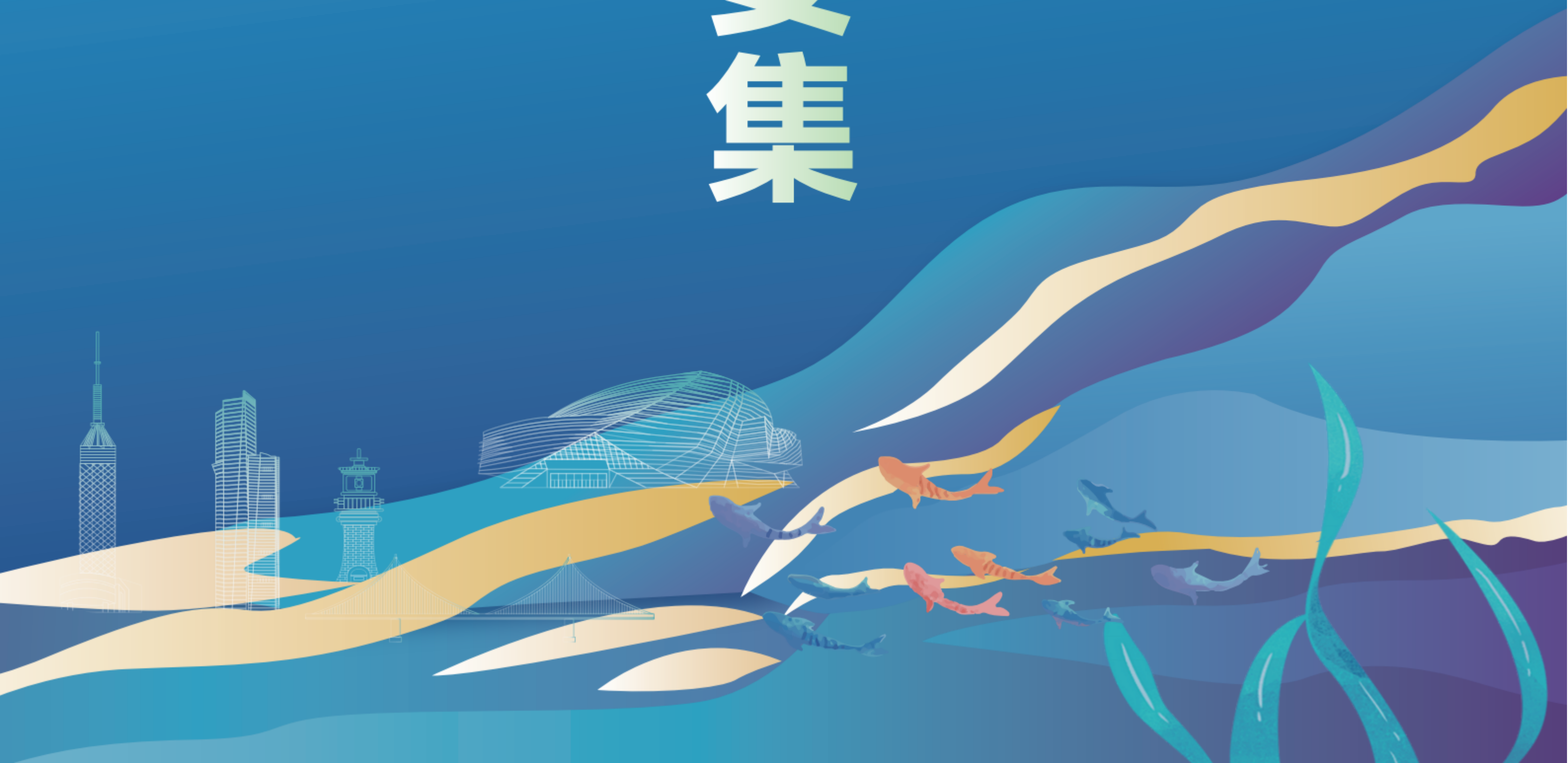
大连海洋大学 DALIAN OCEAN UNIVERSITY

科技创新促进渔业高质量发展

2025中国水产学会
范蠡学术大会

论文摘要集



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第一专题 水产绿色健康养殖新技术新模式

翘嘴鳜对不同光谱的趋向行为与生理适应性研究

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摘要：本研究系统评估了翘嘴鳜对红（RL）、黄（YL）、绿（GL）、蓝（BL）、白（WL）五种光谱及黑暗环境（DA）的行为偏好与生理适应性。行为学结果表明，翘嘴鳜对 RL 表现出最强的趋向性，偏好顺序依次为 RL > DA > YL > BL > GL > WL。群体动态分布显示，RL 区在 48 h 内个体占有率最高；DA 区在前 26 h 聚集优势显著，但随后逐渐下降；YL 区个体数量随时间递增。生理指标检测发现，YL 组的 T-AOC 显著升高，且 MDA 水平显著降低。此外，RL 组皮质醇水平显著高于 YL、GL 及 WL 组；5-HT 含量在 RL 和 DA 组中显著高于 BL 组。组织学观察显示，GL 与 WL 组视锥细胞密度显著高于黑暗组；视网膜色素指数在 RL 组最高。转录组分析显示，相比于 DA 组，YL 组神经活性配体-受体相互作用通路被显著激活。综上，翘嘴鳜对长波光谱具有明显行为偏好，其中红光可能诱发应激，而黄光则有效增强机体抗氧化能力。

关键词：光谱，翘嘴鳜，光谱偏好，应激反应，神经活性配体-受体相互作用通路

Response of mandarin fish (*Siniperca chuatsi*) to different light spectra: Behavior and physiological adaptation

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Abstract：This study evaluated the behavioral preferences and physiological adaptations of mandarin fish (S. chuatsi) to different light colors (RL, YL, GL, BL, WL) and darkness (DA). Behaviorally, the fish exhibited the strongest phototaxis toward RL, with the highest proportion consistently found in the RL zone over 48 hours. Initially, the DA group showed significant aggregation, which later declined, while individuals in YL gradually increased. Physiologically, the YL group demonstrated significantly enhanced total antioxidant capacity (T-AOC) and reduced malondialdehyde (MDA) levels. The RL group had markedly higher cortisol levels, while both RL and DA groups showed elevated 5-HT. Histological analysis revealed higher cone cell density in GL and WL groups compared to DA, and the retinal pigment index was highest under RL. KEGG analysis indicated activation of the neuroactive ligand-receptor interaction pathway. In summary, S. chuatsi shows a distinct behavioral preference for long-wavelength light. While RL may induce stress, YL effectively boosts antioxidant capacity.

Key words: Light spectra, Mandarin fish, Spectral preference, Stress response, Neuroactive ligand-receptor interaction

养殖贝类的碳汇功能与可持续发展探索

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摘要：我国贝类养殖产业历史悠久，是最大贝类养殖国家，结合目前全球气候变化问题大背景，以及我国对于碳达峰目标高要求，基于贝类养殖碳汇成本低廉、环境友好等显著优势，养殖贝类在其正常生命活动中发挥着碳汇功能（如特殊的滤食系统及钙化作用等），能够对全球海洋碳汇做出重要贡献。本文聚焦于贝类养殖的碳汇功能、贝类养殖碳汇潜力、贝壳废弃物碳汇功能进行系统性探讨，旨在清晰梳理当前该领域研究现状、核算方法、影响因素以及现存问题，提出未来贝类养殖向多营养层次复合养殖为主，探索更加符合绿色可持续发展的贝类养殖模式以及贝壳废弃物资源化利用方向提供建议，为后续研究与实践提供部分参考依据，助力贝类养殖碳汇领域实现深入探索与发展。

关键词：贝类养殖，碳汇，碳汇核算，碳汇交易，贝壳废弃物

Carbon Sink Function of Farmed Shellfish

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Abstract：China, with its long history of shellfish aquaculture and leading global production, is well-positioned to contribute to its carbon peak goal through this industry. Given the context of global climate change, shellfish aquaculture offers a cost-effective and environmentally friendly carbon sink. Cultured shellfish sequester carbon via their filter-feeding systems and calcification processes. This review systematically explores the carbon sink function of shellfish aquaculture, its potential, and the role of shell waste. We aim to clarify the current research status, accounting methodologies, influencing factors, and existing challenges. Finally, we propose future directions, advocating for Integrated Multi-Trophic Aquaculture (IMTA) models and the resource utilization of shell waste, to provide references for sustainable development and further exploration in this field.

Key words: Shellfish cultivation; Carbon sequestration; Carbon accounting; Carbon trading; Shell waste

稻–青虾–罗氏沼虾高效生态轮作模式研究

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摘要：本模式在保持原有基本粮田不减产的情况下，探索了青虾、罗氏沼虾与稻田轮作综合种养技术，即上半年分别养殖青虾和罗氏沼虾，下半年种稻，充分利用稻田水土资源，并同时降低农药化肥等使用。通过试验测算，本模式利润比单纯种植水稻利润提高 10 倍左右，经济效益显著，且农药使用量减少 80%以上、化肥使用量减少 50%以上，具有较好的生态效益，值得相关地区示范推广。

关键词：青虾；罗氏沼虾；稻田

Study on Efficient Ecological Rotation Model of Rice-Macrobrachium nipponense and Macrobrachium rosenbergii

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Abstract： This model explores the comprehensive planting and breeding technology of rotating Macrobrachium nipponense, Macrobrachium rosenbergii, and rice fields while maintaining the original basic grain fields without reducing production. In the first half of the year, Macrobrachium nipponense and Macrobrachium rosenbergii are raised separately, and then planting rice, fully utilizing the water and soil resources of rice fields while reducing the use of pesticides and fertilizers. Through experimental calculations, the profit of this model is about 10 times higher than that of simply planting rice, with significant economic benefits. In addition, the use of pesticides is reduced by more than 80% and the use of fertilizers is reduced by more than 50%, which has good ecological benefits and is worthy of demonstration and promotion in relevant regions.

Key words: Macrobrachium nipponense；Macrobrachium rosenbergii； rice field

大鳞副泥鳅对高温低氧的生理响应

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摘要：本研究在稻鳅综合种养常见的温度及溶氧条件下（CC：7.5 mg/L、25℃；CG：7.5 mg/L、35℃；DC：1.5 mg/L、25℃；DG：1.5 mg/L、35℃）对大鳞副泥鳅进行 0、24、48、72 h 短期胁迫。转录组分析显示 48 h 鳃组织显著富集 MAPK、HIF-1、IL-17、JAK-STAT 及谷胱甘肽代谢通路，涉及应激、能量代谢、抗氧化和免疫应答。血浆检测发现 CC、CG 组葡萄糖（GLU）显著升高，DC 组 24 h 皮质醇（COR）显著升高，CC 和 DG 组亦呈上升趋势，表明高温低氧下鱼体处于轻度应激，仍以有氧代谢为主并通过糖代谢适应。肌肉 LDH、ATPase 活性下降，低氧组 SDH 活性上升，表明高温低氧胁迫下大鳞副泥鳅体内能量供应不足，有氧代谢能力增强。血浆 SOD、CAT、MDA、GSH-PX 含量上升，血浆 T-AOC 和肝脏 SOD、CAT、T-AOC 活力下降，但肝脏 MDA、GSH-PX 含量上升，说明机体通过提高抗氧化酶的活性缓解胁迫造成的氧化损伤。本研究阐明大鳞副泥鳅在高温低氧下通过调节糖代谢、信号通路和抗氧化系统实现部分适应，为稻田抗逆新品种选育提供理论依据。

关键词：转录组；应激；能量代谢；大鳞副泥鳅

Physiological responses of Paramisgurnus dabryanus to high-temperature and hypoxic stress

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Abstract: In this study, the large-scale loach was subjected to short-term stress for 0, 24, 48 and 72 h under the common temperature and dissolved oxygen conditions of integrated rice-loach culture (CC: 7.5 mg/L, 25℃; CG: 7.5 mg/L, 35℃; DC: 1.5 mg/L, 25℃; DG: 1.5 mg/L, 35℃). Transcriptome analysis revealed that the 48-h gill tissue was significantly enriched with MAPK, HIF 1, IL 17, JAK STAT and glutathione metabolic pathways, involving stress, energy metabolism, antioxidation and immune response. Plasma testing revealed that glucose (GLU) significantly increased in the CC and CG groups, and 24 h cortisol (COR) significantly increased in the DC group. The levels also showed an upward trend in the CC and DG groups, indicating that the fish were in a mild state of stress under high temperature and low oxygen, still mainly engaged in aerobic metabolism and adapted through glucose metabolism. The activities of muscle LDH and ATPase decreased, while the activity of SDH increased in the hypoxic group, indicating that under high-temperature and hypoxic stress, the energy supply in the body of the large-scale loach was insufficient, and its aerobic metabolic capacity was enhanced. The contents of SOD, CAT, MDA and GPx in plasma increased, while the activities of SOD, CAT and T-AOC in plasma T-AOC and liver decreased. However, the contents of MDA and GPx in liver increased, indicating that the body alleviated the oxidative damage caused by stress by increasing the activity of antioxidant enzymes. This study clarifies that large-scale loach achieves partial adaptation by regulating carbohydrate metabolism, signaling pathways and antioxidant systems under high temperature and low oxygen conditions, providing a theoretical basis for the breeding of new stress-resistant varieties in paddy fields.

Key words: RNA-seq; Stress response; Antioxidant capacity; Energy metabolism; Paramisgurnus dabryanus

不同水源罗氏沼虾育苗水体及微生物群落研究

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摘要：为揭示罗氏沼虾（*Macrobrachiumrosenbergii*）不同水源育苗期养殖水体微生物多样性，探索自来水与外塘水育苗的效果，采用 IlluminaHiSeq 高通量测序方法对不同水源罗氏沼虾育苗水体微生物的 16SrRNA 基因的 2 个高变区（V3—V4）进行测序分析，比较了自来水与外塘水罗氏沼虾育苗水体水质及微生物群落结构差异。结果表明：不同水源罗氏沼虾育苗水体的微生物群落结构不同，自来水育苗组中水样和虾苗分别检测出微生物 348 和 261 种，隶属于 21 和 19 个门；外塘水育苗组中水样和虾苗分别检测出微生物 330 和 263 种，分别隶属于 21 和 19 个门。CCA 结果显示大多数核心微生物菌如假丝酵母菌属、盐单胞菌属、嗜冷杆菌属、拟杆菌属等与亚盐、总氮、CODMn 相关性高。研究结果有助于深入探究不同水体微生物的多样性、功能及相互关系, 为罗氏沼虾育苗的健康管理提供科学依据。

关键词：罗氏沼虾；育苗；水体；微生物群落结构

Study on water body and microbial community of Macrobrachium rosenbergii in different water sources

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Abstract： In order to reveal the microbial diversity in the breeding water of *Macrobrachium rosenbergii* in different water sources during the breeding period, and to explore the effect of tap water and external pond water on the breeding of Macrobrachium rosenbergii, two hypervariable regions (v3-v4) of 16SrRNA Gene of microorganisms in the breeding water of Macrobrachium rosenbergii in different water sources were sequenced by illuminahiseq high-throughput sequencing method, and the differences in water quality and microbial community structure between tap water and external pond water were compared. The results showed that the microbial community structure was different in different water sources of Macrobrachium rosenbergii breeding water. CCA results showed that most core microorganisms such as Candida, Halomonas, psychrophilic bacilli and Bacteroides were highly correlated with subsalt, total nitrogen and COD. The results will help to explore the diversity, function and relationship of microorganisms in different water bodies, and provide a scientific basis for the health management.

Key words: Macrobrachium rosenbergii; Seedling raising; Water body; Microbial community structure

免预扩增 CRISPR 旁切信号放大的水产病原快速检测

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摘要：针对目标预扩增带来的耗时与污染风险，本文提出一种新型自放大的 CRISPR 检测方案：以核酸放大器级联合成可触发旁切的中间体，样品仅经热裂解即可直接进入一锅等温反应，约 40 min 完成判读。在代表性病原靶标上，实现 0.18 aM 核酸灵敏度与 1.2 CFU/mL 细菌检出；对 seed 区单碱基错配表现出更高分辨，并在血清等复杂基质中保持稳定特异。与传统“扩增+CRISPR”流程相比，该方法显著简化步骤、缩短决策时间，兼顾超敏、特异与现场可用性，适用于苗种筛查与池塘侧快速决策，能够为水产病原快速检测提供关键技术底座。

关键词：水产病原检测；CRISPR；信号自放大；超敏检测；单碱基分辨

Amplification-free CRISPR collateral amplification for rapid detection of aquatic pathogens

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Abstract： To address the time cost and contamination risk introduced by target pre-amplification, we propose a self-amplifying CRISPR assay: a nucleic-acid amplifier generates intermediates that trigger collateral (trans) cleavage, enabling one-pot isothermal detection directly after heat lysis, with results in ~40 min. On representative pathogen targets, the method achieves 0.18 aM nucleic-acid sensitivity and 1.2 CFU/mL bacterial detection; it shows enhanced single-nucleotide discrimination at seed-region mismatches and maintains high specificity in complex matrices such as serum. Compared with conventional “amplification + CRISPR” workflows, this approach streamlines steps and shortens time-to-decision, while jointly delivering ultrasensitivity, specificity, and field practicality. It is suited to hatchery screening and pond-side rapid decisions, and provides a key technical foundation for rapid detection of aquatic pathogens.

Key words: Aquatic pathogen detection; CRISPR; Self-amplifying signal; Ultrasensitive detection; Single-nucleotide discrimination

养殖密度对虹鳟幼鱼生长性能的影响

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摘要：研究密度对虹鳟（*Oncorhynchus mykiss*）幼鱼生长性能的影响可以为其苗种培育管理提供科学依据。将 60 尾幼鱼(体重 157±32 g)随机分为低密度组（8 尾/桶，30.2±8.7 kg/m^3）和高密度组（12 尾/桶，55.5±1.2 kg/m^3），各 3 个重复。实验鱼分别饲养在同一个循环水养殖系统的 6 个养殖桶中，每天投喂一次（投喂率约为 1.3%），实验持续 14 天，水温 20±2℃。测量每尾鱼的特定生长率（SGR）和每一桶鱼的饵料系数（FCR）。结果：低密度组和高密度组的 SGR 分别为 0.78±0.40 %d^{-1} 和 0.86±0.39 %d^{-1}（p = 0.509）；FCR 分别为 1.64±0.74%和 1.30±0.20%（p = 0.494）。结果表明，增加养殖密度(30.2 kg/m3 ~ 55.5 kg/m^3)对虹鳟的生长性能没有负面影响。

关键词：虹鳟；养殖密度；特定生长率；饵料系数

Effects of Stocking Density on the Growth Performance of Juvenile Rainbow Trout (*Oncorhynchus mykiss*)

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Abstract：Studying the effects of density on the growth performance of rainbow trout (*Oncorhynchus mykiss*) juveniles can provide a scientific basis for the management of fry cultivation.A total of 60 juvenile fish (body weight: 157 ± 32 g) were randomly divided into a low-density group (8 fish per tank, 30.2 ± 8.7 kg/m^3) and a high-density group (12 fish per tank, 55.5 ± 1.2 kg/m^3), with three replicates each. The experimental fish were reared in six tanks within the same recirculating aquaculture system. They were fed once daily (feeding rate approximately 1.3%), and the experiment lasted for 14 days at a water temperature of 20 ± 2°C. The specific growth rate (SGR) of each fish and the feed conversion ratio (FCR) of each tank were measured.The SGR of the low-density group and the high-density group were 0.78 ± 0.40 %/d and 0.86 ± 0.39 %/d, respectively (p = 0.509); the FCR values were 1.64 ± 0.74 and 1.30 ± 0.20, respectively (p = 0.494).The results indicate that increasing the stocking density (from 30.2 kg/m^3 to 55.5 kg/m^3) had no negative impact on the growth performance of rainbow trout.

Key words: Rainbow trout; Stocking density;Specific growth rate; Feed conversion ratio

不同固定化填料对藻菌共生系统尾水净化能力的影响

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摘要：随着海水养殖业的快速发展，尾水中污染物的高效去除成为亟待解决的环境问题，藻菌共生系统以其协同效应展现出显著优势。本研究以海水小球藻 Chlorella sp.为研究对象，通过筛选藻际细菌、优化藻菌比构建藻菌共生体，比较不同载体材质影响模拟养殖尾水中氮磷的去除效率及微生物挂膜的作用机制。结果表明：藻际细菌 *Pseudomonas* sp. ZB_2 显著促进海水小球藻生长，其与 *Chlorella* sp.的最佳生物量干重接种比为 4：1 时，叶绿素 a 含量提升 145.89%，证实藻菌协同效应可强化生物质积累与光合活性；3 种填料均可有效去除氨氮和活性磷酸盐，其中，G 组填料对硝态氮去除率最高，达 79.34%，Y 组和 W 组填料亚硝态氮积累量较低。G 组单位载体生物固定量为 0.042 g·cm-3，具有更高的微生物挂膜效率。本研究实现了对模拟养殖尾水的高效净化，为海水养殖尾水处理新技术提供理论依据，具有重要的应用前景。

关键词：养殖尾水；载体填料；藻菌共生；水处理；微生物群落

The Effects of Different Immobilized Carriers on the Purification Efficiency of Aquaculture Wastewater by Algal-Bacterial Symbiotic System

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Abstract: With rapid marine aquaculture development, efficient pollutant removal is urgently needed. The algal-bacterial symbiotic system shows significant synergistic advantages. Using *Chlorella* sp. and *Pseudomonas* sp. ZB_2 at a 4:1 ratio, chlorophyll a increased by 145.89%, enhancing biomass and photosynthesis. Three carriers effectively removed ammonium and active phosphate; Group G achieved the highest nitrate removal (79.34%) and superior biofilm formation (0.042 $g\cdot cm^{-3}$). This study provides a theoretical basis for new wastewater treatment technologies with promising application prospects.

Key words: Aquaculture wastewater; carrier; algal-bacterial symbiosis; water treatment

生物絮团零换水养殖系统中抗生素的时空动态、关键影响因素与来源追踪研究

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摘要：本研究以华南典型生物絮团零换水对虾养殖场为对象，全程追踪抗生素在“水源—池塘—絮团—饲料”链条中的时空分布与质量平衡。结果显示：①磺胺嘧啶与红霉素为优势抗生素，水源抗生素总量达同期池水的 1.3–3.9 倍（$p<0.05$），贡献超过 90%，饲料输入占比＜15%；②COD 与悬浮物（SS）是驱动抗生素迁移的核心因子，多元回归与冗余分析共同验证其主导作用；③在整个养殖周期内，池水抗生素浓度随养殖阶段递增，但虾体未检出目标抗生素，说明絮团吸附与生物降解可有效阻断其向可食部位传递。基于“水源主导输入—环境因子驱动—絮团阻断传递”的机制认识，提出“水源氧化消毒+益生菌调控”无抗化技术路线，为绿色高效养殖与全球水产品安全提供理论依据与落地路径。

关键词：抗生素；生物絮团；零换水；来源追踪；水产养殖；环境因子

Temporal Dynamics, Key Influencing Factors, and Source Tracking of Antibiotics in a Biofloc Zero-Water-Exchange Aquaculture System

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Abstract: Using a typical biofloc, zero-water-exchange shrimp farm in South China as the model, we tracked the spatiotemporal distribution and mass balance of antibiotics along the “source water–pond–biofloc–feed” continuum. Key findings are: (i) sulfadiazine and erythromycin-H_2O dominated, with total antibiotic concentrations in source water 1.3–3.9-fold higher than in pond water ($p < 0.05$), accounting for >90 % of the system input, whereas feed contributed <15 %; (ii) COD and suspended solids (SS) were the primary drivers of antibiotic mobility, as confirmed by multiple regression and redundancy analyses; (iii) antibiotic levels in pond water increased over the culture period, yet no target antibiotics were detected in shrimp muscle, indicating that biofloc adsorption and biodegradation effectively block their transfer to edible tissues. Grounded in the mechanism “source-dominated input–environment-driven migration–biofloc-obstructed transfer”, we propose an antibiotic-free protocol combining “source-water oxidative disinfection + probiotic modulation”, providing both a scientific basis and implementation path for green and efficient aquaculture and global aquatic product safety.

Key words: Antibiotics; Biofloc; Zero-water-exchange; Source tracking; Aquaculture; Environmental factors

乳突皮海鞘对长鳍篮子鱼幼鱼生长性能、肌肉营养成分和消化酶活性的影响

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摘要：本研究旨在比较不同饵料对长鳍篮子鱼（*Siganus oramin*）幼鱼生长性能、肌肉营养成分和消化酶活性的影响，探求长鳍篮子鱼幼鱼的消化机制，为长鳍篮子鱼生物防治乳突皮海鞘（*Molgula manhattensi*）提供理论依据。本研究进行为期 5 周的养殖实验，采用常规生化分析方法对该鱼肌肉营养学成分和消化酶活性进行测定分析。结果表明，人工饲料组的生长性能和必需氨基酸含量均显著高于乳突皮海鞘组（$P<0.05$），但乳突皮海鞘组的 Arg、Cys 和 Pro 含量均显著高于人工饲料组（$P<0.05$），EAAI 值较低。肌肉脂肪酸分析显示，两组的 EPA+DHA＞20%，乳突皮海鞘组的Σn-3/Σn-6 显著高于人工饲料组（$P<0.05$）。乳突皮海鞘组内源性和外源性消化酶活性都显著高于其他两组（$P<0.05$），尤其淀粉酶和纤维素酶。研究表明，乳突皮海鞘不能满足长鳍篮子鱼的营养需求，且拥有独特的消化机制。

关键词：长鳍篮子鱼；乳突皮海鞘；生长性能；肌肉营养成分：消化酶活性

Effects of Molgula manhattensi on growth performance, muscle nutritional composition, and digestive enzyme activity in juvenile *Siganus oramin*

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Abstract： This study aimed to compare different diets' effects on juvenile *Siganus oramin* growth, muscle nutrients, and digestive enzyme activities, explore its digestive mechanism, and offer a theoretical basis for Molgula manhattensi biological control via this fish. After a 5-week rearing experiment, routine biochemical analyses measured the fish's muscle nutrients and digestive enzyme activities.Results: The artificial feed group had significantly higher growth and EAA content than M. manhattensi group ($P<0.05$); the latter had significantly higher Arg, Cys, Pro but lower EAAI ($P<0.05$). Muscle fatty acids: EPA+DHA >20% in both groups, with M. manhattensi group showing a significantly higher Σn-3/Σn-6 ($P<0.05$). Additionally, M. manhattensi group had significantly higher endogenous/exogenous digestive enzyme activities (especially amylase, cellulase) than others ($P<0.05$).Conclusion: M. manhattensi fails to meet *S. oramin*'s nutritional needs, though the fish has a unique digestive mechanism.

Key words: Siganus oramin；Molgula manhattensi；growth performance；muscle nutritional composition；digestive enzyme activity

低聚糖替代葡萄糖构建生物絮团系统养殖罗氏沼虾对生长、免疫和肠道菌群的影响

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摘要：本研究评估低聚糖构建生物絮团系统对罗氏沼虾生长、免疫性能和肠道菌群的影响。结果显示，与对照组相比，SBOS 组、FS1 组和 FS2 组显著提高罗氏沼虾生长性能（$P<0.05$），FS2 组表现最佳。SBOS 组肠道胰蛋白酶活性显著高于 GLU 组（$P<0.05$）。FOS 组和 FS1 组肠道淀粉酶活性显著高于 GLU 组（$P<0.05$）。FS2 组 Propo、HSP70、TOLL-R、IGFI-R 和 ECR 表达量显著高于 GLU 组（$P<0.05$）。所有实验组 HSP70、NF-κB、TOLL-R 和 ECR 表达量显著高于 GLU 组（$P<0.05$）。16S 测序结果显示，实验组提高放线菌门的丰度，FS2 组显著提高多核杆菌属（*Polynucleobacter*）和 *Nakamurella* 的丰度，并降低葡萄球菌属（*Staphylococcus*）的丰度（$P<0.05$）。

关键词：大豆低聚糖；低聚果糖；微生物群落；生物絮团；罗氏沼虾

Effects of oligosaccharides instead of glucose on growth, immunity, intestinal flora of *Macrobrachium rosenbergii* in biofloc system

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Abstract：This study evaluated the effects ofSBOS andFOS as carbon sources in biofloc technology (BFT) systems on growth, intestinal microbiota, and immune performance of *Macrobrachium rosenbergii*. Compared with the control group, the SBOS group, FS1 group and FS2 groups significantly improved the growth performance of Macrobrachium rosenbergii ($P<0.05$), and the FS2 group performed the best.The intestinal trypsin activity in SBOS group was significantly higher ($P<0.05$). The intestinal amylase activity was significantly higher in the FOS and FS1 groups($P<0.05$). the expression levels of Propo, HSP70, TOLL-R, IGFI-R and ECR in the FS2 group were significantly higher ($P<0.05$). The expression levels of HSP70, NF-κB, TOLL-R and ECR in all experimental groups were significantly higher ($P<0.05$).The results of 16S sequencing showed that the experimental group increased the abundance of Actinomycetes, and the FS2 group significantly increased the abundance of Polynucleobacter and Nakamurella, and decreased the abundance of Staphylococcus ($P<0.05$).

Key words: Soybean oligosaccharides, fructooligosaccharide, microbial community, bioflocs, Macrobrachium rosenbergii

人工礁体缝隙缓解刺参胁迫效应及促进生长的研究

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摘要：刺参是我国北方高产值海水养殖物种。基于其偏好缝隙的习性，人工礁体被广泛应用，但其缓解环境胁迫与促进生长的系统研究仍缺乏。本研究聚焦人工礁体缝隙的调控功能，探究其能否：1）改善高温下空气暴露与疾病胁迫的存活、患病和行为；2）缓解机械扰动后的行为与生理响应；3）预防性减轻操作胁迫；4）提升消化能力与生长性能。结果表明：缝隙显著提高了高温与空气暴露或疾病复合胁迫下刺参的存活率，降低患病率，并改善黏附与蠕动行为。还能缓解机械扰动导致的摄食下降与生理抑制，促进行为恢复。长期在缝隙中养殖可预防性增强刺参对操作胁迫（如空气暴露、机械扰动）的抵抗能力，表现为黏附时间延长、翻正时间缩短等。此外，缝隙养殖显著改善肠道形态（如肌层厚度、黏膜层厚度等），提高胃蛋白酶活性，从而促进刺参生长和增重。研究证实人工礁体缝隙通过提供微生境有效缓解多种胁迫，促进刺参健康生长，为优化养殖模式提供理论依据。

关键词：刺参；缝隙；胁迫；生长

Artificial Reef Crevices Alleviate the Responses to Stress and Promote the Growth in the Sea Cucumber *Apostichopus japonicus*

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Abstract： The sea cucumber *Apostichopus japonicus* is a high-value mariculture species along the northern coast of China. Their preference for crevices has led to the widespread application of artificial reefs in aquaculture. This study focuses on the regulatory function of crevices in artificial reefs, systematically evaluating the role of crevices in artificial reefs in alleviating environmental stress and promoting growth. Results show crevices significantly improved survival and behavior under high-temperature combined stresses (air exposure and disease). They also alleviated behavioral and physiological inhibition post-mechanical disturbance. Long-term crevice habituation enhanced resistance to handling stress, improving adhesion and reducing righting time. Furthermore, crevices improved intestinal morphology and pepsin activity, thereby enhancing growth performance. This study confirms that artificial reef crevices effectively mitigate multiple stressors and promote healthy growth in sea cucumbers, providing a theoretical basis for optimizing aquaculture practices.

Key words: Sea cucumbers; Crevice; Stress; Growth

亲鱼繁殖状态跟踪：红鳍东方鲀体斑识别与生长检测

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摘要：为了提高红鳍东方鲀亲鱼管理水平，利用其体斑特征对个体进行识别，并追踪其体重、体长、体宽和头宽生长变化，结合繁殖记录来监测其繁殖状态。结果显示，红鳍东方鲀胸斑斑纹丰富多样，足以识别 20 个以上不同个体；通过体长体重关系，以及估计性腺指数 eGSI 和体宽头宽比 BHR（Ratio of body width and head width），可以追踪亲鱼繁殖周期变化，并预测繁殖时间。结果表明，红鳍东方鲀亲鱼可通过胸斑特征进行个体识别，进而追踪个体生长和形态变化，评估繁殖状态。

关键词：鱼类福利；亲鱼管理；体斑特征；个体识别；性腺发育

Broodstock reproductive condition prediction:Body colour patten identification and growth measurements in tiger puffer, *Takifugu rubripes*

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Abstract: To enhance the broodstock management of *Takifugu rubripes*, individual identification was conducted based on body spot characteristics, with subsequent tracking of growth variations in body weight, length, width, and head width. This was combined with reproductive records to monitor their reproductive status. The results revealed that the pectoral spot patterns of Takifugu rubripes are sufficiently diverse to distinguish over 20 individuals. By analyzing the relationship between body length and weight, along with estimated gonadosomatic index (eGSI) and the ratio of body width to head width (BHR), cyclical changes in broodstock reproduction could be tracked, enabling prediction of spawning timing. The findings demonstrate that Takifugu rubripes broodstock can be individually identified via pectoral spot characteristics, allowing for the monitoring of individual growth and morphological changes, as well as assessment of reproductive status.

Key words: Takifugu rubripes; Broodstock management; Body colour pattern; Individual identification; Gonadal development

植物源黄酮对水产纤毛虫的体外抗虫作用机制研究及体内抗虫效果评价

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摘要：纤毛虫感染是水产养殖业面临的重大生物威胁。植物源药物因其环境友好、低毒和低成本的优势，成为替代化学药物的研究热点。前期研究发现补骨脂提取物对梨形四膜虫具有显著抑制作用。通过分离筛选，我们鉴定出五种活性黄酮成分，其中补骨脂乙素能诱导嗜热四膜虫产生氧化应激、线粒体损伤和细胞死亡，提示其作用机制可能与线粒体通透性转变有关。基于此，我们构建了包含 55 种植物源黄酮的化合物库，并筛选出 12 种对嗜热四膜虫具有显著活性的黄酮。后续研究将深入探讨这些黄酮对线粒体膜通透性的影响，以阐明其作用机制。此外，研究将进一步评估这 12 种黄酮对多种水产纤毛虫的体外抗虫活性，并以孔雀鱼为模型进行安全性评价。对存活率超过 50%的化合物，将测定其半致死浓度，以筛选出高效低毒的候选药物。最终，我们将通过建立鱼类感染模型，评估优选化合物的体内抗虫效果。本研究旨在为水产纤毛虫防治提供新思路和科学依据，推动绿色渔药的研发。

关键词：植物源黄酮、纤毛虫、抗虫作用机制、水产养殖

Mechanism of Plant-Derived Flavonoids Against Aquatic Ciliates In Vitro and Evaluation of Their Antiparasitic Efficacy *In Vivo*

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Abstract： Ciliate infections pose a significant threat to aquaculture. Plant-based pharmaceuticals present eco-friendly alternatives for combating these infections. In our study, extracts from Psoralea corylifolia have demonstrated notable anti-parasitic activity. we isolated five flavonoids, with Isobavachalcone identified as a compound that induces mitochondrial damage in Tetrahymena thermophila via permeability transition. From a library of 55 flavonoids, we identified 12 with strong anti-ciliate activity. We plan to investigate their mitochondrial effects to elucidate the underlying mechanisms. These compounds will be tested against multiple aquatic ciliate species. Utilizing guppy models, we will assess the safety of these compounds and determine the lethal concentrations for those exhibiting over 50% survival rates. Additionally, a fish infection model will be employed to evaluate in vivo efficacy.This research endeavors to offer novel insights and a scientific foundation for the prevention and treatment of aquatic ciliates, thereby advancing the development of eco-friendly fishery drugs.

Key words: plant-derived flavonoids;ciliate ; anti-parasitic mechanisms;aquaculture

刺参摄食行为和贴壁行为的初步研究

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摘要：刺参是具有重要经济价值的水产物种，其水产养殖管理在很大程度上依赖于对行为的理解。摄食行为和贴壁行为是刺参重要的行为。因此，研究摄食行为和贴壁行为对于提高刺参养殖生产效率具有重要意义。在摄食行为研究中，探讨了多巴胺的调控机制。结果表明，注射多巴胺能显著提升刺参的摄食量，其作用机制在于延长了摄食时间，而非增加摄食频率。鉴于芽孢杆菌可有效产生多巴胺，进一步研究发现，在饲料中添加芽孢杆菌同样能通过延长摄食时间，显著提高刺参摄食量。在贴壁行为研究中，比较了偏好贴壁与不贴壁个体的差异。发现偏好贴壁的刺参摄食能力更强，表现为摄食量更大、觅食时间更短及摄食时间更长；同时，它们还表现出更强的耐高温能力。而偏好不贴壁的个体则具有更高的淀粉酶活性和摄食频率，暗示其消化效率更高。基于以上发现，建议在增养殖过程中增设垂直礁体以满足贴壁个体的需求，并在礁体外滩面投喂饲料以促进不贴壁个体的摄食。

关键词：刺参；摄食行为；贴壁行为；多巴胺；芽胞杆菌；CTmax

Preliminary study on feeding and adherence behavior of sea cucumber *Apostichopus japonicus*

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Abstract： *Apostichopus japonicus* is an important aquatic economic species in China. The management of its aquaculture largely depends on the understanding of its behaviors. Therefore, it is important to explore feeding behavior and adherence behavior of sea cucumbers. In the study of feeding behavior, the regulatory mechanism of dopamine was investigated. The results showed that injecting dopamine could significantly increase the feeding intake of sea cucumbers. The mechanism of action was that it prolonged the feeding duration rather than increasing the feeding frequency. Further research found that dietary Bacillus could also significantly increase the food intake of sea cucumbers by prolonging the feeding time. In the study of adherence behavior, it was found that sea cucumbers that preferred to adhere had stronger feeding ability and stronger heat tolerance. While those preferred not to adhere had higher amylase activity and feeding frequency, suggesting higher digestive efficiency. Therefore, we have provided corresponding suggestions to optimize the aquaculture management model.

Key words: sea cucumber, feeding behavior, adherence behavior, dopamine, Bacillus subtilis, CTmax

盐碱胁迫对罗氏沼虾生长、生理生化及转录表达的影响

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摘要：本研究开展了盐度和碳酸盐碱度对罗氏沼虾苗的 LC50、LOEC 研究，探究了罗氏沼虾对盐碱胁迫响应机制。结果显示, 盐度对罗氏沼虾虾苗的 96 h-LC50 为 27.1，96 h-LOEC 为 16.5；碳酸盐碱度对罗氏沼虾虾苗的 96 h-LC50 为 230.7 mg/L，96 h-LOEC 为 96.6 mg/L；盐碱交互作用表现出协同效应。罗氏沼虾幼苗鳃和肝胰腺中 AKP 和 Na+-K+-ATPase 活性随胁迫时间延长呈先降后升的趋势, 鳃中 Ca2+-ATPase 则呈现相反的变化趋势；肝胰腺中 SOD 活性在胁迫中期(72 h 和 120 h)达到最低水平。转录组分析结果显示，鳃组织中四次跨膜蛋白、脂肪醛脱氢酶、次级活性跨膜转运蛋白相关基因在盐碱胁迫下表达上调，表明罗氏沼虾可能通过协同增强鳃的离子转运和提高肝胰腺的碳水化合物跨膜转运来适应盐碱环境。

关键词：罗氏沼虾，盐碱胁迫，生理生化，代谢通路，渗透压调节，离子转运

The effects of saline-alkali stress on the growth, physiology, biochemistry and transcriptional expression of *Macrobrachium rosenbergii*

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Abstract：This study conducted a relevant investigation on the LC50 and LOEC of *Macrobrachium rosenbergii* in relation to salinity and alkalinity, and explored the response mechanism to salt and alkali stress. Results showed that the 96 h-LC50 of salinity was 27.1, with a 96 h-LOEC of 16.5, whereas the 96 h-LC50 of alkalinity was 230.7 mg/L, with a 96 h-LOEC of 96.6 mg/L. Salt-alkali interaction exhibited synergistic effects. Enzyme activity analysis revealed initial decreases followed by increases over time for alkaline phosphatase and Na^+-K^+-ATPase activities, whereas Ca^{2+}-ATPase activity exhibited the opposite pattern. Transcriptomic analysis revealed distinct responses to saline-alkaline stress. Up-regulated genes associated with tetraspanin,fatty aldehyde dehydrogenase, and secondary active transmembrane transporters. These results suggest that M. rosenbergii adapts to saline-alkaline environments through coordinated osmotic regulation strategies. This study provides scientific evidence for understanding the adaptation mechanisms of M. rosenbergii in saline-alkaline environments.

Key words: *Macrobrachium rosenbergii*; salt-alkaline stress; physiological and biochemical; metabolic pathways; osmotic regulation; ion transport

光棘球海胆筏式养殖适宜密度初步研究

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摘要：为探索光棘球海胆筏式养殖养苗期的适宜养殖密度，本研究在辽宁大连小王家岛海域开展实验。使用规格 1×0.66×0.52m 的塑料筐，投放平均壳径 15.64mm、体重 2.14g 的苗种，设置 1500、2000 和 2500 只/筐三个密度组，于 5m 水层养殖 6 个月。结果显示，2000 只/筐组的成活率（43.14%）和出苗总重量（7809.21g）最高，但与其余两组无显著差异（$P>0.05$）。该组出苗量为 863 只/筐，显著高于 1500 只/筐组（409 只，$P<0.05$）。1500 只/筐组的平均体重达 10.72g，显著高于 2000 只/筐组（9.08g）和 2500 只/筐组（8.89g）（$P<0.05$）。研究表明，在光棘球海胆筏式养苗过程中，1500 只/筐密度可获得更优个体规格，而 2000 只/筐密度有利于提高出苗量。建议根据养殖目标选择适宜密度，以提升经济效益。本研究结果为开发光棘球海胆筏式养殖新模式提供了技术参考。

关键词：光棘球海胆；养苗期；筏式养殖；养殖密度

A Preliminary Study on the Optimal Stocking Density for Raft-Based Culture of the Sea Urchin *Strongylocentrotus nudus*

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Abstract： Stocking Density Optimization in Raft Culture of *Strongylocentrotus nudus*. This study investigated optimal stocking density for nursery-phase Strongylocentrotus nudus in raft culture near Xiao Wangjia Island, Dalian. Juveniles (mean diameter: 15.64 mm; weight: 2.14 g) were reared in plastic crates (1.0×0.66×0.52 m) at 5 m depth for six months at 1500, 2000, and 2500 individuals/crate. The 2000-individual/crate group showed highest survival (43.14%) and total weight (7809.21 g), though not statistically significant ($P>0.05$). Its yield (863 individuals/crate) significantly exceeded the 1500-individual group (409 individuals, $P<0.05$). Conversely, the 1500-individual group achieved significantly higher average weight (10.72 g) than the 2000 and 2500-individual groups (9.08 g and 8.89 g, $P<0.05$). Results demonstrate 1500 individuals/crate optimizes individual growth, while 2000 individuals/crate maximizes yield. Density selection should align with production goals to enhance profitability, providing technical guidance for raft-based S. nudus aquaculture.

Key words: The sea urchin Strongylocentrotus nudus;Nursery Phase;Raft aquaculture;Stocking density

氮循环菌群驱动下的生物絮团系统氮动态与氮平衡：促进对虾高效可持续养殖

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摘要：生物絮团技术（BFT）通过微生物活动原位回收氮废物，为对虾养殖提供了一种可持续替代方案。然而，商业规模系统中氮循环菌群驱动氮动态与平衡的机制尚不明确。本研究在凡纳滨对虾商业化 BFT 系统中整合了氮平衡分析、宏基因组测序和对虾生产性能指标。经过 56 天养殖，系统在有限水交换（2%-8%/天）下实现产量 7.87 kg/m³ 、饲料系数 1.17 和成活率 94.3%。氮平衡显示：38.1%的输入氮被对虾吸收，20.2%以硝酸盐形式存在于水体，15.0%随絮团排出，26.6%以气体形式损失。宏基因组分析发现以变形菌门和拟杆菌门为主的稳定氮循环菌群，关键功能基因（如 amoA、nirK、nosZ）表明系统存在活跃的硝化与反硝化作用。相关性分析证实氮循环菌群调控无机氮形态和絮团水平，从而提升氮利用率。我们提出了一个机制模型，强调异养同化和耦合的硝化-反硝化作用是氮去除和系统稳定的关键驱动因素。这些发现为优化 BFT 系统氮管理提供了实用策略，推动对虾养殖的可持续发展。

关键词：生物絮团技术，氮循环，宏基因组学，对虾养殖，可持续水产养殖

Nitrogen Dynamics and Balance Driven by Nitrogen-Cycling Bacteriome in a Commercial Biofloc System for Sustainable Shrimp Production

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Abstract：Biofloc technology (BFT) represents a sustainable alternative to traditional shrimp farming by recycling nitrogenous wastes through microbial activity. However, the mechanisms underlying nitrogen (N) dynamics and balance driven by N-cycling bacteriomes in commercial-scale systems remain poorly understood. This study integrated N balance analysis, metagenomic sequencing, and shrimp performance metrics in a commercial BFT system for *Penaeus vannamei* over 56 days. Results showed efficient shrimp production with a yield of 7.87 kg/m³, FCR of 1.17, and survival rate of 94.3%, while maintaining limited water exchange (2%–8% daily). Nitrogen balance revealed that 38.1% of input N was recovered in shrimp biomass, 20.2% accumulated as nitrate in water, 15.0% discharged as bioflocs, and 26.6% was lost as gas. Metagenomic analysis identified a stable yet dynamic N-cycling bacteriome dominated by Proteobacteria and Bacteroidetes, with key functional genes (e.g., amoA, nirK, nosZ) indicating active nitrification and denitrification. Correlation analyses confirmed that N-cycling bacteria regulated inorganic N species and biofloc levels, enhancing N utilization efficiency. We propose a mechanistic model highlighting the roles of heterotrophic assimilation and coupled nitrification–denitrification as key drivers of N removal and system stability. These findings provide practical strategies for optimizing N management in BFT systems, promoting sustainable and efficient shrimp production.

Key words: Biofloc technology，Nitrogen cycling，Metagenomics，Shrimp aquaculture，Sustainable aquaculture

基于多维度分析的不同养殖模式对香螺生长及相关生理生态指标影响的研究

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摘要：为解决黄渤海区域香螺（*Neptunea arthritica cumingii*）自然资源减少的产业瓶颈，明确其最优人工养殖模式，本研究以香螺为对象，开展 120 d 养殖实验（每 40 d 取样），对比吊笼、池塘、室内三种模式对其生长、组织结构、酶活性及肠道菌群的影响。结果显示，生长与结构上，吊笼组增重率、存活率显著高于其他两组（$P<0.05$），120 d 时肠绒毛形态最优，吸收能力更强；酶活性方面，吊笼组鳃组织丙二醛含量最低、过氧化氢酶活性最高，肝脏谷胱甘肽及肠道超氧化物歧化酶、脂肪酶活性均显著更优（$P<0.05$），抗氧化与消化效率突出；肠道菌群中，三组核心优势菌均为绿脓杆菌，吊笼组与池塘组存在 8 条显著差异二级代谢通路（$P<0.05$）。综上，吊笼养殖模式综合表现最优，可为香螺人工养殖产业提供科学依据。

关键词：养殖模式；生长；酶活；组织结构；肠道菌群

Study on the Effects of Different Aquaculture Modes on the Growth and Related Physiological and Ecological Indicators of *Neptunea arthritica cumingii* Based on Multi-Dimensional Analysis

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Abstract：To address the industrial bottleneck of declining natural resources of *Neptunea arthritica cumingii* in the Bohai and Yellow Sea regions and identify its optimal artificial culture mode, this study conducted a 120-day culture experiment (with sampling every 40 days) using Neptunea arthritica cumingii as the research object. The experiment compared the effects of three culture modes—cage culture, pond culture, and indoor culture—on the growth, tissue structure, enzyme activity, and intestinal microflora of the species.The results showed the following: In terms of growth and structure, the weight gain rate and survival rate of the cage culture group were significantly higher than those of the other two groups ($P<0.05$). At 120 days, the intestinal villi of the cage culture group exhibited the optimal morphology and stronger absorption capacity. Regarding enzyme activity, the cage culture group had the lowest malondialdehyde content and the highest catalase activity in gill tissue; additionally, the glutathione content in the liver, as well as the superoxide dismutase and lipase activities in the intestine, were significantly superior ($P<0.05$), indicating outstanding antioxidant and digestive efficiency. For intestinal microflora, Pseudomonas aeruginosa was the core dominant bacterium in all three groups. There were 8 significantly different secondary metabolic pathways between the cage culture group and the pond culture group ($P<0.05$).In conclusion, the cage culture mode showed the best comprehensive performance, which can provide a scientific basis for the artificial culture industry of Neptunea arthritica cumingii.

Key words: aquaculture modes; growth; enzyme activity; tissue structure; intestinal microflora

盐度驱动下铁碳人工湿地脱氮效能与微生物组动态的互馈机制研究：面向海水养殖尾水处理

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摘要：针对铁碳人工湿地（Fe-C-CWs）中盐度驱动的氮去除机制在水产养殖尾水处理中的研究尚不充分。通过为期 155 天的四组盐度试验（S0、S10、S20、S30），结果表明 S20 组对总氮（84.9±3.1%）、硝酸盐（81.8±2.5%）和铵氮（79.3±3.0%）的去除效果最优，显著优于其他组别（$P < 0.05$）。宏基因组学分析显示，S20 组显著富集了反硝化类群（海硫杆菌属(*Halothiobacillus*)、长杆菌属(*Prolixibacter*)），并上调了氮循环基因（*nirB*、*nrfA*、*nrfH*、*hao*）与铁循环基因（*feoA*、*feoB*），揭示了微生物组成与生物地球化学循环过程的功能协同作用。首次应用于 Fe-C-CWs 的双同位素标记（$\delta^{15}N_{NO2}/\delta^{18}O_{NO2}$）证实盐度介导了路径转换：含盐组以亚硝酸盐氧化为主导，S20 组尤为显著，而 S0 组则以还原作用为主。酶谱分析验证了所有组别中硝化、反硝化与厌氧氨氧化途径的同步运行，其活性呈现显著的盐度依赖性调控。S20 组表现出显著的酶促增强效应，其中核心氮循环酶——亚硝酸盐氧化还原酶（NXR: 8.79 ± 0.67 U/g）、硝酸还原酶（NAR: 18.13 ± 1.19 U/g）和亚硝酸还原酶（NIR: 6.74 ± 0.47 U/g）活性较 S0 组提升 16.00~32.18%（$P < 0.01$）。这种酶协同效应表明盐度优化了异化铁还原与氮转化过程的耦合。生态网络分析揭示了微生物门级水平（特别是变形菌门(Proteobacteria)与浮霉菌门(Planctomycetota)）的显著相互作用。本研究表明，S20 盐度能强化铁碳基质与微生物的互作关系，从而提升 Fe-C-CWs 对水产养殖尾水中氮污染物的去除效能。研究结果为深入理解 Fe-C-CWs 内部运行机制提供了理论依据。

关键词：铁碳人工湿地；盐度；水产养殖尾水；氮去除；宏基因组学

Salinity-driven trade-offs between nitrogen removal and microbiome dynamics in Fe-C-CWs toward saline aquaculture tailwater management

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Abstract： Salinity-driven nitrogen removal mechanisms in iron-carbon CWs (Fe-C-CWs) remain poorly understood for aquaculture tailwater management. Through a 155-day trial under four salinities (designated as S0, S10, S20, and S30), result showed that S20 achieved optimal removals of total nitrogen (84.9±3.1%), nitrate (81.8±2.5%), and ammonium (79.3±3.0%), significantly outperforming other groups ($P < 0.05$). Metagenomics revealed that S20 significantly enriched denitrifying taxa (Halothiobacillus, Prolixibacter) and upregulated nitrogen cycling genes (nirB, nrfA, nrfH, hao) and iron cycling genes (feoA, feoB), highlighting the functional synergy between microbial composition and biogeochemical cycling processes. Dual isotope signatures (δ15NNO2/ δ18ONO2) first applied in Fe-C-CWs confirmed salinity-mediated pathway shifts: nitrite oxidation dominated in saline groups, especially in S20 versus reduction in S0. Enzymatic profiling substantiated the concurrent operation of nitrification, denitrification, and anammox pathways across all groups, with activities exhibiting significant salinity-dependent modulation. S20 demonstrated remarkable enzymatic potentiation, where core nitrogen-cycling enzymes including nitrite oxidoreductase (NXR: 8.79 ± 0.67 U/g), nitrate reductase (NAR: 18.13 ± 1.19 U/g), and nitrite reductase (NIR: 6.74 ± 0.47 U/g) showed 16.00~32.18% higher than S0 ($P < 0.01$). This enzymatic synergy suggests salinity-optimized coupling between dissimilatory iron reduction and nitrogen transformation processes. Ecological network analysis revealed significant interactions among microbial phyla, particularly between Proteobacteria and Planctomycetota. This study demonstrates that S20 can enhance interaction between Fe-C matrix and microorganisms, thereby improving the efficiency of Fe-C-CWs in removing nitrogen pollutants from aquaculture tailwater. These findings offer theoretical insights for further understanding the internal operational mechanisms of the Fe-C-CWs.

Key words: Iron-carbon CWs (Fe-C-CWs); Salinity; Aquaculture tailwater; Nitrogen removal; Metagenomic

光照条件对藻菌共生系统处理海水养殖尾水的影响

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摘要：围绕水产绿色健康养殖需求，本研究以海水小球藻与复合菌剂构建藻菌共生系统，系统探讨了光照条件（光谱、光强、光周期）对海水养殖尾水处理效能的影响。结果表明，红光（660 nm）最有利于促进生物质积累与脱氮除磷，叶绿素 a 含量较白光提高 54.8%，NH_4^+-N 和 NO_3^--N 去除率分别达 94.49%和 93.76%，并提升了反硝化相关菌属丰度。在 300 $\mu mol\cdot m^{-2}\cdot s^{-1}$光强下，系统生物质产量与脱氮性能最优，Chl a 含量达 7.28 mg/L，NH_4^+-N 去除率接近完全；而过高光强（400 $\mu mol\cdot m^{-2}\cdot s^{-1}$）则引起光抑制。16L:8D 光周期进一步强化系统稳定性与污染物去除能力，PO_4^{3-}-P 可在 2 天内完全去除，藻菌代谢活性增强，氮代谢通路基因表达上调。综上，通过优化光照条件，本研究构建了高效、稳定的藻菌共生尾水处理系统，为实现水产养殖尾水氮磷资源化与可持续发展提供了技术支撑。

关键词：藻菌共生系统；海水养殖尾水；光照调控；脱氮除磷；绿色养殖

Effects of light conditions on the treatment of mariculture tail water by algae-bacteria symbiotic system

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Abstract： Focusing on green aquaculture, this study developed an algae-bacteria system with marine Chlorella and composite bacteria, examining how light conditions affect mariculture wastewater treatment. Red light (660 nm) best enhanced biomass and nutrient removal, increasing chlorophyll a by 54.8% versus white light. NH_4^+-N and NO_3^--N removal reached 94.49% and 93.76%, respectively, enriching denitrifying bacteria. At 300 $\mu mol\cdot m^{-2}\cdot s^{-1}$, biomass and nitrogen removal were optimal, with Chlorella at 7.28 mg/L and nearly complete NH_4^+-N removal. Higher intensity (400 $\mu mol\cdot m^{-2}\cdot s^{-1}$) caused inhibition. A 16L:8D photoperiod strengthened system stability, removed PO_4^{3-}-P within two days, and upregulated nitrogen metabolism genes. Optimized lighting thus creates an efficient algae-bacteria system, supporting sustainable aquaculture through nutrient recycling.

Key words: Algae-bacteria symbiotic system; Mariculture tail water; Light regulation; Nitrogen and phosphorus removal; Green aquaculture

循环水系统中光照周期对日本对虾(*Penaeus japonicus*)生长及血清生化指标的影响

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摘要：光照是循环水养殖系统中的关键环境因子，研究其对水产动物的影响是实现健康高效养殖的核心环节。为优化循环水养殖的光环境管理，本研究探讨了 0L:24D 至 24L:0D 五种光照周期对日本对虾（*Penaeus japonicus*）的影响。结果表明：24L:0D 组的增重率（WGR）和特定生长率（SGR）最高（$P<0.05$），12L:12D 组次之。血清指标显示，12L:12D 组的皮质醇（COR）和葡萄糖（GLU）含量最低，且生长性能良好，表明其处于低应激状态并保持稳健生长；而持续光照或黑暗条件下，抗氧化酶活性及脂质代谢指标出现应激性波动。综合生长与健康指标分析表明，尽管持续光照能最大化生长速度，但 12L:12D 周期能在促进良好生长的同时，更有效地维持机体代谢稳定和健康状态，是实现健康高效养殖的较理想光照模式。本研究为对虾循环水养殖的光照策略提供了实践依据。

关键词：日本对虾； 光照周期 ；循环水养殖系统； 生长性能 ；血清生化

Effects of Photoperiod on Growth and Serum Biochemical Parameters of *Penaeus Japonicus* in Recirculating Aquaculture System

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Abstract： As a critical environmental factor in recirculating aquaculture systems (RAS), light management plays a vital role in achieving healthy and efficient aquaculture. This study evaluated the effects of five photoperiods (0L:24D to 24L:0D) on Penaeus japonicus. Results indicated that the 24L:0D group exhibited the highest weight gain rate (WGR) and specific growth rate (SGR) ($P < 0.05$), followed by the 12L:12D group. Serum biochemical analysis revealed the lowest levels of cortisol (COR) and glucose (GLU) in the 12L:12D group, along with satisfactory growth, suggesting low stress and steady growth. In contrast, continuous light or darkness induced stress-related fluctuations in antioxidant enzyme activities and lipid metabolism. Although 24L:0D promoted maximum growth, the 12L:12D photoperiod achieved an optimal balance between growth performance and physiological health, making it preferable for sustainable RAS-based Penaeus japonicus culture. These findings support practical light management strategies for Penaeus japonicus aquaculture.

Key words: Penaeus japonicus; photoperiod; recirculating aquaculture systems; growth index; serum biochemical parameters

夏眠期刺参肠道菌群与宿主共代谢特征研究

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摘要：为探究刺参夏眠适应机制，本研究基于 16S 高通量测序与非靶向代谢组学，分析夏眠期刺参肠道菌群结构与代谢变化。结果显示，夏眠显著降低肠道菌群丰度与多样性，但主要菌门构成未变，相对丰度发生显著演替：变形菌门由 86.59%降至 48.71%，拟杆菌门由 2.03%升至 8.06%，疣微菌门由 1.13%升至 19.65%。共现网络表明夏眠后菌群网络节点、边数与正相关作用比例下降，模块化程度上升，*Enterorhabdus*、*Dubosiella* 等成为高中心性类群。代谢组学识别 232 种差异代谢物，包括丝氨酸、油酸酰胺等 155 种上调，异戊酸、花生四烯酸等 77 种下调，主要涉及不饱和脂肪酸与氨基酸代谢通路。整合分析表明 271 种代谢物与高中心性菌群显著相关。研究表明，刺参通过增强肠道菌群稳定性，促进氨基酸与不饱和脂肪酸代谢，优化营养利用以适应夏眠。本研究为无脊椎动物热应激响应机制提供理论参考。

关键词：夏眠；刺参；肠道菌群；共代谢

Research on the Characteristics of Co-metabolism between intestinal flora and Host in *Apostichopus japonicus* during Aestivation Period

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Abstract： To investigate the adaptation mechanisms of sea cucumbers (*Apostichopus japonicus*) during aestivation, this study utilized 16S high-throughput sequencing and untargeted metabolomics to analyze the intestinal microbiota structure and metabolic changes. The results showed that aestivation significantly reduced the richness and diversity of the intestinal microbiota, while the composition of the dominant phyla remained unchanged, with significant shifts in relative abundance: Proteobacteria decreased from 86.59% to 48.71%, Bacteroidetes increased from 2.03% to 8.06%, and Verrucomicrobia increased from 1.13% to 19.65%. Co-occurrence network analysis revealed a decrease in the number of nodes, edges, and the proportion of positive correlations in the microbial network after aestivation, along with an increase in modularity. Genera such as Enterorhabdus and Dubosiella became highly central taxa. Metabolomic analysis identified 232 differential metabolites, including 155 upregulated (e.g., serine, oleamide) and 77 downregulated (e.g., isovaleric acid, arachidonic acid), primarily involved in unsaturated fatty acid and amino acid metabolism pathways. Integrated analysis indicated that 271 metabolites were significantly correlated with highly central microbial taxa. The study demonstrates that sea cucumbers enhance intestinal microbiota stability, promote amino acid and unsaturated fatty acid metabolism, and optimize nutrient utilization to adapt to aestivation. This research provides theoretical insights into the thermal stress response mechanisms of invertebrates.

