基酸评分（AAS）均显著高于冰鲜鱼组（$P<0.05$）。饲料组肌肉必需氨基酸指数（EAAI）高于冰鲜鱼组。饲料组性腺异亮氨酸、亮氨酸AAS评分和异亮氨酸、亮氨酸、CS评分低于冰鲜鱼组；EAAI指数高于冰鲜鱼组。饲料组肌肉DHA、EPA、n6-PUFA及n3-PUFA比例均显著高于冰鲜鱼组（$P<0.05$），性腺中DHA显著高于冰鲜鱼组、EPA显著低于冰鲜鱼组（$P<0.05$）。综上所述，饲料组肌肉和性腺的EAAI指数高，其蛋白质品质较高，说明饲料组成对拟穴青蟹的品质影响显著，可通过调整饲料配方提高青蟹的品质。

关键词：拟穴青蟹；饲料来源；肌肉；性腺；营养组成

Effects of Different Diets on Nutrient Composition of *Scylla paramammosain*

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Abstract: *Scylla paramammosain* with similar body weights were divided into two groups fed with formulated feed and frozen fish respectively for 42 days. After the experiment, muscles and gonads were separated. The components of the muscles and gonads were measured. The results showed that there were varying degrees of differences in the components of the muscles and gonads between the two groups. The total amino acid (TAA), essential amino acid (EAA), and flavor amino acid (FAA) in the muscles of the feed group were higher than those in frozen fish group ($P<0.05$). The essential amino acid index (EAAI) of the muscles in feed group was higher than that in frozen fish group. The proportions of DHA, EPA, n6-PUFA, and n3-PUFA in the muscles of feed group were higher than those in frozen fish group ($P<0.05$), while the DHA in the gonads was higher and the EPA was lower than that in frozen fish group ($P<0.05$). In sum, the results suggest that the composition of feed has a significant impact on the quality of crabs, and the quality of crabs can be improved by adjusting the feed formula.

Key words: *Scylla paramammosain*; different bait; muscle; gonad; nutritional composition

急性盐碱胁迫下大口黑鲈的耐受性以及血清生理响应

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摘要：本研究以大口黑鲈（*Micropterus salmoides*，56.30±0.64 g）为对象，通过 96 h 急性胁迫实验，分析其盐（0-20 ppt NaCl）/碱（0-40 mmol/L 碱度 $NaHCO_3$）耐受性，测定血清脂代谢、免疫酶及抗氧化指标，结合存活率评估阈值。结果显示，急性盐胁迫下其耐受范围为 0～10ppt，与淡水组相比，血清中低密度脂蛋白胆固醇（LDL-C）、高密度脂蛋白胆固醇（HDL-C）含量，酸性磷酸酶（ACP）、天门冬氨酸氨基转移酶（AST）及总抗氧化能力（T-AOC）显著升高（$P<0.05$）。与淡水组相比，高浓度碱胁迫（20mmol/L）较低浓度组 HDL-C 含量和 AKP 活性显著升高（$P<0.05$）。结果表明，急性盐胁迫显著影响大口黑鲈的脂质利用，并诱导急性肝损伤、刺激抗氧化系统；急性碱胁迫改善肝损伤并提高免疫酶活性。为大口黑鲈盐碱水养殖的耐受阈值提供理论参考。

关键词：大口黑鲈；急性盐胁迫；急性碱胁迫；耐受性；生化指标

Tolerance and Serum Physiological Responses of Micropterus salmoides Under Acute Saline-alkali Stress

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Abstract: The study investigated the tolerance thresholds of *Micropterus salmoides*(56.30 ± 0.64 g) under acute salt (0–20 ppt NaCl) and alkali (0–40 mmol/L $NaHCO_3$) stress over 96 hours. Serum lipid metabolism markers, immune enzymes, and antioxidant capacity were measured, alongside survival rates, to evaluate stress responses. Results showed that under acute salinity stress, the tolerance range was 0–10 ppt. Compared with the freshwater group, serum levels of LDL-C, HDL-C, ACP, AST, and T-AOC were significantly elevated. Compared with the freshwater group, high-concentration alkalinity stress significantly increased HDL-C levels and AKP activity compared to lower concentrations. These findings indicate that acute salinity stress significantly alters lipid metabolism, induces acute liver injury, and activates the antioxidant system in largemouth bass. In contrast, acute alkalinity stress mitigates liver damage and enhances immune enzyme activity. This study provides a theoretical reference for tolerance thresholds in saline-alkaline aquaculture of *Micropterus salmoides*.

Key words: *Micropterus salmoides*; Acute salt stress; Acute alkali stress; Survival rate; Biochemical indicators

雨生红球藻源虾青素微胶囊对黄河鲤生长、抗氧化系统及肌肉品质的影响研究

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摘要：为进一步验证虾青素微胶囊对黄河鲤（*Cyprinus carpio*）生长、生理和营养价值的影响以及对微胶囊技术在水产养殖中的可行性和安全性进行评估，本实验采用微囊技术包埋藻源天然虾青素和合成虾青素，空微囊为对照，配合普通饲料对黄河鲤进行连续 6 周的投喂试验，并对其生长、肌肉品质和抗氧化系统进行评价。研究结果表明：（1）天然虾青素组和人工合成虾青素组的增重率、特定生长率和肥满度显著高于对照组（$P < 0.05$）；（2）添加虾青素增强了黄河鲤肝胰脏组织的抗氧化水平，总过氧化物歧化酶活性显著提高（$P < 0.05$），肝胰脏组织丙二醛含量显著降低（$P < 0.05$）；（3）添加虾青素使肌肉营养品质更好，具体体现在肌肉粗蛋白含量显著升高、粗灰分含量显著降低（$P < 0.05$）、肌肉持水性能增强等方面。整体看来，本研究进一步揭示天然源优于合成虾青素，且初步证明自制虾青素微囊在水产养殖中的生物安全性。

关键词：虾青素，微囊，鲤，抗氧化，生物安全

Effects of astaxanthin microencapsulated from *Haematococcus pluvialis* on the growth, muscle quality, antioxidant system, and related gene expression of *Cyprinus carpio*

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Abstract: In order to further verify the influence of astaxanthin microcapsules on the growth, physiology and nutritional value of Yellow River Carp, and to evaluate the feasibility and safety of microencapsulation technology in aquaculture, this experiment used microencapsulation technology to embed natural astaxanthin and synthetic astaxanthin from algae, and used empty microcapsules as control and common feed to feed Yellow River Carp for 6 weeks, and evaluated its growth, muscle quality and antioxidant system. The results show that the natural astaxanthin group has great advantages in growth, antioxidant performance and muscle nutritional quality. On the whole, this study further reveals that natural sources are superior to synthetic astaxanthin, and preliminarily proves the biological safety of self-made astaxanthin microcapsules in aquaculture, which provides reference for green aquaculture.

Key words: Astaxanthin, Microcapsules , *Cyprinus carpio*, Antioxidant, Biosafety

基于组学测序分析大口黑鲈嗅觉响应的分子机制

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摘要：为开发大口黑鲈高效环保诱食剂并解析其嗅觉响应机制，本研究先通过体视显微镜、HE 染色及电镜观察其嗅囊表型，再经触球与行为轨迹实验筛选诱食剂，最后结合转录组及 miRNA 测序揭示分子机制。结果显示：大口黑鲈嗅囊呈 F 型辐射状排列，嗅觉上皮分布纤毛与微绒毛神经元；摇蚊幼虫和醋糟均能显著诱发其趋向行为，但作用机制存在差异。摇蚊幼虫主要激活经典嗅觉转导通路，同时显著下调免疫应答、免疫球蛋白复合物等免疫相关通路，推测机体通过资源重分配优先支持摄食行为；值得注意的是，醋糟虽富集免疫识别通路，但整体免疫反应却被抑制。这提示其或作为一种警示性气味，机体通过主动抑制免疫消耗来优化能量配置，旨在优先保障探索与趋食行为。本研究明确了两种诱食剂的诱食效果及分子机制差异，为解析鱼类嗅觉响应机制及大口黑鲈高效诱食剂开发提供数据支持与理论基础。

关键词：大口黑鲈；嗅囊；诱食剂；行为反应；转录组测序；miRNA 测序

Analysis of the Molecular Mechanism of Olfactory Response in Largemouth Bass (*Micropterus salmoides*) Based on Omics Sequencing

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Abstract: To develop efficient and environmentally friendly attractants for largemouth bass (*Micropterus salmoides*) and elucidate its olfactory response mechanism, this study began by examining the olfactory sac phenotype using stereomicroscopy, HE staining, and electron microscopy. Attractants were then screened through a touching-ball test and behavioral trajectory experiments, followed by integrated transcriptome and miRNA sequencing to reveal the molecular mechanisms. The results showed that the olfactory sac of largemouth bass exhibits an F-type radial arrangement, with the olfactory epithelium containing both ciliated and microvillus neurons. Both chironomid larvae and vinegar residue significantly induced attractive behaviors, albeit through distinct mechanisms. Chironomid larvae primarily activated classical olfactory transduction pathways while significantly downregulating immune-related pathways such as immune response and immunoglobulin complexes, suggesting that the organism reallocates resources to prioritize feeding behavior. Notably, although vinegar residue enriched immune recognition pathways, the overall immune response was suppressed. This indicates that vinegar residue may function as a ‘warning’ odor, prompting the organism to actively suppress immune expenditure to optimize energy allocation, thereby prioritizing exploratory and foraging behaviors. This study clarifies the attractant effects and differential molecular mechanisms of the two attractants, providing data support and a theoretical foundation for understanding the olfactory perception mechanisms in fish and developing efficient attractants for largemouth bass.