Key words: Aestivation;Apostichopus japonicus; intestinal flora; Co-metabolism

热应激下虹鳟（*Oncorhynchus mykiss*）肠道微生物群重塑与肠道屏障破坏的温度依赖性

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摘要：热应激通过破坏宿主生理功能和肠道稳态，严重威胁水产养殖物种。本研究通过生化、组织学、分子和微生物组学方法，研究了虹鳟（*Oncorhynchus mykiss*）在中度（21°C）和重度（24°C）热应激下的肠道反应。结果显示，21°C 下抗氧化反应增强，而 24°C 下氧化损伤加剧，MDA 水平升高。组织学分析显示，24°C 下肠道损伤和细胞凋亡加重。基因表达分析表明，热休克蛋白和硫氧还蛋白显著诱导，屏障基因（OCLN、ZO1）表达双相变化，提示肠道屏障受损。微生物群分析发现，24°C 下肠道菌群重构，菌群丰富度下降，β多样性改变，耐热和厌氧菌（如肠球菌、裂殖芽孢杆菌）富集，相关功能通路涉及能量代谢和氨基酸合成等。研究表明，24°C 是生理临界点，增加氧化应激，破坏肠道屏障并促进菌群失衡，凸显虹鳟在热应激下，尤其是肠道健康方面的脆弱性。

关键词：肠道微生物学；组织病理学；肠道；虹鳟；热应激

Heat stress in rainbow trout (*Oncorhynchus mykiss*): Intestinal dysregulation linking histopathology, oxidative stress, and microbiome-host dynamics

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Abstract：Heat stress disrupts aquaculture species by impacting physiology and gut health. This study examined the intestinal responses of rainbow trout (*Oncorhynchus mykiss*) under moderate (21°C) and severe (24°C) heat stress using biochemical, histological, molecular, and microbiome methods. At 21°C, antioxidant responses were enhanced, while 24°C caused oxidative damage. Histopathological analyses showed greater intestinal injury and apoptosis at 24°C. Gene expression indicated compromised gut integrity, with elevated heat shock proteins and changes in barrier genes (OCLN, ZO1). Microbiota analysis revealed reduced gut diversity and increased stress-tolerant, anaerobic, biofilm-forming bacteria (e.g., *Enterococcus, Lysinibacillus*). These findings highlight 24°C as a tipping point that worsens oxidative stress, damages gut integrity, and promotes dysbiosis, increasing rainbow trout's vulnerability to heat stress, particularly in gut health.

Key words: Gut microbiology; Histopathology; Intestine; Rainbow trout; Thermal stress

北方地区刀鲚大棚越冬试验

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摘要：刀鲚在北方寒冷地区的越冬过程中，低温胁迫导致高死亡率，严重限制了养殖产业的发展。本研究旨在通过暖棚与加热棒相结合的技术，优化越冬环境，提升成活率并完善养殖管理措施。试验采用聚乙烯池、玻璃钢池和帆布池三种养殖模式，通过暖棚控制水温，同时监测水质参数、病害发生及鱼体生长情况。水质管理通过泼洒活化菌液和合理换水实现，病害防治采用提高盐度控制水霉病，并使用头孢曲松（2 ppm）治疗杀鲑气单胞菌感染。即使在外界气温降至-24 ℃的条件下，水温仍能维持在 14 ℃左右，显著降低了低温对鱼类的胁迫。帆布池成活率最高（99.03%），显著优于聚乙烯池和玻璃钢池，实现了整体成活率 63.52%。暖棚与加热棒技术为北方寒冷地区刀鲚越冬提供了一种科学有效的解决方案。帆布池在降低鱼体损伤和提高成活率方面表现最佳。本研究为寒冷地区鱼类越冬养殖提供了技术支持，为水产养殖业的可持续发展提供了重要参考。

关键词：刀鲚；越冬养殖；暖棚；病害防治；北方地区

Overwintering culture experiment of Coilia nasus in greenhouse in northern China

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Abstract： For Coilia nasus overwintering in cold northern regions, low-temperature stress causes high mortality, limiting aquaculture. This study optimizes overwintering conditions, improves survival, and refines management via warm sheds + heating rods.The experiment used three tanks: polyethylene, FRP, canvas. Warm sheds controlled water temperature; water quality, diseases, fish growth were monitored. Water quality: activated bacterial solution + proper water changes. Diseases: increased salinity for saprolegniasis, ceftriaxone (2 ppm) for Aeromonas salmonicida.Even at -24 ℃ external temp, water temp stayed ~14 ℃, reducing cold stress. Canvas tanks had highest survival (99.03%)—better than polyethylene/FRP—with 63.52% overall survival.Warm sheds + heating rods offer a scientific solution for Coilia nasus overwintering in cold north. Canvas tanks best reduced fish damage and boosted survival. This study supports cold-region fish overwintering and provides key references for sustainable aquaculture.

Key words: Coilia nasus; overwintering aquaculture; greenhouse shelter; disease control; northern regions

高温应激通过改变粘膜完整性、免疫信号和微生物群落破坏凡纳滨对虾的肠道功能稳态

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摘要：本研究将凡纳滨对虾持续暴露于 33°C 的高温应激下 7 天，研究了肠道功能稳态的变化。结果表明，高温应激导致肠上皮脱落和粘膜损伤，以及粘液屏障的破坏。氧化应激相关基因如 ROMO1、Nrf2、GPx 和 HO1 表达上调，而 SOD 表达下调；免疫基因如 Crus 和 proPO 表达上调，而 ALF、Pen3 和 Lys 表达下调；炎症基因（JNK 和 NF-κB）和自噬基因（Atg3、Atg12、Beclin1 和 Hsc70）的表达均上调。肠道微生物多样性未显著变化，但群落组成的丰度受到扰动，特别是有害细菌（弧菌属和发光杆菌属）和有益细菌（拟杆菌属、芽孢杆菌属、乳酸杆菌属和乳酸球菌属）的稳态。此外，肠道微生物群的磷酸转移酶系统功能增强，而 N-聚糖生物合成和糖胺聚糖降解等功能减弱。这些结果表明，高温应激通过诱导粘膜损伤、诱导免疫反应、激活氧化应激、炎症和自噬信号通路以及重塑微生物群落，破坏了肠道功能稳态。

关键词：对虾；高温；肠道；生理反应；微生物群

High-temperature stress impairs the intestinal functional homeostasis of *Litopenaeus vannamei* by altering mucosal integrity, immune signaling, and microbial community

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Abstract: This study continuously exposed *Litopenaeus vannamei* to high-temperature stress at 33°C for 7 days and investigated the changes in intestinal functional homeostasis. The results showed that high-temperature stress led to intestinal epithelial detachment, mucosal damage, and disruption of the mucus barrier. The expression of oxidative stress-related genes such as ROMO1, Nrf2, GPx, and HO1 was upregulated, while the expression of SOD was downregulated; the expression of immune genes such as Crus and proPO was upregulated, while the expression of ALF, Pen3, and Lys was downregulated; the expression of inflammatory genes (JNK and NF-κB) and autophagy genes (Atg3, Atg12, Beclin1, and Hsc70) was upregulated. Although intestinal microbial diversity did not change significantly, the abundance of community composition was disturbed, particularly the homeostasis of harmful bacteria (*Vibrio* and *Photobacterium*) and beneficial bacteria (*Bacteroides*, *Bacillus*, *Lactobacillus*, and *Lactococcus*).

Key words: Shrimp; High temperature; Intestine; Physiological response; Microbiota

金鳟与虹鳟肝脏对模拟运输胁迫的响应差异：抗氧化、能量代谢与转录组表达谱分析

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摘要：金鳟为虹鳟突变品系，以金色色素沉着及抗逆性差异为特征，是鲑科鱼类应激反应研究的独特模型。为探究其与虹鳟（WR）的肝脏抗氧化能力、能量代谢、病理学及转录组差异，对两种鳟鱼（1000±5.5 g）开展 6 小时模拟运输实验（振动 20-30 Hz、密度 300 kg/m³），每种鱼设对照（CG）和运输组（TG），每组 6 尾（酶活检测 n=6 / 组 / 种；转录组分析 TG 中 n=3 / 种）。运输应激致两者肝脏氧化损伤，但金鳟更严重。虹鳟则增强糖酵解活性、优先无氧代谢以适应。病理显示金鳟肝损伤更重。转录组筛选出 322 个差异表达基因（DEGs）（141 上调、181 下调）：它们富集于氧化应激、脂肪酸降解等通路。研究证实，运输应激通过“炎症 - 凋亡”网络影响生理功能，11 个 DEGs 的 qRT-PCR 验证佐证了 RNA-seq 可靠性，为鲑科鱼类运输差异化抗应激管理提供依据。

关键词：虹鳟；金鳟；肝脏；运输应激适应；响应差异

Differential Responses of Golden Trout and Rainbow Trout Livers to Simulated Transport Stress: A Comparative Analysis of Antioxidant, Energy Metabolism, and Transcriptome Profiles

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Abstract： Golden trout, a rainbow trout (Oncorhynchus mykiss) mutant with golden pigmentation and distinct stress resistance, is a unique salmonid stress research model. A 6-hour simulated transport experiment (20-30 Hz vibration, 300 kg/m³ density) was performed on golden trout and rainbow trout (WR, 1000±5.5 g), with control (CG) and transport (TG) groups (6 fish/group; enzymatic assay: n=6/group/species; transcriptome: n=3/species in TG).Transport stress induced hepatic oxidative damage in both, with golden trout more severely affected. WR adapted via enhanced glycolysis and prioritized anaerobic metabolism, while golden trout showed worse liver lesions pathologically. Transcriptome identified 322 differentially expressed genes (DEGs: 141 up-, 181 downregulated), enriched in oxidative stress, fatty acid degradation and other pathways.The study confirmed transport stress impacts physiology via the "inflammation-apoptosis" network. qRT-PCR validation of 11 DEGs confirmed RNA-seq reliability, providing a basis for differential anti-stress management of salmonids during transportation.

Key words: Rainbow trout; Golden trout; Liver; Transport stress adaptation; Response differences

银鲳间歇性禁食过程中补偿生长分子调控机制的研究

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摘要：银鲳在间歇性禁食过程中表现出显著的加速生长。为研究该背后的调控机制，我们建立了银鲳完全补偿生长的间歇性禁食模式，并进行了转录组和代谢组测序。基于组学分析发现，在饥饿后，大量脂类、氨基酸被分解录用；在复投后，许多合成代谢被启动。基于组学及定量结果，发现 IGF1-IGFBP3 复合物可能在整个过程起着关键调节作用。构建银鲳肌肉细胞间歇性禁食模型，筛选出 9h 低营养/3h 正常培养（S9R3）下产生细胞活性完全补偿恢复效应，在该模型中 qPCR 验证 IGF1-IGFBP3 上下游基因，发现这些基因表达趋势与鱼体中类似。在模型中敲降 IGF1-IGFBP3 上下游基因，在大多数实验组中，细胞活性没有恢复，但在 IGF1R 敲降组中部分恢复。与对照组相比，仅在 NC 组和 siRNA-IGF1R 组中，S9R3 组的与合成代谢相关的正向调节基因上调。基于上述结果，我们发现银鲳间歇性禁食后的补偿生长主要是由于 IGF1 的在饥饿过程中与 IGFBP3 结合后大量累积，在恢复后 IGF1 与 IGFBP3 解离后大量产生游离 IGF1 促进合成代谢，进一步提高饲料的转化率，最终产生补偿生长效应。

关键词：银鲳；间歇性禁食；补偿生长；代谢调控；

Research on the Molecular Mechanisms Regulating Compensatory Growth in Silver Pomfret During Intermittent Fasting

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Abstract： Silver pomfret exhibits remarkable accelerated growth during intermittent fasting. To further investigate the mechanisms, we established a full compensatory growth model and conducted RNA-Seq analyses of the fish. Based on our RNA-Seq and qPCR analysis, we identified that IGF1-IGFBP3 complex may play a critical role in regulation in this process. To test it, we developed a fasting-recovery cell model and analyzed expression of genes associated with IGF1. We employed RNAi to knock down expression levels of GHR, IGF1, IGFBP3, and IGF1R. In most experimental groups, there was no recovery of cell activity; however, partial compensatory recovery was observed in siRNA-IGF1R group. The anabolism positive regulatory genes were up-regulated in S9R3 group compared to control only within NC and siRNA-IGF1R groups. These findings suggest that there is significant accumulation of IGF1-IGFBP3 complex during fasting periods. Following re-feeding, free IGF1 dissociates from this complex to promote anabolic processes without AMPK inhibition, thereby facilitating accelerated growth.

Key words: Silver Pomfret; Intermittent Fasting; Compensatory Growth; Metabolic Regulation

第二专题 水产生物技术与遗传育种

杂交扇贝闭壳肌杂种优势的遗传调控机制初探

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摘要：本研究以海湾扇贝（♀）与紫扇贝（♂）杂交子代（海紫 F_1 ）为材料，针对其闭壳肌重呈现 231.06%超强杂种优势的现象，采用多组学方法系统解析杂种优势的遗传调控机制。重点从线粒体 DNA（mtDNA）拷贝数变化及线粒体-细胞核互作角度探究海紫 F_1 横纹肌发育优势的成因。结果表明：海紫 F_1 横纹肌中线粒体呈母系遗传，mtDNA 拷贝数显著提升至 238.05 个/细胞，电镜观察结果支持这一发现；相关性分析显示，mtDNA 拷贝数与横纹肌重量、横截面积、肌纤维数量及 ATP 含量均呈显著正相关；进一步机制研究表明，mtDNA 拷贝数增加和线粒体基因高效表达共同促使肌纤维增粗（优势率 103.25%）和增生（优势率 45.10%）。结果提示，线粒体功能增强是海紫 F_1 杂种优势的重要驱动因素，线粒体与核基因组之间的互作协调了肌肉性状的显著改良。该研究为海洋贝类杂种优势机制提供了新视角，对扇贝遗传育种实践具有重要指导意义。

关键词：杂种优势；闭壳肌；线粒体动态；核质互作

A Preliminary Study on the Genetic Regulatory Mechanism of Heterosis in the Adductor Muscle of *Hybrid Scallops*

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Abstract：This study investigated hybrid F_1 scallops (*bay* ♀ × *Peruvian* ♂) exhibiting exceptional heterosis (231.06%) in adductor muscle weight. Multi-omics analyses revealed significantly increased mtDNA copy number (238.05/cell) under maternal inheritance, supported by microscopy. mtDNA copy number correlated positively with muscle weight, cross-sectional area, fiber number, and ATP content. Increased mtDNA copy number and enhanced mitochondrial gene expression jointly promoted muscle fiber hypertrophy (103.25%) and hyperplasia (45.10%). Enhanced mitochondrial function and mitochondria-nucleus interactions are key drivers of heterosis, providing new insights into molluskan heterosis and guidance for genetic breeding.

Key words: Heterosis; Adductor muscle; Mitochondrial dynamics; nu-mt interaction

runx2b 基因调控鱼类肌间刺形成的分子机制研究

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摘要：肌间刺是由肌膈间的肌腱骨化而来，仅存在低等真骨鱼类中,降低鱼类经济价值。为明确鱼类肌间刺形成的关键细胞群，我们首先利用单细胞转录组测序技术(scRNA-seq)明确了野生型斑马鱼肌肉组织(含肌间刺)的 18 个细胞 cluster，筛选到了与肌间刺形成相关的肌腱祖细胞，肌腱分化细胞，成熟肌腱细胞和成骨细胞，拟时序分析结果表明肌间刺是由肌腱祖细胞分化为肌腱分化细胞，再分化为成骨细胞而形成的。根据表达模式筛选出了 10 个在成骨细胞类群中高表达且与肌间刺形成的关键基因。最终发现 runx2b 基因突变斑马鱼肌间刺完全缺失，且其他骨骼的形成、个体生长、肌肉脂肪酸和氨基酸组成成份等性状没有受到显著影响。单细胞测序分析发现斑马鱼 runx2b 基因突变体的肌肉组织（不含肌间刺）中成骨细胞的数量是显著减少，在个体和细胞水平明确了 TGF-β/BMP signaling pathway 在肌间刺形成过程中发挥重要调控作用。

关键词：肌间刺，鱼类，scRNA-seq，runx2b，基因编辑，肌腱细胞-成骨细胞谱系

MOLECULAR MECHANISM OF RUNX2B REGULATING THE FORMATION OF INTERMUSCULAR BONES

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Abstract： Intermuscular bones (IBs), the small bone embedded in muscle, are commonly found in major freshwater cultured fish species, and affect consumption, food processing, and export earnings. The molecular mechanism of IBs in teleosts remains not fully understood. Single-cell RNA sequencing (scRNA-seq) showed 18 distinct cell types were defined in wild-type zebrafish. Differentiation trajectories showed that IBs are derived from tendons and that a core tendon-osteoblast cell lineage is related to IB formation and selected out 10 key genes. Function analysis showed that runx2b-/- mutants completely lost IBs. scRNA-seq analysis in runx2b-/- and runx2b+/+ zebrafish revealed the role of osteoblasts in IB formation. In addition, differentially expressed genes were enriched in the transforming growth factor β pathway after runx2b deletion. This study provides evidence for the crucial role of runx2b regulation in IB formation. Genetic breeding can target runx2b regulation and generate strains of commercial fish species without IBs, which can improve the safe consumption and economic value.

Key words: IBs，teleosts, runx2b, scRNA-seq, tendon-osteoblast cell lineage, gene editing

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

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

单环刺螠耐高温性状全基因组关联分析及全基因组选择研究

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摘要：单环刺螠（*Urechis unicinctus*）是一种新兴趣的高经济价值水产物种，富含蛋白质和必需氨基酸，营养价值与海参媲美。其主要分布于我国环渤海沿岸，夏季高温威胁其生存，制约养殖业发展。鉴定耐高温相关 SNP 及候选基因，对选育耐高温新品种具有重要意义。本研究对 180 个个体进行全基因组重测序，获得 17,693,070 个高质量 SNP 用于全基因组关联分析（GWAS），鉴定出 209 个耐高温相关 SNP 和 318 个候选基因。精细定位（Fine-mapping）发现关键变异，经 Sanger 测序验证与耐高温性状显著相关。RNA 干扰（RNAi）实验表明，干扰 CAD 和 KLHL15 基因后个体耐高温能力显著降低。七种基因组选择（GS）模型比较显示，RRBLUP 模型最适合单环刺螠耐高温性状基因组预测。本研究为阐明耐高温分子机制、开展标记辅助选择及培育耐高温新品种奠定了基础，将促进养殖业可持续发展。

关键词：单环刺螠

关键词：单环刺螠；GWAS；SNP；高温耐受；CAD；KLHL15；RNAi；GS

Genome wide association study and genomic selection of heat tolerance in Urechis unicinctus

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Abstract： Urechis unicinctus is an emerging aquaculture species with high economic value. It is rich in protein and essential amino acids, with nutritional value similar to sea cucumbers. High summer temperatures threaten its survival and limit aquaculture development. Identifying SNPs and candidate genes will aid breeding for improved summer adaptation and expanded cultivation. We performed whole genome resequencing of 180 individuals, obtaining 17,693,070 high quality SNPs for GWAS. We identified 209 heat tolerance related SNPs and 318 candidate genes. Fine-mapping identified causal variants, and Sanger sequencing validated a key SNP significantly associated with heat tolerance. RNA interference of CAD and KLHL15 genes significantly reduced heat tolerance, confirming their important functions. Comparison of seven genomic selection models showed RRBLUP was most suitable for genomic prediction of heat tolerance. These results provide a foundation for understanding heat tolerance mechanisms and breeding heat tolerant varieties, accelerating aquaculture development for U. unicinctus.

Key words: Urechis unicinctus; GWAS; SNP; heat tolerant; CAD; KLHL15; RNAi; GS

基于生理学、转录组和代谢组综合分析，揭示不同体重的三倍体虹鳟鱼脂肪沉积、代谢和免疫的变化

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摘要：体尺是鱼类一个显著的重要性状，体重是影响鱼类代谢的主要因素之一。对不同体重（SRT，0.61± 0.19kg; MRT，1.39± 0.27kg; LRT，2.58± 0.38kg）的三倍体虹鳟的血清生化指标、转录组和代谢组进行了研究。结果表明：SRT 组 SOD 含量显著高于 LRT 组（$P<0.05$），蛋白质羰基含量显著低于 LRT 组（$P>0.05$）。vdac3、plin1、lpl 和 adipoqa 等 DEG 可能与三倍体虹鳟鱼的脂肪沉积和免疫力密切相关。代谢组学分析显示，LRT 组与 MRT 组中的差异丰度代谢物（DAM）在“氨基酸生物合成”途径中显著富集（$P<0.05$），而 LRT 组与 MRT 组中的 DAM 在“氨基酸生物合成”途径中显著富集（$P<0.05$）。SRT 组在“5-羟色胺突触”通路上明显富集（$P<0.05$）。MRT 组与 SRT 组相比，DAM 在“脂肪酸代谢”和“脂肪酸降解”等途径中显著富集（$P<0.05$）。

关键词：三倍体虹鳟，转录组学，代谢组学，关联分析

Integrative analysis of physiology, transcriptome, and metabolome reveals the alterations in fat deposition, metabolism and immunity of triploid rainbow trout (*Oncorhynchus mykiss*) with different body weights

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Abstract： Body size is an evident and significant property of fish, and body weight is one of the major elements influencing fish metabolism. In this study, the serum biochemical parameters, transcriptomes and metabolomes of triploid rainbow trout with different body weights (SRT, 0.61±0.19 kg; MRT, 1.39±0.27 kg; LRT, 2.58±0.38 kg) were examined. The results revealed that the SOD content in the SRT group was significantly greater than that in the LRT group ($P<0.05$), and the protein carbonyl level was significantly lower than that in the LRT group ($P>0.05$). Oil red O staining of muscle tissue revealed that LRT had greater level of lipid deposition than MRT and SRT. The results of KEGG pathway annotation of differentially expressed genes (DEGs) revealed that the DEGs vdac3, plin1, lpl and adipoqa may be closely related to fat deposition and immunity in triploid rainbow trout. Metabolomic analysis revealed that the differentially abundant metabolites (DAMs) in the LRT vs. MRT group were significantly enriched in the “amino acid biosynthesis” pathway ($P<0.05$).

Key words: Triploid rainbow trout, transcriptomics, metabolomics, association analysis

赤眼鳟补体因子 D 基因鉴定及抗 GCRV 感染作用初探

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摘要：赤眼鳟（*Squaliobarbus curriculus*）对草鱼呼肠孤病毒（GCRV）表现出极强的抵抗能力。为探究其分子机制，本研究聚焦于补体因子 D（ScDF），该丝氨酸蛋白酶是补体替代途径的关键调控因子。分子克隆显示，ScDF 基因编码一个 250 个氨基酸的蛋白质。生物信息学分析发现，ScDF 在 Asn139 处有一个独特的 N-糖基化位点，这在草鱼（CiDF）中不存在。尽管其催化三联体及底物结合残基均保守，且与 CiDF 氨基酸同源性达 94.4%，该结构差异仍具有重要意义。组织表达分析表明，ScDF 在肝脏中组成性高表达，其次为心脏。在 GCRV 感染赤眼鳟肾细胞（SCK）后，ScDF 转录在 6 hpi 即急剧上调至 438 倍（$p < 0.001$），反应早于草鱼中 CiDF 的峰值（168 hpi）。功能实验证实，过表达 ScDF 可抑制病毒衣壳基因（VP2、VP5、VP7）表达并上调干扰素调节因子 IRF9；重组 ScDF 激活干扰素和补体 C3 通路。这些结果表明，ScDF 的快速诱导和免疫激活是杠铃抗 GCRV 的基础，为抗病毒育种提供了见解。

关键词：赤眼鳟；草鱼呼肠孤病毒；赤眼鳟补体因子 D；早期免疫反应；结构表征

Molecular Characterization and Antiviral Function Against GCRV of Complement Factor D in Barbel Chub (*Squaliobarbus curriculus*)

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Abstract： The barbel chub (*Squaliobarbus curriculus*) exhibits strong resistance to grass carp reovirus (GCRV). This study investigates complement factor D (DF), a key protease in innate immunity. We cloned ScDF, which encodes a 250-aa protein containing a unique N-glycosylation site (Asn139) not found in grass carp DF (CiDF). ScDF retains critical catalytic residues and shows 94.4% identity with CiDF. It is highly expressed in the liver and heart. Upon GCRV infection, ScDF transcription increased 438-fold at 6 hpi—much earlier than CiDF in grass carp. Overexpression of ScDF suppressed viral genes (VP2, VP5, VP7) and enhanced IRF9. Recombinant ScDF activated interferon and complement C3 pathways. These results indicate that rapid ScDF induction and immune activation underlie barbel chub's GCRV resistance, offering insights for antiviral breeding.

Key words: barbel chub; GCRV; ScDF; early response; structural characterization

基于转录组与代谢组解析墨西哥湾扇贝南北养殖群体应对高温胁迫的调控机制

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摘要：墨西哥湾扇贝（*Argopecten irradians concentricus*）是我国南方重要的贝类养殖品种，具有优良的耐高温性状。本研究以中国南部湛江种群（SM）与自湛江引种、在烟台繁育了四代的北方种群（NM）为对象，探讨两个群体耐高温机制的异同。结果显示，SM 组的 96h 高温半致死温度（31.81±0.14℃）显著高于 NM 组（29.25±0.06℃）（$p < 0.05$）。转录组分析表明，NM 组上调基因主要富集于能量和代谢相关通路，而 SM 组富集于抗逆相关通路。代谢组进一步揭示 SM 组具有更丰富的代谢调控模式。通过加权基因共表达网络分析（WGCNA）分析鉴定出 GPX1、CYP2B5 和 PLA2G4A 三个关键基因。联合分析发现代谢物白三烯 C4（Leukotriene C4）在 NM 和 SM 组中均显著富集，且与上调基因 CAT 呈显著正相关。生理学表明高温胁迫下 SM 组具有更强的抗氧化防御能力。

关键词：墨西哥湾扇贝；高温胁迫；转录组学；代谢组学；血细胞；酶活性

Comparative transcriptomic and metabolomic analyses reveal different tolerance mechanisms to heat stress in two geographic populations of *Argopecten irradians* concentricus

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Abstract：The bay scallop southern subspecies, *Argopecten irradians* concentricus, well known for its high temperature tolerancet. In this study, we investigated the mechanisms underlying heat stress tolerance in two geographically distinct populations of A. i. concentricus, the southern population (SM) from Zhanjiang in southern China and the northern population (NM), which was originally transplanted from Zhanjiang and reared for 4 generations in Yantai waters. NM displayed reduced heat tolerance compared to SM. Comparative transcriptomic analyses, NM predominantly up-regulated energy and metabolic pathways, including carbohydrate, amino acid, and lipid metabolism, whereas SM enhanced the expression in immune-related pathways. Metabolomic profiling indicated more complex metabolic alterations in SM than NM. Weighted Gene Co-expression Network Analysis (WGCNA) identified key genes strongly associated with heat stress, including GPX1, CYP2B5, and PLA2G4A. Physiological analyses demonstrated that SM possessed stronger antioxidant defenses and immune parameters than NM.

Key words: Argopecten irradians concentricus; heat stress; transcriptomic; metabolomic; haemocyte; enzymatic activity

虾青素对青海湖裸鲤生长性能、抗氧化能力、免疫功能和转录水平的影响

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摘要：为阐明虾青素诱导的青海湖裸鲤碱性胁迫响应机制，并为虾青素在该鱼种饲料中的应用提供理论依据。将初始平均体重 21.02 ± 1.15 克的 900 尾幼鱼分为 5 组，每组设 3 个重复，每个重复 60 尾。对照组（AS0）饲喂基础饲料，实验组分别添加 25 mg/kg（AS25）、50 mg/kg（AS50）、100 mg/kg（AS100）或 200 mg/kg 虾青素（AS200）。培养 8 周后，分析饲料中虾青素对青海湖裸鲤生长性能、抗氧化能力及免疫功能的影响。随后对添加最佳剂量虾青素的鱼种进行碱性胁迫实验，从转录组水平分析饲料中虾青素对青海湖裸鲤抗碱性胁迫能力的作用。与 AS0 组相比，AS50 组的特定生长率、肝体比和脂肪含量显著更高，AS200 组的增重率达到峰值。转录组分析显示，肝脏组织中的差异表达基因在新霉素、卡那霉素和庆大霉素生物合成途径、铁死亡及类固醇生物合成通路中显著富集。

关键词：虾青素；青海湖裸鲤；抗氧化剂；免疫应答；转录组

Effects of dietary astaxanthin on growth performance, antioxidant capacity, immune function and transcription level of *Gymnocypris przewalskii*

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Abstract： To clarify the alkaline-stress response mechanism of Gymnocypris przewalskii induced by astaxanthin, and to provide theoretical basis for the application of astaxanthin in the diet of *G.przewalskii*.A total of 900 juvenile G.przewalskii with an initial average body weight of 21.02 ± 1.15 g were divided into 5 groups with 3 replicates per group and 60 fish per replicate. The control group (AS0) was fed a basal diet, and the experimental diets were supplemented with 25 mg/kg (AS25), 50 mg/kg (AS50), 100 mg/kg (AS100), or 200 mg/kg astaxanthin (AS200). After 8 weeks of culture, the effects of dietary astaxanthin on the growth performance, antioxidant capacity, and immune function of G.przewalskii were analyzed. We subsequently conducted alkalic stress experiments on G.przewalskii fed the optimal amount of supplemental astaxanthin to analyze the effects of dietary astaxanthin on the alkalic stress resistance of G.przewalskii at the transcriptome level.

Key words: astaxanthin; Gymnocypris przewalskii; antioxidant; immune response; transcriptome

“福瑞鲤 2 号”遗传特性及其种质利用

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摘要：“福瑞鲤 2 号”是运用多性状综合选育技术培育出的生长快、成活率高的国审水产新品种，每代遗传进展 7%。从基因组进化角度探明“福瑞鲤 2 号”具有更强生长、适应和存活力的分子机理。通过转录组分析，鉴定出了与肌肉生长相关的关键基因。在“福瑞鲤 2 号”中克隆得到 igf3 基因两个亚型，建立 igf3 基因被敲降的鲤活体模型，获得了差异表达的 lncRNAs 和 mRNA。获得了“福瑞鲤 2 号”早期发育 6 个主要阶段的 microRNA 和 lncRNA-mRNA 表达谱。通过全基因组关联分析（GWAS）解析 6 个锦鲤品种与 2 种体色“福瑞鲤 2 号”的遗传结构，挖掘到与体色差异显著相关的 18 个 SNP 位点。转录组和蛋白组联合分析在“福瑞鲤 2 号”和从江田鱼中发现大量与能量代谢和骨骼肌肉发育相关的差异基因和蛋白。“福瑞鲤 2 号”可用于锦鲤、稻田鱼等的改良。

关键词：福瑞鲤 2 号，遗传特性，种质，利用

Genetic characteristics of FFRC no. 2 strain common carp and its germplasm utilization

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Abstract： FFRC No. 2 (FR) strain common carp (Cyprinus carpio) is a nationally approved new aquaculture variety with a primary objective to improve the growth and survival rates. Genomic evolution analysis explained the improved growth rate and survival rate of the FR strain. Transcriptomic analysis revealed several key genes related to muscle growth Full-length sequences of two igf3 subtypes (igf3a and igf3b) were cloned from FR, and the knockdown model was established by RNA interference yielding differentially expressed lncRNAs and mRNAs. The microRNA and lncRNA-mRNA profiles of six important embryonic development stages FR were obtained. The GWAS analysis resolved population structure of six koi strains and two color FR strains, and identified several SNPs that were significantly related to skin color variation. Transcriptome and proteome analyses revealed differential genes and proteins related to energy metabolism and skeletal muscle development in FR. FR germplasm can be used for the improvement of koi carp and rice fish.

Key words: FFRC no. 2 strain common carp, genetic characteristics, germplasm, utilization

刺参骨片发生规律及其分子机制研究

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摘要：为探究刺参骨片发生规律和分子机制，本研究先进行形态学观察，结果显示，刺参大耳状体时已产生骨片（X 状体），五触手时大量出现。樽型至五触手过渡过程，X 状体分化为桌形体和花纹状体。桌形体骨片随着年龄呈“先发育再退化”。其次，针对骨片形成的两个关键时期进行转录组测序，差异表达分析揭示 Nitrogen metabolism、Vascular smooth muscle contraction 和 ECM-receptor interaction 等信号通路在骨片形成中起核心调控作用，筛选出 CA2、ELC-2、COL1A2、papilin-like 等基因。RNAi 敲降 papilin-like 基因后桌形体四周出现刺状突起，证明其对骨片形态建构有作用。本研究为不同发育时期刺参骨片形态学研究奠定基础，并为进一步研究刺参骨片分子机制提供理论依据。

关键词：刺参；骨片；转录组测序；分子机制

Development Patterns and Molecular Mechanisms of Ossicle in *Apostichopus japonicus*

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Abstract： The ossicles, crucial calcified structures in *Apostichopus japonicus*, begin forming at the auricularia stage as X-shaped structures, proliferating significantly during the pentactula stage. They differentiate into table-shaped and rose-shaped ossicles during the doliolaria-to-pentactula transition, with table-shaped ossicles showing developmental degeneration. RNA-Seq revealed nitrogen metabolism, vascular smooth muscle contraction, and ECM-receptor interaction pathways as core regulators. Functional validation identified papilin-like gene as critical for ossicle morphogenesis, as its knockdown induced spiny protrusions on table-shaped ossicles. This study elucidates ossicle development dynamics and molecular mechanisms, providing a foundation for further research.

Key words: *Apostichopus japonicus*；ossicle；transcriptome sequencing；molecular mechanism

Beta–Hexosaminidase A 基因的两个亚型在日本沼虾卵巢发育中的功能分析

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摘要：β-己糖胺酶 A（Hexosaminidase）在配子识别中具有重要作用，但其在甲壳动物中的功能未知。本研究在日本沼虾中发现两个β-己糖胺酶 A 亚型（Mn-HexA1 和 Mn-HexA2）。Mn-HexA1（1641bp）和 Mn-HexA2（1473bp）分别编码 546 和 490 个氨基酸，具有五个相同功能结构域，但氨基酸相似性仅为 58.43%。表达分析显示 Mn-HexA1 表达量显著高于 Mn-HexA2，且在肝胰腺中表达最高，繁殖季节显著上调。两个基因在卵巢和肝胰腺发育 2 期达到峰值。RNA 干扰实验表明，沉默 Mn-HexA1 和 Mn-HexA2 均显著促进卵巢发育（第 13 天实验组 III 期比例分别为 67.49%和 55.49%，对照组 36.91%），且 Mn-HexA1 沉默效果更强。结果表明 Mn-HexA 基因抑制卵巢成熟，且 Mn-HexA1 的抑制作用强于 Mn-HexA2。

关键词：日本沼虾；β-己糖胺酶 A；卵巢发育

Functional Characterization of Two β-Hexosaminidase A Isoforms During Ovarian Development in *Macrobrachium nipponense*

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Abstract： In Macrobrachium nipponense, two β-hexosaminidase A isoforms (Mn-HexA1 and Mn-HexA2) were identified and characterized. Mn-HexA1 (1641 bp, encoding 546 aa) and Mn-HexA2 (1473 bp, 490 aa) share five functional domains but exhibit only 58.43% amino acid similarity. Expression analysis revealed consistently higher Mn-HexA1 levels across all tissues and developmental stages. Both genes showed hepatopancreas-specific enrichment and breeding season upregulation, with peak expression at ovarian/hepatopancreas stage 2. RNAi demonstrated that silencing either isoform accelerated ovarian development, with Mn-HexA1 knockdown showing stronger effects (67.49% vs 55.49% stage III transition). These results establish Mn-HexA genes as negative regulators of ovarian maturation, with Mn-HexA1 exhibiting dominant inhibitory function.

Key words: Macrobrachium nipponense；β-hexosaminidase A；Ovarian development

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 based on whole genome resequencing. This study provides a reference for the selection and breeding of hypoxia-tolerant seahorse.

Key words: Hippocampus abdominalis; hypoxia; tuft gills

低温胁迫下红鳍东方鲀垂体代谢反应及氧化应激适应机制

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摘要：为探究低温诱导红鳍东方鲀雄性化过程中温度对垂体的影响，本研究通过 13℃、45 天的慢性低温胁迫实验，系统分析了垂体在代谢、氧化应激及细胞凋亡等方面的响应机制。代谢组学结果显示，垂体的差异代谢物主要富集在氨基酸代谢信号通路上，其中 GSH 及其合成前体等氨基酸含量发生显著变化；ROS，MDA 等氧化应激指标均呈现先上升后下降的趋势；TUNEL 及凋亡基因 qPCR 结果一致，表明垂体细胞凋亡水平随胁迫进程先升高后回落；组织学分析显示肌肉组织出现肌细胞萎缩和间隙增大，肌肉发育相关基因的表达变化进一步证实低温显著抑制肌肉生长发育。因此本研究推测，红鳍东方鲀在遭受慢性低温胁迫后，垂体可通过强化氨基酸代谢途径缓解鱼体氧化应激反应，且鱼体已呈现逐渐适应低温胁迫的生理趋势，但肌肉生长发育仍受明显抑制。本研究结果可为解析红鳍东方鲀对低温胁迫的生理适应机制提供理论支撑，并为后续深入探究垂体低温响应机制奠定基础。

关键词：红鳍东方鲀、垂体、低温胁迫、氧化应激、细胞凋亡

Metabolic responses and oxidative stress adaptation mechanisms of the pituitary gland in the Tiger Puffer under low-temperature stress

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Abstract： To investigate the pituitary response under chronic low-temperature stress during masculinization in Tiger Puffer, this study analyzed metabolic, oxidative stress, and apoptotic changes in the pituitary. Metabolomics revealed that differential metabolites were enriched in amino acid metabolism pathways, with significant alterations in GSH and its precursors. Levels of oxidative stress markers and pituitary cell apoptosis supported by TUNEL and apoptosis-related gene expression initially increased but later decreased, suggesting gradual physiological adaptation. However, muscle tissue exhibited atrophy and enlarged intercellular spaces, and muscle development-related gene expression confirmed significant suppression of muscle growth. These findings indicate that the pituitary mitigates oxidative stress via enhanced amino acid metabolism, facilitating acclimation to low temperature, while muscle development remains impaired. This study provides insight into the physiological adaptation of Tiger Puffer to low temperature stress and a basis for further research on pituitary regulation.

Key words: Tiger Puffer, pituitary gland, low-temperature stress, oxidative stress, apoptosis

多组学解析卵形鲳鲹抗刺激隐核虫调控机制

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摘要：卵形鲳鲹（*Trachinotus ovatus*）是中国南方沿海重要的经济鱼类，然而刺激隐核虫（*Cryptocaryon irritans*）严重制约了其养殖产业的健康发展。为解析卵形鲳鲹抗虫性状的遗传基础，比较分析了刺激隐核虫敏感组和抗性组的差异。转录组分析结果显示，敏感组与抗性组间共鉴定出2031个差异表达基因（DEGs），这些差异基因主要富集于脂质代谢和氨基酸代谢等通路。非靶向代谢组学分析共鉴定出461种显著差异代谢物，包括295种上调代谢物和166种下调代谢物，类固醇激素生物合成、α-亚麻酸代谢和花生四烯酸代谢是受感染影响最显著的代谢通路。全基因组关联分析鉴定出10个显著的SNP与抗刺激隐核虫性状有显著相关性，其位于7号、8号、16号、19号、21号和23号染色体。这些结果对确定抗刺激隐核虫的分子机制具有重要的指导意义。

关键词：卵形鲳鲹、全基因组关联分析、转录组、代谢组、刺激隐核虫

Multi-omics reveal mechanisms of Cryptocaryon irritans Resistance in Golden Pompano (*Trachinotus ovatus*)

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Abstract：The golden pompano (*Trachinotus ovatus*) is a key economic species in Southern China, but its aquaculture is threatened by Cryptocaryon irritans infections. To decipher the genetic basis of resistance, we compared sensitive and resistant fish using an integrated multi-omics approach. Our analyses revealed 2,031 differentially expressed genes linked to metabolic pathways and 461 significantly altered metabolites, most notably affecting steroid hormone and fatty acid metabolism. A genome-wide association analysis also pinpointed 10 significant SNPs on chromosomes 7, 8, 16, 19, 21, and 23 linked to resistance. These results offer important guidance for understanding the molecular mechanisms of defense against C. irritans.

Key words: *Trachinotus ovatus*, Genome-wide association study, Transcriptome, Metabolome, Cryptocaryon irritans,

虾夷扇贝野生与养殖群体生长分化分析及相关基因筛选

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摘要：虾夷扇贝（*Mizuhopecten yessoensis*）是我国北方重要的养殖物种，但其种质资源面临退化问题。为探究野生与养殖群体间的生长差异机制，本研究比较了小平岛野生群体（YS）与龙王塘养殖群体（YZ）的闭壳肌重量，发现 YS 显著高于 YZ（YS:24.48g vs YZ:21.17g，$P<0.001$）。转录组分析显示，YS 群体中差异表达基因共 1066 个（上调 289 个、下调 777 个）。GO 和 KEGG 分析表明，差异基因主要富集于细胞代谢、催化活性及吞噬体、氨基酸合成等通路。基于分析结果，筛选出 NOTCH1、ANK 和 VLDLR 三个生长相关候选基因，经验证并推测其功能：NOTCH1 可能通过细胞信号与分化负向调控生长；ANK 可能通过能量代谢影响组织发育；VLDLR 可能通过脂质运输与能量供应调控肌肉生长。综上所述，本研究从表型与分子层面揭示了生长差异机制，为生长调控网络解析及分子育种提供了依据。

关键词：虾夷扇贝；生长分化；转录组；差异表达基因；功能富集

Analysis of Growth Differentiation and Screening of Related Genes in Wild and Cultured Populations of *Mizuhopecten yessoensis*

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Abstract: *Mizuhopecten yessoensis* is an important aquaculture species in China, but its germplasm is deteriorating. To elucidate growth variation mechanisms between wild and cultured populations, we compared adductor muscle weights, finding a significantly higher value in the wild (YS) group than in the cultured (YZ) group (YS:24.48g vs YZ:21.17g,$P<0.001$). Transcriptomic analysis revealed 1,066 differentially expressed genes (DEGs) in YS. These DEGs were enriched in cellular metabolism, catalytic activity, and pathways such as phagosome and amino acid biosynthesis. Three candidate genes—NOTCH1,ANK,and VLDLR—were identified and validated. NOTCH1 may negatively regulate growth via cell signaling, ANK likely influences tissue development through energy metabolism, and VLDLR potentially modulates muscle growth via lipid transport. This study provides phenotypic and molecular insights into growth disparities, offering a basis for understanding regulatory networks and molecular breeding.

Key words: *Mizuhopecten yessoensis*; growth variation; transcriptome; differentially expressed genes; functional enrichment

鱼类多组学数据库构建

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摘要：鱼类多组学数据的爆发式增长正重塑渔业和水产养殖领域的基础研究与应用研究。我们系统整合和分析了 88 种鱼类的基因组、转录组、表观基因组和蛋白质组数据集。通过基因组分析，我们鉴定出 1.37 亿个 SNP 和 4552 万个 Indel。通过整合 9797 个 RNA 测序、293 个单细胞 RNA 测序及 840 个 miRNA 测序数据集，我们在多种物种的不同组织中定量分析了 187 万个 mRNA、28 万个 lncRNA、19 万个 circRNA 及 6068 种成熟 miRNA。通过整合 1563 个表观测序数据集，我们提供了组蛋白修饰、染色质可及性、DNA 甲基化和染色质相互作用的全基因组图谱。此外，我们还整理了 270 万条基因注释条目，鉴定同源基因，注释 192107 个转录因子，构建了转录因子调控网络与基因共表达网络，并进行了 RNA 跨物种保守性分析。最终，我们搭建了 iFish 数据库平台，支持交互式浏览、可视化与数据下载。

关键词：多组学分析、数据库构建

Construction of Fish Multi-Omics Database

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Abstract： The explosive growth of fish multi-omics data is reshaping fisheries and aquaculture research. We present iFish, a rigorously curated resource integrating genome, transcriptome, epigenome and proteome data for 88 species. From whole-genome sequencing we called 137.04 million SNPs and 45.52 million indels. By re-analysing 9797 bulk RNA-seq, 293 single-cell RNA-seq and 840 miRNA-seq datasets we quantified 1.87 million mRNAs, 287873 lncRNAs, 197554 circRNAs and 6068 mature miRNAs. Integration of 1563 epigenomic datasets yielded genome-wide maps of histone modifications, chromatin accessibility, DNA methylation and 3-D chromatin interactions. We additionally curated 2.7 million gene annotations, identified orthologues, annotated 192107 transcription factors (TFs), built TF regulatory and co-expression networks, and evaluated non-coding RNA conservation across species. All data are freely accessible through the iFish database (https://gonglab.hzau.edu.cn/iFish), a user-friendly platform supporting interactive browsing, visualization and download.

Key words: Multi-omics analysis；database construction

基于三种分子标记的中国南部养殖与自然点带石斑鱼群体遗传学研究

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摘要：为系统评估点带石斑鱼种质资源现状，本研究整合中国南部沿海自然与养殖群体，综合利用线粒体 DNA、微卫星与单核苷酸多态性三种分子标记，系统解析其遗传结构与分化特征，为资源保护与育种管理提供依据。研究对两类群体进行多维度遗传分析。结果显示：野生与养殖群体的遗传多样性水平相近，核苷酸多样性、期望杂合度与观察杂合度等指标均较为一致。群体间分化方面，自然群体内部与养殖群体内部均呈现较低的遗传分化水平，而自然群体与养殖群体之间则存在中等程度的遗传分化。结构分析进一步表明，两类群体虽共享部分谱系背景，但已形成各自独立的遗传聚类。本研究证实，点带石斑鱼养殖群体仍维持较高的遗传多样性，但与野生群体之间已产生明显的遗传分化。建议在后续资源管理中，将养殖群体作为独立的遗传管理单元，严格规范增殖放流行为，防止对野生群体造成遗传扰动；同时可在科学调控下引入野生种质，以维持养殖群体的遗传健康与可持续利用。

关键词：点带石斑鱼；分子标记；遗传多样性；种群结构；

Population Genetics of Farmed and Wild Orange-Spotted Grouper (*Epinephelus coioides*) in Southern China Based on Three Molecular Markers

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Abstract： This study assessed the genetic status of the Orange-Spotted Grouper (*Epinephelus coioides*) by integrating wild and cultured populations from southern China using three molecular markers (mtDNA, microsatellites, and SNPs). Genetic diversity was similar between wild and cultured populations, with low differentiation within each group. However, moderate genetic differentiation was observed between wild and cultured populations. Structure analysis revealed shared ancestral lineages but distinct genetic clustering between the two groups. These findings indicate that cultured populations retain considerable genetic diversity but have diverged from wild populations. We recommend designating cultured stocks as separate genetic management units to prevent genetic introgression into wild populations through stock enhancement, while controlled introduction of wild genetic material could help maintain long-term sustainability of cultured stocks.

Key words: Orange-spotted grouper; Molecular markers; Genetic diversity; Population structure

基于 smRandom–seq 技术的微生物单细胞转录组学研究：揭示细菌抗生素耐药机制的新视角

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摘要：本研究首次采用 smRandom-seq 技术，针对细菌单细胞转录组进行深度解析，以揭示细菌在抗生素胁迫下的耐药机制。该技术通过多聚甲醛固定、透化处理、原位逆转录以及液滴微流控等技术，实现了对单细菌 RNA 的高效捕获和测序。实验选取大肠杆菌为研究对象，在 12.5 μg/mL 氨苄西林（AMP）处理下，观察其基因表达模式的动态变化。结果显示，随着 AMP 暴露时间的延长，细菌种群逐渐分化为多个表达模式显著差异的亚群。通过 UMAP 降维分析，成功识别出 10 个关键亚群，并通过差异表达基因（DEGs）分析，揭示了与膜完整性、翻译损伤、ROS 代谢及 DNA 修复相关的关键基因表达特征。进一步研究发现，低代谢活性亚群（如 9 号、10 号亚群）的 ROS 降解基因表达显著降低，而 SOS 反应相关基因（如 recA 和 sulA）表达上调，表明细菌在抗生素胁迫下可能通过调控代谢活性与 DNA 修复机制来适应环境压力。此外，smRandom-seq 技术展现出优于现有方法（如 PETRI-seq 和 microSPLiT）的性能，双胞率低至 1.6 %，物种特异性高达 99.6 %。本研究不仅为细菌单细胞转录组学研究提供了新的技术平台，也为抗生素耐药机制的深入理解及新型抗感染策略的开发提供了重要理论依据。

关键词：smRandom-seq；单细胞转录组；大肠杆菌；抗生素耐药；基因表达异质性

Single-Cell Transcriptomics in Microbial Research Using smRandom-seq Technology: Novel Insig hts into Bacterial Antibiotic Resistance Mechanisms

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Abstract: This study for the first time employed the smRandom - seq technology to conduct an in - depth analysis of bacterial single - cell transcriptomes, aiming to unveil the antibiotic resistance mechanisms of bacteria under antibiotic stress. This technology achieved efficient capture and sequencing of single - bacterial RNA through techniques such as paraformaldehyde fixation, permeabilization, in - situ reverse transcription, and droplet microfluidics.In the experiment, Escherichia coli was selected as the research subject. Under the treatment of 12.5 µg/mL ampicillin (AMP), the dynamic changes in its gene expression patterns were observed. The results showed that as the AMP exposure time prolonged, the bacterial population gradually differentiated into multiple sub - populations with significantly different expression patterns. Through UMAP dimensionality reduction analysis, 10 key sub - populations were successfully identified. And by analyzing differentially expressed genes (DEGs), the expression characteristics of key genes related to membrane integrity, translational damage, ROS metabolism, and DNA repair were revealed.Further research found that in sub - populations with low metabolic activity (such as sub - populations 9 and 10), the expression of ROS degradation genes decreased significantly, while the expression of genes related to the SOS response (such as recA and sulA) was up - regulated. This indicates that bacteria may adapt to environmental stress by regulating metabolic activity and DNA repair mechanisms under antibiotic stress.In addition, the smRandom - seq technology demonstrated superior performance compared to existing methods (such as PETRI - seq and microSPLiT), with a doublet rate as low as 1.6 % and species specificity as high as 99.6 %. This study not only provides a new technical platform for bacterial single - cell transcriptomics research but also offers important theoretical bas is for in - depth understanding of antibiotic resistance mechanisms and development of novel anti - infection strategies.

Keywords: smRandom - seq; single - cell transcriptome; Escherichia coli; antibiotic resistance; gene expression heterogeneity

饲料中添加虾青素对赤点石斑鱼生长、体色、皮肤色素和抗氧化性的影响

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摘要：探究虾青素对赤点石斑鱼生长、体色、皮肤色素和抗氧化性的影响，为虾青素在赤斑石斑鱼饲料中的应用及功效评价提供科学依据。本研究选择初体重约为 6.17±0.26 g，平均全长为 7.84±0.54 cm 的赤点石斑鱼 4500 尾，随机分为 5 组，对照组 AST0、AST100、AST200、AST400 和 AST800（虾青素添加量分别为 0、100、200、400 和 800 mg/kg），每组 3 个重复，每个重复 300 尾，进行为期 90 d 的养殖试验。结果显示，饲料中添加虾青素提高了赤点石斑鱼的体重（BW）、增重率（WGR）、特定生长率（SGR），但与 AST0 相比差异不显著（$P>0.05$），对赤点石斑鱼的存活率（SR）、饲料系数（FCR）和肥满度（CF）均无显著影响（$P>0.05$），AST800 组的 HSI 相比 AST0 显著降低（$P<0.05$）。随着饲料中虾青素添加量的增加，赤点石斑鱼的头部、体侧和尾部的皮肤斑点变橙黄色，腹鳍基部变深红色。鱼鳍上的色素团分布均呈现出，背鳍、臀鳍和尾鳍色素细胞密度较高，胸鳍和腹鳍色素细胞密度较低的规律。发现在饲料中添加 100 mg/kg 及以上的虾青素可增加赤点石斑鱼腹鳍中黄色素细胞和红色素细胞的数量。随着虾青素水平的升高，AST100、AST200、AST400 和 AST800 组赤点石斑鱼鳃盖、背部和腹部皮肤、胸鳍和背鳍的 L*、a*和 b*相比 AST0 显著升高（$P<0.05$）。饲料中添加虾青素显著增加了赤点石斑鱼背部和腹部皮肤的类胡萝卜素浓度（$P<0.05$），AST100、AST200、AST400 和 AST800 组的赤点石斑鱼腹部皮肤黑色素浓度相比 AST0 显著增加（$P<0.05$）。赤点石斑鱼肝脏总抗氧化能力（T-AOC）、过氧化氢酶（CAT）、超氧化物歧化酶（SOD）、谷胱甘肽过氧化物酶（GSH-Px）活性随饲料中虾青素添加量的增加而显著升高（$P<0.05$），丙二醛（MDA）含量随饲料虾青素添加量的升高而显著降低（$P<0.05$）。饲料中添加虾青素可提高体重、增重率和特定生长率，显著改善赤点石斑鱼的体色、内在色素沉着和提高肝脏抗氧化能力。综合生长、体色、皮肤色素含量、抗氧化性的试验数据，赤点石斑鱼饲料中适宜虾青素添加量为 200~400 mg/kg。

关键词：赤点石斑鱼；虾青素；体色；皮肤色素；抗氧化性

云纹石斑鱼(♀)×云龙石斑鱼(♂)回交子代染色体核型及带型分析*

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摘要：为了分析云龙石斑鱼回交 F2 代的染色体核型及带型特征, 揭示其遗传变异规律和染色体结构特性, 系统解析染色体数目、核型组成、异染色质分布及核仁组织区数量, 以云纹石斑鱼 (*Epinephelus moara*)为母本、云龙石斑鱼(*E. moara*♀×*E. lanceolatus*♂)为父本进行回交, 获得正常发育的回交子代 MLBCF2。以回交子代 MLBCF2 为材料, 采用植物血球凝集素(PHA)和秋水仙素体腹腔注射法, 取头肾细胞制备染色体标本, 对其染色体核型、C-带、G-带和 Ag-NORs 进行分析。回交 F2 代染色体 2n=48, 核型组成为 4sm+44t, NF=52。染色体均呈现 C-带阳性, 可分为 4 种类型: 着丝粒 C-带、端粒 C-带、居间 C-带和整体 C-带。在第 1 对染色体显示深染 G-带的部分最多, 深染带数量在 3~9 条之间, 未发现整体深染 G-带, 其带纹在每对染色体上的数目及分布具有明显特征性。间期细胞的 Ag- NORs 数目在不同的细胞中表现出多态性, 数目为 1~3 个, 出现 1 个 Ag-NORs 位点的频率为 39.6%,出现 2 个位点的频率为 56.6%, 出现 3 个位点的频率为 3.8%; 中期细胞的 Ag-NORs 位点则主要出现在第 24 对同源染色体上, 未发现有 Ag-NORs 联合的现象。回交 F2 代染色体结构保守性与变异性并存, 第 24 对染色体的异染色质特征为遗传标记提供了依据。研究结果为石斑鱼杂交育种、种质改良及染色体进化研究提供了重要的细胞遗传学资料。

关键词：云龙石斑鱼回交 F2 代; 染色体; C-带; G-带; Ag-NORs; 带型

光强对刺参棘刺数目的影响及分子响应的研究

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摘要：刺参经济价值高，其体表棘刺数量是重要的品质指标。为探究工厂化养殖中蓝光光强对幼参棘刺生长的影响，本研究将幼参置于 1500 lx、3000 lx 和 4500 lx 蓝光下（自然光 0~450 lx 为对照），养殖 60 天，定期检测棘刺数与体重，采用转录组测序分析棘刺基因表达。结果显示，1500 lx 组在 15~60 天时棘刺数量显著高于对照组和 4500 lx 组，3000 lx 组与其余组无显著差异，4500 lx 组与对照组无差异，表明 1500 lx 是促进棘刺数目增长的有效光强。转录组分析显示，1500 lx 组中有 118 个上调和 107 个下调基因。GO 分析差异基因涉及细胞过程、细胞膜等；KEGG 富集于 Ras 信号通路、脂质代谢途径等。筛选得到 7 个关键基因：*tgf-β1*、*rps13*、*survivin*、*phb2*、*soxb*、*trpml3*、*traf6*。本研究结果为工厂化养殖中通过光强调控改善棘刺性状提供依据。

关键词：刺参；光强；棘刺；转录组分析

Papillae development and molecular responses of the juvenile sea cucumber (*Apostichopus japonicus*) exposed to light intensity

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Abstract： The sea cucumber (*Apostichopus japonicus*) is economically important, with dermal papillae number being a key quality trait. This study investigated how blue light intensity affects papillae growth in juveniles under industrial farming. Animals were exposed to 1500, 3000, or 4500 lx blue light for 60 days, using natural light (0–450 lx) as control. Papillae count and weight were monitored. Results showed the 1500 lx group had significantly more papillae than the control and 4500 lx groups from day 15 to 60. Transcriptome analysis of the 1500 lx group identified 118 upregulated and 107 downregulated genes, enriched in cellular processes, the Ras pathway, and lipid metabolism. Seven key genes (tgf-β1, rps13, survivin, phb2, soxb, trpml3, traf6) were identified. This provides a basis for using light intensity to improve papillae traits in aquaculture.

Key words: *Apostichopus japonicus*; Light intensity; Papillae; Transcriptome analysis

秋刀鱼性腺卵母细胞的特征研究

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摘要：为了掌握秋刀鱼性腺的各区域卵母细胞数量和性腺成熟水平的分布和变化情况，以及性腺成熟水平的影响因素，本文通过差异性分析和相关性分析等统计分析方法对66条性腺的卵母细胞进行了研究。结果显示，性腺各区域细胞数量呈现出两端数量较少，中间数量较多且趋于平缓的趋势；各区域性腺成熟水平呈现出整体波动不大的趋势；66条性腺中，只有5条性腺的部分区域的成熟水平存在显著差异；性腺成熟水平与体长、体重、性腺湿重和GSI均存在相关性，随体长的变化呈现出先上升后下降再上升的趋势，随体重的变化呈现出持续上升趋势，随性腺湿重变化呈现出波动上升趋势，随GSI变化呈现出持续上升趋势。结果表明，秋刀鱼性腺的各区域成熟水平几乎一致，且性腺成熟水平受到了秋刀鱼体长和体重等因素的影响。

关键词：秋刀鱼；性腺；卵母细胞；性腺成熟水平；性腺指数

Study on the Characteristics of Oocytes in the Gonads of Pacific Saury

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Abstract：To investigate the distribution and variation of oocyte numbers and gonadal maturity levels in Pacific saury (*Cololabis saira*), this study analyzed oocytes from 66 gonads using statistical methods including differential and correlation analysis. Results indicated that oocyte counts were lower at the polar regions and higher in the central areas, with relatively stable distribution. Gonadal maturity levels showed minimal fluctuation across regions, with significant differences observed only in partial areas of 5 gonads. Maturity levels were correlated with body length, body weight, gonad wet weight, and GSI: exhibiting an initial increase followed by a decline and subsequent rise with body length, a continuous increase with body weight, a fluctuating upward trend with gonad wet weight, and a steady rise with GSI. These findings demonstrate that gonadal maturity is highly consistent across regions and is influenced by factors such as body length and weight.

Key words: Pacific saury;Gonads;Oocytes;Gonadal maturity levels;Gonadosomatic Index

坛紫菜丝状藻丝和膨大藻丝藻际微生物多样性与代谢组的比较分析

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摘要：中国重要经济海藻--坛紫菜（*Pyropia haitanensis*）的养殖高度依赖丝状体成熟，但在工厂化育苗中仍存在丝状体发育周期长、膨大藻丝形成率低等难题。藻类生长发育与藻际微生物群落密切相关，然而不同丝状体发育阶段的藻际微生物群落变化尚不清楚。本研究采用 16S rRNA、ITS 基因测序及非靶向代谢组学技术，对丝状藻丝和膨大藻丝两个阶段的藻际微生物群落及代谢物进行比较分析。共鉴定出 19 种丰度差异显著的微生物，并与关键代谢物（尤其是表茉莉酸甲酯、吲哚-3-乙酰胺、甲硫氨酸亚砜、β-酪氨酸、5-羟基-L-色氨酸、菜油甾醇、(S)-3-磺基内酯、L-酪氨酸、叶绿素酸酯 a 及脱镁叶绿素酸酯 a）呈显著正相关。结果表明，藻际微生物积极参与丝状体成熟过程中代谢物合成，影响其发育、防御反应、激素水平、硫代谢、蛋白质及光合色素合成。丝状藻丝和膨大藻丝之间的差异微生物是代谢物积累的关键因素，凸显了藻际微生物与代谢物之间的紧密关联。本研究为利用有益微生物促进丝状体成熟提供了理论指导。

关键词：丝状藻丝，膨大藻丝，藻际微生物，代谢物

Comparative analysis of phycospheric microbial diversity and metabolome between filamentous conchocelis and sporangia branchlet of *Pyropia haitanensis*

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Abstract：*Pyropia haitanensis*, an economically important seaweed species in China, relies heavily on conchocelis maturation for its production. However, challenges such as prolonged conchocelis development time and low rate of sporangia branchlet formation persist in the factory breeding of P. haitanensis. The growth and development of algae are closely concerned in phycospheric microbial communities, yet little is known about the variations in these microbial communities across different conchocelis life stages. This study employed 16S rRNA, ITS gene sequencing and untargeted metabolomics to compare and analyze the phycospheric microbial communities and metabolites between filamentous conchocelis and sporangia branchlet stages. We identified 19 microorganisms with significantly different abundances and established a significant positive correlation with key metabolites, particularly methyl epijasmonate, indole-3-acetamide, methionine sulfoxide, beta-tyrosine, 5-hydroxy-L-tryptophan, campestanol, (S)-3-sulfonatolactate, L-tyrosine, chlorophyllide a, and pheophorbide a. These findings suggested that phycospheric microorganisms actively participated in metabolite synthesis during conchocelis maturation, influencing development, defense response, hormone levels, sulfur metabolism, protein, and photosynthetic pigment synthesis. The differential microorganisms between filamentous conchocelis and sporangia branchlet stages were a vital factor in metabolite accumulation, highlighting the interconnectedness between phycospheric microorganisms and metabolites. Our research provided theoretical guidance for utilizing beneficial microorganisms to facilitate conchocelis maturation.

Key words: Filamentous conchocelis; Sporangia branchlet; Phycospheric microorganisms; Metabolites

人工诱导菲律宾蛤仔雌核发育二倍体初步研究

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摘要：菲律宾蛤仔是我国重要海产经济贝类。人工诱导蛤仔雌核发育的紫外线诱导精子遗传失活光照强度为 230-235 μW/cm2，照射梯度为 0、3、6、9、12、15、18、21、24 和 27 s。采用细胞松弛素 B (CB) 诱导染色体二倍体化，CB 的浓度梯度为 0、0.25、0.50、0.75、1.0 mg/L 。研究发现紫外线 (254 nm) 照射强度 230-235 μW/cm2 条件下，照射 9 秒是精子遗传失活的合适剂量。0.75 mg / L 浓度 CB 处理受精卵 20 min 是诱导染色体二倍体化的合适浓度，雌核发育二倍体诱导率为 9.60 ± 5.10 %；本实验以蛤仔担轮幼虫为材料，采用热滴片法开展了菲律宾蛤仔雌核发育二倍体、正常二倍体和单倍体核型分析研究。结果显示，蛤仔正常二倍体和雌核发育二倍体染色体数目为 38 条，单倍体为 19 条。蛤仔正常二倍体和雌核发育二倍体核型公式为 2n=18m+20sm。

关键词：菲律宾蛤仔；雌核发育；胚胎发育；核型分析

Preliminary study on artificial induction of gynogenetic diploid of *Ruditapes philippinarum*

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Abstract： Manila clam is an economically important bivalve species. The light intensity of UV-induced sperm genetic inactivation was 230-235 μW/cm2, and the irradiation gradients were 0, 3, 6, 9, 12, 15, 18, 21, 24 and 27 s. Cytochalasin B (CB) was used to induce chromosome diploidization, and the concentration gradients of CB were 0, 0.25, 0.50, 0.75 and 1.0 mg/L, respectively. Under the condition of UV intensity of 230-235 μW/cm2, irradiation for 9 seconds was the appropriate time for sperm genetic inactivation, and the induction rate was 100%. Treatment of zygotes with 0.75 mg/L CB for 20 min was the optimal concentration for inducing chromosome diploidization, and the induction rate of gynogenetic diploid was 9.60 ± 5.10%. Karyotype analysis results showed that the number of normal diploid and gynogenetic diploid chromosomes was 38, and the number of haploid was 19. The karyotype formula of normal diploid and gynogenetic diploid was 2n =18m+ 20sm.

Key words: Ruditapes philippinarum; Gynogenesis; Embryonic development; Karyotype analysis

光强度和光周期对克氏原螯虾卵巢发育的影响：比较蛋白质组学分析、生长性能和生化

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摘要：通过比较蛋白质组学分析，本研究鉴定了许多参与卵巢发育和卵母细胞成熟的重要蛋白质，如麦芽糖酶、α-磷酸合酶和糖代谢相关途径。研究结果表明光强度的降低促进了克氏原螯虾糖原代谢和能量代谢。在低光照强度下，克氏原螯虾代谢糖分更快，产生更多能量，促进生长。光照强度的降低可能导致克氏对虾能量分配策略的改变，导致能量主要用于生长而不是性腺发育。光周期的减少对克氏原螯虾脂质代谢有抑制作用。克氏原螯虾不能产生正常的营养物质（如 Glu、TC 和 TG），导致卵巢和卵母细胞的成熟受到抑制。本研究结果揭示了光强度和光周期影响克氏原螯虾卵巢发育的分子机制，为进一步研究甲壳动物卵巢和卵母细胞的发育提供重要信息。

关键词：比较蛋白质组学；光照强度；卵巢发育；光周期；克氏原螯虾

Effects of light intensity and photoperiod on ovarian development of *Procambarus clarkii* (Girard, 1852): comparative proteomics analysis, growth performance and biochemical

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Abstract： Through comparative proteomic analysis, this study identified many important proteins involved in ovarian development and oocyte maturation, such as maltase, α-phosphate synthase, and sugar metabolism-related pathways. This study found that light intensity and photoperiod can control the development of ovaries and oocytes in P. clarkii by regulating the expression patterns of important proteins. The decrease in light intensity promoted the glycogen metabolism of P. clarkii and was beneficial to energy metabolism of P. clarkii. Under low light intensity, P. clarkii metabolized sugar faster and produced more energy, promoting the growth of P. clarkii. The decrease in light intensity may lead to changes in the energy allocation strategy of P. clarkii, leading to the energy mainly used for growth rather than gonadal development. The decrease in photoperiod had an inhibitory effect on lipid metabolism of P. clarkii. P. clarkii cannot produce normal nutrients, causing maturation of ovaries and oocytes to be inhibited.

Key words: Comparative proteomics; Light intensity; Ovarian development; Photoperiod; Procambarus clarkii

大黄鱼腹部内膜形成机制解析

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摘要：解析器官形成及功能，对于深入理解鱼类生长发育的复杂调控机制至关重要。鱼类腹部内膜作为生理健康的重要指标，长期以来被忽视。大黄鱼(*Larimichthys crocea*)是我国重要的海水养殖品种，但其腹部内膜形成缺陷常伴随鱼苗高死亡事件的发生。早期研究发现与其他鱼类相比，大黄鱼腹部内膜形态结构具有明显差异。因此，本研究通过划分大黄鱼腹部内膜形成时期，借助切片技术解析其结构组成。再结合单细胞转录组技术绘制大黄鱼腹部内膜单细胞转录图谱，锚定腹部内膜形成的关键基因范围。最后联合多组学和分子试验定位到腹膜形成的关键基因 ma1。本研究通过阐释大黄鱼腹膜形成机制，明确组织功能，进而可能为了解鱼类腹膜发育的共性机制和大黄鱼产业中腹膜形成差异导致鱼苗死亡问题提供理论参考。

关键词：大黄鱼，腹部内膜，发育，ma1

Analysis of the formation mechanism of the abdominal inner membrane of large yellow croaker

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Abstract: Understanding organ formation and function is crucial for revealing the complex regulatory mechanisms underlying fish growth and development. The abdominal membrane, an important indicator of physiological health, has long been overlooked. The large yellow croaker (*Larimichthys crocea*), a key marine aquaculture species in China, often exhibits high larval mortality associated with defects in abdominal membrane formation. Compared with other fish, its abdominal membrane shows distinct morphological features. Here, we defined the developmental stages of abdominal membrane formation and analyzed its structure using histological sectioning. A single-cell transcriptomic atlas was constructed to identify key genes involved in membrane formation, and multi-omics integration with molecular validation pinpointed ma1 as a critical gene for peritoneal development. These findings clarify the molecular basis of peritoneal formation in large yellow croaker and offer insights for understanding fish peritoneal development and reducing larval mortality.

Key words: Large yellow croaker, Peritoneum, Development, ma1

滞长刺参恢复生长期肠道菌群变化及基因转录水平分析

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摘要：刺参（*Apostichopus japonicus*）滞长导致刺参养殖产量损失，因此，滞长刺参恢复生长极为重要。本研究在恢复生长 0 周（T0）、4 周(T2)、12 周（T6）进行 16srRNA 和转录组测序，来探究滞长刺参恢复生长的分子机制。16srRNA 显示，Alpha 多样性表明，T6 菌群丰度最高，T2 次之，T0 最低，三组间均存在显著差异（$P < 0.05$）。恢复生长中，拟杆菌门、厚壁菌门等能量供应相关菌丰度上升，变形菌门等威胁免疫稳态菌丰度下降。转录组显示，T2vsT0，T6vsT2 显著差异基因分别为 2028、829 个。T2vsT0，ND5、RPL27 分别在氧化磷酸化和核糖体通路上调，CTSB、LGMN 在溶酶体通路下调。T6vsT2，LAMA3 在 PI3K-Akt 通路上调，PDHB 在糖酵解和糖异生通路上调。综上，滞长刺参恢复生长与能量供应和免疫稳态相关，此结果为探究滞长刺参恢复生长提供参考。

关键词：滞长刺参；恢复生长；肠道菌群；转录组

Analysis of Gut Microbiota Changes and Gene Transcriptional Levels During the Recovery Growth Period of Stunted Sea Cucumbers(*Apostichopus japonicus*)

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Abstract： This study investigates the molecular mechanisms of growth recovery in stunted sea cucumber (*Apostichopus japonicus*) via integrated 16S rRNA and transcriptomic analysis at 0 (T0), 4 (T2), and 12 (T6) weeks. Alpha diversity of gut microbiota increased significantly throughout recovery. Key microbial shifts included elevated abundances of energy-supplying Bacteroidota and Firmicutes, and a decline in Proteobacteria. Transcriptomics revealed 2,028 and 829 differentially expressed genes in T2vsT0 and T6vsT2, respectively. Early recovery (T2vsT0) involved upregulation of ND5 (oxidative phosphorylation) and RPL27 (ribosome), and downregulation of CTSB and LGMN (lysosome). Late recovery (T6vsT2) featured upregulation of LAMA3 (PI3K-Akt pathway) and PDHB (glycolysis/gluconeogenesis). Our findings demonstrate that growth recovery is driven by synergistic shifts in the gut microbiome and host gene expression to enhance energy metabolism and immune homeostasis.

Key words: Stunted Apostichopus japonicus（*A. japonicus*）; compensatory growth; intestinal microbiota; transcriptomic analysis

基于全基因组关联分析（GWAS）与转录组分析筛选团头鲂（*Megalobrama amblycephala*）营养成分性状相关 SNP 及候选基因

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摘要：鱼肉营养成分决定其品质与经济价值，但针对鱼肉营养优化的遗传选育策略仍较匮乏。本研究以 244 尾团头鲂作为实验群体，基于 50K 芯片及背肌转录组数据，经质检后保留 447,530 个 SNP，对肌肉水分、蛋白质、脂肪、PUFA、DHA+EPA、BCAA 六个营养性状进行 GWAS 分析。结果显示，分别有 4、4、4、8、11、8 个 SNP 与上述性状显著关联。结合转录组数据，根据显著位点基因型对候选基因表达量进行显著性差异分析，鉴定出 133 个差异表达基因，结合基因功能、表达水平及其与表型的关联推测出各性状候选基因：hic1（水分）、eef2k（蛋白质）、fosl2（脂肪）、ndufs4/slc25a5（DHA+EPA）、slc25a44a（PUFA）、psmc5（BCAA）。本研究为鱼肉品质遗传育种提供了关键分子标记与候选基因。

关键词：团头鲂；营养性状；全基因组关联分析；单核苷酸多态性；候选基因

Identification of SNPs and candidate genes associated with nutritional composition traits by GWAS and transcriptome analysis in blunt snout bream (*Megalobrama amblycephala*)

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Abstract： To clarify the genetic mechanisms of muscle nutritional traits in blunt snout bream (Megalobrama amblycephala), this study used 244 individuals. It employed 447,530 high-quality SNPs - from a 50K SNP array and the individuals' dorsal muscle transcriptomic data - to conduct a GWAS. The GWAS focused on 6 key muscle nutritional traits: moisture, CP (crude protein), CF (crude fat), PUFA, DHA+EPA, and BCAA (branched-chain amino acids). Results showed 4, 4, 4, 8, 11, and 8 SNPs were significantly linked to these traits, respectively. By combining transcriptomic data and analyzing candidate gene expression around significant loci, 133 genes with highly significant expression differences across SNP genotype groups were found. Further combining gene function, expression levels, and phenotype links, potential candidate genes for each trait were identified: hic1 (moisture), eef2k (CP), fosl2 (CF), ndufs4 and slc25a5 (DHA+EPA), slc25a44a (PUFA), and psmc5 (BCAA).This study provides useful molecular markers and candidate genes for breeding programs to improve fish meat quality.

Key words: Megalobrama amblycephala; Nutritional traits; GWAS; SNP; Candidate gene

菲律宾蛤仔 LRR 基因家族的鉴定与表达分析

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摘要：富亮氨酸重复序列（leucine-rich repeats，LRR）是模式识别受体（PRRs）的一种，大部分富含 LRRs 的蛋白被发现参与了信号通路的转导，存在于各个物种且参与多个生物学过程，包括生物体的固有免疫反应。LRR 结构域由 LRR 基序组成，每个 LRR 基序通常具有 20~29 个残基，其共同特征是都包括个保守的由 11 个氨基酸残基组成的片段（序列为 LxxLxLxxN/CxL）负责同配体识别，发生蛋白质-蛋白质相互作用。已有研究发现 LRR 基因在水产动物先天免疫中发挥重要作用，研究深入对菲律宾蛤仔 LRR 基因家族进行分析，鉴定出菲律宾蛤仔 LRR 基因家族 58 个基因，热图结果显示溶藻弧菌胁迫 48h 后 RpLRRC15、RpLRRC45 表达显著上调（$P<0.05$）,96h 时 RpLRRC71 显著上调（$P<0.05$）。LRRs 在菲律宾蛤仔受弧菌感染过程中可能发挥着潜在的调节作用。

关键词：菲律宾蛤仔；富亮氨酸重复序列；生物信息学；基因家族

Identification and Expression Analysis of the LRR Gene Family in *Ruditapes philippinarum*

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Abstract：Leucine-rich repeats (LRRs) are a type of pattern recognition receptor (PRRs). Most LRR-rich proteins are involved in signal pathway transduction, exist across species, and participate in multiple biological processes, including organisms' innate immune response.The LRR domain comprises LRR motifs (each typically 20-29 residues). A key feature of these motifs is a conserved 11-amino-acid fragment (sequence: LxxLxLxxN/CxL), which mediates ligand recognition and protein-protein interactions.Prior studies show LRR genes are critical for aquatic animals' innate immunity. An in-depth study of the LRR gene family in Ruditapes philippinarum (Manila clam) identified 58 family genes. Heatmap data revealed: RpLRRC15 and RpLRRC45 were significantly upregulated ($P<0.05$) at 48h post-Vibrio alginolyticus stress; RpLRRC71 was significantly upregulated ($P<0.05$) at 96h. These results suggest LRRs may regulate Ruditapes philippinarum's response to Vibrio infection.

Key words: *Ruditapes philippinarum* (Manila clam); Leucine-rich repeat (LRR); Bioinformatics; Gene family

高温胁迫下中间球海胆的转录蛋白水平响应特征及调控机制研究

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摘要：中间球海胆（*Strongylocentrotus intermedius*）是重要的冷水性经济物种，对温度变化极为敏感。为揭示其高温胁迫下的分子响应机制，本研究采用 RNA-seq 与 DIA 蛋白组学对 25 °C 高温组与 15 °C 对照组肠道进行分析。结果共鉴定出 1413 个 DEGs 和 1484 个 DEPs。高温显著抑制氧化磷酸化及细胞周期相关基因（如 COX6B1、V-ATPase、MCM2）表达，降低能量合成与细胞更新；同时，内质网蛋白加工通路中的 HSP70IV 和 GRP94 等在转录组与蛋白组中均显著上调，协同维持 ER 稳态。此外，自噬相关蛋白 LC3C 和 LKB1 上调促进受损组分清除，caspase-3 介导凋亡移除严重损伤细胞。本研究为阐明中间球海胆及其他棘皮动物的高温胁迫分子调控机制提供重要参考。

关键词：中间球海胆；高温胁迫；转录组；蛋白组

Transcriptomic and Proteomic Responses and Regulatory Mechanisms of Strongylocentrotus intermedius under Heat-Temperature Stress

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Abstract： Strongylocentrotus intermedius, an important cold-water economic species, is highly sensitive to temperature changes. To investigate its molecular responses to high temperatures stress, RNA-seq and DIA proteomics were performed on intestines exposed to 25 °C (H) and 15 °C (C). A total of 1,413 differentially expressed genes (DEGs) and 1,484 differentially expressed proteins (DEPs) were identified in group H vs. Group C. High temperature markedly suppressed the expression of genes associated with “oxidative phosphorylation” and“ cell cycle” pathways, such as COX6B1, V-ATPase, and MCM2, reducing energy production and cellular renewal. Meanwhile, HSP70IV and GRP94 in“protein processing in endoplasmic reticulum” pathway were markedly upregulated at both transcript and protein levels, maintaining ER homeostasis. Autophagy-related proteins LC3C and LKB1 were upregulated to clear damaged components, and caspase-3 mediated apoptosis removed severely damaged cells. These findings provide key insights into high-temperature tolerance mechanisms in S. intermedius and other echinoderms.

Key words: Strongylocentrotus intermedius; high temperature stress; transcriptome; proteome

转录组学和代谢组学的综合应用为中华绒螯蟹（*Eriocheir sinensis*）不同体型的生长提供了见解

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摘要：中华绒螯蟹是广泛分布于北半球水系的水生甲壳类动物。体型大小是决定中华绒螯蟹经济价值的重要指标之一。然而，对该物种体型大小的遗传基础和调控机制的研究有限，仅有少数相关基因报道。因此，有必要研究与其生长相关的调控途径。本研究首先利用转录组学分析和代谢组学测序技术构建了不同体型中华绒螯蟹的基因表达谱和代谢物谱。随后，通过整合组学分析，初步确定了控制河蟹生长和大小的关键基因和调控途径。本研究发现，体型较大的雌蟹消化功能显著增强，主要表现为 trypsin-1 表达上调，提示其在调节蟹的生长发育中可能具有关键作用。有趣的是，APOLPP、RICK a、AGMO、NEPHRIN 以及 REXO1L1P 和 ZCCHC24 等多种组织特异性蛋白通过各自的功能途径间接影响螃蟹的生长发育。此外，ECM 受体相互作用、细胞粘附、PI3K-Akt 信号通路等关键的 KEGG 通路在中华绒螯蟹的生长调控中发挥核心作用。

关键词：中华绒螯蟹，体型，转录组，代谢组

Integrated Application of Transcriptomics and Metabolomics Provides Insights into the Different Body-Size Growth in Chinese Mitten Crab (*Eriocheir sinensis*)

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Abstract: Body size is one of the crucial indicators determining the economic value of E. sinensis. To investigate the regulatory mechanisms of its growth, this study first utilized transcriptomic profiling and metabolomic sequencing to construct gene expression profiles and metabolite profiles of E. sinensis of different body sizes. Subsequently, through integrated omics analysis, the key genes and regulatory pathways involved in controlling the growth and size of crabs were preliminarily identified. This study found that larger female crabs exhibited significantly enhanced digestive functions, primarily reflected in the upregulation of trypsin-1 expression, suggesting its potentially pivotal role in regulating the growth and development of crabs. Interestingly, a variety of tissue-specific proteins such as APOLPP, RICK A, AGMO, and NEPHRIN, indirectly influence the growth and development of crab. In addition, key signaling pathways including ECM-receptor interaction, cell adhesion, and PI3K-Akt were confirmed to play central roles in growth regulation.

Key words: Chinese mitten crab (*Eriocheir sinensis*); body-size; transcriptomics; metabolomics

基于全基因组的虾夷扇贝耐高温及生长相关标记筛选

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摘要：基于对虾夷扇贝（*Mizuhopecten yessoensis*）四个群体（定向选育品系 B、常规选育对照 S、广鹿岛 G、大长山岛 D）共 235 份样本的全基因组重测序分析。群体遗传结构显示三个显著分化的亚群：人工选育亚群 CD、大长山亚群 DD 和大连养殖群体 DL。其中 CD 群体呈现典型人工选择特征，其连锁不平衡衰减半径（337 kb）较半野生群体 G（56 kb）显著扩展 5.02 倍，同时遗传多样性降低，表明经历强正向选择。通过全基因组关联分析，在壳长、壳高、壳宽等生长性状中鉴定出 32 个显著关联 SNP 位点（$P < 1\times10^{-6}$），涉及 9 个功能基因。模型交叉验证锁定基因组区域 NW_018404519.1 和 NW_018408733.1 内的 12 个高置信度 SNPs，调控 3 个贝壳形成基因。耐热性状关联到 LOC110459025、LOC110458077 和 LOC110458487 基因。

关键词：重测序；全基因组关联分析；虾夷扇贝；单核苷酸多态性；耐高温和生长性状

Genome-Wide Identification of Heat Tolerance and Growth-Associated Genetic Markers in Yesso Scallop (*Mizuhopecten yessoensis*)

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Abstract： Based on whole-genome resequencing analysis of 235 individuals from four populations (directed breeding B, conventional breeding control S, Guanglu Island G, and Dachangshan Island D) of the Mizuhopecten yessoensis, the population genetic structure revealed three significantly differentiated subgroups: the artificially bred subgroup CD, the Dachangshan subgroup DD, and the Dalian cultured population DL. The CD subgroup exhibited typical characteristics of artificial selection, with its linkage disequilibrium decay radius (337 kb) being 5.02 times larger than that of the semi-wild population G (56 kb), along with reduced genetic diversity, indicating strong positive selection. Through genome-wide association analysis, 32 significant SNPs ($P < 1\times10^{-6}$) associated with growth traits such as shell length, shell height, and shell width were identified, involving nine functional genes. Model cross-validation pinpointed 12 high-confidence SNPs within the genomic regions NW_018404519.1 and NW_018408733.1, which regulate three shell formation-related genes. Heat tolerance traits are associated with LOC110459025, LOC110458077, and LOC110458487 genes.

Key words: Resequencing; GWAS; Mizuhopecten yessoensis; SNP; high temperature tolerance and growth traits

MNK1 基因与虾夷扇贝耐高温性状的关联分析及其外显子区耐高温 SNP 位点筛选

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摘要：本研究中对同一虾夷扇贝群体进行高温胁迫，按壳开口程度筛选高温不耐受和高温耐受两种扇贝，分析两种扇贝鳃组织中 MNK1 基因相对表达水平，挖掘和鉴定 MNK1 基因外显子区与耐高温性状密切相关的 SNP 位点。高温耐受型中 MNK1 基因的相对表达水平显著低于不耐受型（$P<0.05$）。MNK1 基因外显子区的 c.652A>G、c.659C>A 和 c.686C>A 存在 SNP 位点，均表现出中度多态性($0.25\leq PIC<0.5$)。耐受型 MNK1 基因外显子区的 c.686C>A 位点的优势基因型为 CA，由 CC 突变为 CA 可改变 MNK1 基因 mRNA 的二级结构以及编码蛋白的氨基酸组成，最终导致蛋白空间构象发生改变，提示，c.686C>A 位点的基因型在扇贝耐高温性状形成中发挥重要作用。综上，本研究中所获结果不仅明确了 MNK1 基因与耐高温性状的联系，挖掘和鉴定出的 c.686C>A 位点可为筛选和培育耐高温虾夷扇贝提供新的分子标记参考。

关键词：虾夷扇贝；MNK1；SNP；耐高温性状；关联分析

MNK1 affects thermal tolerance capability via SNP alteration in its coding sequence region in scallops (*Patinopecten yessoensis*)

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Abstract ： High-temperature treatment was performed to obtain high-temperature intolerance individuals(HN)and high-temperature tolerance individuals(HR)from the same lineage of the P.yessoensis.The analysis results showed that: the relative expression of MNK1 in the gills of HR was significantly lower than that of HN($P<0.05$);there are three SNP sites at positions c.652A>G, c.659C>A,and c.686C>A of CDS were different between HN and HR.Further analyses showed that three identified SNPs exhibited a moderate polymorphism($0.25\leq PIC<0.5$).The dominant genotype of the identified SNPs were AG(c.652A>G),CA(c.659C>A),and CA(c.686C>A)in CDS of MNK1 of HR.The predicted secondary structure of the MNK1 mRNA,the amino acid composition and the spatial structure of protein could be altered when the c.686C>A site genotype changing from CC to CA.In conclusion, the results obtained in this study not only clarified the association between the MNK1 expression and the high-temperature tolerance capability in P.yessoensis,but also provide novel biomarkers for selective breeding of with high-temperature tolerance trait.

Key words: Patinopecten yessoensis; thermal tolerance; MNK1; SNP identification; bioinformatics analyses

刺参疣足大小分化的表达调控网络：全转录组与 DNA 甲基化组分析

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摘要：为阐明刺参（*Apostichopus japonicus*）疣足大小的表达调控网络，本研究对刺参不同大小疣足的全转录组和 DNA 甲基化组数据进行了测定。通过 RNA 测序和全基因组亚硫酸氢盐测序技术，分别获得全转录组（16.35G）和 DNA 甲基化组（28.92G）的平均有效数据量。共鉴定出 3,188 个竞争性内源 RNA 网络，包括 3,081 个 lncRNA/mi RNA/mRNA 网络和 107 个 circRNA/ miRNA/ mRNA 网络。甲基化组数据表明，与小疣足相比大疣足中存在 3307 个和 3776 个高甲基化水平的差异甲基化区域；以及 3125 个和 3016 个低甲基化水平的差异甲基化区域。所鉴定的差异甲基化区域主要分布于内含子、启动子或外显子。本研究不仅为阐明调控刺参疣足大小的表达调控网络奠定了坚实的理论基础（尤其从表观遗传学层面），还可以为刺参基于疣足表型的选育研究提供更多的生物标志物开发资源。

关键词：刺参；疣足；大小分化；全转录组；DNA 甲基化组

Expression regulation network in papillae of sea cucumbers: Whole-transcriptome and DNa methylation datasets

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Abstract： To elucidate the expression regulation network of papilla size of sea cucumbers (*Apostichopus japonicus*), the whole-transcriptome and DNA methylome datasets of different sizes of papillae in sea cucumbers were generated. Average clean bases of whole-transcriptome (16.35 G) and DNA methylome (28.92 G) were obtained using RNA sequencing and whole-genome bisulfite sequencing techniques. Methylome data indicate that there were 3,307 and 3,776 differentially methylated regions (DMRs) with high-level methylation as well as 3,125 and 3,016 DMRs with low-level methylation in big papillae compared to small papillae. The identified DMRs were mainly distributed in introns, promotors, or exons. The whole-transcriptome and DNA methylome datasets generated from this study not only established a robust theoretical foundation (especially from the epigenetic aspect) for elucidating expression regulation network determining papilla size in sea cucumbers but also can be a valuable resource of biomarker mining for papilla appearance-based selective breeding in sea cucumbers.

Key words: Sea cucumber（*Apostichopus japonicus*）; papilla; Size differentiation; Whole transcriptome; DNA methylation profile

不同壳色香螺繁殖力比较分析

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摘要：香螺（*Neptunea arthritica cumingii*）是我国黄海、渤海重要的经济贝类，因过度捕捞，野生资源下降，亟需开展繁殖生物学研究以恢复资源。本研究以红棕色（HZ）、黄褐色（HH）、白色（BS）三种壳色香螺为对象，比较其生物学性状与繁殖力差异，构建多元回归方程，并通过转录组与蛋白组联合分析，筛选差异表达基因与蛋白，分析 GO 与 KEGG 功能富集，预测影响繁殖力的分子途径与关键基因。形态学分析显示，湿重、性腺重与产卵量正相关，壳高、壳宽、湿重、性腺重是评估繁殖力的关键指标。转录组分析表明，BS 群体中与性腺发育、生殖细胞发育、卵子成熟及生殖周期相关的基因显著上调。蛋白组学分析显示，激素合成、性腺发育相关蛋白在 BS 群体中上调，调控生殖过程，影响卵子成熟与繁殖周期。本研究为香螺人工繁殖、良种选育及品种改良提供理论依据，促进资源保护与可持续利用。

关键词：香螺；转录组；蛋白组；繁殖力；不同壳色群体

Comparative Analysis of Reproductive Capacity in Different Shell Color Variants of *Neptunea arthritica cumingii*

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Abstract： The whelk (*Neptunea arthritica cumingii*), an important economic shellfish in China's Yellow Sea and Bohai Sea, faces declining wild resources due to overfishing, necessitating research on its reproductive biology for resource recovery. This study focuses on three shell color variants—reddish-brown (HZ), yellowish-brown (HH), and white (BS)—to compare their biological traits and reproductive capacity, constructing a multiple regression equation. Through integrated transcriptomic and proteomic analyses, differentially expressed genes and proteins were identified, followed by GO and KEGG enrichment analyses to predict key molecular pathways and genes affecting reproductive capacity. Morphological analysis revealed that wet weight and gonad weight positively correlate with spawning output, with shell height, shell width, wet weight, and gonad weight serving as key indicators for evaluating reproductive capacity. Transcriptomic analysis showed significant upregulation of genes related to gonad development, germ cell development, egg maturation, and reproductive cycles in the BS group. Pro

Key words: Whelk; Transcriptome; Proteome; Reproductive Capacity; Different Shell Color Populations

不同外源刺激对滁州鲫主要免疫因子表达的影响

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摘要：滁州鲫作为国家地理标志产品，具有高品质和强抗性特点。为探究其主要免疫因子应对不同外源刺激的表达，本研究通过腹腔注射等量 PBS、维氏气单胞菌和 ploy(I:C)处理滁州鲫，在刺激后 6h、12h、24h 和 48h 分别取血液进行主要免疫因子的蛋白表达检测，并取滁州鲫鳃、脾和肠组织进行主要免疫因子的 mRNA 表达检测。结果表明维氏气单胞菌刺激 24h 后，LZM 含量达到峰值且显著高于 ploy(I:C)组；IgM 含量在感染维氏气单胞菌 12h 后不断上升；维氏气单胞菌组在刺激 48h 后，补体 C3 的含量显著高于其他组。外源刺激 48h 后，鳃中维氏气单胞菌组的 IL-1β、IFN-γ和 TGF-β表达量显著高于其他组；外源刺激 6h 后，脾脏中 ploy(I:C)组的 IL-1β、IFN-γ和 TGF-β表达量显著高于对照组；外源刺激 12h 后，肠中 ploy(I:C)组的 IL-1β、IFN-γ和 TGF-β表达量显著高于对照组。

关键词：关键词：滁州鲫；外源刺激；免疫因子；表达变化

Effects of Different Exogenous Stimuli on the Expression of Major Immune Factors in Chuzhou Crucian Carp

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Abstract： Chuzhou crucian carp as a national geographical indication product,is known for its high nutritional quality and strong resistance.To investigate the expression of its major immune factors in response to different exogenous stimuli, Fish was treated with intraperitoneal injections of equal amounts of PBS,A.veronii and poly(I:C).Blood samples were collected at 6h,12h,24h and 48h post-stimulation to detect the protein expression,while gill,spleen and intestinal tissues were taken to detect the mRNA expression.The results showed that 24h after A.veronii,LZM levels peaked and were higher than those in the poly(I:C);IgM levels continuously increased 12h after A.veronii infection;C3 levels in the A.veronii were higher than others 48h post-stimulation.After 48h exogenous stimulation,IL-1β,IFN-γ and TGF-β expression in gill were higher in the A.veronii compared to others;six hours post-stimulation,three genes expression in spleen of the poly(I:C) were higher than the control;twelve hours post-stimulation,three genes expression in intestinal of the poly(I:C) were higher than the control.

Key words: Keywords: Chuzhou crucian carp; Exogenous stimuli; Immune factors; Expression changes

日本沼虾 DHCR24 基因在性腺分化与发育中的功能及作用研究

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摘要：本研究阐明了 Mn-DHCR24 基因在日本沼虾中的作用。通过生物信息学手段分析了 Mn-DHCR24 基因的序列特征及系统发育关系。采用 qPCR 技术确定了该基因在不同组织及发育阶段的表达模式，并通过原位杂交法验证其在精巢中的定位。利用 RNA 干扰技术敲降 Mn-DHCR24 表达后，观察 PL10 和 PL30 阶段性别比例及性腺发育的变化，并通过酶联免疫吸附试验测定了激素水平。结果表明 Mn-DHCR24 在精巢中高表达，对精子成熟和性腺分化具有关键作用。RNAi 实验揭示 Mn-DHCR24 不是控制性别分化的主效基因，但在生殖调控中发挥关键作用，影响了甲壳动物的性激素合成、精子发育及复杂的性别调控网络。这些发现为日本沼虾性比分化的机制提供了重要见解，并为单性别养殖技术开发奠定基础。

关键词：性腺发育，Mn-DHCR24，日本沼虾，RNA 干扰，性别分化，性激素

A study on the functional role of the DHCR24 gene in gonadal differentiation and development of *Macrobrachium nipponense*

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Abstract：This study characterized the role of the Mn-DHCR24 gene in the oriental river prawn. We used bioinformatics to analyze sequence features and phylogenetic relationships of a single Mn-DHCR24 gene. The expression patterns of Mn-DHCR24 across different tissues and developmental stages were determined by real-time PCR, and its localization in testis was determined by in situ hybridization. Additionally, an enzyme-linked immunosorbent assay measured 17α-methyltestosterone levels, and tissue sections were used to characterize gonadal development. The results indicated that Mn-DHCR24 was high expression in testis, which was critical for sperm maturation and gonadal differentiation. RNAi experiments showed the role of Mn-DHCR24 during reproductive regulation rather than as a master gene for sex differentiation. Together, these findings provided valuable insights into the genetic and hormonal mechanisms of gonadal differentiation in M. nipponense, and supported the development of monosex culture technology.

Key words: gonadal development, Mn-DHCR24, Macrobrachium nipponense, RNAi, sex differentiation, sex hormone

基于高通量表型的日本囊对虾耐高温新品系“闽海 2 号”耐高温特性研究

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摘要：日本囊对虾（*Penaeus japonicus*）因品质优良而广泛养殖，但耐热性差限制了产业发展。本研究通过家系选育培育耐高温新品系“闽海 2 号”，并利用自主构建的高通量行为表型监测平台，系统比较其与未选育群体在高温胁迫下的运动与摄食行为差异。结果表明，“闽海 2 号”的耐热性指标（UTT）显著高于未选育群体（$p < 0.05$），且家系内变异较小，表现出稳定的耐热遗传特征。在升温实验中，“闽海 2 号”表现为初期快速响应、中期低能耗维持、末期短暂动员的行为模式，而未选育群体则呈持续高活跃度并逐渐衰退。在 36 ℃条件下，“闽海 2 号”仍能保持较高的摄食量和摄食完成率，显著优于未选育对虾。进一步分析表明，运动速度、加速度及摄食启动等行为指标与耐热性密切相关，可作为早期筛选的重要参考。研究结果表明，耐高温选育显著提升了日本囊对虾的环境适应力，行为表型监测为耐热性评价与遗传改良提供了新思路和技术支撑。

关键词：日本囊对虾，耐高温选育，行为表型，高通量监测，摄食与运动特征

High-Throughput Behavioral Phenotyping of Heat Tolerance in the Selectively Bred Kuruma Shrimp “Minhai No. 2”

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Abstract： The kuruma shrimp (*Penaeus japonicus*) is commercially important but highly vulnerable to heat stress. A heat-tolerant strain, “Minhai No. 2,” was developed through family-based selection and evaluated using a high-throughput behavioral phenotyping platform. Its upper thermal tolerance (UTT) was significantly higher than that of unselected shrimp ($p < 0.05$) with reduced variation, indicating stable heritability. During acute heating, the tolerant strain showed rapid early response, mid-phase energy conservation, and short mobilization before mortality, whereas unselected shrimp exhibited prolonged hyperactivity followed by decline. At 36 °C, “Minhai No. 2” maintained higher feed intake and completion rates. Correlation and machine learning analyses identified locomotor and feeding initiation traits as key predictors of heat tolerance. These results demonstrate that selective breeding effectively enhances thermal resilience in *P. japonicus*, and behavioral phenotyping offers a practical tool for trait evaluation and genetic improvement.

Key words: Penaeus japonicus， Heat tolerance breeding， Behavioral phenotyping，High-throughput monitoring，Feeding and locomotion traits

高温胁迫下虾夷扇贝全基因 DNA 甲基化及基因表达关联分析

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摘要：虾夷扇贝是我国北方重要的养殖贝类，近年来夏季出现大规模死亡现象。为探究扇贝响应高温胁迫的表观调控机制，本研究利用 WGBS 测序技术进行了高温胁迫下虾夷扇贝鳃丝全基因组 DNA 甲基化变化特征及其对基因表达的调控分析。虾夷扇贝鳃丝基因组约有 7%胞嘧啶发生甲基化， mCG 和 mCHH 为主要类型，但 mCG 的甲基化水平明显高于其它类型。随着温度升高，DNA 甲基化水平总体呈现先降低后升高的趋势；共检测到 65583 个差异甲基化区域，该区域基因显著富集到与内质网应激、mRNA 选择性剪切、纤毛运动、能量代谢、DNA 修复、自噬等相关 GO 功能及 KEGG 通路上。与转录组关联分析显示，差异甲基化区域中 266 个基因的表达水平与其 DNA 甲基化水平间存在显著负调控关系，这些基因显著富集到内质网应激相关通路。本研究表明了高温改变了虾夷扇贝基因组 DNA 甲基化分布水平，其通过调控内质网应激在虾夷扇贝响应高温胁迫中发挥了重要作用。

关键词：虾夷扇贝，高温，DAN 甲基化，内质网应激

Genome-wide DNA methylation profile and association analysis with gene expression in *Patinopecten yessoensis* under heat stress

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Abstract： *Patinopecten yessoensis*, a vital aquaculture species in China, has recently suffered massive deaths in summer. To explore the regulatory mechanisms underlying scallop responses to heat stress, the study employed WGBS to analyze genome-wide DNA methylation changes in *P. yessoensis* under heat stress. About 7% cytosines were methylated, with mCG and mCHH being the main types, but mCG methylation levels were higher. As temperature increased, methylation levels exhibited initial decrease followed by increase. 65,583 DMRs were identified, and genes in DMRs were enriched in functions related to ER stress (ERS), mRNA alternative splicing, ciliary motility, and so on. Association analysis with transcriptomic data revealed that 266 genes showed negative regulatory relationships with their DNA methylation levels, and the genes were enriched in ERS-related pathways. The study indicated genomic DNA methylation played an important role in response to heat stress by regulating ERS in *P. yessoensis*.

Key words: Patinopecten yessoensis, high temperature, DNA methylation, ERS

miRNA 作为分子性别开关在栉孔扇贝性别决定中的调控机制解析

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摘要：扇贝作为重要的海洋大宗贝类资源，已成为海水养殖的主导产业。尽管人工繁育技术为贝类养殖发展提供了动力，但性控育种技术仍面临关键瓶颈。因此解析贝类性别遗传调控的分子机制，将为性控育种提供基础和技术支撑。性别决定是生命发育的核心事件，其机制解析是生命科学的热点问题。miRNA 作为命运转化的调控者，在性别决定中发挥关键作用。本研究以海洋经济贝类栉孔扇贝为研究对象，首次绘制了发育时序模式图，确定壳高 3.5 mm 为性别决定的关键时间窗口；进一步基于 Small RNA-seq 技术，首次鉴定出 11 个性别偏好性 miRNAs，其中 1 个新的 novel miRNA 引起了重点关注。通过体外和体内验证，发现其可靶向调控性别决定基因 FOXL2，阻滞卵子发生和卵巢功能维持。有意思的是，过表达组性腺呈现雌转雄的性别转换，该发现首次揭示了 miRNA 在贝类性别决定中的调控作用，为解析贝类性别决定分子机制提供了关键实验证据。

关键词：miRNA；分子开关；栉孔扇贝；性别决定；FOXL2

Deciphering the regulatory mechanism of miRNA as a molecular sex switch in the sex determination of Chlamys farreri

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Abstract： Sex determination is a fundamental process in development and a central question in life sciences. miRNAs, known to regulate cell fate decisions, play critical roles in sex determination. However, the functions of miRNAs in the sex determination regulatory network of shellfish remain poorly understood. This study focuses on the Zhikong scallop, an economically important marine bivalve. We established a developmental timeline for the species and identified the 3.5 mm shell height stage as a critical window for sex determination. Using high-throughput sequencing, we identified 11 sex-biased miRNAs, including a novel miRNA of particular interest. Through in vitro and in vivo experiments, we demonstrated that this novel miRNA targets the key sex-determination gene FOXL2, thereby impeding oogenesis and ovarian maintenance. Remarkably, overexpression of this miRNA induced a female-to-male sex reversal in gonads, for the first time, the regulatory role of miRNA in sex determination in shellfish and provides crucial evidence for unraveling the molecular mechanisms governing this process.

Key words: miRNA; molecular switch; Chlamys farreri; Sex determination; FOXL2

转录分析揭示二倍体、三倍体和四倍体太平洋牡蛎的生长调控机制

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摘要：倍性水平对长牡蛎的表型和生理特性有很大影响。与二倍体相比，三倍体表现出理想的特性，如不育，生长速度更快，肉质得到改善。相比之下，四倍体通常生长缓慢，但这些与多倍体相关的特征背后的机制尚不清楚。本研究旨在通过比较二倍体、三倍体和四倍体牡蛎生长相关表型和基因表达的差异来阐明这些机制。结果表明，与天然免疫反应相关的基因在四倍体中显著上调，而与生物矿化和代谢相关的基因在三倍体中显著上调。这些发现表明，与二倍体和三倍体相比，四倍体牡蛎可能具有更强的先天免疫反应，而三倍体则表现出更好的生长性能。本研究为研究多倍体表型差异相关基因的功能提供了宝贵的资源。

关键词：牡蛎；二倍体；三倍体；四倍体；先天免疫；生长

Transcriptomic Analysis Reveals the Growth Regulatory Mechanisms in Diploid, Triploid, and Tetraploid Pacific Oyster (*Crassostrea gigas*)

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Abstract： Ploidy level exerts profound influences on the phenotypic and physiological traits of *Crassostrea gigas*. Compared to diploids, triploids exhibit desirable characteristics such as sterility, a faster growth rate, and improved meat quality. In contrast, tetraploids often suffer from slow growth, yet the mechanisms underlying these polyploid-associated traits remain unclear. This study aimed to elucidate these mechanisms by comparing differences in growth-related phenotypes and gene expression among diploid, triploid, and tetraploid oysters.The results revealed that genes associated with the innate immune response were significantly up-regulated in tetraploids, whereas genes related to biomineralization and metabolism were markedly up-regulated in triploids. These findings suggest that tetraploid oysters may mount a stronger innate immune response compared to diploids and triploids, while triploids demonstrate superior growth performance. This study provides valuable resources for investigating the functional aspects of genes related to polyploid phenotype differences.

Key words: Crassostrea gigas; diploid; triploid; tetraploid; innate immune; growth

细胞自噬参与青蛤的低盐胁迫应答

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摘要：水体盐度变化是影响滩涂贝类生长和存活的重要环境胁迫，对养殖产量和效益造成不利影响。青蛤是我国沿海重要的经济贝类，2 周盐度胁迫实验发现，在 15‰~35‰海水中其存活率均大于 90%，且在极低盐度 5‰的海水中，存活率仍可达 50%左右。目前，青蛤低盐耐受性的分子机制尚不明确。急性低盐胁迫后青蛤鳃组织的差异转录组分析发现，细胞自噬和溶酶体途径被显著富集；通过 qRT-PCR 进行基因时序性表达分析发现，LC3 和 p62 等多个自噬相关基因表达在低盐胁迫过程中发生显著变化；急性低盐胁迫后青蛤肝胰腺的差异代谢组分析发现，除氨基酸与脂代谢发生显著变化外，与自噬调控相关的 mTOR 通路及 FoxO 通路中的代谢物也发生了显著变化。最后，透射电镜观察发现鳃细胞中的自噬体数量显著增加，综上明确细胞自噬轴参与青蛤的低盐胁迫应答。研究可为青蛤耐低盐种质改良及健康养殖提供重要参考。

关键词：青蛤；低盐胁迫；细胞自噬

Autophagy Mediates the Response of *Cyclina sinensis* to Low-Salinity Stress

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Abstract： Water salinity fluctuation is a critical environmental stressor affecting the growth and survival of intertidal bivalves, exerting adverse impacts on aquaculture yield and efficiency. *Cyclina sinensis* is an economically important bivalve species along the coastal areas of China. Based on a two-week salinity stress test, the clam *Cyclina sinensis* exhibited strong salinity tolerance, with survival rates exceeding 90% at salinities of 15‰–35‰ and about 50% even at 5‰. The transcriptomic analyze revealed that autophagy and lysosome pathways were significantly enriched under acute low-salinity stress. Key autophagy-related genes (e.g., LC3, p62) were notably altered, and metabolites related to autophagy-regulating pathways such as mTOR and FoxO also changed significantly. TEM further confirmed increased autophagosome formation in gill cells. These findings collectively demonstrate the involvement of the autophagy axis in the low-salinity adaptation of C. sinensis, providing insights for genetic improvement and aquaculture practices.

Key words: *Cyclina sinensis*，low-salinity stress，Autophagy

中国南海养殖尖翅燕鱼（*Platax teira*）遗传多样性和群体结构

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摘要：尖翅燕鱼（*Platax teira*）是中国南方的重要经济鱼种。近年来，由于过度捕捞，其野生种群数量大幅减少。2015 年前后，尖翅燕鱼人工规模化育苗技术取得突破，促进了海南、广东等地区尖翅燕鱼养殖规模的扩大。为研究目前中国尖翅燕鱼养殖种群的遗传多样性、近交状况和种群结构，我们采用全基因组重测序技术和高密度 SNP 标记对四个主要养殖种群进行了遗传学分析。共对四个种群（NA、ZP、XL 和 XC）的 109 个个体进行了测序，鉴定出 5,384,029 个高质量 SNPs。结果显示，每个种群的核苷酸多样性（π）在 0.00155 至 0.00165 之间，观察杂合度（Ho）在 0.253 至 0.282 之间，该研究首次分析了中国尖翅燕鱼养殖种群的遗传多样性和种群结构，为建立基础养殖种群和实施遗传改良计划奠定了基础。

关键词：尖翅燕鱼，遗传多样性，群体结构，全基因组重测序，近交系数

Genetic diversity and population structure of farmed longfin batfish (*Platax teira*) in the South China Sea

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Abstract： Longfin batfish (*Platax teira*) is an important economic species in southern China. In recent years, its wild population has significantly declined due to overfishing. Around 2015, breakthroughs in the artificial large-scale seedling technology for P. teira have promoted the growth of its aquaculture scale in regions such as Hainan and Guangdong. To study the genetic diversity, inbreeding status, and population structure of the current P. teira farming populations in China, we performed whole-genome resequencing technology and high-density SNP markers to analyze the genetics of four main farming populations. A total of 109 individuals from four populations (NA, ZP, XL, and XC) were sequenced, identified 5,384,029 high-quality SNPs. The results showed that the nucleotide diversity (π) of each population ranged from 0.00155 to 0.00165, and observed heterozygosity (Ho) ranged from 0.253 to 0.282, which indicated low levels of genetic diversity. The results of the ROH analysis show significant inbreeding in the NA population. This study is the first to analyze the genetic diversity and population structure of the Chinese pointed winged swallow fish aquaculture population, laying the foundation for establishing a basic aquaculture population and implementing genetic improvement plans.

Key words: Platax teira; genetic diversity; population structure; whole-genome resequencing; inbreeding coefficient; runs of homozygosity

基于风味组学和代谢组学分析活饵和配合饲料饲喂下的鳜鱼肌肉风味差异

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摘要：配合饲料替代活饵养殖鳜鱼（*Siniperca chuatsi*）可有效降低养殖成本并减少对自然资源的依赖，但其对肌肉风味的影响尚不明确。本研究联合 GC×GC-TOF MS 与 LC-MS 技术，首次系统比较了活饵与配合饲料养殖下鳜鱼肌肉的风味差异。共鉴定出 65 种差异风味物质，其中 2,3-丁二酮、2-壬烯醛、2-戊基呋喃和 2-辛烯醛为关键风味化合物。代谢组分析发现 139 种差异代谢物，饲料组中苏氨酸、L-高丝氨酸等氨基酸代谢物显著上调，KEGG 富集分析提示甘氨酸、丝氨酸、苏氨酸代谢及氨基酰-tRNA 生物合成是关键代谢通路。关联分析进一步表明，二羟丙酮磷酸、O-磷酸高丝氨酸等前体物质与关键风味化合物显著相关。活饵组鳜鱼肌肉具有更浓郁的坚果、黄油、火腿香和青草清香，而饲料组腥味较轻。二羟丙酮磷酸、L-高丝氨酸、苏氨酸和亚油酸等被确认为重要风味前体。本研究为改善配合饲料养殖鳜鱼的肌肉风味提供了理论依据。

关键词：鳜鱼；风味；风味组学；代谢组学；活饵；配合饲料

Characterising flavour differences in Mandarin fish muscle under live prey and formulated feed diets using flavouromics and metabolomics

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Abstract：Substituting formulated feed for live prey in mandarin fish (*Siniperca chuatsi*) aquaculture can reduce costs and resource dependence, but its impact on muscle flavour remains unclear. This study employed GC×GC-TOF MS and LC-MS to compare muscle flavour between fish fed live prey and formulated feed. We identified 65 differential flavour compounds, including four key substances: 2,3-butanedione, (E)-2-nonenal, 2-pentylfuran, and (E)-2-octenal. Metabolomics revealed 139 differential metabolites, with threonine and L-homoserine significantly upregulated in the feed group. KEGG enrichment highlighted glycine, serine, threonine metabolism and aminoacyl-tRNA biosynthesis as key pathways. Key flavour precursors included dihydroxyacetone phosphate, L-homoserine, threonine, and linoleic acid. Fish fed live prey exhibited stronger nutty, buttery, and grassy aromas, while the feed group showed reduced off-flavours. These findings provide a theoretical basis for improving muscle flavour in feed-based mandarin fish culture.

Key words: Mandarin fish; Flavour; Flavouromics; Metabolomics; Live prey; Formulated feed

整合发育图谱与分子网络分析：金鲳胚胎囊胚–原肠胚死亡窗口期耐受阈值崩溃机制

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摘要：在金鲳孵化阶段，胚胎死亡率高严重制约了其人工养殖发展。本研究通过转录组测序分析了关键发育阶段的胚胎样本，系统解析了胚胎发育过程并揭示了阶段特异性死亡的分子机制。研究发现，胚胎在原肠胚转化期出现油球扩散及形态畸变，死亡率最高。对六个核心发育阶段的聚类分析识别出三个动态模块：早期以基因组激活与细胞增殖为主，中期转向形态发生与代谢适应，后期侧重于器官功能分化。关键信号通路包括 Wnt/Hippo 协调调控、核质运输及能量代谢网络。在原肠胚死亡高峰期，虽然能量生产和结构相关基因上调，但 ECM 受体与 PI3K-Akt 通路紊乱导致增殖-凋亡失衡，同时伴随 AP-1 相关炎症反应及蛋白稳态异常，最终超出胚胎耐受阈值。通过 RT-qPCR 验证的 12 个差异基因与测序结果一致。基于上述发现，提出补充铁硫簇前体与糖原的营养干预策略，为突破规模化育苗瓶颈提供了新方向。

关键词：金鲳；胚胎发育；转录组；死亡机制

Integrated developmental atlas and molecular network analysis: mechanisms of tolerance threshold collapse during the blastula-gastrula mortality window in *Trachinotus blochii* embryos

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Abstract : High embryonic mortality during hatching severely limits hatchery production of *Trachinotus blochii*. This study employed transcriptome sequencing to analyze embryonic development and identify the molecular basis of stage-specific mortality. Peak mortality was observed during the blastula-to-gastrula transition, characterized by oil droplet dispersal and morphological deformation. Analysis defined three developmental modules: early-stage proliferation, mid-stage morphogenesis, and late-stage organ specialization, governed by coordinated Wnt/Hippo signaling, nucleocytoplasmic transport, and energy metabolism. Transcriptomics during lethal phases revealed that despite upregulation of energy and structural genes, critical dysregulation occurred. Disruption of ECM-receptor and PI3K-Akt pathways caused a proliferation-apoptosis imbalance, compounded by AP-1-associated inflammation, ultimately exceeding embryonic tolerance. Based on these findings, a targeted nutritional strategy using iron-sulfur cluster precursors and glycogen is proposed to overcome this major bottleneck in aquaculture.

Key words: *Trachinotus blochii*; embryonic development; transcriptome; mortality mechanisms

miR–3529–3p 调控菲律宾蛤仔（*Ruditapes philippinarum*）黑色素合成的分子机制研究

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摘要：壳色是菲律宾蛤仔的重要经济性状，其中黑色素合成通路在色素形成中起关键作用。近年来，miRNA 在贝类壳色形成中的功能日益受到关注。本研究基于实验室前期构建的白蛤、橙蛤、斑马蛤和白斑马蛤的全转录组数据，发现 miR-3529-3p 在不同壳色个体间显著差异表达，在白蛤中最高、斑马蛤中最低。生物信息学分析预测其 324 个靶基因，KEGG 分析显示主要富集于 MAPK 信号通路、黑色素瘤、泛素介导的蛋白水解等通路。以斑马蛤为材料的体内实验表明，过表达 miR-3529-3p 显著降低黑色素合成关键基因表达、酪氨酸酶活性及黑色素含量，而抑制其表达则产生相反效果。表型观察显示，过表达组条纹变浅，抑制组条纹加深。双荧光素酶报告实验验证 miR-3529-3p 可直接靶向 TYR 基因 3′UTR 并负向调控其表达。本研究揭示了 miR-3529-3p 靶向 TYR 调控菲律宾蛤仔黑色素合成的分子机制，为贝类壳色形成及分子育种提供理论依据。

关键词：菲律宾蛤仔；黑色素；miRNA；靶基因

Molecular mechanism of miR-3529-3p in regulating melanin synthesis in the Manila clam (*Ruditapes philippinarum*)

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Abstract： Shell color is an important economic trait of the Manila clam, in which the melanin biosynthesis pathway plays a key role in pigmentation. MicroRNAs (miRNAs) are vital post-transcriptional regulators involved in shell color formation of mollusks. Based on transcriptome data from four color variants—white, orange, zebra, and white-zebra clams—this study found that miR-3529-3p was differentially expressed, with the highest level in white clams and the lowest in zebra clams. Bioinformatic analysis identified 324 target genes enriched in MAPK signaling, melanoma, and ubiquitin-mediated proteolysis pathways. In vivo assays using zebra clams showed that miR-3529-3p overexpression reduced expression of key melanin genes, tyrosinase activity, and melanin content, whereas inhibition produced opposite effects. Shell stripes became lighter after overexpression and darker after inhibition. Dual-luciferase assays confirmed that miR-3529-3p directly targets the 3′UTR of TYR and negatively regulates its expression. These results reveal that miR-3529-3p modulates melanin synthesis in clams.

Key words: *Ruditapes philippinarum*; melanin; miRNA; target gene

暴露于高温会导致免疫力和代谢大口黑鲈脾脏的性别差异

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摘要：大口黑鲈 (*Micropterus salmoides*) 是重要的淡水经济养殖鱼类。在不同温度和雌雄个体的影响下，其繁殖过程、个体生长速度以及病害成为当前一个重要问题，因此深入了解大口黑鲈的雌雄与生长温度的基因表达差异，对于实现确定养殖性别、养殖水温以及提高养殖效率具有重要意义。为深入了解高温条件下大口黑鲈雌雄个体的免疫和代谢等差异，本研究比较了高温和常温条件下大口黑鲈雌雄个体脾脏转录组，分析其免疫及代谢等相关因子的性别二态性差异：（1）大口黑鲈在不同温度下，高温组相比常温组(C22 vs C32)在代谢和免疫的 terms 均存在较大差异，同时存在多条差异显著的免疫、炎症、代谢相关的 pathways，如 Intestinal immune network for IgA production、Autophagy – animal 等，且这两条 pathways 与大部分免疫、炎症相关的 pathway 相关联。 (2) 进一步对相同温度下的雌雄样本进行差异分析，常温组(C22-F vs C22-M)基本没差异，高温组(C32-F vs C32-M) KEGG 富集分析 Top20 pathways 中与免疫、炎症相关的 pathways 分别有 16 个、18 个，且表达相关性分析差异 DEGs 主要为正相关作用。(3) 进一步对雌雄样本分开进行差异分析，雄性组(C22-M vs C32-M)相比雌性(C22-F vs C32-F)组有更大的差异变化，主要体现在有机营养代谢和凋亡等，KEGG 富集分析 TOP30 雄性组将近一半的有机营养代谢 pathway，而雌性组几乎为零，且雄性组比雌雄组的 Glycolysis/Gluconeogenesis 关联到更多的通路。通过本研究分析推测高温胁迫下会影响大口黑鲈机体的多个代谢和免疫途径，可能通过影响 TNFSF13B 受体的表达，介导 Intestinal immune network for IgA production 调控影响机体的免疫应答，反应，调控 PI3K-Akt signaling pathway、Proteoglycans in cancer 等免疫途径，而高温条件下的雄鱼也显著富集到了 Intestinal immune network for IgA production，使得雄鱼有强于雌鱼的抗病力。本研究对大口黑鲈高温胁迫下免疫、炎症、代谢反应的性别二态性差异分析，可为今后大口黑鲈单性选育提供新的方向，对提高养殖效率具有重要意义。

关键词：大口黑鲈(*Micropterus salmoides*)，高温，免疫，炎症，代谢，性别二态性

High-temperature exposure induces sexually dimorphic immune and metabolic responses in the spleen of *Micropterus salmoides*

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Abstract： As primary producers and important regulators of aquatic ecosystems, submerged plants have important roles in both natural and cultured water bodies. In shrimp and crab freshwater aquaculture, submerged plants can purify the water body, provide natural bait and shelter, reduce stress, improve immunity, reduce diseases, improve production performance, and enhance the quality of the output, thus greatly improving the shrimp and crab aquaculture efficiency. Most of the existing literature focuses on the waterbody restoration function of submerged plants and pays less attention to aquatic organism production indexes, and most of them are successful cases. Especially in terms of adaptive aquatic plants for a specific culture species, how to make technical breakthroughs in planting technology, species selection and matching and combining with other technologies, so as to overcome the project's own constraints, so that submerged plants can be more widely used in promoting the growth of culture species is a topic of great practical significance.

Key words: Largemouth bass (*Micropterus salmoides*), High temperature, Immunity, Inflammation，Metabolism, Sex-based differences;

盐度胁迫对斑点叉尾鮰生长性能、组织学特征及与凋亡、免疫相关基因表达的影响

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摘要：本研究开展 8 周盐度胁迫试验，评估 0–9 psu 对斑点叉尾鮰幼鱼的生长、组织学及凋亡与免疫基因表达的影响。设置对照（0）及 6 盐度组（3、3.8、4.7、5.9、7.3、9），存活率均为 100%。随盐度升高，体长、体重、增重率与特定生长率显著下降，高盐组抑制更强；在 9 psu 时 SGR 降至 0.61%/d、WGR 为 40.86%（$p<0.05$）。组织学上，肠道黏膜褶皱增多、杯状细胞减少；肝细胞更致密，肝小叶间隙扩大。凋亡检测显示，4.7 psu 组肝脏凋亡高于对照与 9 psu，9 psu 组肠道凋亡最高（$p<0.05$）。qPCR 结果表明，肝与肠中 caspase3、caspase8、IFN-I、IL-1β、bax 较对照显著上调；bcl-2 在肝脏随盐度升高下调、在肠道上调。结果为盐碱地条件下该鱼养殖提供理论依据。

关键词：斑点叉尾鮰；生长性能；盐度胁迫

Effects of salinity stress on the growth performance, histological characteristics, and expression of genes related to apoptosis and immunity in channel catfish (*Ictalurus punctatus*)

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Abstract: Salinity is a key driver of fish growth. To evaluate salinity stress in juvenile channel catfish (*Ictalurus punctatus*), we conducted an 8‑ week trial using an equal logarithmic gradient of six salinities (3, 3.8, 4.7, 5.9, 7.3, 9 psu) plus a 0 psu control. Survival was 100% across treatments. Body length, body weight, weight gain rate (WGR), and specific growth rate (SGR) declined with increasing salinity, with the strongest suppression at high levels; at 9 psu, SGR and WGR dropped to 0.61%/day and 40.86% ($p < 0.05$). Histology showed relatively more intestinal mucosal folds but fewer goblet cells; hepatocytes became denser and hepatic lobule gaps widened. Apoptosis peaked in liver at 4.7 psu (vs. control and 9 psu), while intestinal apoptosis was highest at 9 psu ($p < 0.05$). qPCR indicated elevated caspase 3, caspase 8, INF‑ I, IL‑ 1β, and bax in liver and intestine vs. control; bcl‑ 2 decreased with salinity in liver but increased in intestine. These findings inform culture in saline‑ alkali waters.

Key words: Channel catfish, gene expression, growth performance, salinity stress, tissue structures

热应激与复温对洛氏鱥心肌损伤与修复机制的研究

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摘要：洛氏鱥（*Phoxinus lagowskii*）是经济价值较高的冷水性鱼类。随着全球变暖，其规模化养殖受高温应激的限制较大。本研究通过组织学，生理学和转录组学分析，探究了洛氏鱥短期热应激及复温条件下心肌损伤与恢复的潜在机制。研究表明，短期28℃高温胁迫会显著影响洛氏鱥心脏的分子调控与生理状态，JAK-STAT信号通路、TNF信号通路及溶酶体通路相关基因显著上调，同时引发心肌细胞肿胀、肌原纤维断裂等组织损伤，以及氧化损伤。而当水温恢复至18℃并维持48h后，蛋白酶体、剪接体及DNA复制相关通路基因显著上调，心肌细胞损伤，氧化应激水平均得到缓解，且恢复组与对照组相比，类风湿性关节炎、金黄色葡萄球菌感染及细胞周期通路相关基因表达水平更高。本研究明确了拉氏鱥在高温胁迫下的心肌损伤及恢复机制，不仅为该鱼在全国范围内的养殖推广提供了重要参考依据，也为理解冷水性鱼类应对全球变暖的适应策略提供了理论支撑。

关键词：洛氏鱥；热应激；复温；心脏；修复

Study on the mechanisms of heart injury and repair in *Phoxinus lagowskii* under heat stress and rewarming

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Abstract： *Phoxinus lagowskii*, a valuable cold-water fish, faces aquaculture challenges from heat stress due to global warming. This study examined the myocardial injury and recovery mechanisms under short-term heat stress (28°C) and subsequent return to 18°C using histological, physiological, and transcriptomic analyses. Results showed that heat stress activated the JAK-STAT, TNF, and lysosome pathways, induced myocardial lesions such as cell swelling and myofibril disruption, and caused oxidative damage. After 48-hour recovery at 18°C, proteasome, spliceosome, and DNA replication pathways were upregulated, leading to alleviated myocardial injury and oxidative stress. The recovery group also exhibited higher expression of genes linked to rheumatoid arthritis, Staphylococcus aureus infection, and cell cycle compared to controls. These findings offer insights into heat response and recovery in cold-water fish, supporting aquaculture adaptation and understanding of climate change resilience.