Keywords: Largemouth bass; Olfactory sac; Attractant; Behavioral response; Transcriptome sequencing; miRNA sequencing

黄芪多糖通过调控糖脂代谢基因与肠道微生物改善鲤生长性能、抗氧化能力、肌肉营养及糖脂蓄积

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摘要：为探究黄芪多糖（Astragalus polysaccharides, APS）对鲤生长、糖脂代谢及肠道健康的调控作用。本研究以鲤为对象，设置对照组（C）、高糖组（HG）、高脂组（HF）、高糖高脂组（HGHF），及上述高能量饲料组分别添加 0.15%APS 干预组，开展 8 周的养殖试验。结果显示，添加 APS 可显著增强鲤抗氧化能力，降低肝胰脏和肌肉中的糖脂蓄积，恢复肝肠健康。同时，APS 通过优化肌肉中必需氨基酸、呈味氨基酸及多不饱和脂肪酸的组成，提升肌肉品质。在分子机制上，APS 上调多组织中糖脂代谢关键基因的表达，提升鲤代谢能力。此外，高糖高脂饲料降低肠道菌群多样性，增加有害菌，减少有益菌；APS 显著恢复菌群平衡。相关性分析表明，有益菌的丰度与糖脂代谢基因、抗氧化能力关键指标协同上调，与生长性能、糖脂蓄积呈负相关；而有害菌则呈相反的趋势。综上，黄芪多糖可作为一种高效、绿色的饲料添加剂应用于鲤养殖。

关键词：鲤；黄芪多糖；高糖高脂；糖脂代谢；肠道微生物

Astragalus polysaccharides improve the growth performance, antioxidant capacity, muscle nutrition and accumulation of glycogen and lipid in common carp by regulating the genes of glycolipid metabolism and intestinal microbiota

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Abstract: To investigate how Astragalus polysaccharides (APS) regulate growth, glucose-lipid metabolism, and intestinal health in common carp, an 8-week trial used seven groups: control (C), high glucose (HG), high fat (HF), high glucose+high fat (HGHF), and corresponding APS-added groups (HG/HF/HGHF + 0.15% APS). Results showed APS improved antioxidant capacity, reduced glycogen and lipid deposition in hepatopancreas/muscle, restore liver and intestinal health. It also improves muscle quality by optimizing the composition of essential amino acids, flavor amino acids, and polyunsaturated fatty acids in the muscles. APS also up-regulated key glucose-lipid metabolic genes across tissues. High-energy diets reduced intestinal microbial diversity, enriched harmful bacteria, and suppressed beneficial ones; APS effectively restored the gut microbiota balance. Beneficial bacteria correlated positively with metabolic genes and antioxidant activity but negatively with growth and fat accumulation—the opposite for harmful bacteria. Thus, APS is a green scientific feed additive used for carp farming.

Key words: Common carp; Astragalus polysaccharides (APS); High-glucose-high-fat; Glycolipid metabolism; Gut microbiota

脯氨酸通过 *c-Jun*/Claudin3 途径缓解中华鳖肠道紧密连接损伤的分子机制

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摘要：通过营养调控提高紧密连接完整性已成为水产动物肠道损伤防治的有效途径。本研究发现嗜水气单胞菌感染会造成中华鳖肠道/肠上皮细胞氧化应激和紧密连接功能障碍。为验证脯氨酸对肠道紧密连接损伤的缓解作用，设计 6 种脯氨酸梯度饲料，投喂中华鳖 8 周后进行应激处理。结果显示，适宜水平的脯氨酸补充（1.21%）显著缓解了应激处理造成的中华鳖肠道微绒毛、隐窝和紧密连接结构损伤，抑制了紧密连接蛋白的表达。转录组分析发现，脯氨酸补充激活了 *c-Jun* 的转录表达，基因和蛋白表达分析也证实了这一结果。进一步基于中华鳖肠上皮细胞损伤模型进行体外验证，发现脯氨酸孵育显著提高了 *c-Jun* 和 Claudin3 的表达，降低了细胞 ROS 含量和晚凋细胞比例。沉默 *c-Jun* 后，脯氨酸对 Claudin3 的调控作用及紧密连接结构的修复作用均被阻断。综上所述，本研究阐明脯氨酸能通过 *c-Jun*/Claudin3 途径挽救中华鳖肠道紧密连接损伤。

关键词：脯氨酸；中华鳖；肠道；紧密连接

*Proline through c-Jun/*Claudin3 *pathway to mitigate intestinal tight junction injury in Pelodiscus sinensis*

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Abstract: Aeromonas hydrophila infection has been found to induce oxidative stress and disrupt tight junction function in the intestinal epithelium of Chinese soft-shelled turtle (Pelodiscus sinensis). Nutritional intervention through proline supplementation has emerged as a promising strategy to enhance tight junction integrity in aquatic animals. In this study, we investigated the protective effect of dietary proline on intestinal barrier injury. Six experimental diets with graded levels of proline were formulated and fed to turtles for eight weeks, followed by stress challenge. The results showed that appropriate proline supplementation (1.21%) significantly alleviated stress-induced damage to intestinal microvilli, crypts, and tight junction structures, while also suppressing the expression of tight junction proteins. Transcriptomic analysis revealed that proline supplementation activated the transcription of c-Jun. Both mRNA and protein expression analyses confirmed this upregulation. Further in vitro validation using an intestinal epithelial cell injury model demonstrated that proline treatment markedly increased the expression of c-Jun and Claudin3, reduced intracellular ROS levels, and decreased the proportion of late apoptotic cells. However, siRNA-mediated knockdown of c-Jun abolished the regulatory effects of proline on Claudin3 expression and disrupted the restoration of tight junction structure. In conclusion, our findings demonstrate that proline ameliorates intestinal tight junction injury in Pelodiscus sinensis via the c-Jun/Claudin3 signaling pathway.

Key words: Proline; *Pelodiscus sinensis*; Intestine; Tight junction

长期高温胁迫诱导花鲈疏水性胆汁酸蓄积及肠道损伤

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摘要：本研究探讨长期高温胁迫对花鲈胆汁酸代谢及肠道健康的影响。实验分为常温组（27℃，NT）和高温组（35℃，HT），处理 28 天。结果显示，HT 组肠道形态受损，杯状细胞和黏液减少，血清二胺氧化酶活力和脂多糖含量显著上升，*muc2* 基因表达下降，表明肠道通透性增加。同时，促炎因子 il-1β和 tnf-α表达上调，而 tgf-β表达抑制，证实炎症发生。高温还使肠道胆汁酸总量、次级胆汁酸及疏水性胆汁酸水平显著上升，共鉴定出 9 种显著上升的差异胆汁酸，多为 CA、CDCA 及其微生物代谢产物，其中次级疏水性胆汁酸 7-ketoDCA 出现多组织蓄积。结果表明，长期高温诱发花鲈肠道通透性增加和炎症反应，并与胆汁酸代谢紊乱及毒性胆汁酸积累密切相关。

关键词：花鲈；高温胁迫；胆汁酸代谢；肠道健康；7-ketoDCA

Long-term high temperature stress leads to the accumulation of hydrophobic bile acids and intestinal injury in *Spotted seabass* (*Lateolabrax maculatus*)

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Abstract: This study investigates the effects of long-term high-temperature stress on bile acid metabolism and intestinal health in *Spotted seabass*. Fish were exposed to normal (27°C, NT) or high temperature (35°C, HT) for 28 days. Results showed intestinal damage, reduced goblet cells and mucus, increased serum diamine oxidase activity and lipopolysaccharide, and decreased muc2 expression in the HT group, indicating elevated gut permeability. Pro-inflammatory genes (il-1β, tnf-α) were upregulated, while tgf-β was suppressed, confirming inflammation. HT also increased total bile acids, secondary and hydrophobic bile acids, with nine differentially accumulated bile acids identified—mostly CA, CDCA and microbial metabolites—including multi-tissue accumulation of the hydrophobic secondary bile acid 7-ketoDCA. Overall, long-term heat stress induces intestinal barrier dysfunction and inflammation, linked to dysregulated bile acid metabolism and toxic bile acid accumulation.

Key words: *Lateolabrax maculatus*, High temperature stress, Bile acid metabolism, Intestinal health, 7-ketoDCA

肌醇通过调控 *Sel1l* 抑制内质网应激以干预 LPS 诱导的中华鳖肠道紧密连接功能障碍

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摘要：本研究通过腹腔注射 LPS 建立中华鳖肠道损伤模型，发现 LPS 应激可导致中华鳖肠道出现明显的组织病理学损伤，包括微绒毛脱落、紧密连接结构破坏，并伴随 Claudin-1、Occludin 及其调控蛋白 MYLK 的 mRNA 和蛋白表达显著下调。超微结构分析显示内质网发生明显肿胀和碎片化，内质网应激关键基因表达上调，而 *Sel1l* 蛋白表达被抑制。4-PBA 抑制实验证实内质网应激是 LPS 诱发紧密连接功能障碍的重要机制。非靶向代谢组学结果显示，LPS 应激后肠道肌醇含量显著降低，KEGG 分析提示肌醇代谢通路被激活，基因表达分析进一步表明肌醇分解代谢增强、合成代谢减弱。在饲料中补充肌醇后，LPS 应激中华鳖的肠道微绒毛形态和紧密连接结构均得到明显改善。结果表明，LPS 应激通过激活肌醇分解代谢导致肠道肌醇耗竭，进而诱发内质网应激和肠道屏障功能损伤，而外源性肌醇补充可通过缓解内质网应激有效保护中华鳖肠道健康。

关键词：肌醇；中华鳖；肠道；紧密连接

Myo-inositol alleviates LPS-induced intestinal tight junction dysfunction in soft-shelled turtle (Pelodiscus sinensis) by suppressing endoplasmic reticulum stress through the regulation of *Sel11*

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Abstract: This study established a Chinese soft-shelled turtle intestinal injury model via LPS injection. LPS induced severe intestinal damage, including microvilli loss and tight junction disruption, along with downregulated expression of Claudin-1, Occludin and MYLK. Ultrastructural analysis revealed endoplasmic reticulum (ER) swelling and fragmentation, accompanied by *Sel1l* suppression. 4-PBA inhibition assays confirmed ER stress as a key mechanism underlying tight junction dysfunction. Metabolomics showed decreased myo-inositol levels after LPS challenge, with KEGG enrichment indicating activated inositol metabolism pathways. Gene expression analysis further demonstrated enhanced inositol catabolism but impaired anabolism. Dietary myo-inositol supplementation markedly ameliorated intestinal damage and improved barrier integrity. These findings suggest that LPS stress triggers inositol depletion through activated catabolism, leading to ER stress-induced barrier dysfunction, while exogenous myo-inositol protects intestinal health by alleviating ER stress.

Key words: Inositol; *Pelodiscus sinensis*; Intestine; Tight junction

一株鳜鱼源植物乳杆菌的筛选及其应用研究

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摘要：从鳜鱼肠道中筛选出一株植物乳杆菌，具有无溶血性、耐低氧、抗药谱广等优点。为研究在饲料中添加植物乳杆菌对鳜鱼生长性能与代谢的影响，选择体重（10.96±0.7）g 的鳜鱼，随机分为 2 组。对照组（C 组）饲喂基础饲料，试验组在基础饲料中按照 1×108CFU/g 植物乳杆菌（LP 组）进行添加，试验期 56d。结果显示：生长指标上，LP 组增重率和特定生长率显著高于 C 组。全鱼基本营养成分，LP 组粗脂肪显著低于 C 组。肝脏组织形态学与肝脏抗氧化酶显示 LP 组 SOD 和 CAT 酶活水平显著高于 C 组，肝脏损伤程度显著低于 C 组。肠道消化酶结果显示，LP 组脂肪酶活性显著高于 C 组。在肠道菌群结构方面，植物乳杆菌成功定植，肠道菌群的优势菌属结构发生重塑，乳酸乳球菌等有益菌含丰度上调。上述结果表明在饲料中添加植物乳杆菌可提高消化酶活力，提升抗氧化能力，丰富肠道菌群结构多样性，最终提升鳜鱼生长表现。

关键词：植物乳杆菌；鳜鱼；生长性能；抗氧化；肠道菌群

Screening and Application of a Strain of *Lactiplantibacillus plantarum* Derived from *Siniperca chuatsi*

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Abstract: A strain of *Lactobacillus plantarum* was isolated from the intestinal tract of the *Siniperca chuatsi*. To study the effects of *Lactobacillus plantarum* on the growth performance and metabolism of *Siniperca chuatsi*, all fish were randomly divided into two groups. The control group (C) was fed with the basal diet, while the experimental group was supplemented with 1×108 CFU/g *Lactobacillus plantarum* (LP). The results showed that compared with C group, LP group significantly increased weight gain rate and specific growth rate, SOD and CAT enzyme activity levels, and lipase activity, and significantly decreased crude fat content. In terms of the intestinal flora structure, the structure of the dominant bacterial genus in the intestinal flora was reshaped. The abundances of beneficial bacteria such as *Lactobacillus plantarum* and *Lactococcus lactis* increased. These results indicate that adding *Lactobacillus plantarum* to the feed can enhance digestive enzyme activity, improve antioxidant capacity, enrich the diversity of intestinal flora structure, and ultimately improve the growth performance.

Key words: *Lactiplantibacillus plantarum*; *Siniperca chuatsi*; growth performance; antioxidant activity; *intestinal microbiota*

P-AKK 及重组 *Amuc_1100* 乳酸菌对大口黑鲈糖脂代谢的调控作用

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摘要：鱼类对糖耐受性差，长期高糖饲料易引发代谢紊乱与免疫损伤。阿克曼菌外膜蛋白 *Amuc_1100* 可调节宿主糖脂代谢与免疫功能。本研究构建自分泌 *Amuc_1100* 菌株 Am-MG1363。在大口黑鲈中进行 8 周养殖实验验证 Am-MG1363 对其糖脂代谢及免疫调控作用。结果显示，Am-MG1363 上调血清中胰岛素和 HDL-C，下调 GSP、TG、TC 和 LDL-C 水平，减轻肝脏糖原和脂肪堆积。Am-MG1363 下调 *pepck*、*fas* 和 *acc-α*的水平，上调 *hsl* 和 *lpl* 的水平。Am-MG1363 下调大口黑鲈肠道中 *caspase3* 和 *caspase9* 的水平，上调 *occludin* 和 *zo-1* 的水平，增强肠道屏障功能；并下调肠道中促炎因子 *tnf-α*和 *il-8* 的表达，上调抗炎基因 *il-10* 的水平，减轻肠道炎症。添加 Am-MG1363 显著增加厚壁菌门的丰度。综上，Am-MG1363 有效缓解大口黑鲈代谢紊乱并增强肠道屏障。

关键词：大口黑鲈；*Amuc_1100*；糖脂代谢；重组乳酸菌

Regulation of recombinant *Amuc_1100* lactic acid bacteria on glucose and lipid metabolism in largemouth bass

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Abstract: Fish exhibit poor glucose tolerance, high-carbohydrate diets lead to metabolic disorders and immune impairment. Akk outer membrane protein *Amuc_1100* has been shown to modulate host metabolism and immune function. In this study, *Lactococcus lactis* MG1363 was used autonomously to secrete *Amuc_1100*, generating recombinant strain Am-MG1363. 8-week feeding trial was conducted on largemouth bass. The effects of Am-MG1363 on metabolism and immunity were evaluated. Am-MG1363 significantly increased serum insulin and HDL-C levels while reducing GSP, TG, TC, and LDL-C. It attenuated hepatic glycogen and lipid accumulation. Am-MG1363 decreased expression of *pepck*, *fas*, and *acc-α*, while increasing *hsl* and *lpl*. Am-MG1363 administration suppressed the expression of *caspase3*, *caspase9* and elevated *occludin*, *zo-1*. It reduced *tnf-α*, *il-8* and enhanced *il-10* levels. 16S rRNA sequencing revealed that Am-MG1363 increased abundance of Firmicute. Am-MG1363 alleviates high-carbohydrate-induced metabolic dysregulation, enhances intestinal barrier function, attenuates inflammation in largemouth bass.

Key words: Largemouth bass; *Amuc_1100*; Glucose and lipid metabolism; Recombinant lactic acid bacteria

工厂化循环水养殖模式下不同养殖密度对 5-25g 牛蛙生长性能及肝脏健康的影响

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摘要：本研究旨在探究循环水系统中 5g-25g 牛蛙(*Aquarana catesbeianus*)幼蛙的适宜养殖密度。实验设置 200、300、400、500 和 600 只/m²五个密度组，测定生长性能、应激、免疫及肝脏健康等指标。结果表明，300 只/m²和 400 只/m²组的生长性能显著高于其他组。消化酶活性方面，400 只/m²组淀粉酶活性显著高于 500 和 600 只/m²组；400 和 200 只/m²组蛋白酶活性显著高于 600 只/m²组；300 只/m²组脂肪酶活性显著高于 200、500 和 600 只/m²组。肝脏健康方面，200–400 只/m²组肝细胞结构正常，血清 ALT、AST 和 TG 水平最低，肝脏过氧化氢酶（CAT）活性和总抗氧化能力（T-AOC）均显著高于高密度组。综上，在工厂化循环水养殖模式下，牛蛙幼蛙的适宜养殖密度为 300–400 只/m²，该范围可促进生长、增强免疫力与抗氧化能力，并维持肝脏健康。

关键词：牛蛙；养殖密度；生长性能；肝脏健康

The effects of different stocking densities on the growth performance and liver health of 5-25 g bullfrogs in industrial recirculating aquaculture system

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Abstract: This study aimed to determine the optimal stocking density for juvenile bullfrogs (*Aquarana catesbeianus*, 5-25 g) in a recirculating aquaculture system. Five density groups (200, 300, 400, 500, and 600 individuals/m²) were evaluated for growth performance, digestive enzyme activity, stress response, and liver health. Results showed that the 300 and 400 ind./m² groups exhibited significantly higher growth rates ($P < 0.05$). Digestive enzyme analysis revealed that amylase activity was highest at the 400 ind./m² group, protease at the 200 and 400 ind./m²groups, and lipase at the 300 ind./m² group. Liver health was the best maintained at the 200-400 ind./m² groups, showing normal histology, the lowest ALT, AST and TG levels, and the highest antioxidant capacity (CAT and T-AOC). The study recommends 300-400 ind./m² as the optimal density for enhancing growth, immunity, and hepatic function in juvenile bullfrog culture.