Key words: *Phoxinus lagowskii*; Heat stress; Rewarming; Heart; Repair

转录组与蛋白组联合解析香螺繁殖力差异的分子调控机制

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摘要：香螺（*Naptunea cumingii Crosse*）的繁殖能力存在显著差异，这对种群动态、水产养殖和保护工作具有重要影响。然而，这些差异背后的分子机制仍不明确。本研究采用转录组学和蛋白质组学技术，系统分析了高繁殖能力和低繁殖能力个体间的基因与蛋白质表达差异，旨在揭示调控繁殖差异的分子机制。通过比较分析，我们鉴定出 87 个差异表达基因和 282 个差异表达蛋白质。功能富集分析表明，这些基因和蛋白质主要参与 FoxO、Wnt 和 TGF-β等关键信号通路的调控，并与细胞增殖、凋亡和代谢调节等重要生物学过程相关。此外，转录组与蛋白质组数据的整合分析还发现了 6 种可能通过调控多种生理通路来影响繁殖能力的关键分子。研究结果表明，香螺的繁殖差异是由多个基因和信号通路的协同效应共同决定的，这为理解繁殖的分子机制提供了新视角，并为优化人工繁殖和保护策略提供了重要理论指导。

关键词：海螺；生殖能力；转录组；蛋白质组；分子机制

Transcriptome and proteome combined to decipher the molecular regulatory mechanism of reproductive capacity differences in snails

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Abstract： The reproductive capacity of *Naptunea cumingii* Crosse exhibits significant variability, which has important implications for population dynamics, aquaculture, and conservation. However, the molecular mechanisms underlying these differences remain unclear. In this study, we employed transcriptomic and proteomic technologies to systematically analyze gene and protein expression differences in *Naptunea cumingii* Crosse with high and low reproductive capacities, aiming to elucidate the molecular mechanisms regulating reproductive differences. Comparative analysis identified 87 differentially expressed genes and 282 differentially expressed proteins. Functional enrichment analysis revealed that these genes and proteins are primarily involved in the regulation of key signaling pathways, such as FoxO, Wnt, and TGF-β, and are associated with critical biological processes including cell proliferation, apoptosis, and metabolic regulation. Moreover, the integrated analysis of transcriptomic and proteomic data uncovered six potential key molecules that may play crucial roles in regulating reproductive capacity by modulating multiple physiological pathways. Our findings suggest that reproductive differences in *Naptunea cumingii* Crosse are governed by the synergistic effects of multiple genes and signaling pathways, providing new insights into the molecular mechanisms of reproduction and offering important theoretical guidance for the optimization of artificial breeding and conservation strategies.

Key words: Mussels; reproductive capacity; transcriptome; proteome; molecular mechanisms

基于 GWAS 筛选棕点石斑鱼（♀）×鞍带石斑鱼（♂）幼鱼群体抗神经坏死病毒相关候选 SNP 及基因

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摘要：病毒性神经坏死病由神经坏死病毒引发，是危害全球野生和养殖鱼类的一种重要神经致病性疾病。目前已有超过 50 种鱼类被报道感染该病毒，尤其在鱼苗阶段常导致幼鱼和仔鱼死亡率高达 100%。该病的组织病理学病变主要集中于脑部和视网膜组织。石斑鱼（鲈形目，石斑鱼科）作为重要海水经济养殖鱼类，现有 47 个品种实现人工养殖，其中逾 20 个石斑鱼种及其杂交种已被证实易感 NNV。目前尚无有效方法能完全预防该病毒或阻断疫情暴发。本研究通过全基因组关联分析法，对比耐受型与易感型虎龙石斑鱼群体，鉴定出与 NNV 抗性相关的遗传变异及潜在基因。结果显示从 9 条染色体中筛选出 30 个性状关联 SNP，最终确定 19 个与 NNV 抗性相关的候选基因。这些基因为培育抗病石斑鱼种质资源提供了重要依据。

关键词：神经坏死病毒；石斑鱼；全基因组关联分析

Identification of candidate SNPs and genes associated with resistance to nervous necrosis virus in juvenile population from *Epinephelus fuscoguttatus*♀×*E. lanceolatus*♂ using GWAS

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Abstract： Viral nervous necrosis (VNN) arise from nervous necrosis virus (NNV) is a hazardous neuropathogenic disease of wild and cultured fishes worldwide, more than 50 fish species have been reported to be affected by this virus, particularly during the fry stage, and often causes 100% mortality of juvenile and larvae fish. Histopathological lesions of VNN are mainly discovered in the brain and eye. Grouper (Perciformes, Epinephelidae) is an important mariculture economic fish, 47 of them have been aquacultured, it has been reported more than 20 grouper species and grouper hybrids being susceptible to NNV infection. So far, there is no effective way to prevent NNV or stop outbreaks. In the present study, we conducted a GWAS on one resistant and one susceptible Hulong grouper population to discover variants and potential genes linked with NNV resistance. The results showed there were 30 trait-associated SNPs from 9 chromosomes, and 19 candidate genes for NNV resistance were discovered. These genes provide valuable resources for the breeding of disease-resistant grouper fish.

Key words: nervous necrosis virus, grouper, GWAS

黄条鰤肌肉低温胁迫响应的分子机制

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摘要：黄条鰤作为重要经济海洋鱼类，在北方冬季养殖中面临低温环境下的生存挑战。为探究其分子适应机制，本研究采用 RNA 测序技术分析了黄条鰤肌肉组织在急性低温胁迫（10℃）下 6、12、24 小时的转录响应。表达分析显示出时序表达模式，分别在低温处理 6、12、24 小时筛选出 269、863 和 984 个差异表达基因。脂质代谢、碳水化合物代谢和应激反应等关键信号通路被显著富集，其中 Sestrin3 基因的上调表明 AMPK 介导的能量稳态调节参与低温适应调控。本研究为解析黄条鰤低温适应分子机制提供了基础数据，为培育耐低温品种和提升养殖抗逆性提供了潜在靶点。

关键词：黄条鰤 低温胁迫 转录组 肌肉 代谢

Molecular Mechanisms of Low-Temperature Stress Response in the Muscle of Yellowtail Kingfish (*Seriola aureovittata*)

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Abstract： The yellowtail kingfish (*Seriola aureovittata*), a commercially important marine species, encounters significant survival challenges under low-temperature conditions during winter aquaculture in Northern China. To elucidate its molecular adaptation mechanisms, this study employed RNA-Seq to analyze transcriptional responses in muscle tissues under acute cold stress (10 ◦C) at 6, 12, and 24 h. Differential gene expression analysis revealed time-dependent patterns, with 269, 863, and 984 differentially expressed genes (DEGs) identified at 6, 12, and 24 h, respectively. Key pathways were significantly enriched in lipid metabolism, carbohydrate metabolism, and stress response. Sestrin3 upregulation implicated AMPK-mediated energy homeostasis in cold adaptation. This study provide basic data into the molecular strategies underlying cold adaptation in yellowtail kingfish, offering potential targets for breeding cold-resistant strains and improving aquaculture resilience.

Key words: yellowtail kingfish; low-temperature stress; transcriptome; muscle; metabolism

我国黄渤海地区紫石房蛤不同群体遗传分化研究

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摘要：为探明我国黄渤海地区紫石房蛤群体遗传多样性与遗传分化状况，本研究以大连黑石礁、大连獐子岛、烟台长岛和威海荣成 4 个地理群体共 80 个个体作为对象，进行了线粒体基因序列和基因组重测序分析，结果发现：四个群体 COI 和 CYTB 基因分别检测到多态位点 54 个和 18 个，核苷酸多样性指数分别为 0.00768 和 0.00446。群体之间相对遗传距离均小于 0.05，没有出现明显分化；基因组重测序研究中，4 个群体共筛选得到 16810429 个高质量的 SNPs。多样性分析结果显示，群体之间的 Fst 值为 0.0042~0.0177，且差异不显著。系统进化树结果显示，不同地理群体个体无法区分。近 10 年 4 个群体 Ne 规模较小且较稳定。综合来看，我国黄渤海地区紫石房蛤进化历史上经历了种群扩张，且尚未出现明显的遗传分化。本研究结果揭示了我国黄渤海地区紫石房蛤群体遗传多样性及种质资源现状，并为其种质资源保护及利用提供科学依据。

关键词：紫石房蛤，COI，CYTB，全基因组重测序，遗传多样性，遗传分化

Genetic Differentiation among Different Populations of Saxidomus purpuratus in the Yellow and Bohai Seas, China

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Abstract: To investigate the genetic diversity and differentiation of *Saxidomus purpuratus* in Yellow and Bohai Seas, a total of 80 individuals from four geographic populations (Heishijiao in Dalian, Zhangzidao in Dalian, Changdao in Yantai, and Rongcheng in Weihai) were subjected to COI and CYTB mitochondrial gene sequencing and genome resequencing analysis. Mitochondrial data revealed 54 and 18 polymorphic sites, suggesting historical population expansion. Genetic distances were below 0.05. Genomic analysis identified 16,810,429 high-quality SNPs, with low and non-significant pairwise Fst values (0.0042–0.0177). Observed and expected heterozygosity were similar across populations . Phylogenetic trees showed no geographic clustering, and effective population sizes have remained small and stable. Overall, S. purpuratus in this region shows no significant genetic differentiation, providing a scientific basis for its conservation and sustainable use.

Key words: Saxidomus purpuratus, COI, CYTB, genome resequencing, genetic diversity, genetic differentiation

基于血细胞性状多组学联合分析定位鲤维氏气单胞菌抗性相关基因

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摘要：血液指标能客观反映动物机体生理、病理变化等，有助于一些疾病的早期情况鉴定。目前鱼类抗病以预防为主，容易造成细菌耐药性增强、环境污染等问题。因此，加快抗病品种培育对保障鲤养殖业健康绿色发展具有重要意义。本研究通过整合全基因组关联分析、转录组学和基因组选择方法等，系统探究鲤血细胞性状对维氏气单胞菌抗性之间的遗传相关性。对 259 尾健康鲤尾静脉全血测得 12 种血细胞性状，不同样本间存在显著差异，且均呈现中高遗传力。通过全基因组关联分析鉴定出 851 个与血液性状显著相关的 SNP 并注释到 3824 个候选基因。富集分析显示其显著参与免疫相关通路，如 Toll 样受体信号通路等。进一步结合鲤攻毒试验头肾组织转录组，最终确定 11 个核心候选基因，并在个体组织和细胞水平通过荧光定量验证基因表达模式。以上研究确定了鲤血液性状与维氏气单胞菌抗性相关的候选基因，为后续分子机制研究打下基础，是鲤抗病育种的重要基因资源和理论依据。

关键词：鲤鱼，血细胞性状，维氏气单胞菌，全基因组关联分析，转录组

Identification of genes associated with resistance to *Aeromonas verenii* in carp through multi-omics analysis of hematopoietic cell characteristics

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Abstract： Blood indicators play a vital role in early disease detection due to their physiological functions.However, fish disease resistance is mainly based on prevention, which is easy to cause bacterial resistance and other problems.Therefore, accelerating the development of disease-resistant fish varieties is crucial for ensuring the healthy and sustainable growth of carp farming.We analyzed 12 hematological traits in whole blood samples from 259 carp, revealing significant inter-sample variations with moderate to high heritability. Through GWAS, 851 SNPs strongly associated with blood traits were identified. Enrichment analysis highlighted their critical roles in immune-related pathways. Integrating transcriptomic data from head kidney tissues in carp challenge experiments, we identified 11 core candidate genes and validated their expression patterns through RT-qPCR at tissue and cellular levels. These findings elucidate the genetic basis of blood traits and disease resistance in carp, providing crucial genetic resources and theoretical foundations for disease-resistant breeding programs.

Key words: Common carp, Hematological traits, *Aeromonas veronii*, Genome-wide association study (GWAS), Transcriptome

长牡蛎牛磺酸合成酶 ADO 的功能研究及分子标记开发

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摘要：牛磺酸是一种条件必需氨基酸，具有抗衰老和渗透调节等多重生理功能。长牡蛎是牛磺酸的重要来源，但其体内的合成机制尚不明确。本研究鉴定并验证参与牛磺酸合成的半胱胺双加氧酶同源基因 CgADO 的功能并筛选其关键 SNP 位点。结果显示重组 CgADO 蛋白可催化半胱胺生成次牛磺酸；在 HEK293T 细胞中过表达 CgADO 增加牛磺酸含量，RNAi 抑制内源 CgADO 可降低牡蛎闭壳肌中牛磺酸含量。通过 CgADO 测序分析，鉴定出 47 个 SNPs，其中同义突变 c.415T>C 与牛磺酸含量显著相关。CT 型个体的牛磺酸含量及 CgADO 表达水平均显著高于 TT 型。细胞实验表明该突变显著提高 CgADO mRNA 稳定性（MT 半衰期 $t_{1/2}$ ≈2.6 h，WT 半衰期 $t_{1/2}$ ≈4.2 h）。综上 CgADO 在牡蛎牛磺酸合成中发挥关键作用，c.415T>C 通过调控基因表达影响牛磺酸含量，为高牛磺酸牡蛎的分子辅助育种提供了候选标记和理论依据。

关键词：牛磺酸；半胱胺双加氧酶；单核苷酸多态性；同义突变；长牡蛎

Functional study and molecular marker development of taurine synthetase ADO in the Pacific oyster (*Crassostrea gigas*)

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Abstract： Taurine is a conditionally essential amino acid with anti-aging and osmoregulatory functions. The Pacific oyster (*Crassostrea gigas*) is a major dietary source of taurine, yet its biosynthetic mechanism remains unclear. Here, we identified and functionally validated the cysteamine dioxygenase homolog gene CgADO, and screened its key SNPs. Recombinant CgADO efficiently catalyzed cysteamine to hypotaurine. Overexpression of CgADO in HEK293T cells significantly increased taurine levels, whereas RNAi knockdown reduced taurine content in oyster adductor muscle. Sequencing analysis of CgADO revealed 47 SNPs, among which the synonymous c.415T>C was strongly associated with taurine content. Individuals with the CT genotype showed significantly higher taurine levels and CgADO expression than the TT genotype. Cell experiments further confirmed that this mutation markedly enhanced CgADO mRNA stability (MT $t_{1/2}$ ≈ 4.2 h vs WT $t_{1/2}$ ≈ 2.6 h). Overall, CgADO plays a key role in taurine biosynthesis, and c.415T>C serves as a promising marker for molecular breeding of high-taurine oysters.

Key words: Taurine; Cysteamine dioxygenase; Single nucleotide polymorphism; synonymous mutation; *Crassostrea gigas*

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，淡水环境卵巢发育停滞在 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*），芳香化酶(*cyp19a1*)，催乳素（*prl*），昼夜节律相关蛋白(*dexras1*)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), *cyp19a1*, *prl*, and *dexras1* (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

银鲳快速生长与耐低温选育群体研究及相关机制

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摘要：银鲳是我国重要的海水经济鱼类，2016 年本团队成功突破了人工繁育技术。经过连续 3 年，发现养殖个体生长缓慢、耐低温能力较差，制约了其产业化发展。2019，团队开始了银鲳的选择育种计划，旨在选育快长和耐低温的银鲳新品系，以培育出高产、抗逆能力强的优良品种。我们采用多种分析方法，评估了养殖与野生群体的遗传多样性，分析了选育群体形态性状间的相关性并估算了遗传参数。通过转录组和基因组分析，鉴定出 14 个与生长显著相关的 SNP，并在银鲳肌肉细胞系中进行了功能验证。在耐低温研究方面，通过降温与复温过程中的存活率曲线，确定 LT_{50} 为 7.09°C。并系统探究了生理生化、组织学等变化。低温胁迫下，MAPK 信号通路被显著富集，进一步对对 DUSP 进行家族分析，同时对 DUSP1/5 进行功能验证。并结合简化基因组，筛选出了与温度相关的 SNP。本研究结果为银鲳的遗传育种提供了理论基础，支持其水产养殖业的可持续发展。

关键词：银鲳；耐低温；SCD1；DUSP 家族

Research on Breeding of Fast-Growth and Low-Temperature Tolerant Selected Populations of Silver Pomfret (*Pampus argenteus*) and Related Mechanisms

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Abstract： The silver pomfret is an important marine economic fish in China. However, we observed that the farmed individuals exhibited slow growth rates and poor low-temperature tolerance, which constrained industrial development. To address these issues, a selective breeding program was initiated in 2019. We analyzed the correlations among morphological traits and estimated genetic parameters in the selected breeding population. Fourteen growth-related SNPs were identified and functionally validated using a silver pomfret muscle cell line. The LT_{50} was determined to be 7.09°C. Transcriptome analysis revealed significant enrichment of the MAPK signaling pathway under low-temperature stress. Further family analysis was conducted on DUSP genes, with functional validation performed for DUSP1 and DUSP5. Additionally, temperature-associated SNPs were screened using reduced-representation genome sequencing. These findings provide a theoretical foundation for the genetic breeding of silver pomfret and support the sustainable development of its aquaculture industry.

Key words: Silver pomfret; low-temperature tolerance; SCD1 gene; DUSP family.

跨平台蛤仔组学数据融合与批次校正方法研究

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摘要：背景：随着高通量组学技术在贝类研究中的广泛应用，蛤仔的多源组学数据（包括转录组、蛋白组与代谢组）迅速积累。然而，由于实验平台、测序批次及环境胁迫条件差异显著，不同数据集间存在明显的批次效应，导致数据可比性下降，影响下游差异分析与特征识别的可靠性。方法：针对小样本条件下多平台组学数据的异质性与批次偏差问题，本研究提出一种跨平台数据融合与批次校正方法。该方法采用 VAE 深度学习架构，通过多数据集输入与编码器权重共享机制实现特征提取一致性，生成去除批次偏差的潜在表示，经共享解码器映射后，获得批次校正与融合的统一表征数据。结论：本研究建立了一套面向蛤仔组学数据的跨平台融合与批次校正标准流程，实现了异构数据的统一表示。该方法为蛤仔性别分化机制解析、环境胁迫响应及分子育种研究提供了可靠的数据基础与算法支持，对促进贝类组学数据的标准化与综合利用具有重要意义，也为其他水产物种的多组学整合分析奠定了技术基础。

关键词：蛤仔组学；数据融合；批次校正；跨平台分析

Research on Cross-Platform Data Integration and Batch Correction Methods for Ruditapes philippinarum Omics

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Abstract：With the application of high-throughput omics technologies, multi-source omics data have been rapidly accumulated. However, significant differences in experimental platforms and sequencing batches have introduced pronounced batch effects among datasets, affecting the reliability of downstream analysis. To address the heterogeneity and batch bias in small-sample, cross-platform omics data, we propose a cross-platform data integration and batch correction method. The approach employs a deep learning framework, which ensures consistent feature extraction through dataset input and shared encoder weights. The model generates latent representations with reduced batch bias, which are mapped back to the original feature space via a shared decoder to obtain unified, batch-corrected, and integrated data representations. The method provides a reliable data foundation and algorithmic support for studies on sex differentiation mechanisms, environmental stress responses, and molecular breeding of clams. It also offers a technical basis for multi-omics integration in other aquatic species.

Key words: Clam Omics; Data Integration; Batch Correction; Cross-Platform Analysis

基于鳞片光谱信息结合机器学习方法的无损检测技术实时监测活鱼肌肉氨基酸含量的动态变化

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摘要：为实现鱼类高营养品质的精准育种与分级，需对活体营养状态进行实时监测。尽管深度学习驱动的可见/近红外光谱技术已在农产品和屠宰动物检测中广泛应用，但由于活鱼体表的鳞片和皮肤可能对光谱信号产生阻挡效应，该技术的适用性仍面临挑战。为此，本研究开发了一种结合高光谱成像与深度学习模型的无损检测方法，用于预测活体鱼的氨基酸含量。研究结果显示，群体异质性是影响建模精度的最关键因素：当使用全光谱信号和BP-ANN模型时，R^2从训练群体的0.974-0.998下降至验证群体的0.777-0.847，其中反向传播人工神经网络（BP-ANN）模型表现出最优的预测性能，R^2值均超过0.777。进一步通过全鱼体扫描分析，发现下颌部、胸部及腹部肌肉中的总氨基酸含量最高。本研究提出的方法有望在精准育种、投喂调控与品质分级中提供可靠的技术支持。

关键词：可见/近红外高光谱、深度学习、氨基酸、活体鱼、时间-空间分布

Non-invasive and timely monitoring the dynamics of muscular amino acid contents in live fish using deep learning-driven scale hyperspectral imagery

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Abstract： To achieve precise breeding and grading of fish with high nutritional quality, real-time monitoring of live nutrient status is essential. Although visible/near-infrared spectroscopy driven by deep learning has been widely applied in agricultural products and slaughtered animal detection, its applicability remains challenging due to potential signal obstruction from fish scales and skin. This study developed a non-destructive method combining hyperspectral imaging and deep learning models to predict amino acid content in live fish. Results showed that population heterogeneity was the most critical factor affecting modeling accuracy: when using full-spectrum signals and BP-ANN models, R^2 decreased from 0.974-0.998 in the training population to 0.777-0.847 in the validation set. The BP-ANN model demonstrated optimal performance with all R^2 values exceeding 0.777. Full-body scanning revealed the highest total amino acid content in mandibular, pectoral, and abdominal muscles. This method offers reliable technical support for precision breeding, feeding regulation, and quality grading.

Key words: visible/near-infrared hyperspectrum, deep learning, amino acids, live fish, spatiotemporal distribution

大泷六线鱼精子低温冷冻保存方法研究

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大连海洋大学

摘要：为建立大泷六线鱼（*Hexagrammos otakii*）精子的超低温冷冻保存方法，对其精子冷冻保存过程中的稀释液、精子与保护液的稀释比例以及降温步骤进行了筛选优化，并用最优保存方法冻存的精子开展授精试验。结果显示，以鱼用任氏液并添加体积分数为20%的乙二醇抗冻剂为冷冻保护液时，冷冻4 h后复温用海水激活，精子活力为（69.00±2.65）%，精子寿命为（569.67±20.43）s，冷冻保存效果显著高于其他组（$P<0.05$）。当稀释比例为1:3时，复温激活的精子活力和寿命显著高于其他组（$P<0.05$），分别为（75.00±1.0）%和（731.61±64.23）s。降温步骤方面，先在4 ℃平衡30 min后，再在液氮面上5 cm处熏蒸5 min，最后投入液氮的降温步骤保存效果显著高于其他组（$P<0.05$）。最后，通过授精试验检验冻精质量，冻精组平均孵化率达到（56.67±9.29）%。

关键词：大泷六线鱼；精子；低温冷冻；保存

Research on Methods for Cryopreservation of Sperm in *Hexagrammos otakii*

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Abstract： To establish a cryopreservation protocol for sperm of the fat greenling (*Hexagrammos otakii*), the effects of extenders, dilution ratios, and cooling procedures were screened and optimized. Fertilization tests were conducted to validate the protocol. Results showed that using fish Ringer’s solution with 20% (v/v) ethylene glycol as the cryoprotectant led to significantly higher post-thaw sperm motility (69.00 ± 2.65)% and longevity (569.67 ± 20.43 s) compared to other groups ($P < 0.05$). A sperm-to-cryoprotectant dilution ratio of 1:3 further improved motility and longevity to (75.00 ± 1.00)% and (731.61 ± 64.23) s, respectively. The optimal cooling procedure involved equilibration at 4 °C for 30 min, vapor-phase exposure 5 cm above liquid nitrogen for 5 min, and final plunging into liquid nitrogen. This method yielded significantly better sperm quality than other protocols ($P < 0.05$). Fertilization tests confirmed the functionality of the cryopreserved sperm, with a mean hatching rate of (56.67 ± 9.29)%.

Key words: fat greenling; sperm; Cryopreservation; preservation.

SNP 对菲律宾蛤仔干露后快速恢复的作用研究

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摘要：本研究以菲律宾蛤仔（*Ruditapes philippinarum*）为研究对象，研究了硝普钠（SNP，NO 供体）的添加对干露后恢复过程中蛤仔抗氧化酶活力的影响。结果表明：干露胁迫时，蛤仔 SOD、CAT、ASAFR 活力被抑制，GSH 含量下降，Gpx 活力上升（$P < 0.05$）。蛤仔经 48 h 干露后放入含 100μM SNP 的海水中恢复，24h 时 GSH 含量显著高于对照组（未添加 SNP 海水组），48h 和 72h 时 CAT、Gpx 和 ASARF 活力也有小幅提升。恢复过程中蛤仔死亡率与对照组相当（$P>0.05$）。综合以上研究结果，可知干露过程中由于蛤仔呼吸作用被抑制，仅依赖 Gpx 应对干露胁迫。恢复过程中添加 SNP，可在短时间内促使蛤仔抗氧化能力提升，缓解代偿性呼吸作用带来的氧化应激，一定程度上提高蛤仔的耐干露能力。该研究所得结果为蛤仔适应干露的生理学机制，以及提高蛤仔耐干露能力研究提供参考。

关键词：菲律宾蛤仔，干露，抗氧化酶，硝普钠（SNP）

The Role of Sodium Nitroprusside (SNP) Supplementation in Accelerating Recovery of Ruditapes philippinarum after Air Exposure

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Abstract： This study examined how sodium nitroprusside (SNP, a nitric oxide donor) affects antioxidant responses in Manila clams (*Ruditapes philippinarum*) recovering from air exposure. Results demonstrated that air exposure suppressed SOD, CAT and ASARF activities and reduced GSH content ($P < 0.05$), while increasing GPx activity ($P < 0.05$). During recovery in 100 μM SNP seawater, GSH content significantly exceeded controls (without SNP) at 24 h, with modest improvements in CAT, GPx and ASARF activities at 48-72 h. Mortality remained unchanged between groups ($P > 0.05$). Results indicate clams primarily rely on GPx during air exposure, and SNP supplementation during recovery enhances antioxidant capacity, alleviates oxidative stress from compensatory respiration, thereby improving air exposure tolerance. These findings provide valuable insights into the physiological mechanisms underlying air exposure adaptation in clams and offers references for enhancing their desiccation resistance.

Key words: Ruditapes philippinarum, air exposure, antioxidant enzymes, sodium nitroprusside (SNP)

石斑鱼杂交育种进展及杂交生长优势解析

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摘要：金虎杂交斑新品种在胚胎发育时期就已呈现一定的杂交生长优势。对金虎杂交斑胚胎各阶段 DNA 甲基化模式分析中，发现杂交种基因组甲基化率均显著低于亲本纯种。结合 DNA 甲基化 PCA 和聚类分析，综合支持石斑鱼受精及胚胎发育过程中，未经历基因组 DNA 去甲基化过程，而是继承了父本精子甲基化模式，指导胚胎发育。与转录组联合分析中，发现杂交种上调基因数目均明显多于亲本，鉴定到 Wnt 和 Notch 信号调节通路，重要候选基因包含，*notch1*，*wnt5a*，*wnt8b*，*myc*，*bmpr1a*，*igf1r*，*fgfr2*，*egfr*，*fasnh* 和 *foxo1a*。此外，绘制了金虎杂交斑单倍型 T2T 水平基因组图谱，结合多组学优势解析了其生长、性腺发育迟滞性状的分子机制，发现父本亚基因组优势协同 DNA 低甲基化调节脂质代谢通路促进杂交生长优势形成，构建了潜在的分子调解网络。

关键词：金虎杂交斑；杂交生长优势；亚基因组优势；DNA 甲基化模式；单倍型基因组

Progress in hybridization breeding of groupers and analysis of hybrid growth heterosis

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Abstract：The new hybrid species of Jinhu grouper has shown certain hybrid growth heterosis during the embryonic development stage. In the analysis of DNA methylation patterns at each stage of the Jinhu grouper embryos, it was found that the methylation rate of the hybrid genome was significantly lower than that of the parental pure breeds. Combined with DNA methylation PCA and clustering analysis, it was comprehensively supported that during the fertilization and embryonic development process of the groupers, no genome DNA demethylation process occurred, but inherited the methylation pattern of the paternal sperm, guiding the embryonic development. In the combined analysis with the transcriptome, it was found that the number of upregulated genes in the hybrid was significantly higher than that of the parents, and the Wnt and Notch signaling regulatory pathways were identified. Important candidate genes included *notch1, wnt5a, wnt8b, myc, bmpr1a, igf1r, fgfr2, egfr, fasnh,* and *foxo1a*. In addition, the haplotype T2T level gene map of Jinhu grouper was drawn.

Key words: Jinhu grouper; Hybrid growth heterosis; Subgenomic advantage; DNA methylation pattern; Haploid hybrid genome

莱州潮间带和潮下带蛤仔群体的形态差异与遗传分化分析

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摘要：菲律宾蛤仔（*Ruditapes philippinarum*）是我国重要的经济贝类，其表型多样性和遗传结构差异对群体适应与品种选育具有重要意义。然而，同一海域内不同生境条件对其表型变异与遗传分化的影响仍缺乏系统研究。本研究以山东省莱州市同一海区的潮间带与潮下带菲律宾蛤仔群体为研究对象，旨在揭示微生境差异对其形态特征与遗传结构的潜在影响。研究采用形态学测量与高通量 SNP 分子标记相结合的方法，对两个群体的壳形态变异与遗传分化进行联合分析。结果显示，潮间带群体壳形较宽，整体趋向于“壳宽型”；而潮下带群体壳形相对扁平，呈现“扁平型”特征。基于 SNP 数据的群体遗传分析表明，两群体间存在显著遗传分化（FST = 0.279），表明在同一海域内的潮间带与潮下带环境已形成明显的遗传结构差异。综合结果表明，生境差异可能通过长期生态选择驱动菲律宾蛤仔在形态与遗传层面产生协同分化。本研究为理解贝类在局域尺度上的生态适应与种群分化机制提供了新的实证依据，对贝类种质资源保护与栖息地管理具有参考价值。

关键词：菲律宾蛤仔；壳形变异；遗传分化

Morphological Differences and Genetic Differentiation between Intertidal and Subtidal Populations of Ruditapes philippinarum in Laizhou

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Abstract：*Ruditapes philippinarum* is an important bivalve species in China, and its phenotypic and genetic diversity are crucial for population adaptation and selective breeding. However, the influence of microhabitat variation on shell morphology and genetic differentiation within the same sea area remains unclear. In this study, intertidal and subtidal populations from Laizhou, Shandong Province were analyzed using morphological measurements and high-throughput SNP markers. The results showed that intertidal clams had broader and thicker shells, while subtidal clams exhibited flatter shell shapes. SNP-based analyses revealed significant genetic differentiation between the two populations, suggesting that local habitat heterogeneity has contributed to genetic structuring. These findings indicate that long-term ecological selection may have driven coordinated divergence in morphology and genetics. This study provides valuable insights into local-scale ecological adaptation and population differentiation in bivalves, with implications for germplasm conservation and habitat management.

Key words: *Ruditapes philippinarum*; shell morphology; genetic differentiation

红鳍东方鲀 miRNA 在感染哈氏弧菌后的表达调控分析

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摘要：红鳍东方鲀 (*Takifugu rubripes*)是中国重要的经济鱼类，但其养殖过程中易受哈氏弧菌（*Vibrio harveyi*）侵染而造成重大损失。MicroRNA（miRNA）是一类小型非编码 RNA，在调节鱼类感染病原体免疫反应方面发挥着至关重要的作用。然而，关于 miRNA 在红鳍东方鲀抗弧菌感染中的免疫功能的研究仍然较少。本研究采用高通量测序技术对红鳍东方鲀感染哈氏弧菌后脾脏中的 miRNA 进行了测序。经鉴定得到已知 miRNA 106 个，预测到新 miRNA 170 个。对 miRNA 的表达及差异分析共筛选出脾脏中 110 个 miRNA 在感染后显著差异表达。DEmiRNA 的靶基因富集在 JAK-STAT 等多条免疫相关的信号通路中。此外，双荧光素酶报告基因测定和体内过表达实验证实了 miRNA 对靶基因表达的负调控作用。本研究结果初步揭示了红鳍东方鲀在抵御哈氏弧菌侵染时 miRNA 的调控作用。

关键词：红鳍东方鲀；miRNA；哈氏弧菌

miRNA Expression Regulation in *Takifugu rubripes* in Response to Vibrio harveyi Infection

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Abstract： The Japanese pufferfish (*Takifugu rubripes*),a commercially significant fish species in China,suffers significant losses from *Vibrio harveyi* infection.MicroRNAs (miRNAs),a class of small non-coding RNAs,play a crucial role in modulating the immune responses of fish during pathogen infections.However, research on the role of miRNAs in pufferfish resistance to Vibrio infection remains scarce.In this study,high-throughput sequencing technology was employed to sequence miRNAs in the spleen of the pufferfish after infection with *V. harveyi*.The analysis revealed 106 conserved miRNAs and 170 predicted novel miRNAs.110 miRNAs were significantly differentially expressed in the spleen post-infection.The target genes of these DEmiRNAs were enriched in multiple immune-related signaling pathways such as JAK-STAT pathway.A dual-luciferase reporter gene assay and in vivo overexpression experiments confirmed the negative regulatory effect of miRNA on target gene expression.These findings illuminate the regulatory role of miRNAs in the pufferfish's defense against *Vibrio harveyi* infection.

Key words: Japanese pufferfish, miRNA, Vibrio harveyi

五个不同群体虾夷扇贝形态测量分析

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摘要：基于几何形态测量学方法，对俄罗斯(ELS)、龙王塘(LWT)、獐子岛(ZZD)、海洋岛(HYD)和小平岛(XPD)的五个不同群体虾夷扇贝（*Mizuhopecten yessoensis*）进行形态学分析。结果显示：（1）龙王塘(LWT)与海洋岛(HYD)群体中，壳长(SL)对其湿重影响最大，而小平岛(XPD)与獐子岛(ZZD)群体中，壳高(SH)对其湿重影响最大。（2）结合薄板样条函数分析结果显示，俄罗斯(ELS)群体的壳耳较小，壳盘相对较大；龙王塘群体的壳耳较大。小平岛、獐子岛和海洋岛群体间形态差异较小。（3）典型变量分析（CVA）表明，小平岛群体与龙王塘群体，二者远离其他群体；獐子岛、海洋岛和俄罗斯群体互有重叠。分析结果：五个群体虾夷扇贝壳体形态存在显著差异。

关键词：虾夷扇贝；几何形态测量学；表型塑化

Morphometric Analysis of Five Different Populations of Patinopecten yessoensis

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Abstract：Based on the geometric morphometrics method, a morphological analysis was conducted on five different populations of Yesso scallop (*Mizuhopecten yessoensis*) from Russia (ELS), Longwangtang (LWT), Zhangzidao (ZZD), Haiyang Island (HYD), and Xiaoping Island (XPD). The results are as follows:(1) In the LWT and HYD populations, the shell length (SL) had the greatest impact on their wet weight. While in the XPD and ZZD populations, the shell height (SH) had the greatest impact on their wet weight.(2) Combined with the results of thin-plate spline function analysis, the ELS population had smaller shell ears and a relatively larger shell disc; the LWT population had larger shell ears. The morphological differences among the XPD, ZZD, and HYD populations were small.(3) Canonical Variate Analysis (CVA) indicated that the XPD population and the LWT population were both far from the other populations; the ZZD, HYD, and ELS populations overlapped with one another.Analysis conclusion: There were significant differences in shell morphology among the five Yesso scallop populations.

Key words: Mizuhopecten yessoensis；Geometric Morphometrics；Phenotypic Plasticity

不同三倍体牡蛎的生化成分分析与营养价值评价

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摘要：比较了三倍体牡蛎（GG-同源三倍体：长牡蛎♀×长牡蛎四倍体♂；GA-异源三倍体：长牡蛎♀×葡萄牙牡蛎四倍体♂；GGA-异源三倍体：长牡蛎♀×杂交四倍体（长牡蛎♀×葡萄牙牡蛎♂）♂）与二倍体长牡蛎（D组）在常规营养成分、氨基酸和脂肪酸组成上的差异。结果表明：二倍体组的蛋白质和糖原含量显著高于三倍体组（$P < 0.05$），而三倍体组的粗脂肪含量显著更高（$P < 0.05$）。各组共检测出18种氨基酸，二倍体组的总氨基酸、必需氨基酸和风味氨基酸含量均显著高于三倍体组（$P < 0.05$）。在三倍体组中，GA组的总氨基酸、必需氨基酸和风味氨基酸含量最高，且氨基酸组成最均衡。本研究为牡蛎品质评价及高营养品种选育提供了重要参考。

关键词：牡蛎、三倍体、生化组成、营养价值

Analysis of biochemical compositions and evaluation of nutritional value in different triploid oysters

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Abstract： This study investigated the differences of conventional nutrients, amino acids and fatty acids compositions among three triploid oysters (GG-autotriploid: *Crassostrea gigas*♀ × *C. gigas tetraploid*♂, GA-allotriploid: *C. gigas*♀ × *C. angulata tetraploid*♂, and GGA-allotriploid: *C. gigas*♀ × hybrid tetraploid (*C. gigas*♀ × *Crassostrea angulata*♂)♂ groups) compared with diploid *C. gigas* (D group). The results showed that the diploid group had significantly higher contents of protein and glycogen than triploids ($P < 0.05$), while triploids exhibited notably higher content of crude fat ($P < 0.05$). The diploid group presented obviously higher total amino acids, essential amino acids and flavor-enhancing amino acids than triploids ($P < 0.05$). The GA group possessed the highest contents of total amino acids, essential amino acids and flavor-enhancing amino acids among triploids. In the triploid group, the GA group had the highest total amino acid (TAA), essential amino acid (EAA), and flavor-enhancing amino acid content, and the most balanced amino acid composition.

Key words: oyster; triploid; biochemical composition; nutritional value

敲除硒蛋白 W1 促进蛋白质泛素化降解抑制斑马鱼骨骼肌的生长和发育

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摘要：硒蛋白是硒元素发挥生物学功能的重要载体。本课题组前期研究发现硒蛋白 W1（selenow1）基因的表达水平与斑马鱼肌肉的生长发育呈正相关，然而其调控机制尚不清楚。为了阐明其调控机制，本研究使用 CRISPR-Cas9 技术构建了三个靶点的硒蛋白 W1 基因敲除（selenow1-/-）斑马鱼模型。在胚胎期和幼苗期，selenow1 的缺失会显著降低斑马鱼受精卵的存活率，体长、体重以及白肌纤维横截面积均显著低于 wt 斑马鱼。机制研究发现，敲除 selenow1 可调控 PI3K/AKT/FoxO 通路，促进蛋白质泛素化降解，抑制骨骼肌的肥大性生长。此外，体外过表达 Selenow1 能够维持 AKT 蛋白的稳定性。综上所述，我们的研究有助于深入理解 selenow1 在鱼类中的生理学功能及其调控机制，为鱼类分子育种提供靶点。

关键词：斑马鱼；硒蛋白 W1；肌肉生长发育；转录组；PI3K/AKT/FoxO 通路

Loss of selenoprotein W1 inhibits skeletal muscle growth and development in zebrafish (*Danio rerio*) by promoting protein ubiquitination degradation

Chenlei Liao1, 2, Li Wang1, Hongyun Li1, Yiwen Tong1, Danqiu Wei1, Hai Huang2, Xuezhen Zhang1, *
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Key words: Zebrafish; selenow1; muscle growth and development; transcriptome; PI3K/AKT/FoxO pathway

敲除硒蛋白 W1 促进蛋白质泛素化降解抑制斑马鱼骨骼肌的生长和发育

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Key words: Zebrafish; *selenow1*; muscle growth and development; transcriptome; PI3K/AKT/FoxO pathway

金虎杂交斑三倍体生物学特性分析及生长优势性状形成的分子机制研究

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中国水产科学研究院黄海水产研究所

摘要：异源三倍体培育是新种质创制的重要途径。本课题组开展了金虎杂交斑三倍体新种质创制研究，并对其红细胞、核型、形态、生长、发育、营养分析等生物学特性以及生长优势形成的分子机制进行了初步研究。优化静水压诱导参数，发现受精后 6 min、 45 MPa 处理 5 min，三倍体率最高，初步建立了金虎杂交斑三倍体群体。三倍体红细胞表面积为二倍体的 1.54 倍；三倍体染色体核型为 3n=72=1m+2sm+69t，NF=75；形态特征分析表明三倍体有其特有的特征。三倍体较二倍体提高 9.6%，表现出生长速度快的优势；21 月龄三倍体的性腺发育缓慢；肌肉营养成分分析发现三倍体粗蛋白含量较高，表明具有较高的食用价值。组学分析鉴定到与生长性状和性腺发育显著相关的目标模块，识别了一系列与内分泌系统、脂质代谢通路相关的基因，如 *epdr1*、*hp1bp*、*pcdhac*、*cyp2j2* 等。为石斑鱼新种质创制提供了丰富的基础数据。

关键词：金虎杂交斑；三倍体；生物学特性；生长优势性状；分子机制

Analysis of biological characteristics of Jinhu hybrid triploid and research on molecular mechanism of growth advantage traits formation

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Abstract： Heteroploid triploid breeding is an important approach for creating new germplasm. Our research group has conducted studies on the creation of new triploid germplasm of the Jinhu hybrid grouper, and has carried out preliminary research on its biological characteristics as well as the molecular mechanism underlying the formation of growth advantages. It was found that the highest triploid rate was achieved when treated at 45 MPa for 5 minutes at 6 minutes post-fertilization. The karyotype of the triploid was 3n = 72 = 1m + 2sm + 69t, NF = 75; morphological characteristic analysis indicated that the triploid had its own unique features. The triploid showed a 9.6% increase compared to the diploid; the gonad development of the 21-month-old triploid was slow; the triploid had a higher crude protein content. Transcriptome analysis recognized a series of genes related to the endocrine system and lipid metabolism pathways, such as *epdr1, hp1bp, pcdhac, cyp2j2*, etc. This provides rich basic data for the creation of new grouper germplasm.

Key words: Jinhu hybrid; Triploid; Biological characteristics; Growth advantage traits; Molecular mechanism

菲律宾蛤仔南北方群体生长和营养成分差异研究

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摘要：本研究将我国南、北方菲律宾蛤仔（*Ruditapes philippinarum*）群体同时养殖于北方海域，研究同一环境下两个群体的生长和营养成分差异。10个月跟踪监测发现，两个群体生长速率变化趋势相同，但南方群体生长速率显著低于北方群体，容量指数、伸长指数、大部分时间点的凸度指数也显著低于北方群体（$P<0.05$），但南方群体肥满度（0.225±0.049）极显著高于北方群体（$P<0.001$）；在繁殖季节，南方群体软体部丙氨酸和亮氨酸含量（分别为0.840±0.019g/100g，0.691±0.007g/100g）较高，而北方群体赖氨酸和组氨酸含量（0.666g±0.005/100g、0.240±0.005g/100g）较高。南方群体水分、灰分含量显著高于北方群体（$P<0.05$），而总蛋白、总脂肪含量则相反。该研究为蛤仔南北方群体生长差异，以及蛤仔不同群体跨区域养殖研究提供了参考数据。

关键词：菲律宾蛤仔，地理群体，生长，营养成分

Growth Performance and Nutritional Composition of Northern and Southern Populations of the Manila Clam *Ruditapes philippinarum*

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Abstract: The Manila clam Ruditapes philippinarum develops distinct geographic populations due to isolation. This study compared growth and nutritional composition between northern and southern Chinese populations reared under identical northern conditions. During 10-month monitoring, while showing similar growth trends, southern clams exhibited significantly lower growth rates than northern counterparts ($P < 0.05$). Southern clams also showed lower bulk and elongation indices ($P < 0.05$), and mostly lower convexity. Conversely, southern clams had significantly higher condition index (0.225 ± 0.049, $P < 0.001$). Nutritional analysis revealed southern clams contained more alanine and leucine (0.840 ± 0.019 and 0.691 ± 0.007 g/100g), while northern clams had higher lysine and histidine (0.666 ± 0.005 and 0.240 ± 0.005 g/100g). Southern clams showed higher moisture and ash but lower crude protein and lipid contents ($P < 0.05$). This study provides valuable data for understanding geographic divergence and supporting cross-regional aquaculture of R. philippinarum.

Key words: *Ruditapes philippinarum*, geographic population, growth performance, nutritional composition

高碱度下南美白对虾鳃顺式调控反应中 lncRNA 的特异性表达

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摘要：长链非编码 RNA（lncRNA）能够协调转录和转录后的网络调控。然而，关于碱胁迫下甲壳动物 lncRNA 的调控作用仍知之甚少。本研究旨在探讨南美白对虾（*Litopenaeus vannamei*）鳃在不同碱胁迫（C：50 mg/L 和 T：350 mg/L）下 lncRNA 的潜在作用。研究发现了 82 个差异表达 lncRNA（DELs）通过转录水平的顺式或反式模式调控基因表达。顺式功能 DELs 富集于谷胱甘肽代谢、过氧化物酶体和溶酶体等通路；反式功能 DELs 则富集于 Toll 样受体信号通路、过氧化物酶体和溶酶体。我们还获得了由 6 个 DELs 和 11 个 mRNAs 组成的 12 对 DEL-mRNA，这些 DELs 具有正向调控邻近基因的潜力，主要表现为顺式调控方式。沉默实验中，DELs 被发现通过顺式作用在碱胁迫下调控溶酶体通路。这些结果为碱胁迫下虾鳃中 lncRNA 的作用机制提供了新的见解。

关键词：长链非编码 RNA；顺式调控；南美白对虾；鳃；碱胁迫；溶酶体

Specific expression profiles of lncRNAs in cis-regulatory responses to gill in *Litopenaeus vannamei* under high alkalinity

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Abstract： Long non-coding RNA (lncRNA) can coordinate the network regulation of transcription and post-transcriptional processes. However, little is known about their cis-regulatory contributions in crustaceans under alkalinity stress. In this study, the purpose was to explore the potential role of lncRNA in gill of Pacific white shrimp (*Litopenaeus vannamei*) under different alkalinity stress (C: 50 mg/L and T: 350 mg/L). We found 82 differentially expressed lncRNA (DELs) in C and T groups may affect gill stress by regulating gene expression in cis- or trans- mode at transcriptional level. The cis-functions DELs were enriched in several pathways, including Glutathione metabolism, Peroxisome and Lysosome. The trans-functions DELs were enriched in Toll-like receptor signaling pathway, Peroxisome and Lysosome. We also obtained 12 DELs-mRNA pairs consisting of 6 DELs and 11 mRNAs, and DELs have potential for positively affecting their neighboring genes, predominantly in a cis-regulatory manner. These results provide new insights into the mechanism of lncRNA in shrimp gills under alkaline stress.

Key words: lncRNA; cis-regulatory; *Litopenaeus vannamei*; Gill; Alkalinity stress; Lysosome

多维度解析（生化指标 + 转录组 + 代谢组）：潮间带牡蛎短期热应激适应机制的揭示

刘优利，王园园，刘圣，林志华，薛清刚
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摘要：牡蛎能够耐受适度的温度升高，但对海洋热浪这种极端高温事件较为敏感。其在突发温度变化中能否存活，关键在于能否快速启动分子与生理层面的响应。然而，其中涉及的转录调控、代谢过程等潜在机制，仍有待深入解析。本研究通过对熊本牡蛎（*Crassostrea sikamea*）进行 35°C 高温暴露（0-3 小时）处理，探究其生化响应、基因表达模式及代谢变化。结果显示，熊本牡蛎可耐受 45°C 以下温度处理 1 小时，此条件下死亡率极低，且抗氧化酶被显著激活。研究共鉴定出 4442 个热应激响应基因和 420 种差异丰度代谢物。转录组与代谢组的整合分析表明，氨基酸生物合成、半胱氨酸与蛋氨酸代谢及半乳糖代谢通路在此过程中发挥重要作用。本研究筛选出候选基因与代谢物，阐明了牡蛎应对温度波动的适应策略。

关键词：熊本牡蛎，海洋热浪，热激蛋白，差异代谢物，生物标记

Short-Term Heat Stress Adaptation in Intertidal Oysters (*Crassostrea sikamea*): Integrative Biochemical, Transcriptomic and Metabolomic Insights

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Abstract：Oysters can tolerate moderate temperature increases but are vulnerable to extreme thermal events. The ability to mount rapid molecular and physiological response is crucial for surviving sudden temperature changes. However, the underlying mechanisms, including transcriptional and metabolic processes—remain poorly understood. This study via 0-3 hours at 35°C high-temperature exposure to investigate the biochemical responses, gene expression patterns, and metabolic changes in Kumamoto oyster (*Crassostrea sikamea*). The result indicated that *C. sikamea* can withstand lower temperature than 45°C for 1 hour, exhibiting minimal mortality and with antioxidant enzyme highly triggered. Total 4,442 heat shock responsive genes and 420 differentially abundant metabolites were identified. Integrative analysis of transcriptomic and metabolomic revealed the amino acid biosynthesis, cysteine and methionine metabolism, and galactose metabolism pathway playing important roles. This study identifies candidate genes and metabolites, elucidates adaptive strategies of oysters to temperature fluctuations.

Key words: *Crassostrea sikamea*, marine heatwave, heat shock proteins, differentially abundant metabolites, biomarkers

两种不同体色大鳞副泥鳅皮肤转录组分析比较

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摘要：黄金鳅，由大鳞副泥鳅突变体经改良培育而来的养殖品种，凭借金黄或金红色的独特体色，在食用价值之外，还具备极高的观赏价值。因此解析黄金鳅的皮肤体色形成机制，可以为黄金鳅的人工育种提供理论依据。本研究通过高通量测序技术对 2 种体色的大鳞副泥鳅皮肤组织的转录组进行测序和分析，研究结果共筛选 871 个差异表达基因，其中上调表达的基因有 466 个，下调表达的基因有 405 个。对差异表达基因进行功能注释，发现它们涉及细胞过程、代谢过程、结合活性、催化活性、分子转导活性等。KEGG 通路富集分析发现，差异表达基因显著富集在多个信号通路中，如细胞黏附分子、嘧啶代谢、核苷酸代谢等。选取 12 个显著性差异表达的相关基因进行 qRT-PCR 验证，验证结果与测序结果变化趋势基本一致。本研究为深入了解大鳞副泥鳅体色形成的分子机制提供了重要的基础数据和理论依据，也为鱼类体色相关研究提供了参考。

关键词：大鳞副泥鳅；体色；转录组；差异表达基因

Transcriptome Analysis and Comparison of Skin in Two Different Body Color Morphs of *Paramisgurnus dabryanus*

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Abstract：The golden loach, a cultivated variety from *Paramisgurnus dabryanus* mutants, has unique golden/golden-red body color, with edible and high ornamental value. Analyzing its skin color mechanism provides a basis for artificial breeding.This study used high-throughput sequencing to analyze skin transcriptomes of *Paramisgurnus dabryanus* with two body colors. Results: 871 differentially expressed genes (DEGs) screened, including 466 up-regulated and 405 down-regulated.Functional annotation showed DEGs involved in cellular/metabolic processes, binding/catalytic/molecular transduction activities. KEGG analysis indicated DEGs enriched in pathways like cell adhesion molecules, pyrimidine/nucleotide metabolism.Twelve key DEGs were validated by qRT-PCR, with results consistent with sequencing data.This study provides basic data and a theoretical basis for understanding *Paramisgurnus dabryanus* body color mechanism, and a reference for fish body color research.

Key words: *Paramisgurnus dabryanus*；body color；transcriptome；differentially expressed gene

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

菲律宾蛤仔与杂色蛤仔的核型制备及比较分析

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摘要：菲律宾蛤仔（*Ruditapes philippinarum*）与杂色蛤仔（*Venerupis aspera*）的准确鉴定在分类学与遗传育种中至关重要。因此，本研究结合经典细胞遗传学与分子遗传学方法，旨在精确判定两种蛤仔的二倍体染色体数目、进行核型分析。为深入鉴别其二者差异，选取两者担轮幼虫为材料，通过秋水仙素、低渗的方法处理，热滴片及利用 Giemsa 染色液染色，对杂色蛤仔与菲律宾蛤仔染色体中期分裂相及显带特征进行研究。结果表明，杂色蛤仔的染色体数目为 38，核型公式 2n=38=20m+4sm+14t，NF=62，未发现随体及性染色体。菲律宾蛤仔的染色体数目为 38，核型公式为 2n=38=20m+18sm，NF=76。本研究对杂色蛤仔与菲律宾蛤仔进行的核型比较分析，不仅为物种的精准鉴定提供了可靠的细胞遗传学依据，也为其基因组进化研究及优良品种选育奠定了重要基础。

关键词：菲律宾蛤仔；杂色蛤仔；染色体；核型分析

Preparation and Comparative Analysis of Karyotypes of *Ruditapes philippinarum* and *Venerupis aspera*

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Abstract： Accurate identification of *Ruditapes philippinarum* and variegated clam is crucial for taxonomy and genetic breeding. Therefore, this study combined classical cytogenetic and molecular genetic approaches to accurately determine the diploid chromosome number and perform karyotype analysis of these two clam species. To further distinguish their interspecific differences, trochophore larvae of both species were used as experimental materials. After treatment with colchicine and hypotonic solution, followed by the hot drop slide method and staining with Giemsa stain, the metaphase chromosome spreads and banding characteristics of *V. aspera* and *R. philippinarum* were investigated. The results showed that *V. aspera* had a diploid chromosome number of 38, with a karyotype formula of 2n=38=20m+4sm+14t (m: metacentric chromosomes; sm: submetacentric chromosomes; t: telocentric chromosomes) and a fundamental number (NF) of 62; no satellites or sex chromosomes were observed. *R. philippinarum* also had 38 diploid chromosomes, with a karyotype formula of 2n=38=20m+18s, NF=76. The comparative analysis of karyotypes between the variegated clam and the Philippine clam in this study not only provides reliable cytogenetic evidence for precise species identification, but also lays an important foundation for their genome evolution research and breeding of excellent varieties.

Key words: *Ruditapes philippinarum*; *Venerupis aspera*; Chromosome; Karyotype analysis

第三专题 水产养殖动物营养与饲料

饲料中添加枝角类对中华绒螯蟹生长性能及肠道消化酶活性的影响

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摘要：文章旨在探究饲料中添加不同浓度的枝角类对中华绒螯蟹生长性能和肠道酶活性的影响。在为期 7 个月的饲养试验中，采用 3 种不同枝角类添加（0%、5%、10%）的中华绒螯蟹配合饲料（各配合饲料分别命名为：对照组、5%添加组、10%添加组），观察不同枝角类添加下配合饲料对中华绒螯蟹的生长性能、肝胰腺指数、性腺指数及肠道酶活性的影响。结果表明，5%添加组和 10%添加组终末体质量比对照组显著提高 21.62 g 和 31.83 g（P＜0.05）；增重率比对照组显著提高 318.02%和 375.54%（P＜0.05）；特定生长率比对照组显著提高 4.20%和 4.90（P＜0.05）；性腺指数比对照组显著提高 28.16%和 35.98%（P＜0.05）；存活率、饵料系数及肝胰腺指数无显著差异（P＞0.05）。5%添加组和 10%添加组蛋白酶活性分别显著提升 31.42%和 34.3%（P＜0.05），淀粉酶活性分别显著提升 23.8%和 33.3%（P＜0.05）。综上所述，配合饲料中添加枝角类可以改善中华绒螯蟹生长性能和肠道消化酶活性, 在本试验中配合饲料中添加 5%枝角类满足中华绒螯蟹生长所需。

关键词：枝角类; 生长性能; 肠道消化酶活; 中华绒螯蟹

The effects of adding cladocerans to feed on the growth performance and intestinal digestive enzyme activities of *Eriocheir sinensis*

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Abstract： The present study investigates the effects of incorporating different concentrations of cladocerans into the feed on the growth performance and intestinal enzyme activity of *Eriocheir sinensis*. A 7-month feeding trial was conducted using three types of compound feeds with varying levels of cladoceran supplementation (0%, 5%, and 10%). These feeds were designated as the control group, the 5% addition group, and the 10% addition group, respectively. The impacts of different cladoceran concentrations on growth performance, hepatopancreas index, gonad index, and intestinal enzyme activity were evaluated. Results indicated that the final body weight in the 5% and 10% addition groups increased significantly by 21.62 g and 31.83 g, respectively, compared to the control group ($P < 0.05$). Similarly, the weight gain rate rose significantly by 318.02% and 375.54%, while the specific growth rate increased by 4.20% and 4.90%, respectively, relative to the control group ($P < 0.05$). Additionally, the gonad index showed a significant increase of 28.16% and 35.98% in the 5% and 10% addition groups compared to the control group ($P < 0.05$). No significant differences were observed in survival rate, feed coefficient, or hepatopancreas index among the groups ($P > 0.05$).

Protease activity increased significantly by 31.42% and 34.3%, and amylase activity increased significantly by 23.8% and 33.3% in the 5% and 10% addition groups, respectively ($P < 0.05$). In conclusion, the incorporation of cladocerans into compound feed enhances the growth performance and intestinal digestive enzyme activity of E. sinensis. In this experiment, supplementing the compound feed with 5% cladocerans adequately meets the growth requirements of *E. sinensis*.

Key words: Cladoceras; Growth performance; Intestinal digestive enzyme activity; *Eriocheir sinensis*

苦瓜皂苷抑制肝脏胰岛素抵抗缓解鲤高糖不耐受的分子机制研究

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摘要：肝脏胰岛素抵抗（IR）是鱼类在摄食高碳水化合物饲料后常见、严重和典型的伴随状态。这限制了碳水化合物在鱼类（包括鲤鱼）蛋白质节约中的作用。我们的初步研究证明了苦瓜皂苷（Momordica charantia sapin, MCS）作为鲤鱼肝 IR 治疗添加剂的潜力，但其机制有待进一步研究。因此，本研究旨在探讨 MCS 改善 IR 的潜在分子机制。首先，通过腹腔注射方法建立 miR-29a 过表达和沉默模型。在此基础上，对饲喂含 MCS 高碳水化合物饲料的鲤鱼进行间隔 14 d 的 miR-29a 注射干预。MiR-29a 模拟物干预显著降低了体质量增加率，提高了饲料转化率。组织学上，注射 miR-29a mimics 后肝脏出现程序性坏死的特征性表现。注射 miR-29a 模拟物不仅引起肝糖原合成明显下降和肝脏脂质增加，还引起血脂异常。机制上，注射 miR-29a 模拟物通过显著下调磷脂酰肌醇 3-激酶 1 的基因和蛋白表达，从而抑制胰岛素信号通路的活性，从而减少糖酵解和糖原合成，增加糖异生和糖原分解。而 MiR-29a 抑制剂干预可辅助 MCS 促进碳水化合物利用能力。综上所述，MCS 通过 miRNA-29a 靶向 pik3r1 激活胰岛素信号通路，从而改善肝脏 IR 并促进碳水化合物代谢。从改善鱼类碳水化合物利用的角度来看，研究结果为基于 miRNA 的添加剂开发拓宽了视野。

关键词：苦瓜皂苷；肝脏胰岛素抵抗；miR-29a；胰岛素信号通路；糖代谢；鲤鱼

Assessment of the molecular mechanism hiding in Momordica charantia saponins alleviating high-carbohydrate intolerance in common carp through inhibiting hepatic insulin resistance

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Abstract: Liver insulin resistance (IR) is a common, serious and typical concomitant state induced by high-carbohydrate diets for fish, which has limited the role of carbohydrate in protein-sparing effect for fish including common carp (*Cyprinus carpio*). Our preliminary study demonstrates the potential of Momordica charantia saponin (MCS) as a therapeutic additive for common carp liver IR, but the mechanism needs further excavation. Hence, this study focused on the underlying molecular mechanisms of MCS in ameliorating IR. MiR-29a overexpression and silencing models were established via in intraperitoneal injection. Therewith, the miR-29a injection intervention at a 14-day interval was conducted for common carp fed with high-carbohydrate diets containing MCS. MiR-29a mimics intervention significantly reduced mass gain rate and increased feed conversion ratio. Histologically, liver after miR-29a mimics injection presented the signature features of necroptosis. MiR-29a mimics injection not only caused a significant decrease in liver glycogen synthesis and an increase in liver lipids, but also induced abnormal serum lipids. Mechanistically, miR-29a mimics injection restrained activity of insulin signaling pathway through significantly down-regulating the gene and protein expressions of phosphoinositide 3-kinase 1 (pik3r1), thereby leading to decreasing glycolysis and glycogen synthesis and increasing gluconeogenesis and glycogenolysis. MiR-29a inhibitor intervention could assist MCS to promote the carbohydrate utilization ability. Overall, MCS ameliorates liver IR and enhances the carbohydrate metabolism through activation of the insulin signal pathway via miRNA-2 9a targeting pik3r1. From the perspective of the carbohydrate utilization improvement of fish, the results broaden the horizon for the development of miRNA-based additives.

Key words: Momordica charantia saponin (MCS); liver insulin resistance; miR-29a; insulin signal pathway; carbohydrate metabolism; common carp (*Cyprinus carpio*)

饲料蛋白质水平对光唇鱼亲鱼生长及繁殖性能的影响

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摘要：为探究饲料中蛋白质水平对光唇鱼亲鱼生长及繁殖性能影响，将540尾（平均体重34.46±1.28g）2龄光唇鱼亲鱼随机分为6组，每组3个重复，每个重复雌、雄各15尾，分别投喂蛋白质水平为30%、35%、40%、45%、50%和55%的6种等脂等能饲料，试验8周。结果表明：随着饲料中蛋白质含量的增加，光唇鱼亲鱼增重率、特定生长率、性成熟指数、肌肉和卵巢中粗蛋白质、获卵量、孵化率、仔鱼成活率和获苗量均先升高后趋平缓，当饲料中蛋白质含量达45%以上时，以上指标在各饲料组间均无显著差异，而45%蛋白组的增重率、特定生长率、卵巢性成熟指数、获卵量和获苗量均显著高于30%、35%和40%蛋白组；饲料系数、肌肉水分和粗脂肪、卵巢水分和灰分含量均随着饲料蛋白质含量增加先降低后趋平稳；饲料蛋白质含量对亲鱼精巢性成熟指数、肌肉灰分、卵巢粗脂肪和受精率均无显著影响。结论：光唇鱼饲料中适宜的蛋白质水平为45%。

关键词：光唇鱼;蛋白质;生长;繁殖性能

Effects of dietary protein levels on growth and reproductive performance of *Acrossocheilus fasciatus*

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Abstract：To investigate the effects of protein levelson the growth and reproductive performance of *Acrossocheilus fasciatus*, 540 two-year-old *Acrossocheilus fasciatus* were randomly divided into six groups . Each replicate contained 15 female and 15 male fish, fed six feedstuff with protein levels of 30%, 35%, 40%, 45%, 50%, and 55% for an 8-week trial. The results showed that the weight gain rate, specific growth rate, sexual maturity index, crude protein in muscle and ovary, egg yield, hatching rate, fry survival rate, and seedling yield of *Acrossocheilus fasciatus* initially increased and then stabilized. When the protein content in the feed exceeded 45%, there were no significant differences. However, the weight gain rate, specific growth rate, ovarian sexual maturity index, egg yield, and seedling yield of the 45% were significantly higher than those of the 30%, 35%, and 40%. The feed conversion ratio, muscle moisture and fat, ovarian moisture and ash content all decreased and then stabilized. We got conclusion: the optimal protein level in *Acrossocheilus fasciatus* is 45%.

Key words: *Acrossocheilus fasciatus*; protein; Growth; reproductive performance

膳食丁酸钠对大口裂腹鱼（*Micropterus salmoides*）生长性能、消化能力、血液生化指标和氨耐受性的影响

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摘要：本研究探究丁酸钠（SB）对大口裂腹鱼生长性能、消化能力、血液生化指标及氨耐受性的影响。实验中，大口裂腹鱼投喂含 0%、0.50% 和 1.00% SB 的饲料，后进行 96 小时氨胁迫试验。结果显示，饲料添加 SB 可改善生长：增重率提高，GH 和 IGF - 1 基因上调；显著提升血清总蛋白、白蛋白、球蛋白含量，降低甘油三酯、胆固醇及天冬氨酸转氨酶含量。0.50% 和 1.00% SB 组消化能力显著增强，胃蛋白酶、脂肪酶等消化酶活性及绒毛高度、肌肉厚度均增加；抗炎能力提升，IL - 1 和 IL - 8 基因下调。氨胁迫 96 小时后，SB 组累积死亡率显著降低；肝脏氨代谢酶（精氨酸酶、精氨酸琥珀酸合成酶等）和诱导型一氧化氮合酶活性显著提高，神经元一氧化氮合酶活性显著降低。综上，饲料添加 SB 可促进大口裂腹鱼生长，改善其消化能力、血液健康及氨耐受性。

关键词：丁酸钠；生长；消化能力；氨；大口裂腹鱼

Effects of Dietary Sodium Butyrate on Growth Performance, Digestive Ability, Blood Biochemistry, and Ammonia Tolerance of Largemouth Bass (*Micropterus salmoides*)

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Abstract： This study examined sodium butyrate (SB)'s impacts on largemouth bass' growth, digestion, blood health, and ammonia tolerance. Bass were first fed diets with 0.00%, 0.50%, or 1.00% SB, then subjected to a 96-hour ammonia challenge.Results showed SB boosted bass growth (higher weight gain; up-regulated GH and IGF-1 genes), increased serum total protein, albumin and globulin, and reduced triglycerides, cholesterol and aspartate transaminase.The 0.50% and 1.00% SB groups had better digestion (higher activities of pepsin, lipase and other enzymes; thicker intestinal villi and muscle layers) and improved anti-inflammatory capacity (down-regulated IL-1 and IL-8 genes).Additionally, SB lowered cumulative mortality after 96-hour ammonia stress, increased liver ammonia metabolism-related enzyme and inducible nitric oxide synthase activities, and decreased neuronal nitric oxide synthase activity.In conclusion, dietary SB promotes largemouth bass growth and improves their digestion, blood health and ammonia tolerance.

Key words: sodium butyrate; growth; digestive ability; ammonia; *Micropterus salmoides*

花生四烯酸提高大口黑鲈低溶氧耐受能力的机制研究

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摘要：本研究探讨了低溶氧胁迫对大口黑鲈肝脏花生四烯酸（AA）代谢的影响及 AA 补充对低氧应激的缓解作用。通过间歇性低氧胁迫和外源补充 AA 的实验，分析了生理生化、肝脏及鳃组织病理、低氧耐受能力及分子生物学指标。结果表明，低溶氧显著提高了血红蛋白和高铁血红蛋白水平，并促进肝脏血管生成相关基因（*vegfa*、*mmp2*、*jagged*、*notch1*）表达。同时，低氧导致肝脏 T-AOC、SOD、CAT 活性降低，MDA 水平升高，脂质代谢重塑表现为饱和脂肪酸升高、多不饱和脂肪酸减少，AA 含量特异性增加。外源 AA 补充显著降低了大口黑鲈的窒息点（1.08 至 0.5 mg/L），延长了低氧耐受时间，并增强了肝脏抗氧化活性。AA 补充显著提高了肝脏血管生成水平，增加了促血管生成物质 PGE2 和 EETs 含量，并上调了相关基因表达。研究表明，大口黑鲈通过 AA 代谢调控血管生成，适应低溶氧胁迫，为营养干预缓解低溶氧应激提供了理论依据。

关键词：低溶氧胁迫；血管生成；花生四烯酸；大口黑鲈

Mechanism of arachidonic acid enhancing hypoxia tolerance in largemouth bass (*micropterus salmoides*)

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Abstract：This study investigated the effects of hypoxic stress on arachidonic acid (AA) metabolism and its potential role in alleviating hypoxia-induced stress in largemouth bass. Intermittent hypoxic stress and AA supplementation experiments were conducted, analyzing physiological biochemistry, liver and gill tissue pathology, hypoxia tolerance, and molecular biology. Results showed that hypoxia significantly increased blood hemoglobin and methemoglobin levels, induced structural changes in gill tissues, and upregulated hepatic angiogenesis-related genes. Hypoxia also impaired hepatic antioxidant capacity, reduced T-AOC, SOD, and CAT activities, and elevated MDA levels. Lipid metabolic remodeling in the liver resulted in higher saturated fatty acids and lower PUFA, with AA accumulating specifically. Exogenous AA supplementation reduced the asphyxiation point, prolonged hypoxia survival, and enhanced hepatic antioxidant activities. AA supplementation also potentiated hepatic angiogenesis, elevating pro-angiogenic mediators (PGE_2 , EETs) and activating angiogenesis pathway.

Key words: Hypoxia stress; Micropterus salmoides; Angiogenesis; Arachidonic acid

关于幼体香螺最适饲料蛋白质水平的研究：生长、消化酶活性及肝脏代谢

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摘要：香螺是我国黄海、渤海重要的经济贝类，因过度捕捞，野生资源下降，亟需开展繁殖生物学研究以恢复资源。本研究以红棕色（HZ）、黄褐色（HH）、白色（BS）三种壳色香螺为对象，比较其生物学性状与繁殖力差异，构建多元回归方程，并通过转录组与蛋白组联合分析，筛选差异表达基因与蛋白，分析 GO 与 KEGG 功能富集，预测影响繁殖力的分子途径与关键基因。形态学分析显示，湿重、性腺重与产卵量正相关，壳高、壳宽、湿重、性腺重是评估繁殖力的关键指标。转录组分析表明，BS 群体中与性腺发育、生殖细胞发育、卵子成熟及生殖周期相关的基因显著上调。蛋白组学分析显示，激素合成、性腺发育相关蛋白在 BS 群体中上调，调控生殖过程，影响卵子成熟与繁殖周期。本研究为香螺人工繁殖、良种选育及品种改良提供理论依据，促进资源保护与可持续利用。

关键词：香螺；饲料蛋白质；生长；消化酶；肝脏代谢组学；最适需求量

An investigation on the Optimal Dietary Protein for Juvenile Neptunea *arthritica cumingii*: Growth, Digestive Enzyme Activity, and Liver Metabolism

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Abstract: *Neptunea arthritica cumingii* is a key economic bivalve in China's Yellow and Bohai Seas, but its wild resources have declined due to overfishing, demanding urgent reproductive biology research for restoration; this study targeted three of its shell color morphs (red-brown HZ, yellow-brown HH, white BS), comparing their biological traits and fecundity, constructing multiple regression equations, screening differentially expressed genes (DEGs) and proteins (DEPs) via integrated transcriptomic-proteomic analyses, and analyzing GO/KEGG functional enrichments to predict fecundity-related molecular pathways and key genes. Morphological analysis showed wet weight and gonad weight were positively correlated with fecundity, with shell height, shell width, wet weight and gonad weight as key fecundity indicators; in the BS population, transcriptomics revealed upregulated genes related to gonadal/germ cell development, oocyte maturation and reproductive cycles, while proteomics found upregulated proteins associated with hormone synthesis and gonadal development—both regulating reproductive processes and oocyte maturation—providing a theoretical basis for *N. arthritica cumingii* artificial propagation, elite breeding and germplasm improvement, and aiding its resource conservation and sustainable use.

Key words: Neptunea *arthritica cumingii*; Dietary Protein; Growth; Digestive Enzymes; Hepatic Metabolomics; Optimal Requirement

零鱼油条件下不同投喂策略对大菱鲆幼鱼生长性能及体组成的影响

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摘要：以大菱鲆(40.21±0.15)g 为研究对象，探究微藻全部替代鱼油后，投喂策略对幼鱼生长、体组成、肠道消化水平及抗氧化能力的影响。通过在基础饲料(F1)中，添加 5.00%裂壶藻、6.00%拟微绿球藻和 4.00%豆油替代全部鱼油，制成等氮等脂的实验饲料(分为 M1、M0)，其中 F1 组为正对照组，M1 组为实验组，M0 组为负对照组。实验分为 3 个阶段：①15 d，三组分别投喂各自饲料；②15 d，F1 和 M1 组均投喂 F1 组饲料；③50 d，各组投喂各自饲料。第一阶段，三组幼鱼的增重率(WGR)和饲料效率(FE)均无显著性差异；第二阶段，M1 组 WGR 显著高于 F1 和 MO 组，M1 组 FE 显著高于 MO 组；第三阶段，F1 和 M1 组的 WGR 和 FE 均显著高于 MO 组。F1 和 M1 组全鱼粗脂肪含量显著高于 M0 组，M1 和 M0 组肌肉粗脂肪含量显著低于 F1 组。综上所述，采用 M1 组的投喂方式并不会对大菱鲆幼鱼的生长性能产生负面影响。

关键词：大菱鲆；投喂策略；裂壶藻；拟微绿球藻；生长性能；体组成

Effects of different feeding strategies without fish oil on growth and body composition of juvenile turbot (*Scophthalmus maximus*)

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Abstract： Three isonitrogenous and isoenergetic diets were formulated, named separately: F1, M1 and M0. The 80-day feeding experiment was divided into three stages. The first stage was 15 d, three groups were fed their own diet; the second stage was also 15 d, the F1 and M1 groups were fed the diet of F1 group, and the M0 group had not changed; the third stage was 50 d, every group was fed their own diet. The results showed as following: 1) At the first stage, The weight growth rate (WGR) and feed efficiency (FE) no significant differences were found between F1, M1 and M0 groups; At the second stage, the WGR of M1 group was significantly higher than F1 and M0 groups, the FE of M1 group was significantly higher than M0 group ; At the third stage, the WGR and FE of F1 and M1 groups were nosignificantly differences, but significantly higher than M0 group . 2) the muscle crude lipid contents of M1 and M0 groups were significantly higher than F1 group. These results indicate that the feeding strategies of M1 group couldn’t influence the growth performance of juvenile turbot .

Key words: *Scophthalmus maximus*; Feeding strategies; Schizochytrium sp.; Nannochloropsis sp.; Growth performance; Body composition

膳食维生素 E 调节中华鲟幼鱼早期性腺发育过程中下丘脑–垂体–性腺轴功能及抗氧化能力

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摘要：一项为期两个月的饲养试验研究了饲料中添加维生素 E 对中华鲟幼鱼早期性腺发育过程中下丘脑-垂体-性腺轴功能及抗氧化能力的影响。实验设置三种饲料：基础商业饲料作为对照组，另两组分别添加 0.2%和 0.4%维生素 E。结果显示：0.2%维生素 E 组显著提升了幼鱼的终末体重、增重率和特定生长率。虽然组织切片未显示三组性腺结构差异，但维生素 E 显著提高了雄性个体的促性腺激素释放激素浓度，以及雌性个体的睾酮和 11-酮基睾酮水平。同时，维生素 E 促使两性个体中 gnrh2、kiss1 等 HPG 轴关键基因表达量显著上升。在抗氧化指标方面，维生素 E 显著提升了雄性的过氧化氢酶活性和雌性的超氧化物歧化酶活性。0.2%添加组雌鱼获得最高过氧化物酶活性和总抗氧化能力，而 0.4%组雌鱼的丙二醛含量最低。维生素 E 还显著促进了两性性腺中抗氧化相关基因的表达。综合生长与生理指标来看，推荐在中华鲟幼鱼饲料中添加 0.2%的维生素 E。

关键词：维生素 E，中华鲟，下丘脑-垂体-性腺轴，转录组，抗氧化

Dietary Vitamin E Modulates the Hypothalamic-Pituitary-Gonadal (HPG) Axis and Antioxidant Capacity during Early Gonadal Development in Juvenile Chinese Sturgeon (*Acipenser sinensis*)

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Abstract： A two-month feeding trial investigated the effects of dietary vitamin E on the HPG axis and antioxidant capacity in juvenile Chinese sturgeon during early gonadal development. Three diets were tested: a basal control (Con), and two diets supplemented with 0.2% (VE2) or 0.4% (VE4) vitamin E. Results showed that 0.2% vitamin E significantly improved growth performance (FBW, WGR, SGR). While no gonadal morphological differences were observed, vitamin E supplementation significantly increased GnRH levels in males, and testosterone and 11-KT levels in females. Key HPG axis genes (gnrh2, kiss1, kissr1, kissr2, ar, fshr) were up-regulated in both sexes. Vitamin E also enhanced antioxidant capacity: CAT activity increased in males, SOD activity in females, and females fed the VE2 diet showed the highest POD activity and T-AOC, while those fed VE4 had the lowest MDA. Expression of gonadal antioxidant-related genes was up-regulated in both sexes. Based on these benefits, a dietary inclusion of 0.2% vitamin E is recommended for juvenile Chinese sturgeon.

Key words: vitamin E, Chinese sturgeon, HPG axis, transcriptome, antioxidant

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

急性和慢性氨暴露对杂交鲤鱼存活、生长和肠道菌群组成的影响

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摘要：长期低氨环境下鱼类生长耐受阈值的评估对水产养殖至关重要。本研究采用序贯法评估了杂交鲤鱼对急、慢性氨暴露的耐受性。首先通过 96 h 高氨胁迫实验，并基于线性插值（$y=0.0047x-0.4659$, $R^2=0.9448$，y 为累积死亡率，x 为氨浓度），确定了 96 h 半致死浓度（LC_{50}）为 206.38 mg/L 的总氨（TA）。进而根据 LC_{50} 值确定 5 个长期低氨暴露梯度，进行 6 周实验。结果表明，氨浓度＞1.03 mg/L TA 时，采食量与生长性能受到抑制，氨浓度＞4.11 mg/L TA 时，存活率降低。游离氨基酸缺乏不仅影响生长，还会抑制尿素循环中关键酶活性，削弱鱼的氨解毒能力。2.05 mg/L TA 足以引起抗氧化酶活性下降及肝损伤和炎症。长期低氨暴露降低了肠道菌群的丰富度和多样性，增加了 *Levisonia* 等有害菌丰度。*Cetobacterium* 等有益菌丰度的增加可能是对氨毒性的适应性策略。

关键词：氨；生长；存活率；肠道菌群；杂交鲤鱼

Effects of acute and chronic ammonia exposure on survival, growth and intestinal microbiota composition of hybrid carp

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Abstract： Evaluating fish growth tolerance thresholds to long-term low ammonia is critical for aquaculture. This study used the sequential method to assess hybrid carp's acute/chronic ammonia tolerance. Firstly, a 96-h high ammonia experiment, via linear interpolation ($y=0.0047x-0.4659$, $R^2=0.9448$; y=cumulative mortality, x=ammonia concentration), determined 96-h LC_{50} for total ammonia (TA) as 206.38 mg/L. Furthermore, five long-term low ammonia exposure gradients (based on LC_{50}) were tested in a 6-week experiment. Results: Ammonia >1.03 mg/L TA inhibited feed intake/growth; >4.11 mg/L TA reduced survival. Free amino acid deficiency impaired growth and urea cycle enzymes (arginase, argininosuccinate lyase), weakening ammonia detoxification. 2.05 mg/L TA caused reduced antioxidant enzyme activity, liver damage, and inflammation. Long-term low ammonia lowered intestinal microbiota richness/diversity, increased harmful bacteria (e.g., *Levisonia*), while elevated beneficial bacteria (e.g., *Cetobacterium*) may be an ammonia tolerance strategy.

Key words: Ammonia ; Growth ; Survival rate ; Intestinal microbiota ; Hybrid carp

小承气汤通过抑制溶血活性和生物膜形成缓解哈维氏弧菌感染

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摘要：本研究探究中药复方小承气汤对哈维氏弧菌感染的作用及机制。体内实验显示，小承气汤可减轻该菌对日本对虾的肠道损伤，肠道弧菌负荷从 1.72×10^8 CFU/mL 降至 1.23×10^5 CFU/mL，同时保护肠道黏膜完整性，减少上皮脱落。分子对接表明，小承气汤中 12 种生物活性化合物对哈维氏弧菌溶血素（VHH）结合亲和力较高，其中诺米林、芦荟大黄素、柚皮苷、橙皮苷能以剂量依赖方式抑制 VHH 介导的溶血，减少血红蛋白释放。体外实验中，这 12 种化合物还可抑制该菌生物膜形成，64μg/mL 橙皮素抑制率达 89.7%。网络药理学分析发现，47 种活性小承气汤化合物有 378 个潜在靶点，富集于 cAMP 信号传导、TNF 信号传导等途径；蛋白质 - 蛋白质相互作用网络确定 EGFR、HRAS 等为核心治疗靶点。

关键词：小承气汤、哈维氏弧菌、溶血素、生物膜、信号通路

Xiaochengqi Decoction Alleviates *Vibrio Harveyi* Infection by Inhibiting Hemolytic Activity and Biofilm Formation

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Abstract： *Vibrio harveyi* causes severe vibriosis in marine aquaculture, leading to heavy losses. This study tested Xiaochengqi decoction (XCQD) against *V. harveyi* using in vivo, molecular docking, functional, and network pharmacology approaches. XCQD reduced intestinal damage in Penaeus japonicus, lowering Vibrio load from 1.72×10^8 to 1.23×10^5 CFU/mL and preserving gut mucosa. Twelve XCQD compounds showed high/moderate affinity (energy < -8.0 kcal/mol) for *V. harveyi* hemolysin (VHH). Nomilin, aloe-emodin, narirutin, and hesperidin dose-dependently inhibited VHH-mediated hemolysis. XCQD compounds also suppressed biofilm formation, with hesperetin achieving 89.7% inhibition at 64 μg/mL. Network pharmacology identified 378 targets for 47 active compounds in cAMP signaling, TNF signaling, and nitrogen metabolism, with EGFR, HRAS, HSP90AA1, JAK2, MAPK1, and PTK2 as core targets. XCQD acts by inhibiting virulence factors and modulating host-pathogen interactions, showing potential for aquaculture disease management.

Key words: Xiaochengqi Decoction, Vibrio harveyi, hemolysin, biofilm, signaling pathway

饲料中添加纳米硒对青海湖裸鲤生长性能、抗氧化能力、免疫和肠道菌群的影响

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摘要：本研究旨在探讨纳米硒(nano-se)作为膳食补充剂对青海湖裸鲤的影响。结果表明，NSE4 组肝体比、脏体比、脂肪率均显著高于对照组(P<0.05)。NSE4 组呈现最高的比生长率和体重增加率，而 NSE11 组呈现最低的比率。NSE2d、NSE4 和 NSE9 组的存活率较高，而 NSE11 组的存活率最低。日粮中添加适量的纳米硒可以改善青海湖裸鲤的肝脏空泡化、肝细胞肿胀和炎性细胞浸润现象。此外，肠道微生物区系检测结果表明，饲料中添加纳米硒可以提青海湖裸鲤肠道微生物的多样性，增加有益菌的丰度。这项研究将提高我们对纳米硒可能用途的认识，并为提高青海湖裸鲤育种和释放的资源利用效率奠定基础。

关键词：青海湖裸鲤、饲料添加剂、抗氧化能力、免疫反应、肠道健康

Efects of dietary nano-selenium on the growth perfommance, antioxidant capacity, immunity and intestinal microbiota of Tibetan naked carp (*Gymnocypris przewalskii*)

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Abstract： This study aimed to investioate the effects of nano-se as a dietary supplement on *Gymnocypis przewalski*. The results showed that the hepatosomatic ratio, viscerosomatic ratio and fatness were significantly greater in the NSE4 group ($P < 0.05$). The NSE4 group presented the highest specific growth rate and weight gain rate, whereas the NS11 group presented the lowest rates. The survival rate was greater in the NsE2, NSE4, and NSE9 groups, whereas it was lowest in the NSE11 group. Dietary supplementation with an appropriate amount of nano-se can improve liver vacuolation, hepatocyte swelling and inflammatory cellinfltration in *G. przewalski*. in addition. the results of intestinal microbota detection showed that dietay nano-selenium could improve the diversily of the intestinal microbiota and increase the abundance of beneicial bacteria in *G. pzewalski*. This research will enhance our understanding of the possible uses of nano-se and lay the groundwork for increasing the resource efficiency of *G. przewalskii* breeding and release.

Key words: *Gymnocypris przewalskil*, feed additives, antioxidant capacity, immune response, intestinal health

BCO2 在中华绒螯蟹中的序列特征、进化历史及表达模式

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摘要：β-胡萝卜素 9’，10’-加氧酶（BCO2）是类胡萝卜素裂解的重要关键酶。为填补中华绒螯蟹（*Eriocheir sinensis*）中相关研究的空白，本研究从其基因组中鉴定出 BCO2 样基因（BCO2l），并解析其进化历史、基因结构及表达模式。结果表明，EsBCO2l 基因的开放阅读框为 1572 bp，编码 523 个氨基酸。结构分析显示其含有 10 个保守基序及 RPE65 结构域，表明 BCO2 在进化过程中高度保守。系统发育分析表明，BCO1 为祖源基因，随后分化出 BCO2 和 NinaB。Ka/Ks 比值显示十足目甲壳类中 BCO2 受更强的纯化选择（0.014–0.045），低于其他甲壳类（0.112–0.185）。表达分析发现，BCO2l 主要在后肠中高水平表达，且雌性显著高于雄性。

关键词：甲壳类；β-胡萝卜素 9’，10’-加氧酶；基因特征；类胡萝卜素代谢

Sequence characteristics, evolutionary history and expression pattern of BCO2 in *Eriocheir sinensis*

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Abstract： β-carotene 9’,10’-oxygenase (BCO2) is a key enzyme in carotenoid cleavage. To address the lack of research on BCO2 in Eriocheir sinensis, we identified and cloned a BCO2-like gene (BCO2l) from its genome, and examined its evolutionary history, gene structure, and expression profile. The EsBCO2l gene contains a 1572 bp open reading frame encoding 523 amino acids. Structural analysis revealed ten conserved motifs and an RPE65 domain, indicating strong evolutionary conservation. Phylogenetic analysis placed EsBCO2 within the carotenoid cleavage oxygenase (CCO) family, with BCO1 as the ancestral gene and BCO2 and NinaB diverging subsequently. Ka/Ks ratios showed that BCO2 in Decapoda is under stronger purifying selection (0.014–0.045) than in other crustaceans (0.112–0.185). Expression analysis indicated that BCO2l is predominantly expressed in the hindgut, with females exhibiting higher levels than males.

Key words: Crustacean; β-carotene 9’, 10’-oxygenase; Gene characteristics; Carotenoid metabolism

日粮碳水化合物与脂肪比例对乌苏里拟鲿幼鱼生长及健康状况的影响

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摘要：本研究进行了为期 8 周的饲养实验以评估日粮碳水化合物 / 脂质（CHO:L）比例对乌苏里拟鲿幼鱼生长性能、非特异性免疫反应、抗氧化能力和抗病能力的影响。实验鱼被投喂六种等氮等能日粮，其 CHO:L 从 0.89 到 7.02 不等。结果显示， WG 和 SGR 呈先升高后下降的趋势，当 CHO:L 为 2.02 时最高，同时血浆 LZM 活性、补体 3 水平和呼吸爆发活性达到最高值。此外， CHO:L 为 2.02 时，鱼肝脏 SOD 活性、CAT 活性和 TAC 达到最高值，并且 MDA 水平随着 CHO:L 从 0.89 增加到 2.02 而降低，然后趋于平稳。另外，随着 CHO:L 从 0.89 增加到 7.02， TNF-α、IL-1β和 HSP70 的 mRNA 水平均呈现先降低后升高的趋势，且均在 CHO:L 为 2.02 时达到最低值。相反，鱼肝脏 IL-10 的 mRNA 表达水平呈现先升高后降低的趋势，且在 CHO:L 为 2.02 时达到最高值。

关键词：乌苏里拟鲿；生长性能；免疫力；抗氧化能力；抗病力

An evaluation of dietary carbohydrate/lipid ratios on growth and health status of juvenile Ussuri catfish (*Pseudobagrus ussuriensis*)

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Abstract： This study conducted an 8 - week feeding experiment to assess the effects of dietary carbohydrate/lipid (CHO:L) ratios on growth performance, non - specific immune response, antioxidant capacity, and disease resistance of juvenile *Pseudobagrus ussuriensis*. Experimental fish were fed six isonitrogenous and isoenergetic diets with CHO:L ratios ranging from 0.89 to 7.02. Results showed that WG and SGR first increased then decreased, peaking at a CHO:L ratio of 2.02. At this ratio, plasma LZM activity, complement 3 level, and respiratory burst activity also reached maximum values. In addition, at a CHO:L ratio of 2.02, liver SOD activity, CAT activity, and TAC of the fish were highest. MDA level decreased as CHO:L ratio rose from 0.89 to 2.02, then stabilized. Furthermore, as CHO:L ratio increased from 0.89 to 7.02, mRNA levels of TNF - α, IL - 1β, and HSP70 all first decreased then inccreased then decreased, reaching the highest value at a CHO:L ratio of 2.02.

Key words: Pseudobagrus ussuriensis; growth performance; immunity; antioxidant capacity; disease resistance

饥饿及复投喂对中间球海胆肠道结构及微生物群落的影响

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摘要：本研究探讨饥饿及复投喂对中间球海胆(*Strongylocentrotus intermedius*)肠道结构与微生物群落的影响。经过各 60 天(d)饥饿和复投喂实验，记录其肠结构变化，并用 16S rRNA 测序技术，分析微生物变化。结果表明，在饥饿过程中，性腺体重比 GSI 由(12.51±0.22)% 降至(7.32±0.23)%，复投喂后恢复至(12.72±0.83)% ($P<0.05$)；实验总过程，门水平拟杆菌门与变形菌门交替占优，纲水平γ-变形菌纲和拟杆菌纲波动，目、科、属水平从肠杆菌类逐步转为拟杆菌类；饥饿胁迫过程中，除代谢通路外其他一级通路丰度均较低；复投喂第 15 天(R15)时其代谢及环境信息处理通路丰度上升；在 30-45 天(R30-R45)时碳水化合物代谢通路丰度升高，契合拟杆菌功能。本研究揭示了海胆动态调控肠道微生态应对饥饿胁迫的适应性机制，为理解海胆营养应激策略提供了理论价值。

关键词：中间球海胆；饥饿胁迫；复投喂；16S rRNA 测序；肠道菌群

Effect of Starvation and Refeeding on Intestinal Structure and Microbial Community in *Strongylocentrotus intermedius*

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Abstract： This study examined the effects of starvation and re-feeding on the intestinal structure and microbiota of *Strongylocentrotus intermedius*. Over 60 days of starvation and 60 days of re-feeding, intestinal changes and microbial shifts were analyzed using 16S rRNA sequencing. Results showed that the gonad-to-body weight ratio (GSI) decreased from (12.51±0.22)% to (7.32±0.23)% during starvation and recovered to (12.72±0.83)% after re-feeding ($P<0.05$). Bacteroidota and Proteobacteria dominated alternately at the phylum level, while Gammaproteobacteria and Bacteroidia fluctuated at the class level. Lower taxonomic levels showed a shift from Enterobacterales to Bacteroidales dominance. During starvation, non-metabolic pathways had low abundances. At R15 of re-feeding, metabolic and environmental information processing pathways increased. From R30 to R45, carbohydrate metabolic pathways rose, aligning with Bacteroidales functionality. This study highlights sea urchins' adaptive regulation of gut microecology under starvation stress, offering insights into their nutritional stress responses.

Key words: Strongylocentrotus intermedius; Starvation stress; Re-feeding; 16S rRNA sequencing; Intestinal microbiota

添加海带烫煮液对微拟球藻培养系统水质与生长的影响

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摘要：为探究海藻加工废弃物资源化利用对微藻培养的潜在价值，通过在标准 BG11 培养基中添加不同比例（0%、5%、10%、15%、20%）的海带烫煮液，分别为 A、B、C、D 和 E 组，每组设 3 个平行，进行为期 10 天的批次培养实验，定期检测各组微拟球藻的藻细胞密度、叶绿素含量、可溶性糖含量、可溶性蛋白含量等营养与生长指标；并同步分析了水体中氨氮（TAN）、亚硝酸氮(NO2--N)等水质指标的动态变化情况。藻初始接种密度为 0.5 × 106 cells/mL。结果表明：添加海带烫煮液能够显著提高微拟球藻的藻细胞密度($P < 0.05$)；同时，可溶性糖以及可溶性蛋白含量随着海带烫煮液浓度增加而增加，但浓度过高时各项指标也会有所下降。本试验条件下，微拟球藻培养的适宜海带烫煮液添加比例为培养基体积的 10%。此外，添加烫煮液可缓冲培养体系中 pH 波动，维持更稳定的碱性环境，但高浓度添加会引发营养失衡与生长抑制。

关键词：微拟球藻；海带烫煮液；水质；生长；营养

The influence of adding kelp boiling liquid on the water quality and growth of the microalgae Pyramimonas pseudoeugeneus culture system

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Abstract：To investigate the potential value of utilizing seaweed processing waste for microalgae cultivation, different proportions (0%, 5%, 10%, 15%, 20%) of kelp scalding solution were added to standard BG11 medium, designated as Groups A, B, C, D, and E, respectively. Each group consisted of three replicates. A 10-day batch culture experiment was conducted, with regular monitoring of nutritional and growth indicators including algal cell density, chlorophyll content, soluble sugar content, and soluble protein content for Microcystis in each group. Concurrently, the dynamic changes in water quality indicators such as total ammonia nitrogen (TAN) and nitrite nitrogen (NO_2^--N) in the culture medium were analyzed. The initial inoculation density was 0.5×10^6 cells/mL. Results indicated that adding kelp boiling liquid significantly increased Microcystis algal cell density ($P < 0.05$). Simultaneously, soluble sugar and soluble protein content increased with rising kelp boiling liquid concentration, though all indicators declined at excessively high concentrations. Under the conditions of this experiment, the suitable addition ratio of kelp boiling solution for microalgae cultivation is 10% of the volume of the culture medium. In addition, adding boiling solution can buffer pH fluctuations in the culture system and maintain a more stable alkaline environment, but high concentration addition can cause nutrient imbalance and growth inhibition.

Key words: Microcystis; kelp cooking liquid; water quality; growth; nutrition

牛蛙不同发育阶段生理生化、肠道菌群特征及饲料添加剂对其影响的研究

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摘要：本研究系统探究了牛蛙生长发育中肠道菌群的作用及外源添加剂调控机制。研究发现，蝌蚪开口摄食阶段，外源营养期肠道菌群中 *Firmicutes* 丰度上升，伴随肝脏脂质积累及脂代谢基因（PPAR-γ、FAS）表达增强，提示菌群与脂代谢密切相关。变态发育过程中，肠道菌群由 *Proteobacteria* 为主转向 Firmicutes 与 *Fusobacteriota* 富集，功能上碳水化合物代谢路径增强，且变态后菌群结构趋近爬行类，反映其对陆生适应的生态演变。此外，饲料中添加丁酸梭菌或复方中草药可提升机体抗氧化能力与免疫力，调节炎症因子表达，并优化肠道菌群结构，如增加 *Firmicutes*、降低 *Bacteroidota*。研究结果为通过靶向调控肠道微生态以提升牛蛙健康水平和养殖可持续性提供了理论依据与实践路径。

关键词：牛蛙，肠道微生物，生长发育阶段，脂质代谢，外源饲料添加剂

Physiological and Biochemical Characteristics, Gut Microbiota Dynamics Across Developmental Stages in Bullfrogs and the Effects of Feed Additives

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Abstract： This study investigated the gut microbiota's role in bullfrog development and the effects of exogenous additives. In tadpoles, the shift to active feeding increased gut Firmicutes abundance, which correlated with hepatic lipid accumulation and upregulation of lipid metabolism genes (PPAR-γ, FAS). During metamorphosis, the gut microbiota transitioned from *Proteobacteria* to *Firmicutes*/*Fusobacteriota* dominance. This post-metamorphic community exhibited enhanced carbohydrate metabolism and converged towards a reptile-like structure, suggesting an adaptation for terrestrial life. Dietary supplementation with Clostridium butyricum or compound Chinese herbs improved systemic antioxidant capacity and immunity, modulated inflammatory responses, and optimized gut microbiota by increasing *Firmicutes* and reducing Bacteroidota. These findings provide a scientific basis for promoting bullfrog health and sustainable aquaculture through targeted gut microbiome regulation.

Key words: Aquarana catesbeiana, gut microbiota, growth and development stages, lipid metabolism, exogenous feed additives

饲料色氨酸水平对大口黑鲈幼鱼需要量、生长性能、免疫应答和脑轴转录分析的研究

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摘要：进行为期 60 天的养殖试验，研究在饲料中添加实测值分别为 0.29%（对照）、0.33%、0.41%、0.48%、0.59%、0.66%（干重）的色氨酸水平对大口黑鲈幼鱼生长性能、免疫应答和脑转录分析的影响。研究结果表明，以 WGR 和 FCR 指标为基准，进行二次回归分析，确定大口黑鲈幼鱼的色氨酸最适需要量分别为 0.47%和 0.45%。全鱼体成分无显著差异。随替代水平增加，血清 TC、TP 和 GLU 呈下降趋势（$P< 0.05$）。0.41%水平组的 ALT、AST 和 ALP 显著高于对照组（$P< 0.05$）。血清中 SOD 和 GSH 在 0.41%水平组酶活性最高（$P< 0.05$）。*il-10* 的表达水平在 0.66%水平组显著低于对照组，tgf-β的表达水平在 0.59%水平组显著高于对照组（$P< 0.05$）。收集 0.33%和 0.48%水平的大口黑鲈脑组织进行转录组学分析，RNA-seq 共筛选出 612 个差异基因。

关键词：大口黑鲈幼鱼；色氨酸；生长性能；免疫功能；转录分析

Dietary tryptophan levels on requirements, growth performance, immune response and brain axis transcriptional analyses in juvenile largemouth bass (*Micropterus salmoides*)

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Abstract: A 60-day aquaculture trial was conducted to investigate the effects of adding tryptophan at levels of 0.29% (control), 0.33%, 0.41%, 0.48%, 0.59%, and 0.66% (dry weight) to feed on the growth performance, immune response, and brain transcriptomic analysis of juvenile largemouth bass. Results indicated that based on WGR and FCR metrics, secondary regression analysis determined optimal tryptophan requirements for juvenile black bass at 0.47% and 0.45%, respectively. No significant differences were observed in whole-body composition. With increasing substitution levels, serum TC, TP, and GLU showed a decreasing trend . The ALT, AST, and ALP levels in the 0.41% group were significantly higher than the control group . Serum SOD and GSH enzyme activities were highest in the 0.41% group . IL-10 expression levels were significantly lower in the 0.66% group , while TGF-β expression levels were significantly higher in the 0.59% group . Brain tissue at 0.33% and 0.48% levels was collected for transcriptomic analysis. RNA-seq identified a total of 612 differentially expressed genes.

Key words: Juvenile largemouth bass; tryptophan; Growth performance; Immune function; transcriptional analyse

基于文献可视化分析技术的桑叶研究进展与现状

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摘要：为全面了解和掌握桑叶的研究进展与现状，以中国知网期刊数据库（CNKI）和 Web of Science 数据库（WoS）作为文献数据来源，利用 CiteSpace 软件对 1996~2024 年桑叶的研究进展与现状进行可视化分析，梳理桑叶研究的发展脉络和热点方向。结果显示，桑叶研究总体上经历探索、发展、繁荣三个时期，涉及的作者和机构较多，主要为中国学者和中国机构，研究的热点方向主要集中于桑叶多糖的提取工艺优化、桑叶作为饲料添加剂对不同动物生长性能的影响以及桑叶生物活性成分在生物医学中的应用等。桑叶已形成以中国为核心的多学科交叉研究体系，研究热点从基础提取工艺向高值化利用（如饲料资源和生物医学）拓展。未来需加强国际合作，深化活性成分作用机制解析及产业化应用研究，以推动桑叶资源的综合开发。

关键词：桑叶；CiteSpace；研究进展；可视化分析

Research Progress and Current Status of Mulberry Leaf Based on Literature Visualization Analysis Technique

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Abstract： In order to comprehensively understand and grasp the research progress and current situation of mulberry leaves, the China National Knowledge Infrastructure journal database (CNKI) and Web of Science database (WoS) were used as literature data sources. CiteSpace software and the analysis tools provided by CNKI were employed to visualize the research progress and current situation of mulberry leaves from 1996 to 2024. The development trend and hotspot direction of mulberry leaf research were sorted out by analyzing the annual publication volume, authors, institutions, keyword knowledge graph, and citation frequency. The results showed that mulberry leaf research generally went through three periods of exploration, development, and prosperity. There are many researchers and institutions focus their study on mulberry leaves, especially Chinese scholars and Chinese institutions. Currently, the hotspots of mulberry leaf research mainly includes extraction process optimization of mulberry leaf polysaccharides, the effects of mulberry leaves as feed additives on the growth performance of different animals, as well as the composition of mulberry leaf extracts and their application in biomedicine. Mulberry leaf has formed a multidisciplinary cross-research system with China as the core, and the research hotspots are expanding from the basic extraction process to the high-value utilization (e.g. feed resources and biomedicine). In the future, it is necessary to strengthen international cooperation, deepen the analysis of the mechanism of action of active ingredients and industrialization application research, in order to promote the comprehensive development of mulberry leaf resources.

Key words: mulberry leaf; citespace; research progress; visualization analysis

短小芽孢杆菌 SE5 肽聚糖和脂磷壁酸对斜带石斑鱼豆粕诱导型肠炎的改善作用研究

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摘要：本研究旨在探究短小芽孢杆菌 SE5 肽聚糖(PG)和脂磷壁酸(LTA)对斜带石斑鱼豆粕诱导型肠炎的改善作用。试验设置对照组：LSM 组(18%豆粕)和 HSM 组(36%豆粕)；试验组：饲喂高豆粕饲料 4 周后，在高豆粕饲料中添加短小芽孢杆菌 SE5 提取的 PG(SPG 组)、LTA(SLA 组)和 PG+LTA(SPL 组)以及全程添加 PG(PG 组)、LTA(LTA 组)和 PG+LTA(PLA 组)。结果显示：与 LSM 组相比，HSM 组石斑鱼生长性能显著降低，炎症增加，肠道健康受损。与 HSM 组相比，各试验组逆转了以上现象，且 PLA 组效果更优。此外，PLA 组可以有效改善肠道菌群结构，增加有益菌的丰度，降低潜在致病菌的丰度。RNA-seq 分析表明，PLA 组肠道差异基因主要富集在细胞生长、死亡相关通路。综上，高豆粕饲料中添加 *B. pumilus* SE5 来源的 PG 和 LTA 可以改善豆粕诱导的肠道炎症，且二者存在协同效应。

关键词：花鲈；短小芽孢杆菌 SE5；肽聚糖；脂磷壁酸；肠道健康

Alleviating effects of peptidoglycan and lipoteichoic acid derived from Bacillus pumilus SE5 on soybean meal-induced enteritis in *Epinephelus coioides*

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Abstract： This study aimed to investigate the alleviating effects of peptidoglycan (PG) and lipoteichoic acid (LTA) extracted from Bacillus pumilus SE5 on soybean meal (SBM)-induced enteritis in Epinephelus coioides. The trial set two control groups: LSM group (18% SBM) and HSM group (36% SBM); six trial groups: after four weeks on HSM feed, PG (SPG group), LTA (SLA group), and PG+LTA (SPL group) from B. subtilis SE5 were added. Additionally, PG, LTA, and PG+LTA were fed throughout the trial period (PG, LTA, and PLA groups). Results revealed that HSM group significantly reduced growth performance, induced intestinal inflammation, and impaired gut health in comparison to the LSM group. Compared with the HSM group, all trial groups reversed the above phenomena, and the PLA group had a better effect. Additionally, PLA group enriched beneficial gut bacteria while suppressing potential pathogens. RNA-seq analysis indicated that DEGs were enriched in cell growth/death pathways in PLA group. Collectively, *B. pumilus* SE5-derived PG and LTA synergistically alleviate SBM-induced enteritis.

Key words: *Epinephelus coioides*; Bacillus pumilus SE5; Peptidoglycan; Lipoteichoic acid; Intestinal health

不同生境来源日本鳗鲡肌肉脂肪酸营养比较分析

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摘要：本研究通过分析江苏河道、长江口、嵊泗三个生境下日本鳗鲡肌肉组织的脂肪酸组成，探讨了不同生境来源鳗鲡的脂肪酸营养状况。结果显示，三个生境的日本鳗鲡肌肉脂肪酸含量存在明显差异。江苏地区的鳗鲡样本中 DHA 含量较高(最高达 17.57%)，且 DHA/EPA 比率平均高于其他地区，表明该生境可能更有利于 Omeg3-3 脂肪酸的积累。长江口水域鳗鲡 EPA 和 DHA 含量波动较大，部分样本显示较高的 PUFA 比例，但整体脂肪酸组成较为均衡。嵊泗周边水域鳗鲡肌肉则表现出较低的 EPA 和 DHA 含量，且 PUFA/SFA 比率相对较低，其脂肪酸营养价值可能略逊于其他地区。江苏河道水域鳗鱼的 N-3PUFA/N-6PUFA 比率较高，反映了其潜在的抗炎和健康益处。生境差异显著影响了日本鳗鲡的脂肪酸谱，朱来会结合不同生境的环境因子、饵料组成和性腺发育期等进一步探讨不同来源鳗鲡肌肉脂肪酸组成差异的原因。

关键词：日本鳗鲡；脂肪酸组成；生境差异；营养评价；Omega-3 脂肪酸

Comparative Analysis of Muscle Fatty Acid Nutrition in Japanese Eels from Different Habitats

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Abstract：This study analyzed the fatty acid composition in the muscle of Japanese eels from three habitats: Jiangsu rivers, Yangtze Estuary, and Shengsi. Results revealed distinct differences among habitats. Jiangsu eels showed the highest DHA content (up to 17.57%) and a higher average DHA/EPA ratio, indicating a superior capacity for omega-3 accumulation. Eels from the Yangtze Estuary had variable EPA and DHA levels but a generally balanced fatty acid profile. In contrast, Shengsi eels exhibited lower EPA and DHA content and a lower PUFA/SFA ratio, suggesting reduced nutritional value. The higher n-3/n-6 PUFA ratio in Jiangsu eels also points to greater health benefits. Habitat significantly influences eel fatty acid profiles, warranting further research into environmental and dietary factors.

Key words: Japanese eel; fatty acid composition; habitat differences; nutritional assessment; Omega-3 fatty acids

干扰 *gs* 和 *gls* 基因对布氏鲳鲹道基因表达和代谢途径的影响

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摘要：先前的研究表明，在饲料中添加外源谷氨酰胺可以促进金鲳的生长发育。本研究利用 RNA 干扰技术实现了对活金鲳 *gs* 和 *gls* 基因的持续抑制。经过 52 天的干扰实验，我们分析了金鲳的生长发育、肠道形态、消化和抗氧化酶活性以及肠道转录组。干扰显著抑制了金鲳的发育，与对照组相比，干扰组的肠道直径、绒毛长度、宽度和肌肉层大大减小。肠道酶活性的测量显示，在干扰后，金鲳的 LPS 含量显著降低，抗氧化相关酶活性降低。转录组分析表明，在 *gs* 和 *gls* 基因敲除后，生长相关的丝氨酸代谢途径和脂质代谢途径以及免疫炎症相关途径显著富集。共表达 mRNA 网络分析显示，与嘌呤从头合成和辅酶 Q 氧化还原酶家族相关的基因显著富集。这些发现为控制布鲁氏菌的肠道健康和农业实践提供了重要见解。

关键词：布氏鲳鲹，谷氨酰胺，肠道，RNA 干扰，转录组

The effects of interfering with gs and gls genes on intestinal genes expression and metabolic pathways in *Trachinotus blochii*

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Abstract： Previous research has demonstrated that the addition of exogenous glutamine in feed can enhance the growth and development of *Trachinotus blochii*. This research utilized RNA interference technology to achieve sustained suppression of the *gs* and *gls* genes in live *T. blochii*. After 52 days of interference, we analyzed the growth and development of *T. blochii*, intestinal morphology, digestive and antioxidant enzyme activity, and intestinal transcriptome. The development of *T. blochii* was markedly inhibited by interference, with the intestinal diameter, villus length, width, and muscle layer in the interference group being greatly reduced compared to the control group. Measurements of intestinal enzyme activity showed a significant decrease in LPS content in *T. blochii* following interference, and antioxidant-related enzyme activities were lowered. Transcriptome analysis indicated that following the knockdown of the *gs* and *gls* genes, there was a significant enrichment of growth-related serine metabolism pathways and lipid metabolism pathways, as well as immune inflammation-related pathways. Co-expression mRNA network analysis revealed a significant enrichment of genes associated with purine de novo synthesis and the coenzyme Q oxidoreductase family. These findings offer significant insights for the control of intestinal health and agricultural practices of *T. blochii*.

Key words: Trachinotus blochii, Glutamine，intestine ，RNA interference, Transcriptome

膳食红辣椒粉对中间球海胆生长、抗氧化和免疫功能、肠道微生物群及相关基因表达的影响

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摘要：在可持续水产养殖理念的推动下，本研究评估了在饲料中添加不同比例（0–2%）红辣椒粉（*Capsicum annuum*）对中间球海胆 (*Strongylocentrotus intermedius*) 为期 50 天的影响。结果显示，红辣椒粉显著促进了生长并降低了饲料系数（FCR）（$P < 0.05$），其中 1.0% 组效果最佳。添加红辣椒粉可改善性腺颜色，提高性腺的蛋白质和脂质含量，并增强消化、免疫和抗氧化酶活性，同时降低丙二醛（MDA）水平。1.0% 组的微生物多样性最高，优势菌群（如厚壁菌门 *Firmicutes*）相对丰度增加，而潜在致病菌减少。与免疫和抗氧化相关的基因上调，促炎和应激相关基因下调。总体而言，1.0% 红辣椒粉补充能够优化肠道微生物群，增强抗氧化与免疫功能，减轻氧化应激，从而促进生长、改善性腺品质并提升刺参整体健康水平。

关键词：中间球海胆；红辣椒粉；生长性能；抗氧化能力；免疫反应；肠道菌群

Effects of dietary red pepper powder on growth, antioxidant and immune functions, intestinal microbiota, and related gene expression in Strongylocentrotus intermedius

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Abstract： Driven by sustainable aquaculture goals, this study evaluated dietary red pepper powder (*Capsicum annuum*) supplementation (0–2%) over 50 days on Strongylocentrotus intermedius. Red pepper powder significantly promoted growth and reduced FCR ($P < 0.05$), with 1.0% showing optimal results. It improved gonadal color, increased protein and lipid content, and enhanced digestive, immune, and antioxidant enzyme activities while lowering MDA levels. The 1.0% group had the highest microbial diversity and a higher abundance of beneficial bacteria (e.g., Firmicutes), with fewer pathogens. Immune- and antioxidant-related genes were upregulated, and pro-inflammatory genes downregulated. Overall, 1.0% supplementation optimized intestinal microbiota, improved antioxidant and immune functions, reduced oxidative stress, and enhanced growth and gonadal quality in S. intermedius.

Key words: Strongylocentrotus intermedius; Red pepper powder; Growth performance; Antioxidant function; Immune response; Intestinal microbiota

鹅脱氧胆酸通过 FXR–NF–κB 途径缓解泥鳅肝脏炎症的作用机制研究

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摘要：本试验旨在探究饲料中添加鹅脱氧胆酸（Chenodeoxycholic acid，CDCA）调控 FXR-NF-κB 信号轴缓解α-萘基异硫氰酸酯（ANIT）诱导泥鳅（*Misgurnus anguillicaudatus*）胆汁淤积性肝炎的作用机制。将 360 尾（IBW：6.13±0.01）g 泥鳅分为 CON 组、ANIT 组、CDCA 组和 ANIT+CDCA 组，饲喂 8 w。结果表明，CDCA 能够显著缓解 ANIT 诱导的胆汁淤积性肝炎，表现为血清 ALT、AST、TBIL 和 DBIL 水平明显下降。组织形态学与 HE 染色结果显示，CDCA 改善了 ANIT 引起的胆囊颜色改变、肝脏淤血和肝脏病理损伤。在分子层面，CDCA 调节多个胆汁酸代谢相关基因（*cyp7a1*、*cyp8b1*、*fxr*、*shp* 和 *lxr*）的表达，影响关键胆汁酸转运蛋白（*bsep*、*ntcp* 和 *mrp3*）的功能，并改善胆固醇与脂质代谢相关基因（*npc1l1*、*hgmcr*、*ldlr*、*abcg5* 和 *srebps*）的紊乱状态。进一步机制研究表明，CDCA 通过激活 FXR 信号通路，显著提升 FXR 蛋白表达，进而抑制 NF-κB 蛋白活化及其下游相关基因（*nf-κb*、*il-6*、*tnf-α*、*il-1β*）的表达，并上调抗炎因子 *il-10* mRNA 表达，从而有效缓解肝脏炎症。综上所述，CDCA 主要通过调控 FXR-NF-κB 信号轴，协同调节胆汁酸代谢及炎症反应，进而缓解 ANIT 诱导的胆汁淤积性肝炎。

关键词：鹅脱氧胆酸；泥鳅；胆汁淤积；肝炎；α-萘基异硫氰酸酯

Chenodeoxycholic Acid Alleviates Hepatic Inflammation in Loach by Modulating the FXR-NF-κB Pathway

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Abstract： This experiment aimed to investigate the mechanism by which dietary supplementation with chenodeoxycholic acid (CDCA) modulates the FXR-NF-κB signaling axis to alleviate α-naphthylisothiocyanate (ANIT)-induced cholestatic hepatitis in loach (*Misgurnus anguillicaudatus*). A total of 360 loaches (initial body weight: 6.13 ± 0.01 g) were divided into four groups: CON, ANIT, CDCA, and ANIT + CDCA, and fed for 8 weeks. The results showed that CDCA significantly alleviated ANIT-induced cholestatic hepatitis, as evidenced by marked reductions in serum levels of ALT, AST, TBIL, and DBIL. Histomorphological and HE staining analyses revealed that CDCA ameliorated ANIT-induced changes in gallbladder color, hepatic congestion, and pathological liver damage. At the molecular level, CDCA regulated the expression of multiple bile acid metabolism-related genes (*cyp7a1*, *cyp8b1*, *fxr*, *shp*, and *lxr*), influenced the function of key bile acid transporters (*bsep*, *ntcp*, and *mrp3*), and improved the disordered expression of cholesterol and lipid metabolism-related genes (*npc1l1*, *hgmcr*, *ldlr*, *abcg5*, and *srebps*). Further mechanistic studies indicated that CDCA activated the FXR signaling pathway, significantly upregulating FXR protein expression, which in turn suppressed the activation of NF-κB protein and the expression of its downstream genes (*nf-κb*, *il-6*, *tnf-α*, and *il-1β*), while upregulating the mRNA expression of the anti-inflammatory factor *il-10*, thereby effectively mitigating hepatic inflammation. In conclusion, CDCA alleviates ANIT-induced cholestatic hepatitis primarily by modulating the FXR-NF-κB signaling axis to coordinately regulate bile acid metabolism, lipid homeostasis, and inflammatory responses.

Key words: Chenodeoxycholic acid; Misgurnus anguillicaudatus; Cholestasis; Hepatitis; α-naphthylisothiocyanate

小球藻对金虎斑生长、营养品质、免疫及肠道菌群的影响

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摘要：微藻因其营养成分丰富，被视为可替代鱼粉、鱼油及豆粕的可持续饲料资源，研究微藻添加对养殖生物的功效至关重要。本研究以金虎斑为研究对象，探究饲料中添加小球藻对金虎斑生长、营养品质、免疫及肠道菌群的影响。实验设置高浓度藻液 HC、低浓度藻液 LC、藻粉 CP 及对照组 CON。14 d 时，HC 组的体重较对照组高 14.66%，增重率高 153.21%；28 d 时 LC 组体重最高，饲料系数最低，增重率较对照组高 5.47%，CAT 和 GSH 活性提升；微藻添加可提高金虎斑粗脂肪含量，增强肠道α-淀粉酶活性，同时显著影响金虎斑肠道微生物组成，变形菌门、厚壁菌门为主为金虎斑在门水平上的优势菌群；而在属水平上，HC 组富集不动杆菌属，CP 组富集乳杆菌属和纤乳酸菌属。本研究为微藻为水产饲料中微藻的添加提供了科学的实践依据，对推动绿色养殖具有重要参考价值。

关键词：金虎斑；小球藻；生长性能；营养指标；免疫；肠道菌群

The effects of Chlorella on the growth, nutritional quality, immunity and intestinal flora of hybrid grouper

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Abstract：This study explored the effects of dietary Chlorella supplementation on growth, nutritional quality,immune response,and gut microbiota in *Epinephelus fuscoguttatus*♀×*Epinephelus tukula*♂.Four diets were tested: high-concentration algal liquid HC,low-concentration algal liquid LC, algal powder CP, and a control CON.By day 14, the HC group showed a 14.66% higher body weight and a 153.21% increase in weight gain compared to CON.At day 28, the LC group achieved the highest body weight and lowest feed conversion ratio,with elevated CAT and GSH activities.Microalgae supplementation raised crude fat content,enhanced intestinal α-amylase activity,and shifted gut microbiota, enriching Acinetobacter in HC and *Lactobacillus*/*Ligilactobacillus* in CP. These results support microalgae as a sustainable aquafeed ingredient.

Key words: *Epinephelus fuscoguttatus*♀×*Epinephelus tukula*♂; Chlorella; Growth performance; Nutritional indicators; Immunity; Intestinal flora

黄芩素靶向 Keap1 调控 PINK1–线粒体途径缓解氨氮所致的鲤鳃肝损伤

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摘要：氨氮造成鱼类鳃组织结构严重病变，损伤氧摄取功能。黄芩素能够重塑鳃组织结构，并在多胁迫下维持器官健康。然而，黄芩素对氨氮胁迫的缓解作用仍不明确。本研究建立黄芩素干预鲤氨氮胁迫模型，并在体外分离培养鲤原代肝细胞、EPC 细胞。结果显示黄芩素能够降低氨造成的 ROS 和 MDA 累积，并以剂量依赖性增加抗氧化物酶活性。黄芩素提高氨造成的膜电位（MMP）和 ATP 下降，减少线粒体 ROS 累积，且 ROS 抑制剂（NAC）的处理能缓解膜电位下降。氨以剂量依赖性抑制 PINK1/Parkin 途径，增加自噬基因 p62 的表达，黄芩素处理有效缓解上述现象。分子对接发现 Keap1 与黄芩素具有很强的结合能力，同时 BAI 能够降低氨造成的 Keap1 累积，并增加 Nrf2 的核移位。应用 Keap1 和 Nrf2 的 siRNA，发现其能够调控 PINK1/Parkin 途径。结果揭示了黄芩素通过靶向 Keap1 调控 PINK1-线粒体途径缓解氨氮胁迫损伤。

关键词：氨氮胁迫；黄芩素；PINK1-线粒体途径；Keap1/Nrf2 途径

Baicalein targets Keap1 to alleviate ammonia-nitrogen stress via PINK1-mitochondrial signaling in carp

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Abstract： Ammonia nitrogen causes lesions in the gill structure of fish. Baicalein can reshape the structure of gill tissue. However, the alleviation effect of baicalein on ammonia nitrogen stress is still unclear. The study showed that baicalein could reduce the accumulation of ROS and MDA caused by ammonia and increase the activity of antioxidant enzymes in a dose-dependent manner. Baicalein increased the decrease of membrane potential and ATP caused by ammonia, reduced the accumulation of mitochondrial ROS. Ammonia inhibited the PINK1 / Parkin pathway and increased the expression of autophagy gene p62. Baicalein treatment effectively alleviated the above phenomenon. Molecular docking showed that Keap1 had a strong binding ability with baicalein, and BAI could reduce the accumulation of Keap1 caused by ammonia and increase the nuclear translocation of Nrf2. Using siRNAs of Keap1 and Nrf2, we found that they can regulate the PINK1 / Parkin pathway. The results revealed that baicalein alleviated ammonia nitrogen stress damage by targeting Keap1 to regulate PINK1-mitochondrial pathway.

Key words: Ammonia nitrogen stress; Baicalein; PINK1-mitochondrial signaling; Keap1/Nrf2 pathway

饲料甜菜碱对高糖诱导的翘嘴鳜（*Siniperea chuatsi*）氧化应激缓解作用机制研究

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摘要：为探究甜菜碱添加对高糖饲料诱导的翘嘴鳜氧化应激的影响，本研究对翘嘴鳜分别投喂对照组（NC）、甜菜碱组（BET，1%）、高糖组（HC, 20%）和高糖+甜菜碱组（BET+HC）饲料，进行为期 8 周的室内循环水体系养殖实验。研究结果显示，无论相比于 NC 组或 HC 组，饲料甜菜碱均显著提高鳜的特定生长率。相较于 CON 组，HC 组鳜肝脏内质网应激、自噬和细胞凋亡相关基因的表达水平显著增加，且总抗氧化能力 T-AOC 水平显著降低，表明高糖饲料显著诱导鳜内质网应激、细胞凋亡和氧化应激的产生。相比于 HC 组，HC+BET 组鳜肝脏内质网应激相关基因 atf4、becn1，细胞凋亡相关基因 bax 的表达量显著降低，表明饲料甜菜碱添加通过减轻内质网应激等途径缓解了高糖诱导的鳜内质网应激、细胞凋亡及氧化应激。综上，饲料甜菜碱添加对鳜生长及高糖诱导的氧化应激具有缓解作用，为淡水鱼对饲料糖的高效利用提供了新的策略。

关键词：翘嘴鳜；甜菜碱；高糖；氧化应激；内质网应激

Dietary betaine attenuates hepatic oxidative stress, endoplasmic reticulum stress-induced autophagy and apoptosis in mandarin fish (*Siniperea chuatsi*) fed high carbohydrate diets

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Abstract: This study investigated the effects of dietary betaine supplementation on high-carbohydrate diet-induced oxidative stress in mandarin fish (Siniperca chuatsi). Fish were fed one of four diets for 8 weeks: control (NC), betaine (BET, 1%), high-carbohydrate (HC, 20%), or high-carbohydrate with betaine (BET+HC). Results showed that betaine significantly enhanced specific growth rate compared to both NC and HC groups. The HC group exhibited up-regulated expression of hepatic genes related to endoplasmic reticulum (ER) stress, autophagy, and apoptosis, along with decreased total antioxidant capacity (T-AOC), indicating induced oxidative stress. In contrast, the BET+HC group showed significant down-regulation of ER stress-related genes (atf4, becn1) and pro-apoptotic gene bax compared to the HC group. These findings demonstrate that dietary betaine alleviates high-carbohydrate-induced ER stress, apoptosis, and oxidative stress, while improving growth, providing a strategic approach to enhance carbohydrate utilization in freshwater aquaculture.