Key words: *Aquarana catesbeiana*; Stocking density; Growth performance; Liver health

萝卜硫素缓解嗜水气单胞菌诱导的鲤鱼肝脏损伤机制研究

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摘要：本研究旨在通过转录组学方法探究萝卜硫素（SFN）对嗜水气单胞菌（*A. hydrophila*）所致鲤鱼肝损伤的缓解机制。对照组（C 组）不感染 *A. hydrophila*，饲喂普通商品饲料。其余 4 组分别为 A 组（*A. hydrophila*+0mg/kg SFN），T1 组（*A. hydrophila*+10mg/kg SFN），T2 组（*A. hydrophila*+15mg/kg SFN），T3 组（*A. hydrophila*+20mg/kg SFN），实验鱼喂养 8 周。结果表明，与 A 组相比，补充 SFN（15 和 20 mg/kg）可通过抑制 NF-κB 信号通路显著降低肝脏肿瘤坏死因子-α (TNF-α)、白细胞介素-1β (IL-1β)和 IL-6 水平，并提高 IL-10 水平（$p < 0.05$）。此外，与 A 组相比，SFN 可提高鲤鱼肝脏 IgM 水平、C3 和 C4 含量（$p < 0.05$），从而增强鲤鱼的先天性和适应性免疫能力。转录组学分析结果表明，补充 SFN 后，主要上调 *rxr*、*ppar-γ*、*vcap-1* 和 *el* 脂肪分解基因的表达，而下调了 *apoa-IV*、*acc*、*acba-1* 和 *cpt-1* 脂肪合成基因的表达水平。这些差异表达基因（DEGs）通过 KEGG 功能分析主要富集在抗原加工和呈递，以及 AMPK 和 PPAR 信号通路。综上所述，投喂适量的（15 mg/kg） SFN 可缓解由 *A. hydrophila* 造成的黄河鲤肝脏炎症损伤，并通过 AMPK 和 PPAR 信号通路，抑制脂肪生成基因，促进脂肪分解基因表达，改善 *A. hydrophila* 诱导的脂质代谢异常。

关键词：嗜水气单胞菌，脂质代谢，萝卜硫素，鲤鱼

Sulforaphanin ameliorates the damage of the *Cyprinus carpio* liver induced by *Aeromonas hydrophila* via activating AMPK pathway

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Abstract: This study aimed to investigate the protective effect of different doses of sulforaphane (SFN) on the liver injury of *Cyprinus carpio* (*C. carpio*) caused by *Aeromonas hydrophila* (*A. hydrophila*). The control group (C group) was not infected with *A. hydrophila* and fed with the commercial feed. The other different groups were attacked by *A. hydrophila* and fed four SFN graded diets A group (*A. hydrophila*+0mg/kg SFN), T1 group (*A.hydrophila*+10mg/kg SFN), T2 group (*A. hydrophila*+15mg/kg SFN)，T3 group (*A. hydrophila*+20mg/kg SFN) for 8 weeks. The results showed that after addition appropriate SFN (15 mg/kg) could significantly reduce the levels of pro-inflammatory factors (TNF-α, IL-1β, IL-6) and increase the levels of anti-inflammatory factors (IL-10, TGF-β). Additionally, the results showed that the contents of C3, C4, MPO and IgM in the liver of *C. carpio* increased with dietary SFN, which suggested that dietary SFN supplementation could improve the innate immunity and adaptive immunity of fish. The results of transcriptomics indicate that the differentially expressed genes (DEGs) of the SFN supplementation mainly increased the expression of *rxr*, *ppar-γ*, *vcap-1* and *el* genes, but the levels of *apoa-IV*, *acc*, *acba-1* and *cpt-1* gene expressions were down-regulated. In conclusion, feeding appropriate amount of SFN (15 mg/kg) could inhibit lipogenic genes and promote the expression of lipolysis genes through AMPK and PPAR signaling pathways, and improve the abnormal lipid metabolism induced by *A. hydrophila*.

Key words: *Aeromonas hydrophila*, Lipid Metabolism, Sulforaphane, *Cyprinus carpio*

从指标评估到优化决策:合成虾青素 vs 天然虾青素对凡纳滨对虾着色、生长和健康的影响

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摘要：本研究比较了合成虾青素（Syn）与三种天然来源（海洋细菌 Mb、微藻 Hp、酵母 Pr）在凡纳滨对虾养殖中的效果。通过 56 天试验，结合 ANOVA、PCA、PLS-DA 和 TOPSIS 方法，评估了 80 项指标。结果显示：合成虾青素在类胡萝卜素含量、消化率和代谢参数上表现更优，而天然虾青素则在体色、抗氧化、抗应激能力、血清酶活性和风味物质方面更具优势。尽管两者综合评分相近，但各具特点，表明组合使用可能效果更佳。研究通过数学建模优化出两种最佳配比：合成组合为 0.011 g/kg Hp、1.2 g/kg Syn 和 26.34 g/kg Pr（虾青素比例 0.5:60:39.5）；天然组合为 0.12 g/kg Hp 和 63.07 g/kg Pr（比例 5.4:94.6）。该框架为水产饲料配方的营养效率、成本效益和品质提升提供了实践指导，通过数据驱动方法促进了行业可持续发展。

关键词：虾青素；凡纳滨对虾；综合评价

From indicator evaluation to optimization decision: Effects of synthetic vs. natural astaxanthin on pigmentation, growth, and health in *Penaeus vannamei*

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Abstract: This study evaluates synthetic (Syn) and natural astaxanthin (from bacteria *P. carotinifaciens* [Mb], microalgae *H. pluvialis* [Hp], and yeast *X. dendrorhous* [Pr]) in *P. vannamei* over 56 days. Using ANOVA, PCA, PLS-DA, and TOPSIS, 80 indicators were analyzed. Results showed Syn excels in carotenoid content, digestibility, and metabolism, while natural sources enhance coloration, antioxidant/anti-stress capacity, serum enzymes, and flavor.Optimal blends were identified: Syn blend (0.011 g/kg Hp + 1.2 g/kg Syn + 26.34 g/kg Pr; astaxanthin ratio 0.5:60:39.5) and natural blend (0.12 g/kg Hp + 63.07 g/kg Pr; ratio 5.4:94.6). The findings support tailored feed formulations for improved nutrition, cost-efficiency, and sustainability in aquaculture.

Key words: Astaxanthin source; *Penaeus vannamei*; Comprehensive evaluation; Optimization decision

木聚糖酶提高尼罗罗非鱼病原菌抵抗力的机制初探

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摘要：本研究以尼罗罗非鱼（4.09±0.02g）为实验对象，探讨了肠道微生物及其代谢物与罗非鱼的免疫状态之间的相互作用。结果表明，添加木聚糖酶提高了罗非鱼对嗜水气单胞菌的抵抗力。转录组结果表明，il-17d 信号通路,在木聚糖酶组显著富集。肠道菌群及代谢组分析结果表明，木聚糖酶能够增加肠道菌群中 *Allobaculum stercoricanis* 的丰度，同时能够增加肠道中的丁酸水平。 体外实验表明，*Allobaculum stercoricanis* 发酵上清液和丁酸盐可以提高肠道上皮细胞产生 il-17d 的能力，而敲降 il-17d 降低了罗非鱼的病原体抵抗力。结合肠道细胞模型和双荧光素酶报告基因检测，结果发现丁酸通过抑制 HDAC3 的表达，来激活肠上皮细胞中 il-17d 的转录。综上所述，木聚糖酶通过调节肠道菌群组成，提高丁酸盐水平，来增加肠上皮细胞中的 il-17d 表达，进而增强罗非鱼的病原菌抵抗力。

关键词：病原菌抵抗力；木聚糖酶；肠道菌群；短链脂肪酸；组蛋白去乙酰化

Xylanase enhances gut microbiota-derived butyrate to exert immune-protective effects in a histone deacetylase-dependent manner

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Abstract: To validate the immune-protective effects of xylanase, Nile tilapia was used as the model and fed with xylanase. The results showed that dietary xylanase improved the survival rate of Nile tilapia when they were challenged with *Aeromonas hydrophila*. The transcriptome analysis showed significant enrichment of il-17d signaling pathway in the xylanase group. High-throughput sequencing revealed that dietary xylanase directly promoted the proliferation of *Allobaculum stercoricanis* and increased the butyrate level in fish gut. Further experiment verified that butyrate supplementation enhanced the expression of il-17d and reg3g in the gut. The knockdown experiment of il-17d confirmed that il-17d is necessary for butyrate to protect Nile tilapia from pathogen resistance. Flow cytometry analysis indicated that butyrate increased the abundance of IL-17D+ intestinal epithelial cells in fish. Mechanistically, butyrate functions as an HDAC3 inhibitor, enhancing il-17d expression and playing a crucial role in pathogen resistance.

Key words: Pathogen resistance, xylanase, intestinal microbiota, short-chain fatty acids, histone deacetylation

桑叶多糖缓解团头鲂脂质代谢障碍的作用机制研究

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摘要：本研究旨在探讨桑叶多糖（MLPs）对高脂（HF）饲料诱导的团头鲂幼鱼肠道损伤的保护机制。本试验共设置两个组：高脂组（HF）和高脂+桑叶多糖（MLPs）组（HF-MLP）。RNA-seq 分析发现差异表达基因（DEGs）显著富集于 ER 功能和脂质代谢通路（$P<0.05$）。MLPs 有效降低由甘油三酯积累提高的 ERS 标志物（bip,chop）水平，有助于恢复 ER 膜功能，并提高肠道抗氧化能力（$P<0.05$）。MLPs 恢复肠道屏障完整性，下调 tlr4/nf-κb 通路相关基因的表达（P<0.05），并通过增加 *Muribaculaceae* 和 *Bacteroidales* 等菌群的丰度，改善 HF 饲料诱导的肠道菌群失调。MeRIP-seq 和 RNA-seq 联合分析发现，关键基因 bnip3 表达模式为“高甲基化-高表达”，而 nlrp1 为“高甲基化-低表达”。本研究为 MLPs 在水产动物脂代谢与氧化损伤防护中的应用提供理论基础。

关键词：桑叶多糖；团头鲂；高脂；肠道；多组学

A study on the role of mulberry leaf polysaccharides in alleviating impaired lipid metabolism in the *Megalobrama amblycephala*

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Abstract：This study explores the potential protective role of mulberry leaf polysaccharides (MLPs) in mitigating intestinal damage induced by high-fat (HF) diet in *Megalobrama amblycephala* juveniles. Two dietary groups were tested for multi-omics analysis: HF group and HF-MLP group (1.00g MLPs/kg HF diet). RNA-seq analysis identified significant enrichment of DEGs in the ER function and lipid metabolism pathways (P<0.05). MLPs supplementation significantly decreased ER stress markers (*bip*, *chop*) induced by triglyceride accumulation, restored ER membrane function (P<0.05). MLPs supplementation restored intestinal barrier integrity and downregulated tlr4/nf-κb pathway-related gene expression (P<0.05). Furthermore, MLPs counteracted HF diet-induced intestinal dysbiosis by increasing the abundance of Muribaculaceae and Bacteroidales. Combined MeRIP-seq and RNA-seq analysis indicated that the expression pattern of bnip3 was Hyper-up and that of nlrp1 was Hyper-down. This study provides theoretical foundation for the application of MLPs in oxidative damage protection in aquaculture.

Key words: Mulberry leaf polysaccharides, *Megalobrama amblycephala*, High fat, Intestinal, Multi-omics

宿主源贝莱斯芽孢杆菌的绿色开发与抗病应用：机制与策略研究

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摘要：为应对水产养殖中抗生素滥用导致的耐药性与生态风险，本研究系统探索宿主源 贝莱斯芽孢杆菌 的益生与抗病应用价值。从黄河鲤和大口黑鲈肠道中分离并筛选出 R71003 与 FLU-1 两株代表性菌株。R71003 具备强酸胆耐受性和高温稳定性，可分泌多种消化酶，对多种病原菌表现显著抑菌活性，且安全性高。创新引入葡萄糖酸钠助剂，显著增强其体外增殖与肠道定植能力，进而改善宿主消化酶活性和肠道微生态稳态。与此同时，从 FLU-1 中纯化得到抗菌肽 LCI，揭示其多靶点抑菌机制，包括破坏细胞膜、抑制生物膜形成、结合 DNA 并削弱运动性。饲喂试验证明，FLU-1 或 LCI 可显著提升大口黑鲈对嗜水气单胞菌感染的存活率并降低病原负荷。整体上，本研究构建了“合生元制剂”和“抗菌肽添加剂”两条技术路径，阐明了宿主源益生菌在耐受性、定植性、肠道健康调控及多靶抗菌作用方面的机制，为水产绿色水产养殖提供解决方案。

关键词：益生菌；贝莱斯芽孢杆菌；抗菌肽；定植；抗感染

Green Development and Antimicrobial Application of Host-Derived *Bacillus velezensis*: Mechanisms and Strategies

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Abstract: To address antibiotic overuse in aquaculture and its associated risks, this study evaluated the probiotic and antimicrobial potential of host-derived Bacillus velezensis. R71003 and FLU-1, were isolated from the intestines of yellow river carp and largemouth bass. R71003 showed strong tolerance to acid, bile, and heat, secreted digestive enzymes, exhibited broad-spectrum antibacterial activity, and was safe. Addition of sodium gluconate markedly enhanced its proliferation and intestinal colonization, improving host enzyme activity and microbial homeostasis. From FLU-1, a ~5.2 kDa antimicrobial peptide (LCI) was purified, which acted through multiple mechanisms: disrupting membranes, inhibiting biofilm, binding DNA, and reducing motility. Feeding trials demonstrated that FLU-1 or LCI significantly increased survival of largemouth bass challenged with *Aeromonas hydrophila* and reduced pathogen load. Overall, this study developed two strategies—“synbiotic formulation” and “antimicrobial peptide additive”—and offering a green solution for antibiotic-free aquaculture.

Key words: Probiotics；*Bacillus velezensis*；Antimicrobial peptide；Colonization；Anti-infection

不同形式的丁酸梭菌对大口黑鲈摄食行为调控及肠道健康的作用

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摘要：前期研究从鱼类肠道分离出一株丁酸梭菌 LZK-08，并评估其活菌（CB）、灭活菌（P-CB）、破碎物（Ly-CB）及发酵上清液（CFS）对大口黑鲈摄食的影响。结果显示：（1）各处理组摄食积极性与摄食量均显著高于对照组（$p<0.05$），CFS 组自第三周起摄食量显著上升（$p<0.05$），摄食响应时间由对照组的 45 秒缩短至不足 0.5 秒；（2）CB 组显著提高了增重率（$p<0.05$）；（3）CB 与 CFS 组均显著上调下丘脑 *npy*、*orexin* 等促摄食基因，下调抑食基因 *pacap*（$p<0.05$）；（4）仅 CB 组显著提升肠道消化酶活性（$p<0.05$），而各处理组抗氧化酶活性均显著增强（$p<0.05$）。表明活菌与发酵上清液均可通过脑肠轴调控摄食行为，但活菌的促生长作用具有代谢产物不可替代的机制。

关键词：丁酸梭菌；大口黑鲈；摄食行为；肠道健康

Effects of Different Forms of Clostridium butyricum on Feeding Behavior Regulation and Intestinal Health in Largemouth Bass (*Micropterus salmoides*)

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Abstract: A strain of Clostridium butyricum LZK-08 was previously isolated from fish intestine. Its effects on largemouth bass (Micropterus salmoides) feeding were evaluated using viable cells (CB), pasteurized cells (P-CB), cell lysate (Ly-CB), and cell-free supernatant (CFS). Key results include: (1) All treatments significantly increased feeding motivation and intake compared to the control ($p<0.05$), with CFS showing notably higher intake from week 3 ($p<0.05$) and reducing feeding response time from 45s to <0.5s; (2) Only CB significantly improved weight gain rate ($p<0.05$); (3) Both CB and CFS significantly up-regulated hypothalamic appetite-stimulating genes (npy, orexin) and down-regulated pacap ($p<0.05$); (4) CB alone significantly enhanced digestive enzyme activity ($p<0.05$), while all treatments boosted antioxidant enzymes ($p<0.05$). Conclusions: Both live bacteria and CFS modulate feeding via the brain-gut axis, but live CB exerts unique growth-promoting effects beyond its metabolites.

Keywords: *Clostridium butyricum*; Largemouth Bass; feeding behavior; intestinal health

亚硝酸盐胁迫对凡纳滨对虾肠道健康的影响

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摘要：本研究将凡纳滨对虾分别暴露于 1 mg/L 和 5 mg/L 的亚硝酸盐胁迫 48 h，探究了其肠道健康的变化特征。结果表明，亚硝酸盐胁迫会损伤对虾肠道黏膜，5 mg/L 亚硝酸盐诱导的生理变化较 1 mg/L 更为显著。抗氧化（*ROMO1*、*Nrf2*、*SOD*、*GPx*、*HSP70*）、内质网应激（*Bip*、*XBP1*）、免疫（*proPO*、*Crus*、*ALF*、*Lys*）、炎症（*JNK*、*TNF-α*）及凋亡（Casp-3、Casp-9）相关基因的相对表达水平均有所升高。此外，亚硝酸盐通过诱导糖代谢、脂质代谢、三羧酸循环及电子传递链相关基因转录，激活肠道能量代谢。肠道菌群组成的稳态也受到干扰，尤其是部分有益菌属丰度下降。研究表明，亚硝酸盐胁迫可通过破坏肠道黏膜完整性、干扰生理稳态及菌群结构，从而损伤对虾的肠道健康。

关键词：对虾；亚硝酸盐；肠道；生理响应；微生物群落

Effects of nitrite stress on the intestinal health homeostasis of Pacific white shrimp (*Litopenaeus vannamei*)

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Abstract: In this study, the shrimp *Litopenaeus vannamei* were separately exposed to 1 and 5 mg/L of nitrite stress for 48 h, and then the variations in intestinal health were investigated. The results showed that nitrite stress damaged intestinal mucosa, and 5 mg/L of nitrite induced more obvious physiological changes than 1 mg/L. Specifically, the relative expression levels of antioxidant (*ROMO1*, *Nrf2*, *SOD*, *GPx*, and *HSP70*), ER stress (*Bip* and *XBP1*), immunity (*proPO*, *Crus*, *ALF*, and *Lys*), inflammation (*JNK* and *TNF-α*), and apoptosis (Casp-3 and Casp-9) genes were increased. Additionally, intestinal energy metabolism was activated by inducing glucose metabolism, lipid metabolism, tricarboxylic acid cycle, and electron transfer chain gene transcription. Further, the homeostasis of intestinal microbiota composition was also disturbed, especially the abundance of some beneficial genera. These results reveal that nitrite stress could damage the intestinal health of *L. vannamei* by destroying the mucosal integrity, physiological homeostasis and microbial community structure.

Key words: shrimp; nitrite; intestine; physiological response; microbial community

氨氮胁迫抑制西伯利亚鲟幼鱼摄食的作用机制研究

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摘要：氨氮是水环境常见的危害因子，抑制鱼类摄食，但作用机制不明。为探究氨氮抑制鱼类摄食的机制，本研究将西伯利亚鲟幼鱼暴露于 0、5、10 和 15 mg/L 氨氮中 14 天。结果显示，日摄食量和累计摄食量均显著下降，15 mg/L 组肝体指数（HSI）和脏体指数（VSI）显著降低。第 14 天血氨浓度显著升高，神经毒性标志物 AchE 显著上升，下丘脑损伤明显，脑中超氧化物歧化酶（SOD）活性显著升高。转录组及 qPCR 分析显示，促食欲因子刺鼠相关蛋白（*agrp*）和神经肽 Y（*npy*）显著下调，抑食欲因子阿黑皮素原（*pomc*）、可卡因-苯丙胺调节转录肽（*cart*）和促肾上腺皮质激素释放因子（*crf*）明显上调。本研究为解析氨氮对水生动物的毒理机制，尤其是探究其对鱼脑功能和摄食行为的损害奠定基础。

关键词：西伯利亚鲟；氨氮胁迫；摄食量；摄食调控

Study on the Mechanism of Ammonia-N Exposure Inhibiting the Feeding of *Siberian Sturgeon* Juvenile

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Abstract: Ammonia-N is a common toxic factor in aquatic environments, which inhibits fish feeding, but its mechanism remains unclear. This study conducted experiments exposing Siberian sturgeon (Acipenser baerii) juveniles to ammonia-N (0, 5, 10, and 15 mg/L) for 14 days. The results revealed a significant reduction in both daily and cumulative food intakes. Obviously decreased HSI and VSI at 15 mg/L group. On the 14th day, serum ammonia concentration was significantly increased, and neurotoxic marker acetylcholinesterase (AchE) was also significantly increased. It was showed that the brain tissue was demonstrated damage and the activity of SOD was significantly increased. RNA-seq analysis and qPCR indicated that appetite-promoting factors *agrp* and *npy* were significantly down-regulated, while appetite-suppressing factors *pomc*, *cart*, and *crf* were significantly up-regulated. This study provides the knowledge for deeper understanding of the toxicological mechanism of ammonia-N on aquatic animals, particularly its detrimental effects on fish brain function and feeding behavior.