Key words: mandarin fish; betaine; high carbohydrate; oxidative stress; ER stress

饲料中添加丁酸衍生物对中间球海胆生长性能、短链脂肪酸和肠道菌群的影响

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摘要：本研究旨在探讨丁酸衍生物（丁酸钠，三丁酸甘油酯）作为饲料添加剂对中间球海胆生长性能、短链脂肪酸和肠道菌群的影响。设置四种饲喂组合: 海带组(KF)，基础饲料组(BF)，丁酸钠组(BFB)，三丁酸甘油酯组(BFT)，饲喂 56d 后，结果表明，与实验起始组（CK）相比，各组壳径、壳高、肠道宽度和黏膜宽度等数值均显著增加；除 KF 组，各组的性腺重和 GSI 均显著增加。BFT 组除壳径外，各生物学性状变化最大(p＜0.05)，而 KF 组除黏膜层宽度外，变化最小(p＜0.05）。此外，各组短链脂肪酸(SCFAs)总含量均呈显著下降趋势(p＜0.05)，BFT 组含量显著高于与 CK 组(p＜0.05)。16SrRNA 测序表明，添加丁酸衍生物可以提高肠道微生物群落丰度和多样性，对海胆免疫有增强作用。本研究揭示丁酸衍生物对海胆生长及肠道菌群的影响，为海胆新型配合饲料的开发与绿色健康养殖提供一定的理论价值。

关键词：中间球海胆；丁酸衍生物；短链脂肪酸；肠道菌群；16SrRNA 测序

Effects of dietary butyric acid derivatives on growth performance, short-chain fatty acids profiles and intestinal microbiota of *Strongylocentrotus intermedius*

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Abstract： This study investigated the effects of butyric acid derivatives (sodium butyrate and tributyrin) as dietary additives on the growth performance, short-chain fatty acids (SCFA) porfiles and intestinal microbiota of sea urchin Strongylocentrotus intermedius. Five feeding groups were established: CK , KF, BF, BFB, and BFT. After 56 days of feeding, the shell diameter, shell height, intestinal mucosal（MU）and total width were significantly higher in all experimental groups than in CK group. Gonad weight and gonado-somatic index (GSI) also inceased significantly in all groups except KF group. The most pronounced improvement were ovserved in the BFT group (except shell diameter), whereas the KF group showed the weakest reponses (except MU width) . Total SCFAs levels decreased significantly across all groups, but remain higher in BFT than in CK group . Moreover, 16S rRNA sequencing indicated that butyrate derivatives enhanced the richness and diversity of the gut microbiota and exerted an immune enhancement.

Key words: Strongylocentrotus intermedius; butyric acid derivatives, short-chain fatty acids; intestinal microbiota; 16S rRNA sequencing.

柞蚕免疫蛹粉对中间球海胆关键经济性状及肠道菌群的影响

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摘要：柞蚕免疫蛹粉（IPP）含有多种活性物质，我们推测其有作为海胆饲料添加剂的潜力。开展了 60d 的试验，研究 IPP 对中间球海胆经济性状及肠道菌群的影响。试验设置海带组和四种含有不同浓度的 IPP 饲料组，分别为 0%IPP（对照组）、0.5%IPP、1.0%IPP 和 1.5%IPP 组。试验表明 IPP 对海胆存活率无显著影响（$P>0.05$）。研究发现添加 1.0% IPP 表现出最高增重率为 77.33%，显著高于对照组（$P<0.05$）。添加 IPP 显著提高了海胆性腺的生长，并通过增加性腺的硬度等来提高其质量（$P<0.05$）。海胆体腔液中超氧化物歧化酶和过氧化氢酶等酶活性较海带组显著升高（$P<0.05$）。添加 IPP 后海胆肠道内厚壁菌门、拟杆菌门丰度增加，弧菌科的丰度减少。这表明添加 IPP 可能会提高海胆的消化功能和肠道健康。总体而言，添加 IPP 可提升海胆部分经济性状和抗氧化能力。本研究为海胆的健康养殖提供了理论依据。

关键词：中间球海胆；柞蚕免疫蛹粉；性腺质量；肠道菌群；抗菌肽

Effects of Tussah Immunoreactive Pupa Powder on Key Economic Traits and Gut Microbiota of the Sea Urchin *Strongylocentrotus intermedius*

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Abstract： Tussah immunoreactive pupa powder (IPP) is composed of various active substances. We speculated that it has the potential to serve as a feed additive for sea urchins. Therefore, we conducted a 60d experiment to examine the effects of IPP on key economic traits and gut microbiota of *S. intermedius*. We prepared a kelp group and four types of feed containing 0% (the control group), 0.5%, 1.0%, and 1.5% IPP. The results indicated that IPP had no significant impact on the survival of sea urchins ($P > 0.05$). Firstly, the 1.0% IPP group had the highest body weight gain rate, significantly higher than that of the control group ($P < 0.05$). Secondly, added IPP significantly improved the growth and quality of sea urchin gonads ($P < 0.05$). Thirdly, added IPP significantly improved the activities of SOD, CAT, and POD ($P < 0.05$). Lastly, added IPP increased the abundance of Firmicutes and Bacteroidetes, and reduced the abundance of Vibrio. This manuscript provides a theoretical reference for the healthful aquaculture of *S. intermedius*.

Key words: Strongylocentrotus intermedius; IPP; antimicrobial peptides; gonad quality; gut microbiota

多巴胺调控长牡蛎壳形成机制研究

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摘要：贝类通过形成坚硬的外壳，来保护自己免受捕食、支持组织并防止干燥。多巴胺（DA）作为一种兴奋型神经递质在贝类幼体发育及贝壳形成过程中发挥着重要作用。本研究发现，DA 处理后，长牡蛎多巴胺 I 型受体（CgDRD1）表达量上调，酪蛋白激酶 2（CgCK2）的活性升高，而下游转录因子 CgCREM 的磷酸化水平降低，几丁质酶（CgChitinase）活力显著降低，进而影响壳几丁质框架的形成。注射多巴胺受体 1 抑制剂（SCH23390）后， CgCK2 的活性显著降低，而 CgCREM 磷酸化水平升高，外套膜中几丁质酶（CgChitinase）活力显著升高。本研究阐明了 DA 通过激活 DRD1-CK2-CREM 信号通路调控贝壳几丁质框架形成的机制，为长牡蛎养殖业应对壳损伤挑战提供了科学依据和潜在解决方案。

关键词：长牡蛎；多巴胺；几丁质；酪蛋白激酶 2；几丁质酶

Research on the Mechanism of Dopamine Regulating the Formation of Shells in *Crassostrea gigas*

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Abstract：Shellfish protect themselves from predation, support tissue and prevent dryness by forming a hard shell. Dopamine (DA), as an excitatory neurotransmitter, plays an important role in the development of shellfish larvae and shell formation. This study found that after DA treatment, the expression of dopamine type I receptor (CgDRD1) in Crassostrea gigas was upregulated, the activity of casein kinase 2 (CgCK2) was increased, while the phosphorylation level of the downstream transcription factor CgCREM was decreased, and the activity of chitinase (CgChitinase) was significantly reduced, which in turn affected the formation of shell chitin framework. After injection of a dopamine receptor 1 inhibitor (SCH23390), the activity of CgCK2 was significantly reduced, while the phosphorylation level of CgCREM was increased, and the activity of CgChitinase in the mantle was significantly increased. This study clarified the mechanism by which DA regulates the formation of chitin framework in shells by activating the DRD1-CK2-CREM signaling pathway, providing scientific basis and potential solutions.

Key words: *Crassostrea gigas*; Dopamine; Chitin; Casein kinase 2; Chitinase

α－酮戊二酸及其环状内酯通过改善线粒体功能缓解碳酸型碱胁迫对异育银鲫生长和代谢的负面影响

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摘要：本研究评估了α-酮戊二酸及其环状内酯对碳酸型碱胁迫下异育银鲫生长和代谢的影响。试验设计 5 种等氮等脂饲料：基础饲料饲喂淡水组，基础饲料及含 0.5%、1.0% AKG 和 0.5%、1.0% AKGD 的饲料分别饲喂 5 个碱胁迫组，养殖持续 8 周。结果表明，1.0% AKGD 组增重率显著高于 CA 组，且与 CK 组无显著差异。在氨代谢方面，碱胁迫导致 CA 组血氨和尿素氮水平显著升高，而 AKG 和 AKGD 的添加有效改善了该状况。在营养代谢方面，碱胁迫显著上调了糖异生、脂分解和蛋白质合成相关基因的表达，而 1.0% AKGD 组逆转了该变化。在线粒体功能方面，1.0% AKGD 组显著上调了线粒体合成、融合和自噬相关基因的表达，并下调了线粒体分裂相关基因的表达。综上，碳酸型碱胁迫抑制了异育银鲫生长以及氨、糖、脂和蛋白质代谢，而饲料中添加 1%AKGD 通过促进线粒体合成、融合、自噬并抑制分裂，缓解了碳酸型碱胁迫的负面影响。

关键词：异育银鲫；碳酸型碱胁迫；α-酮戊二酸；氨代谢；营养代谢；线粒体功能

α-Ketoglutarate and its cyclic lactone alleviate the negative effects of carbonate alkalinity stress on the growth and metabolism of gibel carp by improving mitochondrial function

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Abstract： This study evaluated the effects of α-ketoglutaric acid (AKG) and its cyclic ester (AKGD) on the growth and metabolism of gibel carp under carbonate-type alkaline stress. Five isonitrogenous and isolipidic diets were formulated: a basal diet for the freshwater control (CK) group, and basal diets containing 0.5% or 1.0% AKG or AKGD for five alkaline-stress groups. The trial lasted eight weeks. Results showed that the weight gain rate of the 1.0% AKGD group was significantly higher than that of the alkaline control (CA) group and not significantly different from CK. Alkaline stress significantly increased blood ammonia and urea nitrogen levels, while AKG and AKGD supplementation effectively alleviated these effects. Alkaline stress also upregulated genes related to gluconeogenesis, lipolysis, and protein synthesis, which were reversed by 1.0% AKGD. Furthermore, 1.0% AKGD promoted mitochondrial biogenesis, fusion, and autophagy, and inhibited fission. Overall, dietary 1.0% AKGD mitigated alkaline stress–induced growth and metabolic disorders by enhancing mitochondrial function.

Key words: Gibel carp; Carbonate alkalinity stress; α-Ketoglutarate; Ammonia metabolism; Nutritional metabolism; Mitochondrial function

紫贻贝肉冻存时间及投喂频率对中间球海胆生长和性腺指 数的影响

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摘要：紫贻贝肉与海带搭配投喂中间球海胆可以有效促进其体重增长和性腺发育。为降低饵料成本，本研究选用冻存24个月和2个月的两种不同价格的紫贻贝肉（陈贝肉和鲜贝肉）搭配新鲜海带，并设计3种间隔搭配方式（贝肉：海带投喂天数分别为2：3、2：6、2：9）对中间球海胆进行投喂，比较了各实验组海胆体重增长和性腺发育的差异。结果表明，鲜贝肉：海带=2:6实验组的性腺指数（19%）、陈贝肉：海带=2:6组（17%）均显著高于对照组（只投喂新鲜海带，15%）（$P < 0.05$）；壳径（$p<0.05$，对照组平均值为52mm，陈贝肉组时为54mm，鲜贝肉组达到了55mm）和体重（$p<0.05$ 对照组平均值为51g，陈贝肉组时为58g，鲜贝肉组达到了61g，由此可见鲜贝肉比陈贝肉更能提升性腺指数；但在天数比为2：3时实验组与对照组无明显区别，故得出结论：新鲜贝肉比陈年贝肉更能促进中间球海胆的体重，壳径和性腺的增长。

关键词：紫贻贝；中间球海胆；生长；性腺指数

Effects of Mytilus galloprovincialis Meat Storage Time and Feeding Frequency on Strongylocentrotus intermedius Growth and Gonad Index

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Abstract： Feeding Strongylocentrotus intermedius with Mytilus galloprovincialis meat combined with kelp significantly enhances growth and gonad development. To reduce costs, this study tested combinations of fresh kelp with either "aged" (24-month-frozen) or "fresh" (2-month-frozen) mussel meat under three feeding schedules (mussel:kelp days = 2:3, 2:6, 2:9). The fresh mussel:kelp (2:6) group achieved the highest gonad index (19%), followed by aged mussel:kelp (2:6) (17%), both significantly exceeding the kelp-only control (15%) ($P < 0.05$). Test diameter and body weight also increased significantly: controls averaged 52 mm/51 g, aged mussel groups 54 mm/58 g, and fresh mussel groups 55 mm/61 g ($P < 0.05$). Fresh mussel outperformed aged mussel across all metrics. No significant improvement occurred at the 2:3 ratio. Fresh M. galloprovincialis meat (particularly at 2:6 ratio) more effectively promotes S. intermedius growth and gonad development than aged alternatives.

Key words: Purple mussel，Intermediate sea urchin，Growth Refers to somatic increase in size/weight， Gonad Index

三种微生态制剂对中间球海胆生长性能的影响

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摘要：为探究三种微生态制剂对中间球海胆生长性能的影响。选取初始体质量 1.05g 的健康海胆幼苗，分别在养殖水体中施加沼泽红假单胞菌、植物乳杆菌及 EM 复合菌，每组设 1×10^4、1×10^5 和 1×10^6 CFU/mL 三个浓度梯度，并设空白对照组，实验周期 63 天。结果显示，在特定生长率方面，1×10^5 和 1×10^6 浓度组沼泽红假单胞菌实验组的 SGR（0.0222%/d、0.0226%/d）均显著高于对照组（0.0199%/d）($P < 0.05$）。该菌在 1×10^5 和 1×10^6 浓度下平均体重（84.61 g、87.04g）亦显著高于对照组（73.60 g）($P < 0.05$）。各组养殖水体中氨氮与亚硝酸盐含量均无显著差异，但植物乳杆菌各组水体磷含量均显著高于对照组 ($P < 0.05$）。研究表明，适量添加沼泽红假单胞菌可有效促进中间球海胆生长，具有良好应用潜力。

关键词：中间球海胆 微生态制剂 特定生长率 平均体重

Effects of Three Probiotics on the Growth Performance of *Strongylocentrotus intermedius*

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Abstract： This study investigated the effects of Rhodopseudomonas palustris, *Lactobacillus plantarum*, and a composite EM preparation on the growth of *Strongylocentrotus intermedius* (initial weight: 1.05 ± 0.01 g). Over 63 days, Each probiotic was tested at three concentrations: 1×10^{4} , 1×10^{5} , and 1×10^{6} CFU/mL, alongside a blank control group.The specific growth rate (SGR) in the 1×10^{5} and 1×10^{6} CFU/mL R. palustris groups (0.0222 %/d and 0.0226 %/d, respectively) significantly exceeded the control (0.0199 %/d) ($P < 0.05$). Final body weights in these groups (84.61 ± 0.92 g and 87.04 ± 3.95 g) were also significantly higher than the control (73.60 ± 1.53 g) ($P < 0.05$). While water ammonia-nitrogen and nitrite showed no significant differences, However, water phosphorus content was significantly higher in all L. plantarum groups compared to the control ($P < 0.05$). Results indicate that supplementing with Rhodopseudomonas palustris at appropriate concentrations (recommended range 1×10^{5} – 1×10^{6} CFU/mL) can effectively promote the growth of S. intermedius, indicating good application potential.

Key words: Strongylocentrotus intermedius; probiotics; specific growth rate; average body weight

三种多毛类饵料对凡纳滨对虾雌雄亲虾繁殖性能、生化指标及组织学的影响

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摘要：双齿围沙蚕是亲虾繁育阶段营养强化中唯一被广泛使用的多毛类物种。本研究以双齿围沙蚕为对照，引进富齿岩虫和多齿围沙蚕 2 个多毛类新物种，分析其分别单独作为亲虾饵料对凡纳滨对虾亲虾繁殖性能、生理生化指标及组织学的影响。结果显示，投喂富齿岩虫的雌性亲虾性成熟率、交配率、受精卵总量、孵化率均显著最高（$P<0.05$）。在雄性亲虾中，富齿岩虫组在性腺指数、精荚重量和精子数量上均显著最高，而精子黑化率显著最低（$P<0.05$）。其次，富齿岩虫组在雌雄亲虾肝胰腺和血清组织中抗氧化和免疫能力均显著高于其它组（$P<0.05$）。在肝胰腺、血清和性腺组织中雌二醇、卵黄蛋白原、睾酮含量富齿岩虫组均显著最高。此外，富齿岩虫组中卵母细胞面积、精小管数量、精子密度和精子团、初级精荚层面积均为最大。结果表明，富齿岩虫是一种优于双齿围沙蚕的新型饵料，其较高的粗蛋白和ΣPUFAs水平可最大地提升亲虾的繁殖性能、及抗氧化和免疫能力。

关键词：凡纳滨对虾亲虾，多毛类，繁殖性能，生化指标，组织学

Effects of three polychaetes on reproductive performance, biochemical indices and histology in the female and male Pacific white shrimp, *Litopenaeus vannamei* broodstock

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Abstract：*Perinereis aibuhitensis* is the only polychaete species that has been used in the process of nutrient enrichment in the breeding stage of *Litopenaeus vannamei* broodstock. In this study, two new polychaete species, Marphysa maxidenticulata and Perinereis nuntia, were introduced and compared with *P. aibuhitensis* into *L. vannamei* broodstock. Results showed the *M. maxidenticulata* group had the highest maturity rate, mating rate, number of fertilized eggs and nauplii, hatching rate, spermatophore weight, and sperm count ($P < 0.05$). Moreover, the antioxidant and immune ability of the M. maxidenticulata group were significantly highest ($P < 0.05$). On biochemical indices, the M. maxidenticulata group showed the highest level of estradiol, vitellogenin and testosterone ($P < 0.05$). In addition, area of mature oocytes, the sperm density, sperm mass and primary spermatophore layers were the largest in the *M. maxidenticulata* group. The results showed that M. maxidenticulata is a potential new fresh-live diet for female and male *L.vannamei* broodstock.

Key words: *Litopenaeus vannamei* broodstock, Polychaete, Reproductive performance, Biochemical indices, Histology

微颗粒饲料添加 5 种新型原料对大口黑鲈仔稚鱼生长性能、消化酶活性、肝肠结构和抗应激能力的影响

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摘要：本试验旨在研究微颗粒饲料添加 5 种新型原料对大口黑鲈仔稚鱼生长性能、消化酶活性、肝肠结构和抗应激能力的影响。试验选取 2880 尾初始体重为（0.07±0.01）g 的健康大口黑鲈，随机分为 6 组，每组 4 个重复，每个重复 120 尾。进口商业饲料作为对照组（MI 组），试验组在基础饲料分别添加 4% 钝顶螺旋藻粉（SP 组）、发酵蚯蚓膏（FEP 组）、豆奶宝（SO 组）、毕赤酵母（PP 组）和黑水虻酵素（BSFE 组）的等脂等氮饲料，试验期 33 天。结果表明与 MI 组相比，SP、FEP 和 PP 组的溶失率显著升高（$P<0.05$）；MI 和 FEP 组容重显著低于其它组（$P<0.05$）。与 MI 组相比，BSFE 组的终末体长、终末体重、增重率有升高趋势 ($P>0.05$)，SP 和 SO 组增重率和特定生长率显著降低（$P<0.05$），MI、PP 和 BSFE 组的脏体比、肝体比显著低于 SP、FEP 和 SO 组（$P<0.05$）。MI、PP 和 BSFE 的粗蛋白质显著高于 SP、FEP 和 SO 组；MI、FEP 和 BSFE 组的粗脂肪显著高于 SP、SO 和 PP 组（$P<0.05$）。4）与 MI 组相比，FEP 和 SO 组肠道碱性磷酸酶显著升高（$P<0.05$）。MI 和 BSFE 组的葡萄糖低于其它组（$P<0.05$）。6）MI、FEP、PP、BSFE 组肝脏细胞排列整齐，肠道组织结构清晰完整。MI 组绒毛宽度高于其它组（$P<0.05$）。7）应激前，与 MI 相比，SO 组碱性磷酸酶升高，SP 和 FEP 组总抗氧化能力升高（$P<0.05$）；应激后，SO 组存活率最低，PP 组的总抗氧化能力显著高于 BSFE 组（$P<0.05$）。

关键词：蛋白原料饲料；大口黑鲈仔稚鱼；生长性能；肝肠健康；抗应激能力

Effects of Five New Materials added to Microdiet on the Physical Properties, Growth Performance, Digestive Enzyme Activity, Liver and Intestinal Structure, and Stress Resistance of Largemouth Bass（*Micropterus salmoides*) Larvae and Juveniles

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Abstract: The purpose of this experiment was to study the effects of five new materials added to microdiet on the growth performance, digestive enzyme activity, liver and intestinal structure, and stress resistance of largemouth bass larvae and juveniles. 2880 healthy largemouth bass with an initial body weight of (0.07±0.01) g were selected for the experiment and randomly divided into 6 groups, with 4 replicates in each group and 120 fish per replicate. Imported commercial feed was used as the control group (MI group), while the experimental group was fed with 4% spirulina platensis (SP group), fermented earthworm paste (FEP group), soycomil (SO group), pichia pastoris (PP group), and black soldier fly enzyme (BSFE group) in the basic diet for 33 days. The results showed that: Compared with the MI group, the dissolution rates of SP, FEP, and PP groups were significantly increased ($P<0.05$). The bulk density of the MI and FEP groups was significantly lower than that of the other groups ($P<0.05$). Compared with the MI group, the BSFE group showed an increasing trend in final body length, final body weight, and weight gain rate($P>0.05$), while the weight gain rate, and specific growth rate in SP and SO groups were significantly decreased ($P<0.05$); the viscerosomatic indices and hepatosomatic indices of the MI, PP, and BSFE groups were significantly lower than those of the SP, FEP, and SO groups (*P*<0.05). The crude protein content of MI, PP, and BSFE groups was significantly higher than that of SP, FEP, and SO groups(*P*<0.05); The crude lipid content of MI, FEP, and BSFE groups was significantly higher than that of SP, SO, and PP groups(*P*<0.05). The alkaline phosphatase activity in the intestine of FEP and SO groups was significantly increased (*P*<0.05). The glucose content of the MI and BSFE groups was significantly lower than that of the other groups (*P*<0.05). The liver cells in the MI, FEP, PP, and BSFE groups were arranged neatly, and the intestinal tissue structure was clear and complete. The villus width in the MI group were significantly higher than those in the other groups. Before stress, compared with MI, alkaline phosphatase was significantly increased in the SO group, total antioxidant capacity was increased in the SP and FEP groups(*P*<0.05). After stress, the survival rate in the SO group was significantly lower than that in other groups, and the total antioxidant capacity in the PP group was significantly higher than that in the BSFE group (*P*<0.05).

Key words：microdiet; new materials; largemouth bass larval and juveniles; growth performance; liver and intestinal health; stress resistance

饲料中添加维生素 B1 对杂交鳢仔稚鱼生长、肠道消化、糖代谢及免疫抗氧化能力的影响

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摘要：本试验旨在研究饲料维生素B$_1$（VB$_1$）水平对杂交鳢（*Channa maculate*♀×*Channa argus*♂）仔稚鱼生长、肠道消化、糖代谢及免疫抗氧化能力的影响。选取初始体重为（0.20±0.00）g的杂交鳢 1200 尾，随机分为 5 组，每组 4 个重复，每个重复 60 尾。饲养于室外养殖系统水体体积为 50 L的尼龙网箱中，分别饲喂VB$_1$添加量为 0（T1）、10（T2）、20（T3）、30（T4）、40（T5） mg/kg 的 5 种等氮等脂饲料。试验期 28 d。结果表明：T2 组的增重率和特定生长率均显著高于其它组（$P<0.05$），饵料系数显著低于T1 和T5 组（$P<0.05$），T2 及T3 组蛋白质沉积率显著大于T1 组；T2 和T3 组肝脏转酮醇酶含量显著大于T1、T4 和T5 组（$P<0.05$），乳酸脱氢酶活性在T2 组时显著大于T1、T4 和T5 试验组（$P<0.05$）；T2 和T3 组肠道胰蛋白酶和脂肪酶活性均显著大于T1 组（$P<0.05$）；T2 和T3 组肝脏碱性磷酸酶、酸性磷酸酶及溶菌酶活性均显著大于T1 组（$P<0.05$），T2-T5 组总抗氧化能力显著大于T1 组（$P<0.05$），T2 组肝脏丙二醛含量显著小于T1 组（$P<0.05$）。综上所述，饲料中添加适宜的VB$_1$通过促进机体糖代谢能力和抗氧化能力来提高杂交鳢仔稚鱼的生长性能。以杂交鳢仔稚鱼的增重率、肝脏中VB$_1$含量和转酮酶活性为评价指标，通过折线模型分析得出，饲料中VB$_1$最适需要量分别为 8.70 mg/kg、9.61 mg/kg和 9.72 mg/kg。

关键词：维生素 B1；杂交鳢仔稚鱼；生长性能；消化酶活性；抗氧化；糖代谢

Effects of dietary vitamin B1 on growth, intestinal digestion, immune antioxidant capacity, and glucose metabolism in hybrid snakehead (*Channa maculate*♀×*Channa argus*♂) larvae

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Abstract: This study investigated the effects of dietary vitamin B$_1$ (VB$_1$) levels on growth performance, intestinal digestion, immune-antioxidant capacity, and glucose metabolism in hybrid snakehead (*Channa maculate* ♀ × *Channa argus* ♂) larvae.A total of 1,200 fish with initial body weight of (0.20±0.00) g were randomly allocated into five groups with four replicates each (60 fish per replicate). The fish were reared in 50 L nylon cages in an outdoor aquaculture system and fed five isonitrogenous and isolipidic diets containing 0 (T1), 10 (T2), 20 (T3), 30 (T4), and 40 (T5) mg/kg VB$_1$ for 28 days. Results showed that the T2 group had significantly higher weight gain rate and specific growth rate than other groups ($P<0.05$), with significantly lower feed conversion ratio than T1 and T5 groups ($P<0.05$). Protein retention rate in T2 and T3 groups was significantly higher than in T1 group. Hepatic transketolase activity in T2 and T3 groups was significantly greater than in T1, T4 and T5 groups ($P<0.05$), while lactate dehydrogenase activity in T2 group was significantly higher than in T1, T4 and T5 groups ($P<0.05$). Intestinal trypsin and lipase activities in T2 and T3 groups were significantly higher than in T1 group ($P<0.05$). Hepatic alkaline phosphatase, acid phosphatase and lysozyme activities in T2 and T3 groups were significantly greater than in T1 group ($P<0.05$). Total antioxidant capacity in T2-T5 groups was significantly higher than in T1 group ($P<0.05$), while hepatic malondialdehyde content in T2 group was significantly lower than in T1 group ($P<0.05$). In conclusion, optimal dietary VB_1 supplementation improved growth performance by enhancing glucose metabolism and antioxidant capacity in hybrid snakehead larvae. Broken-line regression analysis based on weight gain rate, hepatic VB_1 content and transketolase activity indicated the optimal dietary VB_1 requirements were 8.70 mg/kg, 9.61 mg/kg and 9.72 mg/kg, respectively.

Keywords: Vitamin B1; Hybrid snakehead larvae; Growth performance; Digestive enzyme activity; Antioxidant capacity; Glucose metabolism

饲料中添加维生素 C 对杂交鳢仔稚鱼生长性能、消化酶活性和抗氨氮胁迫能力的影响

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摘要：本试验旨在研究饲料维生素C（VC）水平对杂交鳢（*Channa maculate*♀×*Channa argus*♂）仔稚鱼的生长、消化和抗氨氮胁迫能力的影响。选取初始体重为（0.20±0.00）mg的杂交鳢 1440 尾，随机分为 6 组，每组 4 个重复，每个重复 60 尾。饲养于室外养殖系统水体体积为 50 L的尼龙网箱中，分别饲喂VC添加量为 0（AA1）、60（AA2）、120（AA3）、180（AA4）、240（AA5）、320（AA6） mg/kg 的 6 种等氮等脂饲料。试验期 28 d。结果表明：AA3-AA5 组的增重率和特定生长率均显著高于AA1 组（$P<0.05$），饵料系数显著低于AA1 和AA6 组（$P<0.05$）；AA3-AA6 组肠道胰蛋白酶显著大于AA1 和AA2 组（$P<0.05$），AA2-AA4 及AA6 组肠道脂肪酶显著大于AA1 组（$P<0.05$）；AA2-AA6 组肝脏碱性磷酸酶活性显著大于AA1 组（$P<0.05$），AA3-AA5 组肝脏酸性磷酸酶活性显著大于AA1、AA2 和AA6 组（$P<0.05$），AA3-AA6 组肝脏溶菌酶活性显著大于AA1 和AA2 组（$P<0.05$），AA3-AA5 组总抗氧化能力显著大于AA1 和AA2 组（$P<0.05$），AA3-AA4 组丙二醛含量显著小于AA1 组（$P<0.05$）。氨氮胁迫后，杂交鳢仔稚鱼的存活率在AA4 组时最高，显著高于AA1、AA2、AA5 和AA6 组（$P<0.05$）。综上所述，饲料中添加适宜的VC通过提高其消化和免疫抗氧化能力促进杂交鳢仔稚鱼生长。以增重率、肝脏中VC含量和胁迫存活率为评价指标，通过折线模型分析得出，杂交鳢仔稚鱼对饲料VC水平的最适需求量分别为 185.22 mg/kg、201.32 mg/kg和 177.63 mg/kg。

关键词：维生素 C；杂交鳢仔稚鱼；生长性能；消化酶活性；氨氮胁迫

Effects of dietary vitamin C on growth performance, digestive enzyme activity, and ammonia nitrogen stress resistance in hybrid snakehead (*Channa maculate*♀×*Channa argus*♂) larvae

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Abstract: This experiment aimed to investigate the effects of dietary vitamin C (VC) levels on the growth, digestion, and ammonia stress resistance of hybrid snakehead (*Channa maculate* ♀ × *Channa argus* ♂) larvae. A total of 1,440 hybrid snakehead larvae with an initial body weight of (0.20 ± 0.00) mg were randomly divided into six groups with four replicates each (60 fish per replicate). The fish were reared in 50 L nylon cages in an outdoor aquaculture system and fed six isonitrogenous and isolipidic diets containing 0 (AA1), 60 (AA2), 120 (AA3), 180 (AA4), 240 (AA5), and 320 (AA6) mg/kg VC for 28 days. Results showed that the AA3-AA5 groups exhibited significantly higher weight gain rate and specific growth rate than AA1 ($P<0.05$), with significantly lower feed conversion ratio than AA1 and AA6 groups ($P<0.05$). Intestinal trypsin activity in AA3-AA6 groups was significantly higher than AA1 and AA2 ($P<0.05$), while intestinal lipase activity in AA2-AA4 and AA6 groups was significantly greater than AA1 ($P<0.05$). Hepatic alkaline phosphatase activity in AA2-AA6 groups was significantly higher than AA1 ($P<0.05$), with AA3-AA5 groups showing significantly greater acid phosphatase activity than AA1, AA2 and AA6 ($P<0.05$). AA3-AA6 groups had significantly higher

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hepatic lysozyme activity than AA1 and AA2 ($P<0.05$), while AA3-AA5 groups demonstrated significantly greater total antioxidant capacity than AA1 and AA2 ($P<0.05$), with AA3-AA4 groups showing significantly lower malondialdehyde content than AA1 ($P<0.05$). After ammonia stress challenge, the survival rate was highest in AA4 group, significantly exceeding AA1, AA2, AA5 and AA6 groups ($P<0.05$). In conclusion, dietary VC supplementation at appropriate levels improved growth performance by enhancing digestive capacity and immune-antioxidant ability in hybrid snakehead larvae. Broken-line regression analysis based on weight gain rate, hepatic VC content and post-stress survival rate indicated the optimal dietary VC requirements for hybrid snakehead larvae were 185.22 mg/kg, 201.32 mg/kg and 177.63 mg/kg, respectively.

Keywords: Vitamin C; Hybrid snakehead larvae; Growth performance; Digestive enzyme activity; Ammonia nitrogen stress.

饲料中添加 3 种益生菌对牛蛙幼蛙生长性能、免疫能力和肠道健康的影响

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摘要：为评估 3 种益生菌在牛蛙养殖中对牛蛙幼蛙生长性能、免疫能力和肠道健康的影响。在饲料中添加不同益生菌[无（对照组 Control Group, CG）、3.05×10^7 CFU/g 丁酸梭菌（*Clostridium butyricum*, CB）、0.95×10^7 CFU/g 凝结芽孢杆菌（*Bacillus coagulans*, BC）0 和 0.2% 酿酒酵母（*Saccharomyces Cerevisiae*, SC）]饲养牛蛙幼蛙（7.04±0.02）g 36 d。结果显示:1)CB 蛋白质沉积率（PDR）显著提高（$P<0.05$），饲料系数（FCR）显著下降（$P<0.05$）。2）试验组肝脏、肠道胰蛋白酶和肠道脂肪酶、Na^+-K^+-ATP 酶活性均高于 CG。3）试验组肝脏和肠道溶菌酶（LZM）、超氧化物歧化酶（SOD）、谷胱甘肽过氧化物酶（GSH-Px）均显著高于 CG（$P<0.05$），SC 碱性磷酸酶（AKP）显著高于 CG（$P<0.05$）；CB 和 BC 肝脏总抗氧化能力（T-AOC）显著高于 CG（$P<0.05$）；CB 组肝脏过氧化氢酶（CAT）和丙二醛（MDA）显著低于 CG（$P<0.05$）。4）试验组肠道绒毛高度、绒毛宽度显著高于 CG（$P<0.05$），CB 和 BC 肠道肌层厚度显著高于 CG（$P<0.05$）。5）试验组有益菌丰度有增加趋势。综上，饲料中添加 CB、BC 和 SC 均可一定程度地改善幼蛙的生长、提高其消化酶活性和免疫抗氧化能力，调节肠道菌群，其中添加丁酸梭菌效果较好。

关键词：牛蛙；丁酸梭菌；凝结芽孢杆菌；酿酒酵母

Effects of Dietary Probiotic Supplementation on Growth Performance, Immune Function,and Intestinal Health in Juvenile Bullfrogs (*Aquarana catesbeiana*)

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Abstract: To evaluate the effects of three probiotics on growth performance, immune capacity, and intestinal health of juvenile bullfrogs in aquaculture, different probiotics were supplemented in the feed: no probiotics (Control Group, CG), 3.05×10^7 CFU/g *Clostridium butyricum* (CB), 0.95×10^7 CFU/g *Bacillus coagulans* (BC), and 0.2% *Saccharomyces Cerevisiae* (SC). Juvenile bullfrogs (initial weight 7.04 ± 0.02 g) were reared under these conditions for 36 days. The results showed that: 1)The protein deposition rate (PDR) was significantly increased ($P < 0.05$), and the feed conversion ratio (FCR) was significantly reduced ($P < 0.05$) in the CB group. 2) The activities of hepatic and intestinal trypsin, intestinal lipase, and Na^+-K^+-ATPase were higher in the treatment groups compared to the CG group. 3) Lysozyme (LZM), superoxide dismutase (SOD), and glutathione peroxidase (GSH-Px) levels in the liver and intestine were significantly higher in the treatment groups than in CG ($P < 0.05$). Alkaline phosphatase (AKP) in the SC group was significantly higher than in CG ($P < 0.05$). The total antioxidant capacity (T-AOC) in the liver of CB and BC groups was significantly higher than that in CG ($P < 0.05$). Catalase (CAT) and malondialdehyde (MDA) levels in the liver of the CB group were significantly lower than those in CG ($P < 0.05$). 4) Intestinal villus height and width were significantly greater in the treatment groups compared to CG ($P < 0.05$). The intestinal muscularis thickness in CB and BC groups was significantly higher than that in CG ($P < 0.05$). 5) An increasing trend in beneficial bacterial abundance was observed in the treatment groups. In conclusion, dietary supplementation with CB, BC, and SC could moderately improve growth performance, enhance digestive enzyme activity and immune-antioxidant capacity, and modulate intestinal microbiota in juvenile bullfrogs. Among these, *C. butyricum* exhibited the most pronounced effects.

Keywords: *Aquarana catesbeiana*; Clostridium butyricum; Bacillus coagulans; Saccharomyces Cerevisiae

黑水虻虫粉替代饲粮鱼粉对斑点叉尾鮰生长、肝脏和肠道健康及功能的影响

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摘要：本研究通过探究黑水虻虫粉（BSFLM）替代鱼粉对斑点叉尾鮰生长、肝肠健康及生理功能的影响，确立兼顾生长性能与机体健康的最优替代比例。使用 BSFLM 替代 0%（G0）、25%（G25）、50%（G50）、75%（G75）和 100%（G100）鱼粉配制 5 种等氮等脂饲料。选取初重（2.75±0.01）g 斑点叉尾鮰 600 尾，随机分 5 组，每组 3 个重复，每个重复 40 尾，试验周期 56 d。BSFLM 对各组存活率、增重率、蛋白质效率及饲料系数无显著影响；G25 及 G75 组肥满度显著大于 G0 组（$P<0.05$）。G100 组鱼体粗蛋白质和粗灰分显著大于 G0 组（$P<0.05$）。G25 和 G50 组肠道胰蛋白酶、脂肪酶和钠钾 ATP 酶活性显著大于 G0 组（$P<0.05$）。G25 组肠道肌层厚度显著大于 G0 组（$P<0.05$），各组绒毛长度和宽度无显著差异；G100 组肝细胞体积增大，胞质疏松透明。G25 和 G50 组肝脏酸性磷酸酶活性和补体 C3 含量显著低于 G0 组（$P<0.05$）。与 G0 相比，G25 组的肝脏总超氧化物歧化酶和过氧化氢酶活性显著升高，各试验组丙二醛含量显著升高，G25 组蛋白质羰基含量显著降低（$P<0.05$）。G25-G75 组肠道 *ZO*-1 及 *CL*-2 表达量显著高于 G0 组（$P<0.05$）。本试验下，BSFLM 可完全替代斑点叉尾鮰饲料的鱼粉，结合肝肠健康及功能，饲粮中 BSFLM 适宜替代量以 25%-50%为佳。

关键词：斑点叉尾鮰；黑水虻虫粉；肝肠健康及功能；免疫抗氧化

Effects of replacing dietary fishmeal with black soldier fly larvae meal (BSFLM) on growth, hepatic and intestinal health and functions in channel catfish (*Ictalurus punctatus*)

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Abstract: This study investigated the comprehensive effects of replacing fishmeal with black soldier fly larvae meal (BSFLM) on the growth, hepatointestinal health, and physiological functions of channel catfish (*Ictalurus punctatus*), aiming to establish the optimal replacement ratio that balances growth performance and organismal health. Five isonitrogenous and isolipidic diets were formulated by replacing fishmeal with BSFLM at 0% (G0, control group), 25% (G25), 50% (G50), 75% (G75), and 100% (G100). Six hundred channel catfish with an initial body weight of (2.75 ± 0.01) g were selected, randomly divided into 5 groups, with 3 replicates per group and 40 fish per replicate. The trial lasted 56 days. Compared with the control group, BSFLM had no effect on survival rate, weight gain rate, protein efficiency ratio or feed conversion ratio of channel catfish($P>0.05$) . The condition factor was significantly higherin the G25 and G75 groups ($P<0.05$) .Compared with the control group, the whole-body crude protein and crude ash contents were significantly increased ($P<0.05$). Compared to the control group, intestinal trypsin, lipase, and Na^+ -K^+ -ATPase activities were significantly increased in the G25 and G50 groups ($P<0.05$). BSFLM did not affect intestinal villus length or villus width. The muscular layer thickness was significantly greater in the G25 group than in the control($P<0.05$). Hepatocyte volume was significantly enlarged in the G100 group, with cytoplasmic vacuolization and increased transparency.Compared to the control group, hepatic acid phosphatase activity and complement C3 content were significantly decreased in the G25 and G50 groups ($P<0.05$). Compared with the G0 group, hepatic total superoxide dismutase and catalase activities were significantly increased in the G25 group, while malondialdehyde content was significantly elevated in G25-G100 groups. Additionally, protein carbonyl content was significantly decreased in the G25 group ($P < 0.05$). Compared to the control group, intestinal *ZO*-1 and *CL*-2 gene expression levels were significantly increased in the G25-G75 groups ($P<0.05$).Under the conditions of this trial, complete replacement of fishmeal with BSFLM in the diet did not negatively affect the growth of channel catfish. Considering hepatointestinal health and physiological functions, a replacement level of 25%-50% BSFLM is recommended as optimal.

Keywords: Channel catfish (*Ictalurus punctatus*); Black soldier fly larvae meal (BSFLM); Hepatic and intestinal health and functions; Immunity and antioxidant capacity

第四专题 水产病害防治与水产品质量安全

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

鲤转铁蛋白在细菌防御中的作用

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摘要：转铁蛋白(TF) 是一种具有铁结合特性的典型生物大分子蛋白质。TF 蛋白在调节宿主铁稳态和防御病原体入侵中起着至关重要的作用。本研究从鲤(Cyprinus carpio)中鉴定出 CcTF，并对其表达模式和抗菌活性进行了分析。CcTF 在肝脏、脾脏、心脏、头肾、血液、皮肤、肌肉、脑、肾脏、肠、鳃中均有表达，其中在肝脏中表达最高。体外在 LPS 和嗜水气单胞菌（*Aeronmonas hydrophila*）的刺激下，CcTF 在头肾、脾脏、肝脏中 mRNA 表达水平显著上调。同时 CcTF 对 LPS 具有浓度依赖性的结合亲和力，并且表现出对六种致病菌的结合、凝集和抑制特性。构建 *A. hydrophila* 感染原代头肾白细胞的模型，发现 CcTF 可以调节炎症因子表达，减轻炎症反应。此外，CcTF 的过表达后可以调节相关炎症因子，减轻组织损伤，提升了鱼体的抗病能力。总之，本研究的发现表明了 TF 在鲤先天免疫反应中的关键作用。

关键词：鲤；血清转铁蛋白；嗜水气单胞菌；炎症反应；抗感染

The Role of Transferrin in the Bacterial Defense of common Carp (*Cyprinus carpio*)

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Abstract： Transferrin (TF) is a prototypical biological macromolecule protein known for its iron-binding properties. TF proteins play a crucial role in modulating host iron homeostasis and defending against pathogen invasion. In this study, we identified TF from common carp (*Cyprinus carpio*) and proceeded to analyse its expression pattern and antimicrobial activity. The predominant expression of CcTf has been observed to be in the liver. CcTF demonstrated a concentration-dependent binding affinity for LPS, exhibiting binding, agglutination, and inhibition properties against six pathogenic bacteria. A model of primary head kidney white blood cells infected with *A. hydrophila* was constructed. The study revealed that CcTF could modulate the expression levels of inflammatory factors. Furthermore, the overexpression of CcTF resulted in an enhancement of the disease resistance of the fish. In conclusion, in this study, these findings suggest that CcTF plays a critical role in the innate immune response of common carp.

Key words: *Cyprinus carpio*, Tf, *Aeromonas hydrophila*, inflammatory response, antibacterial

claudin–3 基因在尼罗罗非鱼抗无乳链球菌感染血脑屏障中的防御作用

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摘要：【目的】克隆尼罗罗非鱼 claudin-3 基因并分析其在无乳链球菌刺激后的表达，以探讨其在抗感染中的作用。【方法】根据已公布序列设计引物进行克隆，利用生物信息学和 qPCR 分析其组织分布及感染后的表达变化，并构建体外血脑屏障模型研究其在脑膜炎过程中的功能。【结果】获得 648 bp 全长序列，编码 216 个氨基酸，分子量 23.3 kD，等电点 8.12。该基因在肝脏、头肾和脑中表达较高，感染后呈现组织特异性的动态表达变化。【结论】claudin-3 在尼罗罗非鱼抗无乳链球菌感染中发挥重要作用，尤其在维持血脑屏障功能方面具有关键意义。

关键词：尼罗罗非鱼；claudin-3 基因；无乳链球菌；血脑屏障；防御

Expression pattern of claudin-3 gene in *Oreochromis niloticus* in *Streptococcus agalactiae* infection and its role in blood-brain barrier defense

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Abstract：【Objective】Clone and characterize Nile tilapia claudin-3 to elucidate its role during *Streptococcus agalactiae* infection.【Methods】The 648-bp ORF (XM_005465025.4) was amplified, and its 216-aa product (23.3 kDa, pI 8.12) was analysed in silico. qPCR quantified basal and post-challenge expression in nine tissues; an in vitro blood–brain barrier (TVEC-01/TA-02) assessed function during meningitis.【Results】Highest basal levels occurred in liver, head-kidney and brain. After challenge, skin, liver, spleen and intestine displayed “up–down–up” kinetics; brain, muscle and head-kidney showed initial suppression followed by recovery.【Conclusion】Claudin-3 is dynamically modulated and essential for tilapia defense, notably in preserving blood–brain barrier integrity against *S. agalactiae*.

Key words: *Oreochromis niloticus*；claudin-3 gene；*Streptococcus agalactiae*；blood-brain barrier；defense

东星斑体表一种鱼蛭的生活史观察和种类鉴定

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摘要：为有效防治困扰海南东星斑养殖业的寄生虫鱼蛭病害，保障东星斑健康生长和产业可持续发展，本研究旨在开展鱼蛭的基础研究，重点聚焦于其形态特征、生活史规律及准确品种鉴定。通过显微胚胎观察记录生活史，通过 COI、NDI、和 18S rDNA 序列等分子生物学方法，进行物种鉴定和亲缘关系分析。结果发现，在 26～33℃水温下，鱼蛭完成一个完整的生活史周期需要 17～18 天，成虫在完成产卵后约 6 天开始陆续死亡。该鱼蛭与已知物种阿鲁加姆锡兰蛭 (*Zeylanicobdella arugamens*i) 的基因序列匹配相似度高达 100%。明确了关键生活史参数，包括卵茧孵化期（7～8 天）、幼蛭至初次产卵期（约 10 天）、完整生活史周期（17～18 天）以及成虫产卵后死亡时间（约 6 天）。这些基础研究结果为后续制定针对性的阿鲁加姆锡兰蛭防治策略提供了重要的科学依据。

关键词：鱼蛭，胚胎发育，COI，NDI，18s rDNA

Life history observation and species identification of a species of leech on the body surface of *Plectropomus leopardus*

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Abstract： In order to determine the types of leech on the body surface of Plectropomus leopardus, three aspects of the study were carried out in this experiment, including the morphological observation, the observation of embryonic development, and the NJ method based on the morphological observation. Species identification of constructed COI, NDI and 18s rDNA phylogenetic trees. When the water temperature of the leech is 26-33 ℃, the egg cocoon incubation period is 7-8 days, and it takes 10 days for the young leech to develop to the first egg laying, that is, a complete life cycle of the leech takes 17-18 days; The leech was observed to start dying 6 days after finishing spawning. These basic research results provide important scientific basis for the subsequent development of targeted prevention and control strategies.

Key words: leeches, embryonic development, COI , NDI , 18s rDNA

硬骨鱼黏膜免疫空间图谱构建：多重探针联用揭示牙鲆鼻黏膜免疫微环境

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摘要：鱼类的嗅觉器官所执行的嗅觉功能几乎涉及所有的生命活动。水环境胁迫使得硬骨鱼进化出鼻相关淋巴组织（NALT），以维持嗅觉器官的结构和稳态。由于缺乏特异性探针，对硬骨鱼 NALT 和鼻黏膜免疫微环境的认识仍处于起步阶段，其中免疫细胞和分子的组成和分布尚不清楚。本研究根据健康牙鲆（*parichthys olivaceus*）的形态学特征，将其鼻黏膜分为 5 个不同的区域，并研究其形态发育特点。多种组织学染色技术显示嗅觉器官中存在丰富的血管、胶原纤维和神经网络。利用各种探针，对鼻黏膜内的先天和适应性免疫细胞和分子进行定位和定量，此外，评估了健康条件下 47 个免疫基因在嗅囊中的基线表达水平。本研究结果揭示了牙鲆鼻黏膜独特的免疫微环境，为硬骨鱼黏膜免疫研究提供了新的视角。

关键词：牙鲆；鼻黏膜；免疫微环境；黏膜免疫

Construction of a Mucosal Immune Spatial Atlas in Teleost Fish: Multiplex Probes Reveal the Immune Microenvironment of the Nasal Mucosa in Flounder （*parichthys olivaceus*）

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Abstract: The olfactory functions performed by olfactory organs of fish are involved in almost all life activities. Continuous microbial exposure in the water has forced teleost fish to evolve nasal-associated lymphoid tissues (NALT) to maintain the structural and functional homeostasis of the olfactory organ. However, the knowledge of the NALT and nasal immune microenvironment of teleost fish is still in its infancy due to the lack of specific probes, in which the composition and distribution of immune cells and molecules are not well known. In this study, the olfactory mucosa of healthy flounder (Paralichthys olivaceus) was divided into 5 different regions based on its morphological characteristics, and multiple histological staining techniques revealed the presence of highly abundant blood vessels, collagen fibers, and nerve networks in the olfactory organ. Using various probes, innate and adaptive immune cells and molecules in the olfactory mucosa were localized and quantified. Additionally, the baseline expression levels of 47 immune genes in the olfactory sacs were assessed.

Key words: Flounder (*Paralichthys olivaceus*); Nasal mucosa; Immune microenvironment; Mucosal immunity

微流控在水产品快检中的应用研究

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摘要：提升水产品安全检测效率是保障食品安全的关键环节。本报告聚焦微流控技术为水产品快速检测带来的革新。报告将重点阐述三个核心层面：首先，在在线一体化前处理方面，探讨微流控芯片如何将复杂的目标物在线吸附、纯化与洗脱等步骤集成化、自动化，极大缩短前处理时间并减少人为误差。其次，在标准品制备层面，重点分析微流控精准加标方法的应用。通过纳升/皮升级的精准流体控制，可实现标准物与待测样品的均匀、定量混合，相较于传统的“药浴法”，该方法具有用量极省、混合均匀度高、重现性好等显著优势。最后，展示基于上述技术的在线一体化检测设备，它将前处理、反应与检测模块无缝集成，真正实现了水产品中危害因子的“样品入-结果出”式现场快速检测。本报告旨在系统论证微流控技术如何通过方法学创新，推动水产品快检技术向高效、精准、自动化的新阶段发展。

关键词：微流控技术、快速检测、在线一体化、在线前处理、抗生素残留

Application of Microfluidics in Rapid Detection of Aquatic Products

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Abstract: Improving the safety detection efficiency of aquatic products is the key link to ensure food safety. This report focuses on the innovation of microfluidic technology for rapid detection of aquatic products. The report will focus on three core aspects : Firstly, in the aspect of online integrated pretreatment, how to integrate and automate the steps of online adsorption, purification and elution of complex targets by microfluidic chips is discussed, which greatly shortens the pretreatment time and reduces human errors. Secondly, at the level of standard preparation, the application of microfluidic precise standard addition method is mainly analyzed. Through the precise fluid control of nanoliter / skin upgrade, the uniform and quantitative mixing of the standard substance and the sample to be tested can be realized. Compared with the traditional ' medicated bath method ', this method has the advantages of extremely low dosage, high mixing uniformity and good reproducibility. Finally, the on-line integrated detection equipment based on the above technology is demonstrated, which seamlessly integrates the pre-processing, reaction, and detection modules, truly realizing the "sample in result out" on-site rapid detection of hazardous factors in aquatic products. This report aims to systematically demonstrate how microfluidic technology can promote the development of fast detection technology for aquatic products towards a new stage of efficiency, precision, and automation through methodological innovation.

Key words: Microfluidics, Rapid detection, Online integration, Online pretreatment、Antibiotic residues

枸橘苷抗副溶血弧菌耐热直接溶血素作用机理的研究

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摘要：副溶血弧菌（*Vibrio parahaemolyticus*，Vp）是一种常见的水产动物致病菌，可引发鱼虾等患病，也可导致人类食源性中毒。Vp具有多种致病因子，其中耐热直接溶血素（TDH）被认为是其最重要的毒力因子之一。通过分子对接及动力学模拟、表面等离子共振（SPR）以及微量热泳动（MST）结果证明枸橘苷能够与TDH特异性结合。Western Blot结果证实，枸橘苷可以阻碍TDH四聚体的形成。位点突变后，枸橘苷对溶血活性的抑制作用降低，证明G12和S92是TDH-枸橘苷的结合位点。亚抑菌浓度的枸橘苷转录组与蛋白组共同分析得出其有4个基因共同上调，22个基因共同下调。本研究结果表明，枸橘苷能够通过抑制TDH四聚体的形成和干扰转录及蛋白生成，从而影响VP毒力，为相关研究提供了新的潜在药物和研发方向。

关键词：副溶血弧菌；枸橘苷；耐热直接溶血素；四聚体

Investigation into the Mechanism of Poncirin Inhibiting Thermostable Direct Hemolysin of *Vibrio parahaemolyticus*

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Abstract： A prevalent infection in aquatic animals, Vibrio parahaemolyticus (Vp) can cause foodborne illnesses in humans as well as disorders in fish and shrimp. Among the various virulence factors that Vp contains, the thermostable direct hemolysin (TDH) is thought to be one of the most significant. Citrusin can bind to TDH selectively, as shown by data from surface plasmon resonance (SPR), molecular docking and kinetic simulations, and micro-swim thermometry (MST). Citrusin prevents the production of TDH tetramers, according to Western Blot research. Citrusin's decreased reduction of hemolytic activity was discovered by site-directed mutagenesis, which also identified G12 and S92 as binding sites for the TDH-citrusin interaction. At subinhibitory citrusin concentrations, transcriptome and proteome studies identified 22 co-downregulated genes and 4 co-upregulated genes. These results suggest that citrusin affects VP pathogenicity by preventing the formation of TDH tetramers and interfering with transcription and protein synthesis, offering new possible therapeutic targets and avenues.

Key words: *Vibrio parahaemolyticus*; Poncirin; Thermostable direct hemolysin; Tetramer

海水青鳉 MYL3 介导赤点石斑鱼神经坏死病毒入侵宿主细胞的分子机制研究

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摘要：鱼类神经坏死病毒作为引发海水鱼类病毒性神经坏死病的重要病原，严重制约着我国海水养殖业的健康发展。深入解析 NNV 入侵机制对于发现新的抗病毒靶点与开发高效抗病毒药物具有重要意义。本研究通过一系列蛋白互作技术证明 MmMYL3 能够与 RGNNV 表面的唯一结构蛋白 CP 直接相互作用。通过调控 MmMYL3 在细胞中的表达水平，进一步证明了 MmMYL3 可在 RGNNV 的感染早期发挥作用，揭示其作为受体的可能性。在明确 MmMYL3 是 RGNNV 新受体的基础之上，我们发现 MmMYL3 能够直接与巨胞饮关键 RTK-MmIGF1R 胞外区结合，并且 MmIGF1R 能够与小 GTP 酶 Rac1、Cdc42 相互作用。说明 MmMYL3 通过 IGF1R-Rac1/Cdc42 信号轴介导 RGNNV 通过巨胞饮入侵细胞。研究结果不仅深化了对 NNV 感染机制的认识，更为鱼类抗病毒药物提供了参考，为经济鱼类疫病防控提供了新的理论基础与应用方向。

关键词：神经坏死病毒，肌球蛋白轻链 3，受体，巨胞饮

Myosin light chain 3 serves as a receptor for nervous necrosis virus entry into host cells via the macropinocytosis pathway

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Abstract： Nodaviridae infections cause severe mortality in insects and fish, with nervous necrosis virus (NNV) posing significant threats to global fish populations. However, the host factors involved in NNV entry remain poorly understood. We identify myosin light chain 3 from marine medaka (Oryzias melastigma) (MmMYL3) as a novel receptor for red-spotted grouper NNV (RGNNV), facilitating internalization via macropinocytosis. MmMYL3 directly binds the RGNNV capsid protein (CP), which dependents on the arm and S domains of CP and the EF-hand2 domain of MmMYL3. In vitro experiments showed that MmMYL3 siRNA, protein, anti-MYL3 antibodies or the arm domain synthetic peptides blocked RGNNV entry. Moreover, in vivo administration of MmMYL3 protein also inhibited RGNNV infection. Ectopic MmMYL3 expression enabled RGNNV internalization into resistant cells. Notably, MmMYL3 facilitated RGNNV internalization through the macropinocytosis pathway via the IGF1R-Rac1/Cdc42 axis. Collectively, our findings underscore MYL3’s crucial role in NNV entry and its potential as an antiviral target.

Key words: nervous necrosis virus, myosin light chain 3, receptor, macropinocytosis

二尖梅奇酵母铁稳态调控基因的初步研究

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摘要：二尖梅奇酵母是引致中华绒螯蟹“牛奶病”的致病真菌，该病致死率高，严重危害河蟹养殖产业。前期研究发现铁元素在该酵母侵染河蟹中发挥重要作用。本研究综合多组学与基因编辑技术，系统解析了该酵母的铁稳态调控网络，重点探究了 MbCcc1 和 MbSfu1 两个关键基因的功能。通过转录组技术，在高铁和低铁胁迫中筛选到 27 个与铁代谢相关基因，构建出铁稳态调控网络。功能研究表明，MbCcc1 作为液泡铁转运蛋白，其缺失导致菌株生长减缓、环境胁迫耐受性下降，毒力减弱，并引起铁摄取基因表达下调，表明其在铁储存与解毒中发挥作用。MbSfu1 作为铁吸收抑制因子，其缺失株生长受限，对金属离子和氧化胁迫敏感，毒力降低，同时铁摄取基因表达上升，表明其负调控铁吸收过程。此外，该基因还参与铜稳态的调控。综上，二尖梅奇酵母通过 MbCcc1 和 MbSfu1 协同维持铁稳态，为针对铁/铜稳态靶点开发“牛奶病”防控策略提供了理论依据。

关键词：二尖梅奇酵母；铁稳态；MbCcc1； MbSfu1

Preliminary study on the Iron homeostasis regulatory genes in *Metschnikowia bicuspidata*

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Abstract： The fungus Metschnikowia bicuspidata causes "milky disease" in Chinese mitten crabs, leading to high mortality and significant economic losses. As iron is a key virulence factor, this study investigated its homeostasis in the yeast using multi-omics and gene editing.Transcriptomic analysis under iron stress identified 27 iron metabolism-related genes, outlining a regulatory network. Functional studies on key genes revealed that MbCcc1, a vacuolar iron transporter, is crucial for iron storage and detoxification. Its deletion impaired growth, stress tolerance, and virulence. MbSfu1, a suppressor of iron uptake, negatively regulates iron absorption; its deletion increased metal sensitivity, reduced virulence, and upregulated iron uptake genes, and it also influenced copper homeostasis.In conclusion, M. bicuspidata maintains iron homeostasis via MbCcc1 and MbSfu1, providing a theoretical foundation for novel disease control strategies targeting these pathways.

Key words: *Metschnikowia bicuspidate*, Iron homeostasis, MbCcc1, MbSfu1

沙塘鳢肠道致病菌 G–2 全基因组测序及信息分析

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摘要：为探明造成养殖沙塘鳢肠道出血的病原菌 G-2 的特性，对 G-2 进行全基因组测序和分析。基因组组分分析和基因功能注释结果显示：G-2 的总基因数为 5 134 个，其中蛋白编码基因 4 977 个，非蛋白编码基因 157 个，非编码基因中 tRNA 基因 107 个，rRNA 基因 42 个，sRNA 基因 8 个；分别有 5 109、3 339、3 362、2 543 个基因在对应的 Nr、SwissProt、COG、KEGG 数据库中获得注释；毒力基因分析表明 G-2 含有多种肠毒素和溶血素基因、InhA 蛋白、磷脂酶及蛋白质毒素，解释了该菌造成养殖沙塘鳢肠道出血的原因。基于 G-2 菌株的 16S rRNA 序列信息构建系统进化树，确定其为苏云金芽孢杆菌。该研究结果为进一步了解苏云金芽孢杆菌的基因组基本功能以及沙塘鳢病害防控奠定了理论基础。

关键词：沙塘鳢；全基因组测序；苏云金芽孢杆菌

Whole genome sequencing and analysis of Bacillus thuringiensis G-2, a pathogenic bacterium in the intestinal tract of *Odontobutis potamophila*

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Abstract： Understanding the biological characteristics and pathogenic mechanism of G-2 through whole genome sequencing and analysis. Using third-generation PacBio RS II sequencing technology combined with second-generation Illumina HiSeq 2000 sequencing technology to analyze the gene function of this bacterium. The analysis of the genome sequencing results of G-2 shows that its total number of genes is 5134, including 4977 protein coding genes and 157 non coding RNA genes. Among the non coding genes, there are 107 tRNA genes, 42 rRNA genes, and 8 sRNA genes; 5 109, 3 339, 3 362, and 2 543 genes were annotated in the corresponding Nr, SwissProt, COG, and KEGG databases, respectively; Analysis of virulence genes revealed that it contains multiple enterotoxin and hemolysin genes, InA protein, phospholipase, and protein toxins. This study lays the foundation for further understanding of the basic function of the genome of Bacillus thuringiensis and the prevention and control of the disease.