Key words: *Acipenser baerii*, Ammonia-N, Food intake, Feeding regulation.

长期盐度暴露下草鱼的生理反应

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摘要：盐度是影响水生生物存活、生长、发育、繁殖等生命活动的重要环境因素。然而，盐度影响鱼类生理反应的相关机制尚不具体。因此，本实验为探究长期盐度胁迫对草鱼(*Ctenopharyngodon idellus*)生理机能变化，设置空白对照组（0 g/L）和实验组（4 g/L、8 g/L）,对草鱼进行为期 60 天的盐度胁迫。结果表明，长期盐度胁迫对 8 g/L 组生长参数有显著不利影响。高盐度显著改变了乳酸 (LA)、总蛋白 (TP) 、总胆固醇(TC)、甘油三酯 (TG) 和谷草转氨酶 (GOT) 水平。同时，高盐度暴露改变了 Mg^{2+}，Ca^{2+}、Na^{+} 和 Cl^{-} 浓度。此外，盐度胁迫诱导了氧化应激导致抗氧化状态发生改变，总的来说，长期高盐胁迫会抑制草鱼生长，草鱼会产生各种生理变化来应对盐度应激。

关键词：盐度胁迫；生长性能；生理反应；草鱼

Physiological Responses in Grass Carp (*Ctenopharyngodon idellus*) under Chronic Salinity Exposure

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Abstract: Salinity is a critical environmental factor affecting the survival, growth, development, and reproduction of aquatic organisms. However, the specific mechanisms through which salinity influences fish physiological responses remain unclear. This study investigated the physiological changes in grass carp (Ctenopharyngodon idellus) under long-term salinity stress (0, 4, and 8 g/L for 60 days). The results demonstrated that prolonged exposure to 8 g/L salinity significantly impaired growth performance. High salinity notably altered levels of lactic acid (LA), total protein (TP), total cholesterol (TC), triglycerides (TG), and glutamic-oxaloacetic transaminase (GOT), as well as the concentrations of Mg^{2+}, Ca^{2+}, Na^{+}, and Cl^{-}. Additionally, salinity stress induced oxidative stress and modified antioxidant status. Overall, long-term high-salinity exposure inhibits grass carp growth and triggers various physiological adaptations to cope with salinity stress.

Key words: Salinity stress; Growth performance; Physiological responses; *Ctenopharyngodon idellus*

不同地区黑斑侧褶蛙生长性能及抗氧化能力对比研究

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摘要：黑斑侧褶蛙（*Pelophylax nigromaculata*）别名黑斑蛙、青蛙等，兼具食用与药用价值，其人工养殖已成为我国南方特种水产重点产业。为探究不同地理种群黑斑蛙在江西的生长及抗氧化差异，实验选取湖南、湖北、安徽、山东、江西五省健康幼蛙，于2025年4-6月在江西九江养殖基地，经相同条件饲养，每两周取样，对比体重、体长、肝重等生长指标，及肝脏中CAT、SOD、GSH-Px三种抗氧化酶活性与肝总蛋白含量。结果显示，五省种群生长速率差异显著（$P<0.05$），江西本地种群增重最快，山东种群最慢；抗氧化指标上，湖北、安徽种群CAT、SOD活性较高，江西种群GSH-Px活性显著更高（$P<0.01$），湖南种群总蛋白含量最高。这些差异或与地理适应性、遗传背景相关，可为黑斑侧褶蛙生态适应机制研究及种群保护提供依据。

关键词：黑斑侧褶蛙；生长性能；抗氧化性能；养殖种群

Comparative Study on Growth Performance and Antioxidant Capacity of *Pelophylax nigromaculata* from Different Regions

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Abstract: To explore the differences in growth and antioxidant capacity of *P. nigromaculata* populations from different geographical regions in Jiangxi, healthy juvenile frogs from five provinces (Hunan, Hubei, Anhui, Shandong, and Jiangxi) were selected. From April to June 2025, the frogs were reared under the same conditions at a breeding base in Jiujiang, Jiangxi. Samples were collected every two weeks to compare growth indicators (body weight, body length, liver weight) as well as the activities of three antioxidant enzymes (CAT, SOD, GSH-Px) and total liver protein content in the liver.The results showed that there were significant differences in the growth rate of the populations from the five provinces ($P<0.05$): the local population in Jiangxi had the fastest weight gain, while the Shandong population was the slowest. For antioxidant indicators, the Hubei and Anhui populations had higher CAT and SOD activities; the Jiangxi population had significantly higher GSH-Px activity ($P<0.01$); and the Hunan population had the highest total protein content. These differences may be related to geographical adaptability and genetic background, and can provide a basis for research on the ecological adaptation mechanism and population protection of *P. nigromaculata*.

Key words: *Pelophylax nigromaculata*; growth performance; antioxidant capacity; breeding population

漏斗型池塘生态循环种养（水产“168+”）技术之尾水处理

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摘要：文章介绍了漏斗型池塘生态循环种养（水产“68”1+）模式尾水治理设计方案，以生态高效、绿色健康创新理念，以“让养鱼环境好、让养的鱼好吃、让养鱼人赚钱”创新目标，实现了亩增产 6 倍以上、增效 40%以上、节水 80%、节地 50%以上四大突破。解决了传统养殖尾水处理和鱼粪收集难题，实现了水资源和鱼粪残饵的循环利用，为 2025 年中央一号文件提出的水产养殖尾水治理提供河南方案。

关键词：168 技术；尾水治理；鱼粪残饵；资源化利用

The Funnel-Type Pond Eco-Recirculating Aquaculture Technology (Aquatic “168+”Model)

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Abstract: This paper elucidates a innovative design for the funnel-type pond ecological recirculating aquaculture model (“168+”). Guided by the principles of ecological efficiency, sustainability, and innovative health-conscious practices, and aligned with the core objectives of "improving aquaculture environments, enhancing fish quality, and increasing farmer profitability," this model has achieved four major breakthroughs: a sixfold increase in yield per mu, over 40% improvement in production efficiency, 80% reduction in water usage, and more than 50% savings in land use. It effectively addresses longstanding challenges associated with tailwater management and fish waste collection in traditional aquaculture, enabling efficient recycling of water resources and reuse of fish excrement and residual feed. The study offers a tailored solution from Henan Province for managing aquaculture tailwater, contributing to the national goals outlined in the 2025 Central No. 1 Document.

Key words: Funnel-type pond; Ecological recirculating aquaculture model; Tailwater treatment; Resource utilization of fish feces and residual feed

大口黑鲈对碱度胁迫的耐受性及其机制研究

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摘要：本研究首先评估了大口黑鲈对碱度胁迫的耐受性，然后分析长期碱度胁迫对大口黑鲈生长性能、生理学、组织学及肌肉品质的影响，最后通过 BSA-seq、转录组、代谢组等多组学联合分析揭示碱度耐受机制。结果表明，大口黑鲈对碱度具有较强的耐受能力，其幼鱼 96 h 半致死浓度为 44.38 mmol/L；高碱度胁迫（28 mmol/L）对大口黑鲈的存活率无显著影响，但却对其生长性能、饲料利用率、生理和组织学产生了不利影响；碱度胁迫有利于改善大口黑鲈肌肉营养品质和质构特性。多组学分析表明，大口黑鲈鳃组织通过调节能量代谢、离子转运和氧化应激等过程来增强耐碱性能；肝脏组织通过增强营养物质代谢、提高抗氧化能力和免疫调节能力，增强离子转运酶活性，从而提高耐碱性能。通过 BSA-seq 分析，共鉴定出 4 个与大口黑鲈耐碱相关的 QTL 区域，筛选出 7 个核心候选基因和 10 个候选 SNP 位点，可作为大口黑鲈耐碱新品种培育的潜在遗传靶点。

关键词：大口黑鲈，碱度，转录组，代谢组，BSA-seq

Tolerance capacity and mechanism of largemouth bass to alkalinity stress

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Abstract: This study first evaluated the tolerance of largemouth bass *Micropterus salmoides* to alkalinity stress, then revealed the tolerance mechanism through multi-omics analysis. The results showed that largemouth bass had a strong tolerance to alkalinity, with a 96-h LC50 of 44.38 mmol/L. The high alkalinity (28 mmol/L) had no significant effect on the survival rate, but had adverse effects on its growth performance, feed utilization, physiology and histology. Alkalinity stress was beneficial to improving the nutritional quality and texture characteristics of muscle. Multi-omics analysis indicated that the gill enhanced its alkalinity tolerance by regulating energy metabolism, ion transport and oxidative stress processes; while the liver enhanced its alkalinity tolerance by strengthening nutrient metabolism, improving antioxidant capacity and immune regulation ability, and increasing the activity of ion transport enzymes. Through BSA-seq analysis, a total of 4 QTL regions related to the alkalinity tolerance were identified, and 7 and 10 key candidate genes and SNPs were screened out.

Key words: Largemouth bass *Micropterus salmoides*, Alkalinity, Transcriptome, Metabolome, BSA-seq

不同稻渔种养模式对稻田水质理化因子的影响

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摘要：稻渔综合种养不仅能稳定提高稻米和水产品产量，还能大幅减少农药和化肥的使用，实现绿色可持续发展。本研究选取了 5 种代表性的稻渔模式（稻鱼、稻虾、稻鳖、稻蛙和稻蟹），并按照不同稻渔品种的生长周期来采样，进行水质的 pH、总氮（TN）、总磷（TP）、总氨氮（TAN）、溶解氧(DO)、化学需氧量（COD）常规指标检测。研究结果表明，稻渔种养模式对水质的影响具有显著特异性。其中稻鳖组、稻蛙组、稻虾组和稻蟹组的 pH 值、氨氮浓度和化学需氧量在温暖季节呈现较大波动，主要与物种的高代谢活动有关。稻鱼组对水质理化因子的影响表现出较好的水体稳定性。较高的溶解氧水平能够加速有机物的分解和硝化作用的充分进行。溶解氧浓度在稻鳖组中显著升高，表明这些物种的活动可能促进了水体的气体交换和氧循环。稻鱼模式表现出较好的生态稳定性；而稻鳖、稻蛙、稻虾和稻蟹模式在温暖季节可能对水质造成较大压力，需加强水质调控和污染防控。

关键词：稻渔综合种养；理化因子；水质调控；生态稳定性

The impact of different rice-fish farming models on the physicochemical factors of paddy water quality

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Abstract: Integrated rice-aquaculture (IRA) boosts rice and aquatic yields stably, cuts pesticide use sharply, and enables green sustainable development. This study chose 5 typical IRA modes (rice-fish, rice-shrimp, rice-turtle, rice-frog, rice-crab), sampled per species' growth cycles, and tested water quality indicators: pH, TN , TP , TAN , DO, COD .Results showed IRA modes had distinct specificity in water quality impact. pH, TAN, and COD in rice-turtle, rice-frog, rice-shrimp, rice-crab groups fluctuated greatly in warm seasons, mainly due to high species metabolism. The rice-fish group showed better water stability on physicochemical factors.Higher DO accelerated organic decomposition and full nitrification. DO rose significantly in the rice-turtle group, suggesting species activities might promote water gas exchange and oxygen cycle. Rice-fish mode had good ecological stability; rice-turtle, rice-frog, rice-shrimp, rice-crab modes may stress water quality in warm seasons, needing enhanced regulation.

Key words: Comprehensive rice-fish integrated farming; physicochemical factors; water quality control; ecological stability

BDE-47 通过整合素介导的氧化应激与炎症通路引发西伯利亚鲟胚胎毒性

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摘要：2,2',4,4'-四溴联苯醚（BDE-47）属持久性有机污染物，对鱼类胚胎发育具有潜在毒性，但作用机制不明。本研究将西伯利亚鲟受精卵暴露于 0.5、5 和 50 μg/L BDE-47。结果表明，BDE-47 显著降低胚胎孵化率与仔鱼存活率，造成胚胎畸形；抗氧化酶 SOD 和 GPx 活性与 MDA 含量显著升高；转录组与分子对接发现 BDE-47 激活整合素信号通路并与其受体（ITG-α5、ITG-α8 和 ITG-α11）强结合；BDE-47 显著上调整合素受体（itg-α5、itg-α8 和 itg-α11）、炎症因子（il-6、tnf-α和 nf-κb）和氧化应激相关基因（gpx、nrf2 和 keap1）的表达。细胞实验发现整合素受体特异性拮抗剂显著逆转 BDE-47 对上述基因表达的影响。本研究揭示了 BDE-47 通过整合素介导的氧化应激与炎症通路发挥胚胎毒性的新机制，为鲟鱼等珍稀鱼类资源保护与多溴联苯醚的生态风险评估。

关键词：2,2’,4,4’-四溴联苯醚；BDE-47；西伯利亚鲟；胚胎发育；整合素

BDE-47 Induces Embryotoxicity in Siberian Sturgeon via Integrin-Mediated Oxidative Stress and Inflammatory Pathways

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Abstract: 2,2′,4,4′-Tetrabromodiphenyl ether (BDE-47), a persistent organic pollutant, impairs embryonic development in fish through unclear mechanisms. Exposure of Siberian sturgeon embryos to 0.5, 5, and 50 μg/L BDE-47 significantly reduced hatching and survival rates, and induced malformations. Elevated activities of SOD and GPx, along with increased MDA content, indicated oxidative stress. Transcriptomics and molecular docking showed BDE-47 activates integrin signaling and strongly binds integrin receptors. Expression of itg-α5, itg-α8, itg-α11, inflammatory markers (il-6, tnf-α, nf-κb), and oxidative genes (gpx, nrf2, keap1) was up-regulated. Cellular experiments have found an integrin receptor-specific antagonist reversed these effects. This study reveals a novel mechanism whereby BDE-47 causes embryotoxicity via integrin-mediated oxidative and inflammatory pathways, providing a reference for the conservation of sturgeon and other rare fish species and the ecological risk assessment of polybrominated diphenyl ethers.

Key words: 2,2′,4,4′-Tetrabromodiphenyl ether; BDE-47; Siberian sturgeon; Embryonic development; Integrins

箱塘联动养殖模式下水环境特征和微生物群落结构研究

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摘要：通过在池塘中布设网箱养殖淡水鱼、网箱外种植常绿矮化苦草（*Vallisneria natans* (Lour.) Hara）养殖中甲壳类动物，构建了箱塘联动生态养殖模式，实现同塘多品种养殖、水环境和水产品质量提升以及养殖增收的目的。本研究通过对箱塘联动生态养殖池塘水环境跟踪监测，旨在探明该生态模式下水质和养殖水体中微生物群落组成特征，结果表明：箱塘联动生态养殖水体中氮和磷的主要存在形态为硝酸盐氮（在总氮中平均占比 72.65%）和磷酸盐（在总磷中平均占比 88.15%），悬浮物和叶绿素 a 含量极低；试验塘养殖水体中优势菌门为 *Proteobacteria*、*Actinobacteriota*、*Bacteroidota*、*Firmicutes* 和 *Verrucomicrobiot*a，优势菌属为 *Unclassified Comamonadaceae*、*hgcI-clade*、*Limnohabitans*、*Mycobact*erium 和 Aurantimicrobi。

关键词：养殖模式; 箱塘联动; 水质特征; 微生物群落组成

Research on Water Environment Characteristics and Microbial Community Structure in Integrated Net-Pond Aquaculture System

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Abstract: By establishing an integrated net-pond ecological aquaculture system—where nets were deployed for freshwater fish culture inside enclosures and *Vallisneria natans* (Lour.) Hara was planted outside to cultivate crustaceans—a multi-species co-culture model was implemented within a single pond. This approach improved water quality, enhanced the quality of aquatic products, and increased overall aquaculture income. Through continuous monitoring of the pond water environment, this study aimed to clarify the characteristics of water quality and the composition of microbial communities in the aquaculture water. Results showed that the dominant forms of nitrogen and phosphorus were nitrate nitrogen (averaging 72.65% of total nitrogen) and phosphate (averaging 88.15% of total phosphorus), with very low concentrations of suspended solids and chlorophyll a. The predominant bacterial phyla included *Proteobacteria*, *Actinobacteria*, *Bacteroidetes*, *Firmicutes*, and *Verrucomicrobota*, while the dominant genera were *Unclassified Comamonadaceae*, *hgcI-clade*, *Limnohabitans*, *Mycobacterium*, and *Aurantimicrobi.*

Key words: farming model; integrated net-pond; characteristics of water quality; microbial community composition

对虾工厂化循环水养殖系统不同水处理单元和肠道微生物群落的时空演替模式研究

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摘要：循环水产养殖系统（RAS）在凡纳滨对虾养殖中广泛应用，微生物对水质净化与对虾生长具有重要作用。为解析系统各单元（养殖区→沉淀区→毛刷区→曝气区→养殖区闭环）水体理化性质及微生物群落动态，本研究通过 16S rRNA 测序，分析了全周期（0、40、60、80 天）不同区域水体及对虾肠道的菌群结构与功能。结果表明，水体中 NH_4^+–N、NO_2^-–N 和 NO_3^-–N 浓度呈先升后降趋势，曝气区最高，活性磷酸盐则持续上升。水体优势菌门为浮霉菌门，而对虾肠道以疣微菌门和芽孢杆菌门为主。随时间推移，对虾肠道中放线菌门和拟杆菌门丰度显著降低，芽孢杆菌门显著上升。肠道微生物多样性显著低于水体，但各水处理单元间水体菌群多样性无显著差异。本研究阐明 RAS 中水处理单元有效降低氮污染物，揭示了水体与对虾肠道微生物的互作模式，为优化对虾工厂化循环水养殖系统提供了理论依据和数据支持。

关键词：凡纳滨对虾；工厂化循环水养殖；微生物群落；水体理化因子

Study on the spatiotemporal succession mode of different water treatment units and intestinal microbial communities in shrimp factory recirculating aquaculture system

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Abstract: Recirculating Aquaculture Systems (RAS) are essential in *Litopenaeus vannamei* farming. This study used 16S rRNA sequencing to analyze microbial communities in water and shrimp intestines across RAS treatment units (culture → sedimentation → biofilter → aeration) at 0, 40, 60, and 80 days. Results indicated that NH_4^+–N, NO_2^-–N, and NO_3^-–N levels increased initially, peaked in the aeration zone, and then decreased, while reactive phosphate rose consistently. *Planctomycetota* dominated water microbiota, whereas shrimp intestines were primarily colonized by *Verrucomicrobiota* and *Bacillota*. Over time, *Actinomycetota* and *Bacteroidota* significantly decreased in shrimp intestines, while *Bacillota* increased significantly. Intestinal microbial diversity was significantly lower than in water, but no notable differences were observed among water treatment units. The findings demonstrate that RAS effectively reduces nitrogenous pollutants and reveal interactions between water and intestinal microbiota, offering valuable insights for system optimization.