Key words: Odontobutis potamophila; Bacillus thuringiensis; bacteria; genome

从饥饿瘦身到精准调控：草鱼脂肪代谢双通路技术探索

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摘要：池塘养殖草鱼常面临腹腔脂肪过度沉积和泥腥味重等产业难题，“降脂”是解决该问题的关键途径。当前行业普遍采用饥饿瘦身（俗称“吊水”）技术，可显著改善鱼体品质，但也会造成约 20%的体重损失，显著增加应激性病害风险。针对这一痛点，本研究从“预防脂肪沉积”和“促进脂肪降解”两个方向开展系统研究。一方面，机制解析发现，养殖草鱼的慢性肠炎可能是诱发腹腔脂肪沉积的重要原因。基于此，筛选并证实脱氧胆酸、黄连素、皇竹草粉等功能性饲料添加剂可有效抑制脂肪沉积。另一方面，从脂滴代谢角度揭示了花生四烯酸–COX–PGF₂ α 信号通路在促进脂滴水解与自噬中的作用，同时，发现肌酸富集可协同增强脂肪降解效率。本研究提出的“双机制调控”策略，有望在保障健康养殖的同时降低损耗率、缩短养殖周期，为草鱼产业提供具有显著应用价值的科学解决方案。

关键词：草鱼；瘦身；品质提升；脂肪代谢；健康养殖

From Starvation-Based Weight Loss to Precision Regulation: Dual-Pathway Technology Exploration for Grass Carp Lipid Metabolism

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Abstract: Pond-cultured grass carp (Ctenopharyngodon idella) often face industry challenges such as excessive abdominal fat deposition and strong muddy odor. "Fat reduction" is a key solution to these problems. Currently, the industry widely adopts starvation-based weight loss (commonly known as "water suspension") technology, which significantly improves fish quality but also results in approximately 20% body weight loss and substantially increases the risk of stress-induced diseases. To address this issue, this study systematically investigates two approaches: "preventing fat deposition" and "promoting fat degradation." Mechanistic Insights: Chronic enteritis in farmed grass carp was identified as a potential major cause of abdominal fat deposition. Based on this, functional feed additives—such as deoxycholic acid, berberine, and Pennisetum sinese Roxb powder—were screened and confirmed to effectively inhibit fat accumulation. Lipid Droplet Metabolism: The study revealed the role of the arachidonic acid–COX–PGF₂ α signaling pathway in promoting lipid droplet hydrolysis and autophagy.

Key words: Grass carp; Slimming; Quality improvement; Lipid metabolism; Healthy aquaculture

中间球海胆（Strongy locentrotus intermedius）对病原体感染的动态分子反应：来自一系列比较转录组分析的见解

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摘要：为探讨海胆对病原菌感染的动态分子反应，以一株海胆黑嘴病病致病菌株感染中间球海胆为研究对象。在感染后不同时间（hpi）采集标本，进行比较转录组分析。结果表明：1)与 0 hpi 相比，其他 hpi 分别鉴定出 771、1437、3477、8417、1566 和 2171 个差异表达基因（DEG）。2)感染后各时间点上表达上调的 DEG 数量均高于表达下调的 DEG 数量。3)Rho-GTPase 主要家族成员与 Caspase 家族成员一样，在感染过程中表现出普遍的上调表达趋势。4)细胞周期和凋亡途径是受影响最大的途径，其 DEG 富集水平在整个检测感染过程中均保持在前 30 和前 50。综上所述，本研究的所有发现将加深我们对海胆响应病原体感染的动态分子表达机制的理解。

关键词：中间球海胆、病原体感染、动态基因表达、比较转录组分析

Dynamic molecular responses of the sea urchin Strongylocentrotus intermedius to pathogen infection: Insights from a serial comparative transcriptome analysis

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Abstract：To explore the dynamic molecular responses to pathogen infection in sea urchins, the sea urchin Strongylocentrotus intermedius were infected by a causative pathogen strain of sea urchin black peristomial membrane disease. Specimens were collected at different hours post–infection (hpi), and comparative transcriptome analysis were performed. The results showed that 1) 771, 1437, 3477, 8417, 1566, and 2171 differentially expressed genes (DEGs) were identified at other hpi compared with the 0 hpi, respectively. 2) The number of upregulated DEGs was higher than that of downregulated DEGs at each time point. 3) Among identified DEGs, main Rho–GTPase family members exhibited a general upregulated expression trend during the examined infection process, the same as Caspase family members. 4) Cell cycle and apoptosis pathways are most affected, the DEG enrichment level of which remained in the top 30 and 50 throughout the infection process. To sum up, all findings will deepen understanding of the dynamic molecular expression mechanisms of sea urchins in response to pathogen infection.

Key words: Strongylocentrotus intermedius、 Pathogen infection、 Dynamic gene expression、 Comparative transcriptome analysis

秦皮乙素作为群体感应抑制剂对鳗弧菌毒力与生物膜的抑制作用

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摘要：鳗弧菌(*Vibrio angulilarum*)可引发水产动物出血性败血症、烂鳃病等疾病，其生物膜形成、运动性、鞭毛合成及毒力因子均受群体感应（QS）调控，抑制 QS 是潜在治疗途径。相比传统抗生素，植物源药物安全性高、残留低且不易产生耐药性。在评估的 33 种天然化合物中，秦皮乙素对鳗弧菌的最小抑菌浓度为 40mg/L。亚抑菌浓度下，它可抑制生物膜和胞外多糖，抑制率分别为 45.84%和 27.23%，使群集和游泳运动直径分别减小 6.67%和 25.76%，还能抑制胞外蛋白酶及溶血活性等毒力因子。RT-qPCR 显示，ompU、vanR、rpoN、vanT、vanO、flaB、hlyU 基因下调；对表达显著下调的 vanR、vanT 进行分子对接及动力学模拟，证实二者与秦皮乙素结合稳定，且 vanT 结合稳定性更强。综上，秦皮乙素是有效的 QS 抑制剂，有望成为防控鳗弧菌感染的新型候选药物，为水产弧菌病防治提供新途径。

关键词：鳗弧菌;秦皮乙素;生物膜;群体感应;水产养殖

The Inhibitory Effect of Esculetin as a Quorum Sensing Inhibitor on the Virulence and Biofilm of *Vibrio anguillarum*

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Abstract： Vibrio anguillarum causes aquatic diseases like hemorrhagic septicemia and gill rot. Its biofilm, motility, flagellar synthesis, and virulence factors are regulated by quorum sensing (QS), making QS inhibition a potential therapy. Vs traditional antibiotics, plant-derived drugs are safer, lower-residue, and less likely to induce resistance. Among 33 tested natural compounds, esculetin's minimum inhibitory concentration against Vibrio anguillarum is 40 mg/L. At sub-inhibitory concentrations, it inhibits biofilm (45.84%) and extracellular polysaccharides (27.23%), reduces swarming (6.67%) and swimming diameters (25.76%), and suppresses virulence factors like extracellular protease and hemolysis.RT-qPCR shows downregulation of ompU, vanR, rpoN, vanT, vanO, flaB, hlyU. Molecular docking/simulations on significantly downregulated vanR/vanT confirm stable binding with esculetin, vanT more stable. In conclusion, esculetin is an effective QS inhibitor, a promising candidate for controlling *Vibrio anguillarum* infections, and offers a new way to prevent/treat aquaculture vibriosis.

Key words: *Vibrio anguilarum*; esculetin; biofilm; quorum sensing; aquaculture

二尖梅奇酵母（*Metschnikowia bicuspidata*）在河蟹（*Eriocheir sinensis*）中的致病性研究

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摘要：二尖梅奇酵母引起的牛奶病对于河蟹产业危害巨大，明确其形态特征对于该病的防控具有重要意义。本研究发现了酵母相、假菌丝相和菌丝相的二尖梅奇酵母并建立了稳定的培养方法及酵母相与菌丝相之间的形态转换过程，同时对三者的致病性进行了比较。研究结果表明，在25℃添加了甘露醇和磷酸氢二钾的V8果汁培养基中可以诱导出假菌丝相二尖梅奇酵母，在37℃添加了乙酰葡糖胺和血清的YPD液体培养基中诱导出菌丝相二尖梅奇酵母，菌丝相在25℃继续培养时又可以转变为酵母相。在不同菌相的致病性比较中，酵母相的黏附力最强，菌丝相的毒力最强，对健康河蟹的致病性都明显高于酵母相和假菌丝相，菌丝组“牛奶病”患病进程加快，血淋巴白浊程度更重。耐药性方面，菌丝相比其他菌相对两性霉素B、氟康唑、伏立康唑、5-氟胞嘧啶药物更为敏感。本研究建立了不同菌相二尖梅奇酵母的培养方法明确了不同菌相的致病性，对于明确二尖梅奇酵母的生活史和防控具有重要意义。

关键词：二尖梅奇酵母、形态转换、致病性、河蟹、牛奶病

Research on Morphological Transformation and Pathogenicity of *Metschnikowia bicuspidata* in Chinese Mitten Crab

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Abstract：“Milky disease”caused by *Metschnikowia bicuspidata* poses a significant threat to the crayfish industry. Clearly understanding its morphological characteristics is crucial for disease prevention and control. In this study, the yeast phase, pseudohyphal, and hyphal of M. bicuspidata were found, and stable cultivation methods were established, as well as the morphological transitions between yeast and hyphal phases were investigated.The results showed that pseudohyphal phase M.bicuspidata. can be induced in V8 juice medium supplemented with mannitol and potassium dihydrogen phosphate at 25℃, while hyphal phase can be induced in YPD liquid medium supplemented with glucosamine and serum at 37℃. Hyphal phase can revert to yeast phase when continued to be cultured at 25℃ Among the different phases, yeast phase exhibited the strongest adhesion, while hyphal phase showed the highest toxicity. This study established cultivation methods for different phases of M.bicuspidata. and clarified their pathogenicity, providing guidance for further understanding the life history of *M.bicuspidata*.

Key words: *Metschnikowia bicuspidata*, morphological transformation, pathogenicity, Chinese mitten crab, milky disease

肽聚糖识别蛋白调控自噬通路增强菲律宾蛤仔抗鳗弧菌的免疫反应

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摘要：PGRP-SC2 作为肽聚糖识别蛋白家族的关键成员，可以特异性识别细菌细胞壁的肽聚糖组分，从而激活宿主的免疫防御反应。本研究发现，菲律宾蛤仔的肽聚糖识别蛋白（定义为 RpSC2）对鳗弧菌、溶藻弧菌、副溶血性弧菌、脾弧菌和创伤弧菌等弧菌具有显著的抗菌活性。结果表明，在弧菌和 LPS 刺激下，RpSC2 mRNA 显著上调。此外，注射重组 RpSC2 蛋白可显著提高蛤仔感染鳗弧菌后的存活率。病理分析显示，RpSC2 重组蛋白可显著增加血细胞数量，增强抗氧化能力（CAT 和 NOS），减少鳗弧菌数量，最终减轻肝胰腺损伤。转录组分析结果表明，在 RpSC2 可能通过溶菌酶通路、自噬通路、NF-κB 通路、泛素介导的蛋白水解和吞噬体通路参与抗鳗弧菌的免疫应答。双荧光素酶和 siRNA 实验结果进一步表明，RpSC2 通过激活自噬信号通路减轻炎症反应。本研究揭示了 RpSC2 在蛤仔中的免疫调节作用，为无脊椎动物免疫学研究提供了新视角。

关键词：菲律宾蛤仔，肽聚糖识别蛋白，免疫反应，鳗弧菌

A peptidoglycan recognition protein enhances immune defense against vibrio infection by regulating the autophagy signaling pathway in *Ruditapes philippinarum*

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Abstract: PGRP-SC2 can specifically recognize the peptidoglycan components of bacterial cell walls, thereby activating the host's immune defense response. This study found that a PGRP-SC2 (defined as RpSC2) from *R. philippinarum* exhibited significant antibacterial activity against Vibrio. The results indicated that the RpSC2 mRNA was significantly upregulated following stimulation with Vibrio and LPS. Additionally, the RpSC2 protein can significantly enhance the survival rate of R. philippinarum following infection with *V. anguillarum*. Pathological analysis revealed that the RpSC2 recombinant protein significantly increased hemocytes, enhanced antioxidant capacity, and decreased the number of *V. anguillarum*, ultimately alleviating hepatopancreas damage. Transcriptome results indicated that RpSC2 might be involved in the immune response against Vibrio through the autophagy pathway. The results of dual-luciferase and siRNA suggest that RpSC2 alleviates the inflammatory response by activating the autophagy pathway. This study reveals the novel immunomodulatory role of RpSC2 in R. philippinarum.

Key words: *Ruditapes philippinarum*, RpSC2, Vibrio, Immune response

mTORC1/C2 信号通路对大菱鲆脂肪合成的影响

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摘要：大菱鲆（*Scophthalmus maximus*）是重要的养殖鱼类，但因饲喂不当，易诱发营养性脂肪肝。mTOR（MammalianTarget of Rapamycin）信号通路是细胞生长代谢的中心协调器。本研究设置正常饲料（脂肪含量 11.69%）组，高脂饲料（脂肪含量 16.58%）组及复方中草药（LS）添加组，分别投喂 14 天，病理切片观察肝脏变化，检测甘油三酯（TG）含量、mTOR 信号通路及脂质合成相关基因的表达变化。结果表明，投喂 14 天高脂饲料后，肝脏有显著脂肪变性，甘油三酯含量、脂质合成相关基因 SREBP1 和 PPARγ、mTORC1 和 mTORC2 的下游效应器 4EBP1 和 AKT 的表达均显著升高。在添加了 LS 后，与高脂组比较，肝脏脂肪变性显著减少，且以上指标均显著下调。本研究为后续探究 mTOR 信号通路对鱼类脂肪合成调控的机制研究提供了理论基础，也为鱼类营养性疾病的防治提供了新思路。

关键词：大菱鲆，营养型脂肪肝，mTOR 信号通路，复方中草药，甘油三酯

The Effects of mTORC1/C2 Signaling Pathway on Fat Synthesis in *Scophthalmus maximus*

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Abstract：*Scophthalmus maximus* is an important aquaculture species, yet improper feeding can lead to nutritional fatty liver disease. The mTOR signaling pathway is vital for cell growth and metabolism. In this study, three feeds were used: normal feed (11.69% fat), high - fat feed (16.58% fat), and feed with compound Chinese herbal medicine (LS). Fish were fed for 14 days, and liver changes were evaluated by pathological sections. Triglyceride content, mTOR signaling pathway activity, and lipid synthesis - related gene expression were measured. After 14 days of high - fat feeding, significant liver fatty degeneration occurred, with increased triglyceride levels and elevated expression of lipid synthesis - related genes and mTORC1 and mTORC2 downstream effectors. Nevertheless, compared to the high - fat group, adding LS reduced liver fatty degeneration and downregulated the above indicators. This study provides a theoretical basis for understanding mTOR signaling pathway regulation of lipid synthesis in fish and new insights into preventing and treating nutritional diseases in aquaculture.

Key words: *Scophthalmus maximus*, nutritional fatty liver, mTOR signaling pathway, compound Chinese herbal medicine, triglycerides

温度对罗氏沼虾感染虹彩病毒的影响及转录组学分析

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摘要：研究设置 5 组不同温度(26、28、30、32、34℃)对罗氏沼虾人工感染 DIV1，并统计其存活率，结果显示温度 34℃能够抑制罗氏沼虾体内的病毒复制，减少死亡并延长其存活时间。对感染 DIV1 24h 和 72h 的罗氏沼虾肝胰腺、鳃及肌肉进行病毒载量测定，结果表明感染 DIV1 的罗氏沼虾在 72h 内病毒迅速增殖，但当水温升高至 30℃及更高温度时其体内的病毒载量明显降低。此外，采集罗氏沼虾不同温度下感染 DIV1 的肝胰腺进行转录组学分析，结果表明共有 8483 个不同差异表达基因，对罗氏沼虾感染 DIV1 后的免疫基因 CAT、Cu/ZnSOD、CTL、ACP 的表达水平进行测定，结果发现当温度为 32℃时这些免疫基因的表达量显著高于其他温度，表明高温能够促进罗氏沼虾的免疫基因表达量增加以抵御病毒入侵。

关键词：温度；十足目虹彩病毒 1；转录组学分析；调控机制；罗氏沼虾

TEMPERATURE ON DIV1 INFECTION IN MACROBRACHIUM ROSENBERGII AND TRANSCRIPTOMIC ANALYSIS

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Abstract: In this study, we set up five experimental groups at different temperatures (26, 28, 30, 32, and 34℃) for artificial DIV1 infection, and calculated its survival rate. The results showed that the temperature of 34℃ significantly inhibited virus replication in M. rosenbergii, decreased mortality, and extended survival duration. The viral load in the hepatopancreas, gill, and muscle of M. rosenbergii infected with DIV1 was determined at 24h and 72h. The results found that the virus rapidly proliferated within 72 hours, however, a notable reduction in the viral load decreased significantly when the water temperature increased to 30℃ or above. In addition, transcriptomic analysis was conducted on hepatopancreas of M. rosenbergii infected with DIV1 at different temperatures, and a total of 8483 differentially expressed genes were identified. Furthermore, the expression levels of immune genes CAT, Cu/ZnSOD, CTL, and ACP in M. rosenbergii infected with DIV1, revealing significantly higher expression at temperature of 32℃ compared to other temperatures.

Key words: Temperature; Decapod iridescent virus 1; Transcriptomic analysis; Regulating mechanism; *Macrobrachium rosenbergii*

两株细菌的鉴定及其作为养殖中间球海胆黑嘴病潜在致病菌的研究

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摘要：黑嘴病是养殖中间球海胆的主要细菌性疾病，常在春冬季暴发。2024 年 1 月，从黄海患病海胆的口膜和肠道中分离得两株与黑嘴病相关的细菌 SIBMPM04 和 SIBMIT01。经革兰氏染色、形态观察、感染及代谢分析，结果表明两者均属弧菌属。16S rRNA 分析显示，SIBMPM04 与深海弧菌相似性为 98.68%，SIBMIT01 与异型弧菌相似性为 98.93%。药敏结果显示，两株菌对氯霉素、氟苯尼考、亚胺培南、卡那霉素、左氧氟沙星和多黏菌素 B 敏感。感染试验证实，两株菌单独感染均可致典型黑嘴病症状，且呈剂量依赖性；联合感染时出现协同致病效应。本研究为海胆黑嘴病病原研究与防控提供参考。

关键词：中间球海胆 黑嘴病 致病菌 菌鉴定 协同治病效应

Identification of two novel bacterial strains as the putative cause of black mouth disease in farmed *Strongylocentrotus intermedius*

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Abstract： Black mouth disease (BMD) is a major bacterial disease of the cultured sea urchin Strongylocentrotus intermedius, usually occurring in spring and winter. In January 2024, two dominant bacterial strains,SIBMPM04 and SIBMIT01, were isolated from the peristomial membrane and intestine of diseased sea urchins from a farming area in the Yellow Sea, China. Gram staining, morphological observation, artificial infection, and metabolic characterization were performed on both strains. Results showed that SIBMPM04 and SIBMIT01 belonged to the genus Vibrio. 16S rRNA gene and phylogenetic analyses revealed 98.68% similarity between SIBMPM04 and Vibrio bathopelagicus, and 98.93% similarity between SIBMIT01 and Vibrio atypicus. Antibiotic susceptibility tests indicated both strains were sensitive to chloramphenicol, florfenicol, imipenem, kanamycin, levofloxacin, and polymyxin B. SIBMPM04 was sensitive to gentamicin and amikacin, while SIBMIT01 was sensitive to norfloxacin and sulfamethoxazole.

Key words: Strongylocentrotus intermedius Black mouth disease Pathogenic bacterial strains Identification Synergistic pathopoiesis effect

海水鱼盾纤毛虫疫苗研制

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摘要：盾纤毛虫对海水鱼工厂化养殖带来严重危害。目前。该病防治主要采用药物治疗方式，然而药物的频繁使用会导致严重耐药反应，对生态环境、鱼体以及人类自身也会造成重大影响。鱼类疫苗的研究与应用有助于保护生态和食品安全，具有广阔的应用前景和经济价值。本研究开展了盾纤毛虫疫苗研究工作，针对大连地区海水鱼类盾纤毛虫病流行病原水滴伪康纤虫，基于鱼粉改良培养基，建立了盾纤毛虫的纯化培养方法，构建了水滴伪康纤虫的冷冻复苏方法，虫株冷冻保藏 12 周仍具有较强活力；分析比较了连续传代水滴伪康纤虫的毒力变化，筛选到 163 个与盾纤毛虫毒力变化相关蛋白，建立了盾纤毛虫毒力复壮方法；制备的水滴伪康纤虫全虫疫苗免疫大菱鲆 28 天后，经过体表擦伤攻毒感染，大菱鲆在 24 小时和 48 小时的相对减虫率分别达到 85.8%、71.5%，表明该全虫疫苗可有效减少盾纤毛虫在鱼体伤口感染。本研究工作为海水鱼寄生虫疫苗研制提供了参考。

关键词：海水鱼、盾纤毛虫、寄生虫、疫苗、水滴伪康纤虫

Development of a Marine Fish Vaccine for Scuticociliate

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Abstract： Scuticociliate pose a serious threat to industrialized marine fish farming. This study investigated scuticociliate vaccines. Targeting Pseudocohnilembus persalinus the epidemiological agent of scuticociliatosis in marine fishes in the Dalian region, a purification and culture method for scuticociliate was established using a fish meal-based modified culture medium. A freeze-thaw method for scuticociliate was also developed, resulting in strains maintaining robust viability after 12 weeks of cryopreservation. The virulence of serially passaged scuticociliate was analyzed and compared, resulting in the identification of 163 proteins associated with scuticociliate virulence, and a method for scuticociliate virulence restoration was established. Twenty-eight days after immunization with the vaccine, the relative parasite reduction rates reached 85.8% and 71.5% at 24 and 48 hours, respectively, demonstrating that the whole-worm vaccine effectively reduces scuticociliate infection in fish wounds. This work provides a reference for the development of vaccines for marine fish parasites.

Key words: Marine fish, scuticociliate, parasites, vaccines, Pseudocohnilembus persalinus

抑制剂组合物对柴油胁迫刺参化皮的抑制效果及转录表达分析

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摘要：随着海上溢油事故频发，柴油污染已成为威胁刺参健康的重要环境因素之一。本研究采用课题组自主研制的抑制剂组合物，评估其在柴油胁迫下对刺参化皮现象的抑制作用。通过化皮面积测定、自溶相关酶及抗氧化酶活性分析，结合转录组学研究，从表型、生理及分子水平系统揭示抑制剂的抑制效果与作用机制。结果显示，抑制剂组合物能显著降低刺参在柴油胁迫下的化皮面积，显著降低自溶酶、组织蛋白酶活性，提高抗氧化酶活性，有效减缓组织自溶和氧化损伤过程，体现出显著的抑制效果。转录组分析进一步揭示其分子作用机制，抑制剂组合物显著激活 Notch 信号、糖胺聚糖生物合成及 ECM 重塑等通路，Fibropellin 家族及胶原蛋白等基因上调，促进组织修复与结构维持；同时，上调 UGTs、CYP1A1 及 GST 类抗氧化酶等基因，富集于外源物代谢和氧化应激防御通路，表明抑制剂组合物增强了刺参的解毒与抗氧化能力；此外，脂肪消化与吸收及烟酰胺代谢等能量代谢途径活跃，也为组织修复与防御提供了能量支持，这充分证明该抑制剂组合物在缓解柴油污染损伤方面的有效性。这些发现为水产养殖环境中制定石油污染防护策略提供了理论依据，是一个非常具有实际意义的课题。

关键词：柴油污染；刺参化皮；抑制剂组合物

Inhibitory Effect of an Inhibitor Combination on Diesel-Induced Skin Ulceration in *Apostichopus japonicus* and Transcript Expression Analysis

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Abstract：With the increasing frequency of offshore oil spill accidents, diesel pollution has become one of the significant environmental threats to the health of *Apostichopus japonicus*. This study evaluated the protective effects of an inhibitor combination developed by our research team on *A. japonicus* under diesel stress.The results showed that the inhibitor significantly reduced the ulceration area of *A. japonicus*, decreased autolytic enzyme activity, and increased antioxidant enzyme activity. Transcriptomic analysis revealed activation of pathways such as Notch signaling, glycosaminoglycan biosynthesis, and ECM remodeling. Upregulation of detoxification and antioxidant genes (UGTs, CYP1A1, GSTs) enhanced detoxification and oxidative stress defense. Additionally, activated energy metabolism pathways supported tissue repair and defense, demonstrating the inhibitor's effectiveness in mitigating diesel-induced damage.These findings provide a theoretical basis for developing oil pollution prevention strategies in aquaculture environments, making it a highly practical and meaningful topic.

Key words: Diesel pollution; Skin ulceration in *Apostichopus japonicus*; Inhibitor combination

基于 MNPs 磁分离—信号输出双重功能的可视化生物传感方法用于检测恩诺沙星

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摘要：分别在 MNP130 和 MNP20 表面修饰抗体和 ENR 抗原，制备 IMNP130 和 MNP20-ENR。样品中的 ENR 被 IMNP130 捕获并占据其表面部分结合位点。然后，加入一定数量的 MNP20-ENR 类似物，竞争性结合 IMNP130 表面剩余的位点，形成“MNP20-ENR-IMNP130”复合物。由于 MNPs 的磁分离速度随其体积的增大而加快，IMNP130 表面结合的 MNP20-ENR 越多，其分离速度越快。在没有 ENR 的情况下，会形成大量的“MNP20-ENR-IMNP130”复合物，导致磁分离后的上清液中只有少量 MNPs 残留，颜色较浅。最后，通过肉眼观察上清液的颜色变化进行定性检测，并通过酶标仪测量 405 nm 处的吸光度值（OD405）或智能手机处理颜色信号实现定量检测。本方法兼具灵敏性、选择性并将检出限降低至 0.18 ng mL-1,检测时间缩短至 25 分钟以内。

关键词：磁性纳米颗粒；恩诺沙星；可视化检测；无需洗涤；智能手机

A washing-less biosensor based on the dual functions of magnetic separation and signal output of magnetic nanoparticles for the rapid and visual detection of enrofloxacin

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Abstract： Herein, a simple and washing-less biosensor that took full advantage of magnetic nanoparticles (MNs), i.e., magnetic separation and signal output, was developed for the rapid and sensitive detection of enrofloxacin (ENR) residues. The surface of MNs with diameters of approximately 20 nm (MN20) and 130 nm (MN130) were modified with ENR and antibodies to prepare MN20-ENR and immunomagnetic nanoparticles (IMN130), respectively. In the absence of ENR, the MN20-ENR analogues were captured on the surface of IMN130, forming “MN20-ENR-IMN130” complexes, which were larger in volume and could be quickly separated in a magnetic field. While in the presence of ENR, the target ENR competed for the binding sites on IMN130 surface, inhibiting the formation of the “MN20-ENR-IMN130” structures. Therefore, the separation speed significantly slowed down. Qualitative or semi- quantitative determination of ENR residues could be achieved via visual observation of the color changes, while quantitative detection was also achieved with the aid of a microplate reader or merely a smartphone.

Key words: Magnetic nanoparticles; Enrofloxacin; Visual detection; Washing-less; Smartphone

芽孢杆菌 D7-HSJ9 发酵软颗粒饲料对罗非鱼的益生菌效应

谢宗省；贾纪鑫；李晓婷；覃玉月；甫佳；李皓琛；彭春艳；刘莹；龚斌#
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摘要：本研究针对海豚链球菌（*Streptococcusiniae*）引发的链球菌病对全球水产养殖业的破坏问题，评估了芽孢杆菌 *Bacillus inaquosorum* D7-HSJ9 发酵软颗粒饲料（FSPF）对尼罗罗非鱼（*Oreochromisniloticus*）抗海豚链球菌能力、生长性能及生理指标的影响。首先通过形态学与基因组学鉴定菌株 D7HSJ9，验证其非溶血、抗生素敏感的安全性，以及产淀粉酶、蛋白酶、纤维素酶的能力和环境适应性；随后设置 3 个 FSPF 试验组（RKL 组：D7-HSJ9 单菌发酵，BL 组：D7-HSJ9 +鼠李糖乳杆菌，BLS 组：D7-HSJ9 +鼠李糖乳杆菌+酿酒酵母）与 1 个未发酵饲料对照组，开展 8 周投喂试验并进行海豚链球菌攻毒实验。结果显示，RKL 组对海豚链球菌的保护率最高（42.86%），且生长性能最优，具体表现为增重率（WGR）、特定生长率（SGR）显著升高，饲料系数（FCR）显著降低；同时该组罗非鱼肠道绒毛宽度增加、消化酶活性提升，肝脏脂肪变性程度减轻，肠道菌群结构优化（病原菌丰度下降、益生菌比例上升）。转录组分析进一步表明，RKL 组免疫相关基因（E3-TRIM39、NLRC3、CTL10、Mx、Ho1）显著上调，免疫抑制基因（LTA4、Plc2、angptl3、VTCN-1、PD1）显著下调。综上，D7-HSJ9 单菌发酵软颗粒饲料可有效增强尼罗罗非鱼的抗病能力与健康水平，为水产养殖绿色病害防控提供了新的饲料方案。

关键词：尼罗罗非鱼；芽孢杆菌属；发酵饲料；转录组学；肠道微生物；代谢组

Probiotic Effects of *Bacillus inaquosorum* D7-HSJ9 Fermented Soft Pellet Feed on Tilapia

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Abstract: The streptococcosis caused by *Streptococcus iniae* kills a variety of economically valuable freshwater and marine fish species and has devastated the global aquaculture industry. This study evaluated the probiotic effects of *Bacillus inaquosorum* D7-HSJ9-fermented soft pellet feed (FSPF) on Nile tilapia (*Oreochromis niloticus*), focusing on resistance to *S. iniae*, growth, and physiology. Strain D7-HSJ9 was identified via morphology and genomics, with confirmed safety (non-hemolytic, antibiotic sensitivity), enzyme production (amylase, protease, cellulase), and environmental adaptability. Three FSPF groups (RKL: D7-HSJ9; BL: D7-HSJ9+*Lactobacillus rhamnosus*; BLS: D7-HSJ9+*L. rhamnosus*+*Saccharomyces cerevisiae*) and a control (unfermented feed) were tested in an 8-week feeding trial, followed by *S. iniae* challenge. RKL showed the highest *S. iniae* protection rate (42.86%), optimal growth (higher WGR, SGR; lower FCR), improved intestinal villus width and digestive enzyme activity, reduced hepatic steatosis, and modulated gut microbiota (decreased pathogen, increased probiotics). FSPF with *Bacillus* D7-HSJ9 modify the complete pelleted feed’s composition, affecting microbial communities and reshaping intestinal microbiota. Transcriptomic analyses revealed upregulated immune genes (*E3-TRIM39*, *NLRC3*, *CTL10*, *Mx*, and *Ho1*) and downregulated immunosuppressive genes (*LTA4*, *Plc2*, *angptl3*, *VTCN-1*, and *PD1*) in RKL. In conclusion, D7-HSJ9-singly fermented FSPF enhances tilapia disease resistance and health, offering a green alternative for aquaculture.

Key word: *Bacillus*; fermentation; gut microbiota; transcriptomic analysis; intestinal metabolome

二尖梅奇酵母高铁还原酶基因的鉴定和功能研究

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摘要：二尖梅奇酵母菌是“牛奶病”的主要病原，高铁还原酶是真菌获取铁的主要途径之一，即还原性铁吸收途径。这类酶主要分布于细胞质膜上，其主要功能是催化不易吸收 $Fe3^+$转变为可以吸收的 $Fe2^+$。本研究在二尖梅奇酵母菌中成功筛选出高铁还原酶家族的基因共 9 个。为进一步了解其响应机制，本研究将结合基因编辑等技术进行研究。对缺失菌株表型分析，发现缺失菌株均能影响二尖梅奇酵母菌的生长性能，对低铁（0 mM）、高铁（2 mM）、低铜（0 mM）和氧化应激（2 mM H2O2）胁迫的敏感性增强。对缺失菌株酶活测定，发现高铁还原酶基因的缺失均能降低其活性。缺铁条件下，缺失和野生菌株均出现了增长趋势和峰值，但缺失菌株显著低于野生菌株。有铁条件下，均未出现增长趋势和峰值。本研究系统阐述了二尖梅奇酵母高铁还原酶家族，初步揭示了二尖梅奇酵母高铁还原酶在不同条件下的响应机制。研究结果为明确水生致病菌对铁的响应机制提供了见解。

关键词：二尖梅奇酵母菌；牛奶病；高铁还原酶；功能研究

Identification and Functional Study of High-Iron Reductase Genes in *Metschnikowia bicuspidata*

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Abstract：*Metschnikowia bicuspidata* is the primary pathogen of "milk disease". High-iron reductase, a key component of fungal reductive iron uptake pathway, is mainly distributed on the cytoplasmic membrane and catalyzes the conversion of poorly absorbable Fe^{3+} to absorbable Fe^{2+}. In this study, 9 high-iron reductase family genes were identified in M. bicuspidata. Using gene editing techniques, phenotypic analysis of deletion strains showed impaired growth performance and increased sensitivity to low iron (0 mM), high iron (2 mM), low copper (0 mM) and oxidative stress (2 mM H_2O_2). Enzyme activity assays revealed reduced activity in deletion strains. Under iron deficiency, both deletion and wild-type strains showed growth trends and peaks, with deletion strains significantly lower than wild-type. No such trends or peaks were observed under iron sufficiency. This study systematically characterized the high-iron reductase family in M. bicuspidata and preliminarily revealed their response mechanisms under different conditions, providing insights into iron response mechanisms of aquatic pathogens.

Key words: *Metschnikowia bicuspidata*; Milk disease; High-Iron reductase; Functional study

基于 CRISPR–DNase I 双重信号放大的水产品中抗生素残留快速检测方法研究

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摘要：水产品中的抗生素残留问题日益严峻。本研究建立了一种 DNase I 辅助的 CRISPR/Cas12a（CRISPR-DNase I）生物传感器用于检测恩诺沙星（ENR）残留。该方法利用 DNase I 和牛血清白蛋白—恩诺沙星标记的金纳米颗粒（AuNPs-DNase I-ENR）与目标物 ENR 竞争性结合免疫磁性纳米颗粒表面的抗体结合位点，并通过 AuNPs-DNase I-ENR 探针降解激活 DNA，将 ENR 识别事件转化为 CRISPR/Cas12a 系统的切割活性，最终通过测量 CRISPR/Cas12a 介导的反式切割所释放的荧光信号实现对 ENR 残留的视觉定性和荧光仪定量检测。该方法充分利用了 AuNPs、DNase I 和 CRISPR/Cas12a 的信号放大能力，极大地提升了对 ENR 的检测灵敏度，检出限降低至 0.04 ng/mL 且具有良好的检测特异性。

关键词：CRISPR；DNase I；抗生素残留；生物传感器；快速检测

Research on rapid detection method for antibiotic residues in aquatic products based on dual signal amplification from CRISPR-DNase I

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Abstract: Antibiotic residues in aquatic products have become one of the important hazardous factors. In this research, a DNase I-assisted CRISPR/Cas12a biosensor was developed for the detection of enrofloxacin (ENR) residues. In this biosensor, target ENR competed with deoxyribonuclease I (DNase I)- and bovine serum albumin-ENR composite-modified gold nanoparticles (AuNPs-DNase I-ENR) for the binding sites on the surface of antibody-modified magnetic nanoparticles. Then, the captured AuNPs-DNase I-ENR degraded the activator DNA in the solution, which inhibited the activation of the CRISPR/Cas12a system. Finally, the fluorescence released by the activated CRISPR/Cas12a system was measured for the quantitative detection of ENR. The dual enzymatic amplification from DNase I and the CRISPR/Cas12a system guaranteed the sensitivity of this method with a low detection limit of 0.04 ng/mL.

Key words: CRISPR; DNase I; antibiotic residues; biosensor; rapid detection

泥蚶 AOX 基因对环境胁迫的响应模式及其功能分析

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摘要：泥蚶（*Tegillarca granosa*）是我国传统养殖贝类之一，通过 RACE 克隆泥蚶 AOX 全长序列，模拟温度、盐度、干露硫化物、重金属镉常见环境胁迫，进一步研究温度及抑制剂 SHAM 联合作用下的功能。结果显示，泥蚶 AOX 基因全长 2504bp，开放阅读框为 1047bp。RT-qpcr 显示 AOX 在泥蚶各组织中均表达，在不同胁迫条件下 AOX 表达量呈现显著的时间及强度依赖性变化：在温度胁迫下被显著诱导，在盐度胁迫中呈短期诱导与长期抑制，在干露及硫化物胁迫下呈时间依赖性上调，而在镉胁迫下被显著抑制。温度及抑制剂联合作用下线粒体钙稳态紊乱与膜电位升高，线粒体活性氧和氧化损伤标志物 4-HNE 的显著积累，ATP/ADP 比率显著降低，并在高温 7 天+SHAM 处理中全部死亡，证明 AOX 是维持机体在高温下存活的关键。综上，泥蚶 AOX 基因具有保守的 AOX 结构特征，对多种环境胁迫存在特异性响应，并通过调控线粒体功能、维持细胞能量稳态及减轻氧化损伤，在泥蚶应对环境胁迫（尤其是温度胁迫）中发挥关键保护作用，本研究为阐明贝类抗逆分子机制提供理论依据。

关键词：泥蚶；AOX；环境胁迫

The response patterns and functional analysis of the AOX gene in mud clamss to environmental stress

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Abstract： The mud clams (*Tegillarca granosa*) is one of the traditional farmed shellfish species in China. By cloning the full-length sequence of mud clams AOX using RACE technology, and simulating common environmental stresses such as temperature, salinity, desulfurization substances, and heavy metal cadmium, further studies were conducted on the functions under the combined action of temperature and inhibitor SHAM. The results showed that the full-length of the mud clams AOX gene was 2504 bp, with an open reading frame of 1047 bp. RT-qpcr revealed that AOX was expressed in all tissues of the mud clams. Under different stress conditions, the expression level of AOX showed significant temporal and intensity-dependent changes: it was significantly induced under temperature stress, showed short-term induction and long-term inhibition under salinity stress, showed time-dependent upregulation under desulfurization and sulfide stress, and was significantly inhibited under cadmium stress. Under the combined action of temperature and inhibitor, mitochondrial calcium homeostasis disorder and membrane potential increase occurred, and the significant accumulation of mitochondrial reactive oxygen species and oxidative damage marker 4-HNE was observed. The ATP/ADP ratio was significantly reduced, and all died after 7 days of high temperature + SHAM treatment, proving that AOX is the key to maintaining the survival of the organism under high temperature. In summary, the mud clams AOX gene has conserved AOX structural characteristics, has specific responses to various environmental stresses, and regulates mitochondrial function, maintains cellular energy homeostasis, and alleviates oxidative damage, playing a key protective role in mud clams's response to environmental stress (especially temperature stress). This study provides a theoretical basis for clarifying the molecular mechanism of shellfish stress resistance.

Key words: Tegillarca granosa；AOX；environmental stress

鳜 irak1 基因在抗嗜水气单胞菌中的表达分析及 SNP 开发

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摘要：白介素-1 受体相关激酶 1（irak1）是鱼类先天免疫的重要调控基因。本研究对鳜鱼（*Siniperca chuatsi*）的 irak1 进行了生物信息学与表达分析。感染嗜水气单胞菌（*Aeromonas hydrophila*）后，irak1 在肝脏和头肾中显著上调（$P < 0.05$）。双重原位杂交显示，irak1 mRNA 与 A. hydrophila DNA 在肝脏中高度共定位。该基因全长 2,264 bp，含有 Death 结构域和 PKC 结构域。共鉴定 4 个 SNP 位点，其χ^2值分别为 2.305（$P = 0.316$）、7.829（$P = 0.02$）、1.314（$P = 0.518$）和 11.369（$P = 0.003$），其中 SNP2 不符合哈代-温伯格平衡。结果表明，irak1 参与鳜鱼抗嗜水气单胞菌免疫调控，其中 SNP4 与抗病性显著相关，可作为鳜鱼抗病育种的潜在分子标记。

关键词：鳜 ；irak1; 嗜水气单胞菌; SNP

Expression analysis of the irak1 gene in Siniperca chuatsi against Aeromonas hydrophila and SNP development

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Abstract: The interleukin-1 receptor-associated kinase 1 (irak1) gene is a key regulator of fish innate immunity. In this study, bioinformatics and expression analyses of irak1 from Siniperca chuatsi were performed. After Aeromonas hydrophila infection, irak1 was significantly upregulated in the liver and head kidney ($P < 0.05$). Double-label in situ hybridization showed strong co-localization of irak1 mRNA and A. hydrophila DNA in the liver. The full-length irak1 (2,264 bp) contained a Death and a PKC domain. Four SNPs were identified; χ^2 values for SNP1–SNP4 were 2.305 ($P = 0.316$), 7.829 ($P = 0.02$), 1.314 ($P = 0.518$), and 11.369 ($P = 0.003$), respectively, with SNP2 deviating from Hardy–Weinberg equilibrium. Overall, irak1 plays a regulatory role in resistance to A. hydrophila, and SNP4 shows a significant association with disease resistance, suggesting its potential as a molecular marker for selective breeding in S. chuatsi.

Key words: Mandarin fish; irak1; Aeromonas hydrophila; SNP

生物素补充对刺参免疫反应、抗氧化能力及抗灿烂弧菌感染的影响

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摘要：刺参（Apostichopus japonicus）是重要的经济性海洋物种，近年受灿烂弧菌（Vibrio splendidus）引发腐皮综合征威胁。生物素（维生素 B7）参与脂肪酸合成、糖异生等代谢，在哺乳动物、鱼类和甲壳类中能改善免疫功能，但在棘皮动物中的作用尚不明确。本研究评估不同浓度（1.0%、1.5%、2.0%）生物素对刺参免疫、抗氧化能力及抗 V. splendidus 感染的影响。短期（21 天）补充中，1.5%组存活率增加 1.6 倍，ACP 和 AKP 活性分别增加 3.6 倍和 2.4 倍，LZM 活性增加 1.2 倍；长期（56 天）补充中，1.5%组存活率增加 1.7 倍，吞噬细胞活性和呼吸爆发力分别为 1.9 倍和 1.8 倍，基因表达（sod、ferritin、hsp70）分别为 2.1 倍、2.0 倍和 1.6 倍。综上，1.5%浓度显著提高了刺参存活率，免疫和抗氧化能力，为防控腐皮综合征及养殖防控策略提供理论依据。

关键词：刺参；灿烂弧菌；生物素；免疫；抗氧化；腐皮综合征

Biotin supplementation enhances immune and antioxidant responses and disease resistance in *Apostichopus japonicus* exposed to *Vibrio splendidus*

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Abstract：*Apostichopus japonicus*, an important marine species, suffers mass mortality from Skin Ulceration Syndrome caused by Vibrio splendidus. Biotin (vitamin B7), a cofactor in carboxylase-dependent pathways, boosts growth, immunity, and antioxidant functions in many animals, but its role in echinoderms is unclear. This study assessed the effects of 1.0%, 1.5%, and 2.0% biotin supplementation on immune and antioxidant responses and resistance to V. splendidus in A. japonicus over 21 and 56 days. Results showed that the 1.5% biotin group had the highest survival rate—1.6 times higher than the control in the short term, with ACP and AKP activities increasing by 3.6 and 2.4 times, and LZM by 1.2 times. Long-term survival ncreased by 1.7 times, with phagocytosis and respiratory burst activity increasing by 1.9 and 1.8 times. sod, ferritin, and hsp70 gene expression increased by 2.1, 2.0, and 1.6 times, respectively. Biotin supplementation, especially at 1.5%, significantly enhanced survival and immunity, offering a potential strategy for managing skin necrosis syndrome in aquaculture.

Key words: *Apostichopus japonicus; Vibrio splendidus;* Biotin; Immunity; Antioxidant; Skin Ulceration Syndrome

基于转录组分析揭示了 CD36 在大菱鲆抗杀鲑气单胞菌感染中的作用

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摘要：大菱鲆（Scophthalmus maximus）是重要的养殖鱼类，病害问题日益加剧。杀鲑气单胞菌（Aeromonas salmonicha）是大菱鲆疖疮病的病原菌之一，为阐明其感染的机制，本研究对杀鲑气单胞菌感染 24 小时后的大菱鲆肝组织进行转录组分析。结果鉴定出 2363 个差异基因，其中上调 1048 个，下调 1315 个。GO 功能分析表明，大多数差异基因被显著富集到生物过程，如细胞大分子生物合成过程、细胞生物合成过程等。KEGG 分析表明，差异基因多富集到免疫和代谢相关通路，如 NOD 样受体信号通路、胰岛素信号通路等。qRT-PCR 验证了测序结果的可靠性。其中，CD36 作为脂蛋白转运受体在感染后 2 小时表达量显著减低，6 小时后又显著升高，并且在肝脏和脾脏中有较高的表达水平，这预示这其是一个免疫与代谢互相调节的关键因子。这为我们后续去探究大菱鲆在应对感染时，免疫-代谢相关性及协同性提供理论依据。

关键词：大菱鲆；杀鲑气单胞菌；肝组织；转录组分析；CD36

Transcriptome Analysis Reveals a Role for CD36 in Scophthalmus maximus against Aeromonas salmonicida

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Abstract： Scophthalmus maximus is a significant cultured fish facing increasingly severe disease challenges, with Aeromonas salmonicha causing furuncles in turbot. A transcriptome analysis of liver tissue from turbot infected with A.salmonicida 24 hours post-infection identified 2,363 DEGs(1048 up-regulated and 1315 down-regulated). GO functional analysis indicated that the DEGs were significantly enriched in biological processes such as the cellular macromolecular metabolism and cellular biosynthesis. KEGG analysis revealed enrichment in immune and metabolic pathways such as the NOD-like receptor and insulin signaling pathways. The qRT-PCR validation corroborated the sequencing results. Notably, the expression of CD36, a key lipoprotein transporter, decreased significantly at 2 hours post-infection and then increased substantially at 6 hours, with elevated levels observed in the liver and spleen. These results underscore the critical role of CD36 in the immune-metabolic interplay and lay the groundwork for investigating the immune-metabolic response to infections in turbot.

Key words: Scophthalmus maximus; Aeromonas salmonidum; Liver tissue; transcriptome analysis; CD36

斜带石斑鱼清道夫受体基因的全基因组鉴定、特征分析及表达分析

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摘要：清道夫受体（Scavenger receptors）是硬骨鱼中介导先天免疫防御的模式识别受体，但其多样性及其在石斑鱼中的功能作用尚未得到充分的研究。通过斜带石斑鱼全基因组挖掘，共鉴定出 13 个 SR 基因，并将其分为 5 个亚类（A、B、F、H、L）。外显子-内含子组织、基序组成、保守结构域和选择压力分析的结果，显示出其高度的类内保守性。在哈维弧菌感染和低盐度胁迫后的表达分析显示，包括 EcSCARA5、EcSCARB1 和 EcSCARF2 在内的 SR 基因以时间和组织特异性的方式显著调节。富集分析表明其与膜相关运输、脂质代谢和免疫途径有关，支持其在应激适应中的潜在作用。这些发现增强了我们对 SR 功能的认识，并为改善水产养殖中鱼类健康的免疫相关策略提供了基础。

关键词：清道夫受体、斜带石斑鱼、哈维弧菌、低盐胁迫

Genome-wide identification, characterization, and expression analysis of scavenger receptor genes in orange-spotted grouper (*Epinephelus coioides*)

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Abstract：Scavenger receptors (SRs) are a diverse group of pattern recognition receptors that mediate innate immune defenses in teleosts, but their diversity and functional roles in Epinephelus coioides have not been fully characterized. Here, 13 SR genes were identified through genome-wide mining and classified into five subclasses (class A, B, F, H, L). Bioinformatic analysis, including exon–intron organization, motif composition, conserved domains and selection pressure analysis, revealed high intraclass conservation. Expression analysis under two distinct challenges — Vibrio harveyi infection and low-salinity stress — revealed that several SR genes, including EcSCARA5, EcSCARB1, and EcSCARF2, were significantly regulated in a time- and tissue-specific manner. Enrichment analyses indicated associations with membrane-related transport, lipid metabolism, and immune pathways, supporting their potential roles in stress adaptation. These findings enhance our understanding of SR function and provide a basis for immune-related strategies to improve fish health in aquaculture.

Key words: Scavenger receptors, Epinephelus coioides, Vibrio harveyi, low-salinity stress

Yorkie 在中华绒螯蟹蜕壳过程中负向调控 Crustin 的表达以影响其免疫防御能力

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摘要：中华绒螯蟹的生长发育需要经历多次蜕壳，而在蜕壳过程中机体易受病原侵袭，但具体的免疫调控机制尚不清楚。本研究聚焦重要免疫信号通路 Hippo 通路的关键下游转录因子 Yorkie（Yki），探究其参与调控中华绒螯蟹蜕壳免疫应答的作用机制。研究结果表明，Yki 在蜕壳前期的 mRNA 表达水平高于蜕壳后期和间期，且蜕皮激素（20E）可显著诱导 Yki 的表达。此外，其血淋巴细胞的菌清除能力在蜕壳前期最弱。病原刺激后，Yki 在不同蜕壳阶段的表达量均显著升高，其中在蜕壳后期的表达量最高，而抗菌肽 Crustins 的表达模式则与其相反。进一步研究发现，抑制 Yki 显著上调了 Crustins 的表达量，同时，NF-κB 的磷酸化水平也被激活。综上所述，本研究发现 Yki 通过抑制 NF-κB 负向调控 Crustins 的表达，进而影响中华绒螯蟹在不同蜕壳阶段的免疫防御能力。研究成果为揭示甲壳动物蜕壳过程中的免疫应答机制提供了新视角。

关键词：蜕壳；免疫应答；Yorkie；抗菌肽；中华绒螯蟹

Yorkie negatively regulates the Crustin expression during molting in Eriocheir sinensis, thereby influencing its immune defense capability

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Abstract： The growth of Eriocheir sinensis involves multiple molting cycles, which render the organism vulnerable to infection. The underlying immune regulatory mechanism remains unclear. This study examines Yorkie (Yki), a key Hippo pathway transcription factor, analyzing its expression after pathogen challenge during molting stages. Yki expression was highest in pre-molt stage, while haemocytes bacterial clearance were weakest. 20E stimulation significantly increased Yki expression. After pathogen challenge, Yki expression also rose, most notably in the post-molt stage. In contrast, antimicrobial peptide Crustins expression was lowest in the late stage. Furthermore, inhibition of Yki upregulated Crustins and activated NF-κB phosphorylation. In conclusion, this study establishes that Yki impairs immune defense in Eriocheir sinensis during molting by suppressing NF-κB to inhibit Crustins expression. These results provide a new framework for understanding immune regulation in molting crustaceans.

Key words: Molting; Immune response; Yorkie; antibacterial peptide; Eriocheir sinensis

CLec-HTM/IgR-Syk-BCL10-mTOR/ERK 信号通路在长牡蛎免疫启动中的作用

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摘要：无脊椎动物通常被认为缺乏适应性免疫，主要依赖固有免疫抵御病原侵染。然而近年来越来越多的研究发现无脊椎动物也存在免疫记忆现象，即再次感染同样病原后表现出更快更强的免疫反应。本研究发现，长牡蛎 CLec-HTM/IgR-Syk-BCL10 信号通路通过调控 mTOR 和 ERK 的磷酸化影响糖酵解途径和组蛋白修饰，进而促进二次刺激中吞噬相关基因（ATPeV、Clathrin）和炎症因子（TNF）的表达，最终增强血淋巴细胞的吞噬活性和炎症反应。本研究揭示了 CLec-HTM/IgR-Syk-BCL10-mTOR/ERK 通路通过调控糖酵解-组蛋白修饰信号轴调控长牡蛎免疫记忆的新机制，为理解和认识无脊椎动物免疫记忆提供了新视角，也为水产动物病害防治提供了新思路。

关键词：长牡蛎、免疫启动、吞噬作用、炎症反应、糖酵解、组蛋白甲基化

The involvement of CLec-HTM/IgR-Syk-BCL10-mTOR/ERK signaling pathway in immune priming of oysters

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Abstract： Invertebrates have traditionally been considered to lack adaptive immunity and primarily rely on innate immune responses to defend against pathogenic infections. However, growing evidence in recent years has revealed that invertebrates can exhibit immune memory, characterized by enhanced and accelerated immune responses upon re-exposure to the same pathogen. This study demonstrates that in the Pacific oyster Crassostrea gigas, the CLec-HTM/IgR-Syk-BCL10 signaling pathway regulates the phosphorylation of mTOR and ERK, thereby influencing glycolytic metabolism and histone modifications. This regulatory mechanism subsequently promotes the expression of phagocytosis-related genes (ATPeV and Clathrin) and inflammatory cytokines (TNF) during secondary challenge, ultimately enhancing hemocyte phagocytic activity and inflammatory responses. Our findings elucidate a novel mechanism by which the CLec-HTM/IgR-Syk-BCL10-mTOR/ERK axis governs immune memory in oysters through a glycolysis–histone modification signaling cascade.

Key words: Crassostrea gigas, Immune priming, Phagocytosis, Inflammation, Glycolysis, Histone methylation

复方中草药对虹鳟鱼肝脏非特异性免疫及免疫相关基因表达的影响

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摘要：虹鳟是重要冷水经济鱼种，其易受传染性造血器官坏死病毒（IHNV）威胁，造成巨大经济损失。本研究评估了饲料中添加不同浓度（0、10、20、30 g/kg）复方中草药（CHMM）对虹鳟免疫及抗 IHNV 能力的影响。结果表明，CHMM 显著提升其 T-SOD、CAT、AST、ALT、ACP、AKP 活性，并降低 MDA 含量($P<0.05$)。同时，显著上调了 NF-κB、TNF-α、IFN-β、IL-1β、JAK1、HSP70 和 HSP90 的表达($P<0.05$)。在 IHNV 感染后，CHMM 组的虹鳟其 T-SOD、ACP、AKP 活性显著升高($P<0.05$)。免疫基因 TNF-α、IFN-β、IL-1β、HSP70 和 HSP90 表达上调($P<0.05$)。值得注意的是，20 g/kg 添加组的 IHNV G 蛋白基因表达量显著低于其他各组($P<0.05$)。综上所述，本研究为其作为虹鳟免疫增强剂的开发应用提供了科学依据。

关键词：虹鳟；复方中草药；抗氧化能力；免疫应答；IHNV

Dietary supplementation of Chinese herbal medicines enhances immune response, and resistance of rainbow trout (*Oncorhynchus mykiss*) to infectious hematopoietic necrosis virus

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Abstract： Rainbow trout is an important cold-water economic fish species that is susceptible to Infectious Hematopoietic Necrosis Virus (IHNV), leading to significant economic losses. This study evaluated the effects of dietary supplementation with different concentrations (0, 10, 20, 30 g/kg) of Compound Chinese Herbal Mixture (CHMM) on the immune response and resistance to IHNV in rainbow trout. The results showed that CHMM significantly enhanced the activities of T-SOD, CAT, AST, ALT, ACP, and AKP ($P < 0.05$). Additionally, it significantly upregulated the expression of NF-κB, TNF-α, IFN-β, IL-1β, JAK1, HSP70, and HSP90 ($P < 0.05$). After IHNV infection, the activities of T-SOD, ACP, and AKP in the CHMM groups were significantly increased ($P < 0.05$). The expression of immune-related genes TNF-α, IFN-β, IL-1β, HSP70, and HSP90 was also upregulated ($P < 0.05$). The expression of the IHNV G protein gene in the 20 g/kg supplementation group was significantly lower than in the other groups ($P < 0.05$). This study supports developing CHMM as an immunostimulant for rainbow trout.

Key words: Rainbow trout; Chinese herbal medicines mixture; Antioxidant; Immune response; IHNV

抗美人鱼发光杆菌噬菌体的筛选及其在银鲳养殖中的应用探究

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摘要：美人鱼发光杆菌美人鱼亚种（PDD）是一种分布广泛、宿主感染谱广且导致银鲳养殖死亡率高的致病菌。在当前水产疾病预防疗法中，噬菌体疗法因其强特异性、快速起效、无毒性和无污染特性而备受关注。本研究从银鲳养殖环境中筛选出二株能特异性裂解 PDD 的噬菌体，并对其生物学特性进行了分析，确认其遗传物质为 DNA。此外，研究还探讨了温度与 pH 值等不同环境条件下噬菌体的作用效果。结果显示，在 28℃至 50℃范围内，噬菌体效价无明显变化；当温度超过 50℃时，效价逐渐降低，并在 80℃时完全失活。在正常海水 pH 条件下，噬菌体活性保持稳定，且能耐受 4 至 10 的 pH 值变化。通过人工感染实验，结果表明所分离的噬菌体对感染 PDD 的银鲳具有一定保护作用。综上，本研究分离筛选出二株生物学特性相对稳定、可特异性裂解 PDD 的噬菌体，为银鲳海水养殖中 PDD 感染的预防策略提供了一定理论依据。

关键词：银鲳；噬菌体；水产养殖；美人鱼发光杆菌；抗菌制剂

Isolation and characterization of bacteriophages for biological control of Photobacterium damselae subsp. damselae in silver pomfret mariculture

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Abstract: In this study, we identified two bacteriophages that can specifically lyse PDD in the silver pomfret culture environment, and we further analyzed their biological characteristics; the genetic material of the bacteriophages was confirmed as DNA. Additionally, we studied the effects of bacteriophages under different environmental conditions such as temperature and pH. The results showed no significant change in phage titer between 28℃ and 50℃, while at temperatures higher than 50℃, the phage titer gradually decreases, and the phage is inactivated at 80℃. Bacteriophage activity remains unchanged under normal seawater pH conditions and can tolerate pH changes within the range of 4-10. In artificical infection experiments, our results indicated that the selected phages had a certain degree of protective effect on silver pomfret infected with PDD. In summary, we isolated and screened two bacteriophages with relatively stable biological properties against PDD, providing a certain theoretical basis for preventive strategies against PDD infection in silver pomfret mariculture.

Key words: Silver pomfret; Bacteriophage; Aquaculture; *Photobacterium*; Antimicrobial agent

乳酸通过 HIF-1α-NF-κB 信号轴参与调控中华绒螯蟹低氧胁迫下抗菌肽表达的作用机制

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摘要：缺氧会严重影响水产动物的免疫防御能力。乳酸作为无氧糖酵解的终产物，在高等动物中已被证实具有免疫调节功能，然而其是否参与调控甲壳动物低氧免疫应答尚不明晰。本研究针对我国重要的水产经济甲壳动物中华绒螯蟹开展了低氧胁迫实验，结果显示，在低氧条件下，乳酸脱氢酶 LDH 的 mRNA 表达量和组蛋白乳酸化（H3k18）水平均显著升高；抑制 LDH 能够显著下调抗菌肽的表达，而激活 LDH 则显著上调抗菌肽表达。进一步研究发现，乳酸能够激活低氧诱导因子 HIF-1α，并促使 HIF-1α通过促进 NF-κB 的核转位进而正向调控抗菌肽的表达。综上所述，本研究初步证实了低氧胁迫增强了组蛋白乳酸化水平和 LDH 的表达，并通过激活 HIF-1α-NF-κB 信号轴进而正向调控抗菌肽的表达。本研究为深入探究甲壳动物在低氧胁迫下的免疫应答机制提供依据，为虾蟹类养殖过程中的病害防控管理提供数据支撑。

关键词：低氧胁迫；乳酸；抗菌肽；免疫应答；中华绒螯蟹

Lactate is involved in the regulation of the expression of antimicrobial peptides through the HIF-1α-NF-κB signaling axis in Chinese mitten crab (*Eriocheir sinensis*) under hypoxia stress.

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Abstract： Hypoxia impairs the immune defense of aquatic animals. Lactate, the end product of anaerobic glycolysis, exhibits immunomodulatory roles in higher vertebrates, yet its function in crustacean hypoxic immune responses remains unclear. This study investigated the Chinese mitten crab (*Eriocheir sinensis*), an economically important crustacean. Under hypoxia stress (DO<2 mg/L), both lactate dehydrogenase (LDH) mRNA expression and histone lactylation (H3K18la) levels were significantly elevated. Inhibition of LDH downregulated Anti-lipopolysaccharide factors (ALFs) expression, whereas its activation enhanced ALFs production. Further research revealed that lactate activates hypoxia-inducible factor-1α (HIF-1α), which promotes NF-κB nuclear translocation, thereby positively regulating ALFs expression. In summary, hypoxia enhances histone lactylation and LDH expression, and activates the HIF-1α–NF-κB axis to upregulate antimicrobial responses. These findings offer insights into the immune mechanisms of crustaceans under hypoxia and support disease management in aquaculture.

Key words: Lactate; Antimicrobial peptides; Hypoxia stress; Immune response; *Eriocheir sinensis*

基于宏基因组和代谢组分析虹鳟在不同养殖水温下感染 IHNV 后肠道内容物的变化

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摘要：IHN 严重危害虹鳟养殖，其致死率与水温密切相关。本研究通过宏基因组与代谢组学联合分析，比较了 12-13℃与 16-17℃下虹鳟感染 IHNV 后肠道菌群与代谢物的响应。结果显示，在 12-13℃感染导致真核生物群落缺失，耶尔森菌科等致病菌显著增多，4087 种肠道代谢物发生改变；而在 16-17℃感染后，链球菌科与乳酸乳球菌显著富集，4259 种代谢物产生变化。两种温度下，免疫相关代谢物 1-十八烷酰-甘油-3-磷酸乙醇胺和 L-谷氨酸均显著上调。同时，与免疫相关代谢物同棉子糖乳球菌、真姬菇和红缘拟层孔菌显著相关。本研究揭示了不同水温条件下虹鳟肠道菌群与代谢物对 IHNV 的响应机制，筛选出具有潜在抗 IHN 能力的有益菌株，为 IHN 的防治提供了新思路。

关键词：虹鳟；IHN; 温度；宏基因组；代谢组

Metagenomic and metabolomic analysis of changes in intestinal contents of rainbow trout (*Oncorhynchus mykiss*) infected with infectious hematopoietic necrosis virus at different culture water temperatures

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Abstract： IHN is a serious threat to rainbow trout aquaculture, and its mortality rate is closely related to water temperature. This study compared gut microbiota and metabolite responses to IHNV infection in rainbow trout at 12–13°C and 16–17°C using metagenomic and metabolomic analyses. The results demonstrated that IHNV infection at 12–13°C led to a loss of eukaryotic communities, a surge in pathogens like Yersiniaceae, and changes in 4087 metabolites, while infection at 16-17°C caused marked enrichment of Streptococcaceae and Lactococcus lactis alongside changes in 4259 metabolites. At both temperatures, 1-octadecanoyl-glycero-3-phosphoethanolamine and L-glutamate were significantly upregulated. Additionally, immune-related metabolites showed significant correlations with Lactococcus raffinolactis, Hypsizygus marmoreus, and Fomitopsis pinicola. This study elucidates the temperature-dependent responses of the trout gut ecosystem to IHNV and identifies potential probiotic bacteria, paving the way for novel IHN control strategies.