Key words: *Litopenaeus vannamei*; Factory recirculating aquaculture; Microbial community; Water physicochemical factors

对虾源益生菌对凡纳滨对虾幼体养殖性能和环境生物安全风险评估

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摘要：本研究分析了对照组和益生菌处理组之间水和虾肠道中虾幼虫培养性能、细菌群落、潜在病原体和抗生素抗性基因的差异，以评估虾源益生菌干酪乳酸杆菌 *HD1* 和地衣芽孢杆菌 *WZ1* 的潜力和环境安全性。补充益生菌显著提高了存活率、生物量和个体重量，同时减少了水体 NH_4^+-N,NO_3^--N、和 PO_4^{3-}-P 浓度。与 CK 相比，水α多样性（丰富度、香农指数等）和拟杆菌门、拟杆菌门和 *Balneolota* 的丰度显著增加，而肠道放线菌门减少。至关重要的是，益生菌没有显著改变肠道微生物多样性、组成、ARG 或潜在病原体。结构方程模型证实，益生菌通过双重途径提高性能：调节水微生物群以减少污染物(水调节)和直接增强肠道微生物稳定性(肠道保护)。研究结果主张使用特定物种的益生菌来平衡生产力和环境健康。此外，不同的益生菌类型对水/肠道微生物结构和幼虾生长有独特的影响，这为我们在对虾幼体培育阶段使用不同种类益生菌组合提供思路。

关键词：南美白对虾；本土益生菌；微生物群落动态；潜在病原体；抗生素耐药基因；环境安全

Risk assessment of shrimp-derived probiotics on culture performance and environmental biosafety of *Penaeus vannamei* larvae

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Abstract: This study evaluated shrimp-derived probiotics *Lacticaseibacillus casei HD1* and *Bacillus licheniformis* WZ1 in *Litopenaeus vannamei* larval culture,assessing production performance,bacterial communities, potential pathogens and antibiotic resistance genes (ARGs) in water and shrimp gut. Probiotic supplementation significantly improved survival,biomass,and individual weight,and reduced concentrations of NH_4^+-N,NO_3^--N and PO_4^{3-}-P in water. Water α-diversity increased, along with higher abundances of *Bacteroidota*,*Bacillota*,and *Balneolota*,while gut *Actinobacterota* decreased.Notably, probiotics did not significantly alter gut microbial diversity, composition, ARGs, or potential pathogens. The results indicate that probiotics enhance performance through dual pathways:modulating water microbiota to reduce pollutants (water regulation)and directly stabilizing gut microbiota (gut protection).The findings support using host-specific probiotics to maximize productivity and environmental health.Differential effects of probiotic types suggest potential for tailored application during larval stages.

Key words: *Penaeus vannamei*; Indigenous probiotics; Microbial community dynamics; Potential pathogens; Antibiotic resistance genes; Environmental safety

利用水产养殖废水培养普通小球藻的可行性研究

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摘要：养殖废水中氮、磷等营养盐易引发水体富营养化，亟需经济高效的处理方法。为此，本研究分析了不同养殖废水的营养盐组成，并利用土塘鲈鱼、工厂鲈鱼和工厂甲鱼三种废水培养普通小球藻，系统评估其生长情况与水质净化效果。结果表明，工厂甲鱼组中小球藻的终末密度显著高于 BG11 对照组，而土塘鲈鱼组显著较低（$P < 0.05$），工厂鲈鱼组则无显著差异（$P > 0.05$）。进一步添加乙酸钠（10 g/L）可显著提高小球藻在工厂甲鱼废水中的生长，其终末密度与叶绿素 a 含量甚至超过同水平碳添加量的 BG11 培养基（$P < 0.05$）。同时，小球藻对废水净化效果显著，总氮去除率与工厂循环水处理无显著差异（$P > 0.05$），且总磷去除率显著更高（$P < 0.05$）。竞争实验还表明，小球藻在不同接种密度下均能有效抑制铜绿微囊藻的生长。综上所述，利用养殖废水培养小球藻不仅可行，并可同时实现水质高效净化。

关键词：养殖废水；废水处理；普通小球藻；种间竞争；氮磷比

Study on the Feasibility of Culturing *Chlorella vulgaris* with Aquaculture Wastewater

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Abstract: Aquaculture wastewater rich in nitrogen and phosphorus often causes eutrophication, requiring economical treatment solutions. This study cultivated *Chlorella vulgaris* in three types of wastewater (pond perch, factory perch, and factory turtle) to assess growth and purification efficiency. The final algal density was highest in turtle wastewater, significantly exceeding the BG11 control ($P < 0.05$), while pond perch wastewater showed the lowest ($P > 0.05$). Adding sodium acetate (10 g/L) further enhanced growth in turtle wastewater, with biomass and chlorophyll-a surpassing carbon-supplemented BG11 ($P < 0.05$). *C. vulgaris* also demonstrated effective purification: total phosphorus removal was significantly higher than in recirculating treatment ($P < 0.05$), while total nitrogen removal showed no significant difference ($P > 0.05$). Additionally, *C. vulgaris* suppressed Microcystis aeruginosa growth across inoculation densities. These findings indicate that culturing *C. vulgaris* in aquaculture wastewater is feasible and enables efficient water purification.

Key words: Aquaculture wastewater；wastewater treatment；*Chlorella vulgaris*；interspecific competition；nitrogen-phosphorus ratio

重力驱动膜低碳处理养殖尾水

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摘要：本研究提出了一种新型的重力驱动膜集成工艺：电絮凝、好氧缺氧和重力驱动陶瓷膜，旨在提高海水养殖废水处理的长期稳定脱氮效率。主要创新包括：（1）协同氮途径：Anammox 和与异养反硝化协同脱氮（出水：总氮<5mg/L）（2）强大的除磷能力：铁絮体结合吸附和化学沉淀强化除磷（出水：总磷<0.05 mg/L）。（3）良好的过滤性能：大孔载体促进了生物膜的发展，减少了滤饼层的形成，同时保持了水的净化效率 COD<15mg/L 和膜通量 10-11LMH。在合成/真实海水养殖废水处理的 140 天运行期间无需清洗。此外，重力驱动膜对海水养殖废水分散和不连续流入的特点表现出很强的系统稳定性和适应性。

关键词：养殖尾水处理；重力驱动膜；氮和磷；Anammox；电絮凝

Electrocoagulation Aerobic-Anoxic Gravity Driven Ceramic Membrane (EC-OA-GDCM) for Mariculture Wastewater Treatment: Enhanced Nitrogen Removal Mechanism

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Abstract: The persistent challenge of achieving sustainable nitrogen removal in high-salinity mariculture wastewater necessitates advanced treatment strategies. This study presents a novel Gravity-Driven Membrane Integration Process: Electrocoagulation, Aerobic-Anoxic and Gravity-driven Ceramic Membrane (EC-OA-GDCM), aiming to improve the long-term and stable nitrogen removal efficiency for mariculture wastewater treatment. Key innovations include: (1) Synergistic nitrogen pathways: the iron-rich environment (Fe3+ generated from EC) facilitated Anammox (Candidatus Brocadia and Candidatus-Kuenenia) and Feammox (Geobacter), working in tandem with heterotrophic denitrification to achieve desirable Total Nitrogen (TN) removal efficiency (effluent: Ammonia (NH3-N)<0.1mg/L and TN<5mg/L). (2) Robust phosphorus removal: Electrocoagulation-derived iron flocs achieved phosphorus removal (effluent: Total Phosphorus (TP)<0.05 mg/L) through combined adsorption and chemical precipitation mechanisms. (3) Great filtration behavior: Macroporous carriers promoted biofilm development, reducing cake layer format.

Key words: Mariculture wastewater treatment; Gravity driven ceramic membrane; Nitrogen and phosphorus; Anammox; Electrocoagulation

饥饿与再投喂对卵形鲳鲹生理生化指标、肠道菌群及转录组的影响

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摘要：饥饿是鱼类常见的应激反应，可导致生长抑制，而再投喂可能引发补偿性生长现象。本研究发现卵形鲳鲹经 7 天饥饿及后续 7 天再投喂处理。本研究旨在探究饥饿与再投喂对卵形鲳鲹肝脏生化指标、肠道微生物组及转录组的影响。结果表明，饥饿导致鱼体出现低血糖和低甘油三酯血症，并显著改变了碳水化合物代谢关键酶的活性：葡萄糖激酶活性升高，而丙酮酸激酶和 6-磷酸果糖激酶活性降低。肠道微生物结果显示在门水平上，变形菌门、螺旋体门和厚壁菌门为优势菌群；在属水平上，优势菌属为短螺旋体属、血螺旋体属和支原体属。转录组结果显示在对照组、饥饿组和再投喂组之间，共鉴定出 227 个显著差异表达的基因。再投喂后出现的补偿性生长与 DEGs 的下调相关，而饥饿效应的消除则与应激反应和碳水化合物代谢相关通路的 DEGs 上调有关。综上所述，本研究通过解析酶活性、肠道菌群和转录组对饥饿-再投喂的响应机制，为卵形鲳鲹的健康养殖提供了理论依据。

关键词：卵形鲳鲹、饥饿、再投喂、微生物、转录组

Starvation and refeeding influence the biochemical index, intestinal microbiota and transcriptomic profiles of golden pompano *Trachinotus ovatus* (Linnaeus 1758)

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Abstract: Starvation is a common stress in fish, starvation and refeeding can cause growth inhibition and compensatory growth. Golden pompanos were starved for 7 days and then fed for another 7 days. The results showed that starvation resulted in a hypoglycemia, low triglyceride concentration and considerably affected the activities of carbohydrate metabolic enzymes. Starvation increased glucokinase activity and decreased pyruvate kinase and fructokinase 6-phosphateactivities, while PK and PFK activities increased after refeeding. Starvation led to increased diversity and altered composition in the intestinal microbiome. The dominant phylum of intestinal microbiota was *Proteobacteria*, *Spirochaetes* and *Tenericutes*. The dominant species at the genus level were *Brevinema*, *Haematospirillum* and *Mycoplasma*. Starvation also led to signifcant alterations in gene expression, with distinct pathways affected at starvation and refeeding. Therefore, this study provides a theoretical support for healthy farming of *T. ovatus* through enzyme activity indicators, gut microbiota and transcriptome response.

Key words: *Trachinotus ovatus*, starvation, refeeding, transcriptome profiles, intestinal microbiome