Key words: Rainbow trout; IHN; temperature; metagenomic; metabolomic

六价铬对鲤鱼血液学指标、氧化还原状态及细胞凋亡的毒性效应

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摘要：近年来，六价铬[Cr (VI)]对水生动物构成潜在威胁。本研究旨在探究 Cr (VI)对鲤血液学指标、消化酶活性、氧化还原状态及细胞凋亡的毒性效应。本研究选取 300 尾鲤，将其随机分为 4 组，分别暴露于浓度为 0 mg/L（对照组）、0.5 mg/L、1mg/L 和 2 mg/L 的 Cr (VI)中，暴露时长均为 28 天。结果显示，六价铬暴露显著降低鲤的血液学指标及血清钙水平，升高血清生化指标，同时降低消化酶活性。此外，Cr (VI)暴露还显著提高鲤体内的氧化应激水平，通过增加丙二醛、活性氧与蛋白质羰基的含量，干扰抗氧化系统的酶活性，最终破坏鲤体内的氧化还原平衡状态。同时，研究发现，Cr (VI)暴露可诱导鲤肠道和肝脏细胞凋亡，且二者的凋亡途径存在差异——肠道细胞凋亡主要与死亡受体途径相关，肝脏细胞凋亡则主要与线粒体途径相关。综上所述，鲤暴露于浓度≥0.5 mg/L 的 Cr (VI)会产生潜在毒性效应。

关键词：六价铬，氧化应激，细胞凋亡，消化酶

Hexavalent chromium-induced toxic effects on the hematology, redox state, and apoptosis in Cyprinus carpio

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Abstract: Recently, hexavalent chromium [Cr (VI)] has posed potential threat to aquatic animals. The objective of this study was to investigate the toxic effects of Cr (VI) on hematology, digestive enzyme, redox state, and apoptosis in Cyprinus carpio. In this study, 300 C. carpio were randomly divided into four groups and exposure to 0, 0.5, 1 and 2 mg/L Cr (VI) for 28 days, respectively. The result showed that Cr (VI) exposure exerted significant toxic effects by reducing in the levels of hematology parameters and serum calcium, increasing serum biochemistry, decreasing digestive enzyme. The Cr (VI) exposure increased oxidative stress levels by increasing the levels of MDA, ROS and PC, interfering with the enzyme activities of antioxidant system and finally breaking the redox state in C. carpio. Additionally, our study found that Cr (VI) exposure induced intestinal and liver apoptosis in different ways was mainly related to death receptor pathway and mitochondrial pathway, respectively. The results suggest that exposed to Cr (VI) above 0.5 mg/L has potential toxic effects in C. carpio.

Key words: Hexavalent chromium, oxidative stress, apoptosis, digestive enzyme

C3 介导自噬–溶酶体途径限制微生物逃逸

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摘要：C3 作为补体系统的关键组分在补体激活中发挥重要作用，可调控吞噬作用、裂解细胞、介导炎症反应并清除免疫复合物。本研究发现，长牡蛎（*Crassostrea gigas*）血淋巴上清中的 *Cg*C3 能够结合多种多糖及微生物，进而与膜受体 *Cg*CD18 相互作用，介导 *Cg*C3 包被的弧菌进入血淋巴细胞。血淋巴细胞内的 *Cg*ATPV1D 能够感知 *Cg*C3 包被的弧菌囊泡，并募集 *Cg*ATG16L1。同时，血淋巴细胞中游离的 *Cg*C3 也能识别并结合胞内入侵的弧菌，进而直接募集 *Cg*ATG16L1。*Cg*ATG16L1 募集 *Cg*LC3 以促进自噬体膜的延伸。随后，自噬体与溶酶体融合形成自噬溶酶体，从而降解 *Cg*C3 包被的弧菌。这些结果共同表明，*Cg*C3 能够结合胞内/胞外微生物，形成胞内 C3-CD18-ATPV1D-ATG16L1-LC3 和 C3-ATG16L1-LC3 微生物相关复合物，进而触发胞内抗菌性自噬-溶酶体途径以清除入侵微生物。

关键词：长牡蛎；补体系统；自噬；免疫效应

C3 restrict the escape of microbes through autophagy-lysosome pathway

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Abstract： As the key component of complement system, C3 plays important roles in complement activation to regulate phagocytosis, lyse cells, mediate inflammation, and clear immune complexes. In the present study, *Cg*C3 in the cell-free hemolymph of the Crassostrea gigas was found to be able to bind various polysaccharides and microbes and then interacted with membrane receptor *Cg*CD18 to mediate the entry of the *Cg*C3-coated Vibrio into hemocytes. *Cg*ATPV1D in hemocytes sensed the *Cg*C3-coated Vibrio vacuole and recruited *Cg*ATG16L1. The free *Cg*C3 in hemocytes could also recognize and bind the intracellular invading Vibrio and then directly recruited *Cg*ATG16L1. *Cg*ATG16L1 recruited *Cg*LC3 to promote the extension of autophagosome membrane. The autophagosome then fused with lysosome to form autolysosome to degrade the *Cg*C3-coated Vibrio. The results collectively demonstrated that *Cg*C3 was able to bind intra/extracellular microbes to form intracellular microbe-associated complexes of C3-CD18-ATPV1D-ATG16L1-LC3 and C3-ATG16L1-LC3, and then trigger intracellular antibacterial autophagy-lysosome pathway to eliminate the invading microbes.

Key words: *Crassostrea gigas*; Complement system; Autophagy; Immune effect

高温胁迫下 CgALDH6A1 对长牡蛎氧化应激反应的调控作用

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摘要：高温胁迫会诱导长牡蛎生成大量丙二醛，严重时甚至会导致长牡蛎死亡。ALDH 可降解 MDA，并且其在增强抗氧化防御能力方面的作用受到广泛关注。本研究在长牡蛎基因组中鉴定出 14 个 ALDH 家族成员，其中 CgALDH6A1 含有 ALDH_F6_MMSDH 结构域，解析了 CgALDH6A1 在高温胁迫下的表达模式以及在室外养殖期间 CgALDH6A1 的 mRNA 转录水平。在注射 CgALDH6A1 siRNA 并 28℃高温胁迫后，MDA 含量显著升高，而 SOD 和 CAT 活性及 T-AOC 均显著下降；同时观察到鳃组织形态紊乱，鳃丝出现明显肿胀。当注射 CgALDH6A1 激动剂并 28℃高温胁迫后，MDA 含量显著降低，而 SOD 和 CAT 活性及 T-AOC 均显著升高，且鳃组织未出现明显形态变化。综上，CgALDH6A1 基因可通过降解 MDA 在调控长牡蛎氧化应激反应中发挥作用，并与抗氧化系统协同作用缓解高温胁迫诱导的氧化应激。

关键词：CgALDH6A1; MDA; 高温胁迫; 长牡蛎

The regulatory role of CgALDH6A1 in the oxidative stress response of *Crassostrea gigas* under high-temperature stress

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Abstract： High temperatures induce the production of a large amount of MDA in the oysters, and even lead to mass mortalities. ALDH degrades MDA and has attracted increasing attention for its role in enhancing antioxidant defense capacity. This study identified 14 ALDH family members in the oyster genome. Among them, CgALDH6A1 harbored a conserved ALDH_F6_MMSDH domain. Following injection of CgALDH6A1 siRNA, the MDA content increased significantly, while the activities of SOD and CAT, and T-AOC decreased significantly under high-temperature stress. Meanwhile, the gill tissue was observed to be disorganized with obvious filament swelling. Following injection of CgALDH6A1 agonist, the MDA content decreased significantly, while the activities of SOD and CAT, as well as T-AOC all increased significantly. However, no obvious morphological change was observed in the gill. These results demonstrated that CgALDH6A1 was key in regulating the oxidative stress response by degrading MDA under high-temperature stress and cooperated with the antioxidant system to reduce oxidative stress.

Key words: CgALDH6A1; MDA; high-temperature stress; Pacific oyster *Crassostrea gigas*

银鲳感染美人鱼发光杆菌的免疫响应及该菌在吞噬体内逃逸机理的研究

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摘要：银鲳（*Pampus argenteus*）是全球重要的海洋经济鱼类，但病害问题严重制约其产业化养殖。目前影响银鲳的病原体主要分为三类：寄生虫（刺激隐核虫、淀粉卵涡鞭虫）、细菌（美人鱼发光杆菌美人鱼亚种、鰤鱼诺卡氏菌）及病毒（虹彩病毒）。其中美人鱼发光杆菌美人鱼亚种（PDD）致死率最高。该菌是一种高毒性、广宿主范围的海洋弧菌，感染常引发严重出血性败血症，但其致病机制与宿主免疫调控网络尚未完全解析。本研究发现在银鲳感染 PDD 过程中，病原会破坏机体免疫与代谢平衡，并在感染中后期显著抑制抗原呈递过程。进一步探究证实，PDD 分泌溶血素 $HlyA_{pl}$ 等毒力因子破坏银鲳吞噬溶酶体膜结构，同时发现银鲳体内存在宿主协同因子-吞噬体相关基因 *gilt-ifi30a* 协助病原实现吞噬体逃逸，从而躲避巨噬细胞清除。此外，银鲳特有的免疫调控缺陷（IFNg 基序缺失导致的 JAK-STAT-GILT 转录调控异常，MHCII 基因家族收缩）使其抗菌能力较弱，导致“病原逃逸-宿主抑制”。

关键词：银鲳；吞噬体；免疫逃逸；溶血素

Preliminary Investigation of the Immune Response and Immune Evasion Mechanisms of Silver Pomfret (*Pampus argenteus*) to Photobacterium damselae subsp. Damselae

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Abstract： The silver pomfret (*Pampus argenteus*) is a commercially important marine fish species, yet disease poses a major challenge to its industrial aquaculture. Among the various pathogens affecting this species-including parasites, bacteria, and viruses-PDD stands out due to its high lethality. PDD is a virulent, broad-host-range marine bacterium often causing hemorrhagic septicemia, this study demonstrates that PDD infection disrupts immune and metabolic homeostasis in silver pomfret and markedly suppresses antigen presentation during mid to late infection stages. Further analysis showed that PDD secretes virulence factors, including hemolysin $HlyA_{pl}$, which damage the phagolysosomal membranes of host cells. In addition, a host co-factor -the phagosome-related gene *gilt-ifi30a* - was found to promote phagosomal escape, helping the pathogen avoid phagocytic clearance. Silver pomfret also exhibits specific immune deficiencies, such as dysregulated JAK-STAT-GILT transcription due to the IFNg motif deletion and a contracted MHCII gene family, which together weaken antibacterial immunity and sustain a cycle of “pathogen evasion and host suppression.”

Key words: Silver Pomfret; Phagosome; Immune evasion; Hemolysin

第五专题 可持续捕捞

基于 COI 基因的东海剑尖枪乌贼群体遗传结构研究

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摘要：本文基于 2023 年 9 月至 2024 年 4 月捕获的剑尖枪乌贼样本，提取其线粒体细胞色素氧化酶亚基 I(COI)基因，研究该物种遗传多样性。分子标记结果表明样本个体可分为三个群体(ES1、ES2 和 ES3)，不同群体均表现出较高的单倍型多样性指数 Hd 和较低的核苷酸多样性指数 Pi，其中 ES2 群体的 Hd 和 Pi 均为最低。分子方差分析(AMOVA)显示，群体间的遗传变异为 89.06%，ES1 和 ES3 之间以及 ES2 和 ES3 之间的遗传分化程度均较大(Fst>0.9)，ES2 与 ES3 间的 Fst 值偏小，三个群体间均存在遗传分化现象。中性检验 Tajima's D 和 Fu ' s Fs 均为负数，三个群体均表现显著性差异(P<0.05)，群体错配分析显示 ES1 群体在历史上发生过种群扩张，推测其扩张时间大约发生在 59.739 万年前。系统进化树显示样本存在较为明显的谱系聚类，三个群体各为一支。

关键词：剑尖枪乌贼；东海海域；COI；遗传多样性；群体遗传结构

Population genetic structure of *Uroteuthis edulis* in the East China Sea based on the COI gene

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Abstract： *Uroteuthis edulis* is a significant economic cephalopod resource utilized by mainland China, Taiwan, and Japan. Understanding the population genetic structure of U.edulis is essential to evaluate the changes of its resource abundance. In this study, we used the COI gene as a marker to evaluate the population structure of U.edulis. Molecular marker analysis indicated that the sampled individuals were categorized into three populations (ES1, ES2, and ES3). All populations exhibited high haplotype diversity indices (Hd) and low nucleotide diversity indices (Pi), with the ES2 population showing the lowest Hd and Pi values. Analysis of molecular variance (AMOVA) revealed that genetic variation among populations accounted for 89.06% of the total variation. The phylogenetic tree illustrated distinct lineage clustering, with each population forming a separate clade.Combined with the biological information, it was observed that the majority of female individuals were larger in size and exhibited high sexual maturity.

Key words: Uroteuthis edulis; East China Sea ; COI; Genetic diversity; Population genetic structure

西北太平洋中上层渔业种类栖息地的协同变化及其对气候变化的响应

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摘要：本研究综合考虑了 6 种时空尺度、4 类联合物种分布模型，以多种角度评估时空尺度对联合物种分布模型影响，并选取最优时空尺度（年、0.25°）和模型（HMSC），厘清西北太平洋中上层种类种间（日本鲭、沙丁鱼和柔鱼）关系、栖息地的分布模式及其对气候变化的协同响应。结果显示，日本鲭与沙丁鱼存在正向的种间关系，而与柔鱼之间则呈现负向的种间关系。对比发现，厄尔尼诺事件下，日本鲭和沙丁鱼具有更宽的适宜的环境生态位宽度，造成其适宜栖息地面积增加；而在拉尼娜事件下，柔鱼具有更宽的适宜的环境生态位宽度，适宜栖息地面积要大于厄尔尼诺期间。研究表明，正向的种间关系能够反映物种对环境因子的相似响应，并揭示它们占据相似生态位的特征。这种对环境响应的一致性导致物种适宜栖息地的同步变化趋势，从而对资源丰度产生潜在影响。此外，物种之间存在正向的种间关系时其栖息地也对 ENSO 具有相似且同步的响应，负向种间关系则表现出异步的响应。

关键词：时空尺度；种间关系；栖息地分布；中上层渔业种类；气候变化

Synergistic Habitat Changes and their response to climate change of Small Pelagic Fish in the Northwest Pacific Ocean

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Abstract: This study evaluated the effects of spatiotemporal scale on joint species distribution models across six scales and four models, identifying the annual scale at 0.25° resolution with the HMSC model as optimal. Based on this framework, we analyzed the interspecific relationships among fishery species in Northwest Pacific—Scomber japonicus, Sardinops melanostictus, and Ommastrephes bartramii—along with their habitat distributions and collective responses to climate variability. Results revealed a positive relationship between S.japonicus and S.melanostictus, but negative relationships of both with O.bartramii. During El Niño, S.japonicus and S.melanostictus exhibited broader environmental niches and expanded habitats, whereas under La Niña, O.bartramii showed a wider niche and larger suitable habitat. These patterns indicate that positive interspecific relationships reflect similar environmental responses and niche overlap, leading to synchronous habitat shifts under ENSO, which may influence resource abundance. Conversely, negative associations correspond to asynchronous responses.

Key words: Spatio-temporal scale，Interspecies relationship，habitat distribution，Mesopelagic fish，climate variability

西北太平洋重要经济种类对捕捞诱导进化的动态响应：不同生活史策略的研究

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摘要：越来越多的研究表明，渔业捕捞会引发鱼类生活史性状的进化，从而影响种群动态。本研究利用基于个体的生态进化模型，探讨了 FIE 在捕捞强度变化期间的影响。我们重点关注西北太平洋四种重要经济鱼种，这些鱼类分别属于不同的生活史策略（远东拟沙丁鱼（JS）（机会主义）、日本鲭（CM）（中间型）、长鳍金枪鱼（AL）（周期策）和大青鲨（BS）（均衡型））。与理论预期一致，我们发现选择性捕捞会促使这些物种向更快的生活史策略演化，而 FIE 会进一步加剧这个变化。在高捕捞强度下，JS 和 CM 的变化速率较为显著，AL 和 BS 则较为缓慢，这一变化使得进化后的物种在捕捞期间能够维持更高的种群数量，特别是对于短生命周期物种而言。但其对生物量的影响则表现出较为复杂的模式，未呈现出一致性。此外，FIE 对种群恢复有着显著的影响，即使捕捞活动停止，进化后的物种仍未能完全恢复，且各个物种的恢复能力与物种的生活史策略密切相关。

关键词：西北太平洋；不同生活史策略；捕捞诱导进化；种群动态；生态进化模型

Dynamic responses of key economic species in the Northwestern Pacific to fisheries-induced evolution: A study on different life history strategies

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Abstract：Increasing evidences suggest that fishing activities can trigger evolutionary changes in fish life history traits and thus affect population dynamics. In this study, an individual-based eco-evolutionary model was applied to investigate the impact of fisheries-induced evolution (FIE) under varying fishing pressures. The study focused on four economically important species in the Northwestern Pacific representing four life history strategies: Sardinops melanostictus (S. melanostictus, opportunistic strategists), Scomber japonicus (S. japonicus, intermediate strategists), Thunnus alalunga (T. alalunga, periodic strategists), and Prionace glauca (P. glauca, equilibrium strategists). As expected, we found that selective fishing drove these species to evolve towards faster life history strategies and that FIE accelerated this evolution. Under high fishing pressures, the rate of change in the life history traits of S. melanostictus and S. japonicus was more pronounced, but T. alalunga and P. glauca showed slower changes. The changes allowed the evolved species to maintain larger population

Key words: Life history strategy; Fisheries-induced evolution; Northwestern Pacific; Eco-evolutionary model; Population dynamics

中国近海捕捞渔获物追溯体系构建研究及行动建议

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摘要：海产品供应链环节众多、高度复杂，实现端到端可追溯性面临显著挑战。建立可追溯体系对保障食品安全、满足法规要求、打击非法捕捞及推动可持续实践具有重要意义。当前，欧洲、美国等地海产品标签法规已较完善，而中国尚未建立强制性追溯标准。本研究聚焦中国近海捕捞—上岸阶段的可追溯管理，识别出当前管理实践、追溯机制及相关法规存在不足。主要挑战包括：制度碎片化与执法资源不足；数据标准不统一形成信息孤岛；验证体系软硬件基础薄弱，设备改装与云平台年均成本较高，中小型渔船经济负担突出。对此提出政策、技术与协同三方面建议，通过政策、技术与协同三轮驱动，我国有望于2035年前建成国家级全链条智能化追溯体系，为实现渔业资源可持续和消费者信任双重目标奠定基础。

关键词：IUU；可追溯；渔业

Research on the Construction of a Traceability System for China's Offshore Fishing Catches and Action Recommendations

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Abstract： The seafood supply chain's complexity challenges end-to-end traceability. Establishing traceability is vital for food safety, regulatory compliance, combating illegal fishing, and sustainability. While the EU and US have mature labeling regulations, China lacks mandatory traceability standards. This study examines China's offshore fishing-to-landing phase, identifying deficiencies in management practices, traceability mechanisms, and regulations. Key challenges include: institutional fragmentation and insufficient enforcement; disparate data standards creating information silos; and weak verification infrastructure with high annual costs for equipment and cloud platforms, disproportionately burdening small-scale fishers. We propose policy, technological, and collaborative recommendations. Through these three drivers, China can establish a national smart traceability system by 2035, supporting sustainable fisheries and consumer trust.

Key words: IUU；Traceability；Fisheries

巴塔哥尼亚海域环境对阿根廷滑柔鱼的空间非平稳性影响效应评估

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摘要：阿根廷滑柔鱼是西南大西洋的重要渔业物种之一，其丰度容易受到海洋环境的影响。传统研究往往假设环境与阿根廷滑柔鱼之间关系具有空间平稳性。然而，越来越多研究认为环境对物种分布的影响效应在空间上存在非平稳性。为探究巴塔哥尼亚海域复杂的海洋环境对阿根廷滑柔鱼资源分布的影响是否存在空间非平稳性，本研究构建了多尺度地理加权回归模型。该模型基于局部回归分析了不同环境因子与阿根廷滑柔鱼单位捕捞努力量渔获量之间的影响关系。模型结果显示，海表面高度、50m 水深温度、叶绿素 a 浓度以及海表面盐度等重要环境因子对阿根廷滑柔鱼 CPUE 的影响均表现出显著的空间异质性。这些环境因子的局部回归系数在空间上呈现出显著差异，尤其在大陆坡及邻近水域，其影响效应更为显著。研究推测，复杂的海洋动力学过程塑造了具有显著的空间异质性的海洋环境，影响了阿根廷滑柔鱼的摄食迁徙，最终导致了环境因子空间影响效应的非平稳性。

关键词：阿根廷滑柔鱼；空间非平稳性；多尺度地理加权回归模型；巴塔哥尼亚大陆架

Assessing the non-stationary spatial effects of environmental conditions on Illex argentinus in the Patagonian region

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Abstract： Illex argentinus is an important fishery species in the southwest Atlantic Ocean. Its abundance is influenced by the marine environment. However, a growing body of research suggests spatial non-stationarity. To investigate the potential spatial non-stationarity between the distribution of I. argentinus and the complex marine environment in the Patagonian Shelf waters, we developed a multi-scale geographically weighted regression model. The model results revealed significant spatial heterogeneity between I. argentinus CPUE and key environmental factors, including sea surface height (SSH), water temperature at 50m depth (T50m), chlorophyll-a concentration (Chl-a), and sea surface salinity (SSS). The local regression coefficients of these environmental factors exhibited significant spatial variation, with effects particularly pronounced on the continental slope and in adjacent waters. This provides evidence that the complex marine dynamic processes have shaped a spatially heterogeneous marine environment, thereby influencing the distribution and feeding migration of I. argentinu.

Key words: Illex argentinus; Spatial Non-stationarity; Multi-scale Geographically Weighted Regression model; Patagonian Shelf

不同内衬网比例的南极磷虾桁杆拖网模型水槽试验水动力性能分析

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摘要：为探究南极磷虾桁杆拖网内衬网的最佳装配比例，实现绿色低碳捕捞目标，本研究以南极磷虾专业捕捞加工船“深蓝”号采用的南极磷虾桁杆拖网为研究对象，基于修正的田内准则制作了大尺度比为 15 的桁杆拖网模型网，并在循环动水槽中开展试验，探究内衬网比例（100%、90%、80%）和重锤质量（0.5、1、1.5、2 kg）对桁杆拖网模型网整体形态、阻力、能耗系数、稳定性的影响。结果表明：（1）当内衬网比例减少，模型网阻力和能耗系数呈下降趋势，网口高度无明显变化；在相同条件下，当内衬网比例减少 20%时，模型网阻力减少 12.02%，能耗系数降低 5.66%。（2）当流速增加，模型网网口高度降低，网具整体收缩，阻力增大。（3）重锤质量的增加与模型网阻力、网口高度和能耗系数呈正相关关系。（4）减少内衬网比例，增加重锤质量，模型网阻力振荡趋于稳定，振幅减小。适当减少内衬网比例并增加重锤质量，有助于降低拖网阻力和能耗。

关键词：南极磷虾桁杆拖网；内衬网比例；重锤质量；水槽模型试验；水动力性能

Hydrodynamic performance analysis of model nets of the Antarctic Krill beam trawl with different liner net ratios in flume tank experiments

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Abstract： experiments were conducted in a circulating flume tank to investigate the effects of liner net proportions and sinker weights on the overall geometry, drag, energy consumption coefficient, and stability.The results indicate the following: (1) A reduction in the liner net proportion led to decreases in drag and energy consumption coefficient, while the net mouth height remained relatively unchanged. Under identical conditions, a 20% reduction in liner net proportion resulted in a 12.02% decrease in drag and a 5.66% reduction in the energy consumption coefficient. (2) With increasing flow velocity, the beam trawl model exhibited a reduction in net mouth height, greater overall contraction and increased drag. (3) Increased sinker weight was positively correlated with drag, net mouth height, and energy consumption coefficient. (4) Reducing the liner net proportion while increasing sinker weight resulted in more stable drag oscillations with reduced amplitude. Appropriately reducing the liner net ratio and increasing the sinker weight can help reduce trawl drag and energy consumption.

Key words: Antarctic Krill beam trawl; liner net ratio; sinker weight; flume tank model experiment; hydrodynamic performance

底栖海洋鱼类的趋光行为是否符合信号适应假说：以黄鳍鲷为例

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摘要：LED 已成为研究鱼类行为不可或缺的工具，不仅在选择性捕捞实践中发挥关键作用，也在生态可持续性倡议中日益受到重视。本研究系统探究了关键光照参数——光谱、强度与时长——对黄鳍鲷（Sparus latus）趋光行为的影响。实验针对黄鳍鲷，在四种光谱条件下开展行为观测，并结合趋光指数（ Ip）与趋避指数（f）进行综合分析。结果表明，黄鳍鲷在不同光谱下均表现出不同程度的趋光性，其响应强度由强至弱依次为：蓝光 > 白光 > 红光 > 绿光。此外，当鱼体从黑暗环境突然暴露于光照时，初期呈现回避行为；但随着光照持续时间延长，趋光行为逐渐增强，表明光照时长是调控趋光反应的重要变量。本研究结果进一步支持“信号–适应假说”（Signal-Adaptation Hypothesis）在黄鳍鲷趋光行为中的适用性。综上，本研究为构建动态化、精准化的光诱策略提供了理论支撑，对推动可持续渔业发展具有重要应用价值。

关键词：鱼类趋光行为、光照时间、光照强度、光谱频率、信号适应假说、黄鳍鲷

Do the Phototactic Behaviors of reef-dwelling demersal marine species Align with the Signal-Adaptation Hypothesis: case of yellowfin seabream

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Abstract： Light-emitting diodes (LEDs) have become indispensable tools for studying fish behavior in both selective fishing practices and ecological sustainability initiatives. This study systematically investigates how key light parameters spectrum, intensity, and duration influence the phototactic responses of yellowfin seabream (Sparus latus). Thus, the behavior of juvenile yellowfin seabream was analyzed under four LED spectral conditions and by integrating the phototaxis index (Ip) and approach-avoidance index (f). The results indicated that yellowfin seabream exhibited varying degrees of phototropism across four spectral frequencies, with responses ranging from strong to weak in the order of blue light, white light, red light, and green light.Furthermore, an initial avoidance response was observed with sudden exposure to light from darkness, while phototaxis progressively intensified with extended exposure, indicating that light duration serves as a significant modulator. Moreover, the findings substantiate the relevance of the Signal-Adaptation Hypothesis in the phototactic behavior .

Key words: Fish phototropic behavior, Illumination , Light intensity, light wavelength, Signal-Adaptation Hypothesis, yellowfin seabream (Sparus latus)

网衣系统动力学快速高保真仿真方法构建研究

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摘要：网衣系统动力学的快速高保真仿真方法对网渔具的数字化优化设计与精准动态控制具有重要意义。本研究以平面网片为对象，加速底层算法效率，采用网目群化方法实现网衣系统的模型降阶，并运用插值映射算法进行保真反演，验证仿真方法的可行性。研究以横纵各 48 目的方形和菱形网片为仿真案例，结果表明，采用批量构造和行处理储存的全局矩阵处理方式、共轭梯度法求解器和半隐式修正拟牛顿迭代法，计算时间由原来的 3200 s 与 5600 s 缩短至 120 s 与 200 s，效率提升约 95%。在 2×2 至 24×24 的网目群化比例范围内，发现群化比例增大将导致网片受力与形变偏差增大。随着群化比例增大，保真度得分逐渐降低。在 3×3 及更精细的群化水平下，方形与菱形网片的多视角网形保真度均超过 0.85，且仿真时间则缩短至 9-20 s。本研究结果为网衣系统动力学仿真提供了高效、高保真的解决方案，可作为数字孪生系统的核心仿真引擎。

关键词：网衣系统；快速仿真；高保真；数字孪生

Rapid High-Fidelity Dynamic Simulation Method of Fishing Nets

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Abstract： Rapid, high-fidelity dynamic simulation of netting systems is crucial for fishing gear optimization and precise dynamic control. We accelerate the core algorithm. Then, Mesh grouping is used for model order reduction, followed by interpolation-mapping-based fidelity reconstruction, thus verifying the feasibility of the simulation method. A square-mesh and a diamond-mesh panel nets both with 48 ×48 meshes as representative cases were tested. Results show that with the batched matrix assembly and row-wise storage, a conjugate-gradient solver, and a semi-implicit modified quasi-Newton iteration, simulation time of two cases were reduced from 3200 s and 5600 s to 120 s and 200 s, respectively, raising the simulation efficiency to 95%. Across 2×2–24×24 groupings, larger grouping increased force and deformation deviations. And fidelity scores decreased as grouping increases, at 3×3 (and finer),fidelity remained> 0.85 for both panels, while total runtime drops to 9-20 s. These results deliver an efficient, high-fidelity net-dynamics solution and a core engine for digital-twin applications.

Key words: Fishing net; Rapid simulation; High fidelity; Digital twin

海龟排除装置（TED）水动力优化以提升拖网性能与生态可持续性

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摘要：本研究通过实验方法，系统分析了格栅间距、安装角度和流速对网囊形态与水动力特性的影响。同时，构建了一种原型遗传算法，用于识别能够在提升水动力性能的同时保持网囊稳定性的最优格栅配置。此外，利用傅里叶分析对水动力作用力的振荡进行时频特征分析。结果表明，安装 TED 后，网囊的平均阻力较空网增加了 29.33%–74.56%；阻力随格栅间距减小、安装角度增大及流速提高而上升。较大的安装角度可提高网囊形态稳定性；而较高的流速会使网囊形态向中心轴收缩。傅里叶分析显示，水动力波动主要受低频分量（0.233–1.06 Hz）主导；由于格栅扰动流场的影响，TED 网囊的功率谱能量较空网高出 68.46%–95.50%。遗传算法在六代内即完成收敛，得到的最优参数组合为：格栅间距 88 mm、安装角度 40°、流速 0.6 m/s。该配置可使阻力降低 45.25%，阻力振荡幅值降低 63.24%，网囊相对稳定性提高 28.76%。

关键词：拖网网囊，海龟释放装置，遗传算法，动水槽试验，阻力优化，可持续渔业

Hydrodynamic Optimization of Turtle Excluder Device (TED) for Enhanced Trawl Performance and Sustainability

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Abstract： The sorting grid called Turtle Excluder Device is one of the most extensively utilized and efficient selective mechanisms in global trawl fisheries, designed to minimize bycatch, enhance the escape success rate of non-target species, and improve the overall selectivity of trawl gear, thereby playing a crucial role in sustainable fisheries management. Therefore, this study experimentally investigated the influence of bar spacing, installation angle, and flow velocity on the codend morphology and hydrodynamic characteristics. A prototype genetic algorithm was developed to identify the optimal sorting grid configuration that improves hydrodynamic performance and maintains the stability of the trawl codend. Fourier analysis is used to analyze the time-frequency contents of the oscillation of hydrodynamic force. The results indicated that the presence of sorting grid inside the codend increases the mean drag force by 29.33%-74.56% compared to an empty codend, with drag force observed to increases with decreasing bar spacing, as well as with increasing installation angle and flow velocity.

Key words: Trawl codend, Turtle Excluder Device, Genetic algorithm, Flume tank experiment, Drag optimization, Sustainable fisheries

用硬组织测定金乌贼年龄的适宜性：以中国东海岸为例

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摘要：金乌贼（*Sepia esculenta*）是中国东部沿海的重要经济头足类，但受过度捕捞、栖息地退化和气候变化影响，其种群面临衰退风险。准确的年龄鉴定对其资源管理具有重要意义。本研究于2021年9—11月在中国东部沿海采集360尾金乌贼，分析角质颚、内壳、眼睛晶体和耳石微结构特征。结果显示，上角质颚矢状切面具有清晰的明暗交替增量环，符合“日增一环”规律，是最可靠的年龄鉴定材料；内壳纵切面显示层片状增量，虽与角质颚的年龄估算结果接近，但不具严格的日周期性，可作为辅助材料；眼睛晶体和耳石的增量结构不清晰，缺乏日周期性，不适用于年龄测定。角质颚、内壳和眼睛晶体的增量数与胴长长呈幂函数关系，三者间相关显著。研究结果为金乌贼的年龄与生长研究提供基础，并为其资源的合理开发与可持续利用提供科学依据。

关键词：金乌贼，硬组织，微结构，年龄，中国东海

Suitability of Hard Tissues for Age Determination in Sepia esculenta: A Case Study from the East coast of China

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Abstract： *Sepia esculenta* is an important commercial cephalopod along China’s eastern coast but faces population decline due to overfishing, habitat loss, and climate change. Accurate age estimation is crucial for resource management. In this study, 360 individuals were collected between September and November 2021, and the microstructures of beaks, cuttlebones, eye lenses, and statoliths were examined. The sagittal section of the upper beak showed clear daily growth increments, making it the most reliable structure for age determination. The cuttlebone exhibited layered lamellae with similar but non-daily increments, serving as an auxiliary material. Growth increments in eye lenses and statoliths were indistinct and unsuitable for aging. Increment numbers in beaks, cuttlebones, and eye lenses showed power relationships with mantle length. These findings provide a foundation for understanding the growth characteristics of S. esculenta and support sustainable resource management.

Key words: Sepia esculenta, hard tissue, microstructure, age determination, East coast of China

第六专题 水生生物资源养护与水域生态修复

全球海洋入侵生物的经济影响和成功机制

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摘要：在全球化背景下，海洋生物入侵日益严重，威胁生态系统稳定并造成巨大经济损失。深入理解入侵的机制与影响对外来种的管理至关重要。然而，目前大多数研究都关注陆地和淡水系统的生物入侵，鲜有研究从全球尺度上分析海洋生物入侵的影响和机制。为填补这一空缺，研究首先聚焦有经济影响数据的海洋入侵物种，评估了海洋生物入侵在全球范围内的经济损失，揭示了海洋生物入侵经济损失在类群和地区之间的变动模式。随后，研究针对全球海洋入侵物种，量化了物种在入侵地占据的环境空间随时间的变动趋势。最后，研究聚焦入侵海洋鱼类，从全球尺度上构建了海洋鱼类的入侵途径，分析了生活史特征对外来鱼类在入侵地占据环境空间的影响。

关键词：外来入侵物种；环境生态位；入侵影响；入侵机制

现生头足类身体形态宏观进化速率与驱动机制研究

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摘要：头足类动物可追溯至约 5 亿年前的晚寒武世祖先，其演化历程由最初的外壳型原始形态逐步过渡至当代物种，形成了多样而复杂的体型结构。尽管其体型特征与适应策略极为丰富，但有关其形态多样化的宏观进化格局及驱动机制仍未得到充分阐明。本研究基于对 161 个现生属体型与形态演化的系统分析，覆盖了长达 4 亿余年的演化历程，并囊括了大部分属级层面的形态变异。研究结果表明，头足类形态多样化经历了四个主要阶段，期间伴随着演化速率与差异度的显著转变。进一步分析显示，形态演化与海水溶解氧、温度及盐度等环境因子之间呈现非线性关联。同时，更广阔的地理分布范围、更宽泛的温度耐受性以及以摄食策略为代表的生态特征，均对形态进化的多样化过程起到了积极的促进作用。总体而言，本研究揭示了气候、生态及生物地理因素在深时尺度上对头足类形态演化所产生的协同作用。

关键词：头足类身体；形态多样化；宏观进化；古气候变化；几何形态测量学

The tempo and drivers of body macroevolution in extant cephalopods

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Abstract：Cephalopods evolved from Late Cambrian ancestors approximately 500 million years ago, progressing from simple, externally shelled forms to modern species with diverse and complex morphologies. Despite their varied body plans and adaptations, the macroevolutionary patterns and drivers of their morphological diversification are not fully understood. We examine body size and shape evolution across 161 extant genera, spanning over 400 million years of evolutionary history and covering most genus-level variation. Analyses reveal four major phases of morphological diversification with shifts in evolutionary rates and disparity. Morphological evolution shows nonlinear relationships with environmental factors such as seawater oxygen, temperature, and salinity. Additionally, wider habitat ranges, thermal tolerance, and ecological traits like feeding strategies contribute to increased morphological diversity. These results reveal the combined influence of climatic, ecological, and biogeographic factors on cephalopod morphology through deep time.

Key words: Cephalopods body, morphology diversification, paleoclimate change, macroevolution, geometric morphometrics

南极犬牙鱼（*Dissostichus mawsoni*）胃中线虫（*Anisakidae*）感染情况及宿主–寄生虫营养相互作用研究

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摘要：鳞头犬牙南极鱼寄生虫的感染情况关乎其作为商业渔业资源的价值，且探究宿主-寄生虫相互作用关系便于理解寄生虫在海洋生态系统中重要作用。故本研究将宿主鱼种的基础生物学信息、摄食及感染情况联系起来，同时利用稳定同位素分析手段，探究寄生虫感染特性及宿主宿主-寄生虫的相互作用关系。研究表明犬牙鱼感染率显著受到特定摄食对象的影响，并通过对胃含物数据进行机器学习分析指明了将寄生虫传递至犬牙鱼体内主要的中间宿主。除摄食外，寄生虫的感染还受到栖息地、性成熟度等因素影响。本研究推测异尖线虫倾向主动吸收来自宿主代谢的产物。研究中支持了寄生虫可能会影响宿主的能量学或代谢特征，以及宿主的生理状况，进而影响宿主的同位素特征的观点；揭示了寄生虫感染会影响宿主生长速率进而影响宿主种群动态的情况；同时指出将寄生虫纳入食物网及渔业模型，有助于提高提高营养动力学的准确性以及基于生态系统的宿主渔业管理。

关键词：营养相互作用、寄生虫、南极犬牙鱼、摄食、食物网

Nematode (*Anisakidae*) infection in the stomach of Antarctic toothfish (*Dissostichus mawsoni*) and host-parasite trophic interactions

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Abstract：Parasites are an important but overlooked component in the marine ecosystem, however, the study on parasites of Antarctic fish, especially Antarctic toothfish (TOA, Dissostichus mawsoni), remains limited. Parasitic infection is closely linked to the economic value of TOA, which is a commercial fishery resource, while the presence of parasites also contributes to the complexity of marine food webs. Investigating host-parasite interactions is thus essential for understanding their important roles in marine ecosystem. Therefore, this study linked baseline biological information, feeding ecology, and infection status of the TOA species, while employing stable isotope analysis to explore the characteristics of parasite infection and host–parasite trophic interactions. The results showed that infection rates in TOA were significantly influenced by specific prey items, and machine learning analysis of stomach-content data identified the principal intermediate/paratenic hosts responsible for transmitting parasites to toothfish. Beyond feeding, parasite infection was also affected by factors.

Key words: Trophic interaction, parasite, toothfish, diet, food web

密斑刺鲀（*Diodon hystrix*）染色体水平基因组组装和注释

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摘要：密斑刺鲀（*Diodon hystrix*），俗称豪猪鱼，是一种珊瑚礁硬骨鱼，其广泛分布在太平洋、大西洋、印度洋和地中海的热带和亚热带水域。然而，目前仍缺乏该物种的高质量参考基因组，这阻碍了密斑刺鲀的生物学和基因组育种的进一步研究。在这里，我们使用 PacBio HiFi、超长读取和 Hi-C 测序将基因组组装到染色体尺度。密斑刺鲀的 713.62 Mb 的基因组中有 98.63%锚定在 23 条染色体上，支架 N50 长度为 31.52 Mb。组装的基因组包含 284.19 Mb 的重复序列，占全部基因组的 39.82%。组装后的基因组的 BUSCO 完整性得分为 97.7%。共鉴定出 23171 个蛋白质编码基因，其中 22221 个进行了功能注释。总之，高质量的参考基因组为开发刺鲀资源提供了有用的基因组工具，并支持未来对该物种的功能基因组学研究。

关键词：密斑刺鲀，基因组，染色体，功能注释

Chromosome-level genome assembly and annotation of the porcupine fish (*Diodon hystrix*)

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Abstract： The porcupine fish (*Diodon hystrix*), a coral reef teleost, is widely distributed in the tropical and subtropical waters of the Pacific, Atlantic, Indian Oceans, and Mediterranean. However, the absence of a high-quality refference genome hinders further research on biology and genomic breeding. Here, we assembled the genome to chromosome-scale using PacBio HiFi, ultra-long reads, and Hi-C sequencing. A total of 98.63% of the 713.62 Mbp genome is anchored into 23 chromosomes, with a scaffold N50 of 31.52 Mb. The assembled genome contained 284.19 Mb of repeat sequences, accounting for 39.82% of the assembly. The assembled genome achieved a BUSCO completeness score of 97.7%, with 23,171 protein-coding genes identified, of which 22,221 were functionally annotated. In summary, the high-quality reference genome provides useful genomic tools for exploiting the genomic resource of D. hystrix and supports the functional genomic study of this species in the future.

Key words: Diodon hystrix，genome，chromosome，functional annotation

基于环境 DNA 宏条形码技术的海南“两江一河”河口海域及三亚珊瑚礁区鱼类多样性研究

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摘要：根据 2024 年 7 月-8 月在海南“两江一河” (南渡江、昌化江、万泉河)河口海域及三亚珊瑚礁分布区 18 个点位的鱼类环境 DNA(eDNA)调查资料，分析了鱼类种类组成和群落结构特征。结果显示，通过 eDNA 宏条形码共检测到 28 目 59 科 108 属 144 种鱼类，其中鱼类群落以鲈形目(Perciformes)鱼类为主，占鱼类种类总数的 25.69%。PCoA 分析结果表明昌化江口和南渡江口、万泉河口及三亚珊瑚礁区之间鱼类群落结构差异明显，分离度较高。RDA 分析表明溶解氧、盐度、亚硝酸盐和水深是鱼类群落区域分布的主要影响因子。Spearman 相关性检验表明磷酸盐与 Shannon 多样性、Simpson 多样性、Pielou 指数显著负相关，溶解氧和 Chao1 和 ACE 指数呈正相关。总体上，本研究表明 eDNA 宏条形码技术能够快速分析鱼类种类组成和分布，其在我国近岸海域鱼类资源监测中是一种极具潜力和重要性的工具。

关键词：环境 DNA 宏条形码；鱼类多样性；高通量测序；河口海域；三亚珊瑚礁区

A Study on Fish Diversity in the Estuary Areas of Three Main Rivers and the Sanya Coral Reef Area in Hainan Island Based on eDNA Metabarcoding Technology

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Abstract：Based on the eDNA metabarcoding survey data of fish in the estuary areas of three main rivers and the Sanya coral reef area during July-August 2024, this study analyzed the fish species composition and community structure characteristics. The results revealed that a total of 144 fish species, belonging to 108 genera, 59 families, and 28 orders, were detected using eDNA metabarcoding method. Among them, the fish community was predominantly composed of Perciformes, accounting for 25.69% of the total fish species. PCoA indicated the fish community structure in the Changhua River estuary showed marked differences and higher separation from those of the Nandu River estuary, Wanquan River estuary, and Sanya coral reef area. RDA indicated that DO, salinity, NO_2^-, and water depth were the primary environmental factors. Overall, this study demonstrates that eDNA metabarcoding technique is capable of rapidly analyzing fish species composition and distribution, rendering it a highly promising and significant tool for monitoring fish resources in coastal waters of China.

Key words: eDNA metabarcoding; fish diversity; high-throughput sequencing (HTS); estuary area; Sanya coral reef area

维生素 D3 对中华鲟糖脂代谢的影响

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摘要：1,25-二羟基维生素 D3 是维生素 D3 的活性激素形式，除了在矿物质体内平衡中发挥作用外，它在多种生理过程中是不可或缺的。然而，其对中华鲟葡萄糖和脂质代谢的调节作用仍未得到充分验证。本研究采用腹腔注射和体外肝细胞培养的方法来研究这些作用。腹腔注射 125（OH）$_2$ D$_3$ 导致血糖（GLU）和甘油三酯（TG）水平显著降低。体外实验表明，用 1,25（OH）$_2$ D$_3$ 处理肝细胞导致细胞 TG 含量降低，并伴有 ATGL 和 HSL mRNA 表达和活性上调。此外，1,25（OH）$_2$ D$_3$ 增强了丙酮酸激酶（PK）的活性，这是一种关键的糖酵解限速酶。线粒体功能的研究表明，1,25（OH）$_2$ D$_3$ 提高了细胞 ATP 水平和乙酰辅酶 a 含量。这些结果表明，1,25（OH）$_2$ D$_3$ 调节中华鲟肝脏中的葡萄糖和脂质代谢，促进线粒体 ATP 的产生，以满足生理能量需求。

关键词：1,25 (OH)$_2$ D$_3$;中华鲟;糖脂代谢;线粒体功能;肝细胞

Effects of Vitamin D3 on Glucose and Lipid Metabolism in Chinese Sturgeon (*Acipenser sinensis*)

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Abstract：Beyond its established role in mineral homeostasis, 1,25-Dihydroxyvitamin D3 , the active hormonal form of vitamin D3, is integral to a variety of physiological processes. However, its regulatory effects on glucose and lipid metabolism in the Chinese sturgeon remains inadequately characterized. This study employed intraperitoneal injection and in vitro hepatic cell culture to investigate these effects. The intraperitoneal administration of 1,25(OH)$_2$ D$_3$ resulted in a significant reduction in blood glucose (GLU) and triglyceride (TG) levels. In vitro experiments demonstrated that treatment of hepatocytes with 1,25(OH)$_2$ D$_3$ led to a decrease in cellular TG content, accompanied by an upregulation in mRNA expression and activity of ATGL and HSL. Furthermore, 1,25(OH)$_2$ D$_3$ enhanced the activity of pyruvate kinase (PK), a key glycolytic rate-limiting enzyme. Investigation of mitochondrial function revealed that 1,25(OH)$_2$ D$_3$ elevated cellular ATP levels and acetyl-CoA content.

Key words: 1,25(OH)$_2$ D$_3$; Chinese sturgeon; Glycolipid metabolism; Mitochondrial function; Hepatic cell

北部湾鱼类物种多样性研究进展

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摘要：系统总结北部湾海域鱼类多样性的研究历程，梳理区域内鱼类物种组成与保护现状，以期为生物多样性保护提供科学依据。通过整合历年来相关调查研究成果，本文整理出北部湾最新鱼类物种记录，并分析其鱼类区系特征。目前，北部湾共记录鱼类 40 目 166 科 503 属 1059 种，主要以暖水性鱼类为主。区系中包含 1 种国家一级保护物种和 9 种国家二级保护物种，另有 54 种鱼类被评估为 IUCN 近危及以上等级，显示出较高的保护关注度。总体来看，北部湾鱼类多样性丰富，但也受到生态保护政策、气候变化等多重因素的影响。未来应加强中越之间的合作与数据库建设，持续拓展调查范围，深入推进区域鱼类多样性的保护与可持续利用，同时加快中国鱼类数据库的构建，以更有效地支撑生物多样性管理工作。

关键词：南海西北部；鱼类；物种多样性；生态保护；研究概况

Review of Fish Species Diversity in the Beibu Gulf

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Abstract： This study reviews the research history of fish diversity in the Beibu Gulf, summarizes species composition and conservation status, and provides a scientific basis for biodiversity conservation. By integrating past survey results, we compiled an updated checklist of fish species in the region and analyzed their faunal characteristics. To date, 1,059 species representing 40 orders, 166 families, and 503 genera have been recorded, dominated by warm-water fishes. The fauna includes one species under first-class national protection and nine under second-class protection, as well as 54 species assessed as Near Threatened or above by the IUCN, highlighting high conservation concern. Overall, the Beibu Gulf supports rich fish diversity, but it is subject to multiple pressures, including ecological policies and climate change. Future work should strengthen cooperation between China and Vietnam, expand survey coverage, and promote database development, thereby advancing conservation and sustainable use of regional fish diversity and accelerating the establishment of a national fish database.

Key words: northwestern South China Sea; fish; species diversity; ecological conservation; research overview

维生素 D3 对中华鲟性腺发育的影响

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摘要：本研究采用腹腔注射和体外垂体细胞培养来研究这些影响。腹腔注射 1,25（OH）$_2$ D$_3$ 导致雌性中华鲟幼鱼血浆 FSH、LH 和 E2 水平显著升高，但对雄性中华鲟没有显著影响。性腺转录组分析显示，在添加 1,25（OH）$_2$ D$_3$ 的实验组中存在多个差异表达基因（DEGs）。通过 KEGG 通路分析发现，这些基因对氧化磷酸化、花生四烯酸代谢、卵巢类固醇生成及卵母细胞减数分裂等过程产生显著影响。性腺代谢组分析表明，1,25（OH）$_2$ D$_3$ 通过磷酸戊糖途径和甘油磷脂代谢途径促进中华鲟的葡萄糖与脂质代谢。总体而言，这些研究结果表明，1,25（OH）$_2$ D$_3$ 能够调节中华鲟性腺激素水平，并通过调控葡萄糖与脂质代谢来满足性腺发育的能量需求。本研究为维生素 D3 调控中华鲟性腺发育过程中葡萄糖与脂质代谢的机制提供了重要基础性见解。

关键词：中华鲟，维生素 d3，性腺发育

Effects of Vitamin D3 on gonadal development in Chinese Sturgeon (*Acipenser sinensis*)

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Abstract： This study employed intraperitoneal injection and in vitro pituitary cell culture to investigate these effects. The intraperitoneal administration of 1,25(OH)$_2$ D$_3$ resulted in a significant increasing plasma FSH ,LH and E2 levels in female Juvenile Chinese Sturgeon. Gonadal transcriptome analysis revealed a number of DEGs in the 1,25(OH)$_2$ D$_3$ -supplemented groups with KEGG pathway analysis highlighting impacts on oxidative phosphorylation, arachidonic acid metabolism, ovarian steroidogenesis, and oocyte meiosis.indicating that 1,25(OH)$_2$ D$_3$ may play a role in enhancing reproductive signaling pathways. Gonadal metabolome analysis revealed that 1,25(OH)$_2$ D$_3$ promote glucose and lipid metabolism in Chinese sturgeon by pentose phosphate pathway and glycerophospholipid metabolic pathway, Overall, these research results indicate that 1,25(OH)$_2$ D$_3$ can regulate the levels of gonadotropins in Chinese sturgeon and fuel the energy requirements for gonadal development by regulating glucose and lipid metabolism.

Key words: Chinese Sturgeon，Vitamin D3，gonadal development

基于耳石形态对新疆叶尔羌河三种裂腹鱼类的鉴定分析

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摘要：为探究中国新疆塔里木河水系叶尔羌河三种土著裂腹鱼属鱼类（塔里木裂腹鱼、宽口裂腹鱼和厚唇裂腹鱼）的耳石形态特征及差异，本研究共分析 93 尾（塔里木裂腹鱼 27 尾、宽口裂腹鱼 39 尾、厚唇裂腹鱼 27 尾）样本，通过 6 项耳石基础形态参数（耳石面积、耳石最大半径、耳石最小半径、耳石周长、耳石长、耳石宽），推导得出 6 个形态因子（F1-F6）和 7 个形态指数（RO、FF、CI、RE、EL、RR、AR）。结合耳石 77 个傅里叶系数的判别分析显示，三种鱼类间存在显著形态差异。所有物种的耳石形态与标准体长均呈显著幂函数关系，决定系数 R^2 介于 0.409-0.749 之间。对 7 项传统耳石形态指标的主成分分析（PCA）解释了 81.243% 的变异，物种总体鉴别率达 81.65%；进一步对 77 个傅里叶谐波值进行主成分分析后，鉴别精度显著提升，前 3 个主成分累计解释 77.49% 的总变异，鉴别率达 100.00%。聚类分析将塔里木裂腹鱼与厚唇裂腹鱼聚为一支，再与宽口裂腹鱼聚类，表明三者间存在明显形态分化。耳石形态指数与椭圆傅里叶分析均适用于区分不同鱼类的表型单元，本研究首次将耳石形态应用于裂腹鱼属鱼类鉴定，深入阐述了物种分布与演化历史，为裂腹鱼属鱼类的物种鉴定、系统分类提供参考，也为制定有效的物种保护措施、促进物种及重要栖息地的可持续管理提供科学依据。

关键词：裂腹鱼类；耳石形态分析；椭圆傅里叶变换；物种鉴别

Identification of Schizothorax species in Yarkand River, (Xinjiang, China) based on otolith morphology

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Abstract： This study explored the morphological characteristics and differences of the otoliths in three native species, Schizothorax biddulphi, S. eurystomus and S. curvifrons, in the Yarkand River of the Tarim River, Xinjiang, China. A total of 93 specimens (27 S. biddulphi, 39 S. eurystomus, and 27 S. curvifrons)were analyzed using six basic otolith morphological parameters (OA, Rmax, Rmin, OP, OL, OW) to derive six factors (F1, F2, F3, F4, F5, F6) and seven indices (RO, FF, CI, RE, EL, RR, AR) for morphological assessment. A discriminant analysis incorporating 77 Fourier coefficients of the otoliths revealed distinct morphological differences among the species. A significant power function relationship between otolith morphology and standard length was observed across the species, with R2 values ranging from 0.409 to 0.749. Principal component analysis (PCA) of 7 traditional otolith morphological indicators explained 81.243% of the variance, yielding an overall species discrimination rate of 81.65%. Further PCA of 77 Fourier harmonic values enhanced the discrimination accuracy.

Key words: Schizothorax; otolith morphological analysis; elliptic Fourier transform; species discrimination

鸭绿江径流对虾夷扇贝幼虫输移路径的影响研究

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摘要：虾夷扇贝（*Patinopecten yessoensis*）是中国北方的重要经济贝类，其幼虫在鸭绿江径流的影响下，能够被输送到数百公里之外，导致输移路径的不确定性。本文旨在通过数值模拟探讨鸭绿江径流对虾夷扇贝幼虫的时空分布及输移路径的影响，为天然幼虫采集提供依据。采用有限体积法（FVCOM）构建北黄海的三维水动力模型，同时结合潮汐、温度、盐度等因素进行验证。在此基础上，构建虾夷扇贝的个体模型（IBM），模拟幼虫的生物-物理耦合特征。模拟结果表明，虾夷扇贝幼虫在鸭绿江径流影响下，主要向西南的老铁山迁移，并形成高密度附着区。与无鸭绿江输入情况相比，有流域作用时幼虫的输移路径和最终分布明显不同。本研究为虾夷扇贝幼虫的分布特征提供了有效预测模型，结合水动力学特征，为海洋生态研究及养殖管理提供了重要的实证依据。希望本研究能为后续的虾夷扇贝资源管理和可持续发展提供参考。

关键词：虾夷扇贝、鸭绿江径流、数值模拟、输移路径、生物物理耦合模型

Effects of the Yalu River Runoff on the Transport of Yesso Scallop Larvae

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Abstract： Yesso scallop (*Patinopecten yessoensis*) is a significant economic shellfish in northern China. The larvae, farmed in Changhai County, Dalian, are transported hundreds of kilometers due to the Yalu River runoff, leading to uncertainty in their movement paths. Thus, predicting the spatiotemporal distribution patterns of Yesso scallop larvae is crucial for guiding natural seed collection. This study employs numerical simulation to explore the migration routes and distribution of scallop larvae influenced by the Yalu River runoff. Utilizing the FVCOM (Finite-Volume Coastal Ocean Model), a three-dimensional hydrodynamic model of the North Yellow Sea was established, considering factors like river runoff, tides, temperature, and salinity. Verification against measured data confirmed the model's accuracy. Based on these observations and accounting for survival rates and climatic changes, an individual-based model (IBM) was developed. By integrating the super-individual method and Lagrangian particle tracking, the study constructed a bio-physical coupling model to predict larval distributio

Key words: Yesso scallop、Yalu River runoff、Numerical simulation、Transport pathways、Bio-physical coupling model

基于贝叶斯状态空间剩余产量模型的南海蓝圆鲹资源评估

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摘要：蓝圆鲹（*Decapterus maruadsi*）是中国南海的中上层重要经济鱼种，由于气候环境变化和人类活动的多重因素，南海蓝圆鲹种群数量波动明显，该渔业资源的养护和可持续开发，需要资源状态的有效评估和科学合理的管理建议。本文基于1990—2023年渔获量、捕捞努力量等渔业生产数据，使用贝叶斯状态空间剩余产量模型对南海蓝圆鲹种群进行了资源评估，并通过敏感性分析、回溯性分析等对模型的稳定性和适应性进行了进一步的探索。资源评估结果显示：2023年南海蓝圆鲹生物量为64万吨，种群最大可持续产量MSY为49万吨，高于2023年的渔获量（36万吨）；2023年生物量略高于获得MSY所需的生物量水平BMSY，捕捞强度低于获得MSY所需的强度（B2023/BMSY=1.08，F2023/FMSY=0.66），表明当前种群处于健康状态，但补充型过度捕捞的风险已经升至30%。

关键词：南海；中上层种类；蓝圆鲹；JABBA

Stock assessment of South China Sea Japanese scad Based on Just Another Bayesian Biomass Assessment

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Abstract： The Japanese scad (*Decapterus maruadsi*) is a key mid-to-upper-layer economic fish species in the South China Sea. Its population fluctuates significantly due to climate change and human activities. Effective resource assessment and science-based management are essential for its conservation and sustainable exploitation. Using fishery production data (catch and effort) from 1990 to 2023, this study applied a Bayesian state-space surplus production model to evaluate the Japanese scad population. Sensitivity and retrospective analyses were conducted to explore the model's stability and adaptability. Results show that in 2023, the biomass was 640,000 tons, with a maximum sustainable yield (MSY) of 490,000 tons, exceeding the actual catch of 360,000 tons. The 2023 biomass slightly exceeded the level required for MSY (B2023/BMSY = 1.08), and fishing intensity was below the MSY level (F2023/FMSY = 0.66), indicating a healthy population. However, the risk of recruitment overfishing has risen to 30%.

Key words: South China Sea; Pelagic fish; Japanese scad; JABBA

中国海水硅藻新记录——类嗜寒舟形藻

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摘要：通过 18S rDNA 和 rbcL 序列分析和系统分析对采集的底栖硅藻样品进行分子鉴定。结果显示，在辽宁省大连市采集的底栖硅藻样品中发现 1 个新记录种—类嗜寒舟形藻(*Navicula criophiliforma Witkowski*, Riaux-Gobin & Daniszewska-Kowalczyk)。光镜和扫描电镜观察结果显示，该种壳面呈线形披针形，壳面顶端尖圆形，壳缝简单，呈线形，近缝端膨大呈水滴状，稍偏向壳体一侧，远缝端延伸成钩状，弯向一侧，中轴区狭，中心区形状不规则，壳面中部胸骨略微隆起，壳面横线纹由单列的投币口状的孔纹组成，中央区横线纹略为平行排列，在接近两末端处略呈会聚状，横线纹 10 μm 内 11~13 条，符合舟形藻属特征。

关键词：舟形藻属；新记录种；鉴定；海洋底栖硅藻

A new recorded diatom species in China—— Navicula criophiliforma Witkowski, Riaux-Gobin & Daniszewska-Kowalczyk

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Abstract： In order to enrich the diversity of benthic diatoms in the Yellow Sea, a systematic sampling survey was carried out along costal of this area. The morphological characteristics and ultrastructure of benthic diatom samples were observed in detail by light microscope and scanning electron microscope, and 18S rDNA and rbcL sequence analysis and phylogenetic analysis were identified. A new recorded species, Navicula criophiliforma Witkowski, Riaux-Gobin&Daniszewska-Kowalczyk, was found in the intertidal zone of Heishijiao in Dalian, Liaoning Province. The results show that: (1) valves linear lanceolate with rather acutely roundedapices. (2) The raphe fissures are simply straight, the proximal raphe end is slightly enlarged, drop-like, and inclined to the valve sid, the terminal raphe end extends into a hook shape. (3) The axial area is narrowly linear and the central area is irregularly circular. Sternumslightly elevatedin the valve middle. (4) Transapical striae composed of apically oriented slit-likeareolae, which are arranged radially in the middle and gather at both ends.

Key words: Navicula; new record species; identification; marine benthic diatoms

鲫不同地理种群的生长特征及其环境影响因子研究

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摘要：为探究鲫(*Carassius auratus*)生长特征与环境因子的关系，研究选取地理环境具有显著差异的 7 个湖泊(松花湖、乌梁素海、衡水湖、洪泽湖、高邮湖、太湖和洱海)。基于体长-体重关系、生长系数 k、渐进体长 L_∞及拐点年龄 t_1等生长参数流量化不同水域鲫的生长发育情况，并进一步结合曼特尔检验(Mantel Test) 、斯皮尔曼相关分析(Spearman) 和冗余分析(RDA)等多种方法，解析环境因子对其生长的影响。结果表明：(1)不同种群间平均体长、平均体重存在显著差异(P<0.05)；生长指数 b 介于 2.96—3.15，纬度较低的湖泊，鲫呈现匀速生长，纬度较高的湖泊，呈现正异速生长。(2)所有种群均表现为快速生长型(k>0.2)；渐进体长 L_∞为 243.50—278.25 mm；松花湖和乌梁素海拐点年龄 t_1在 2 龄以上，其余均在 1 龄左右；生长性能指数 ϕ' 处于 4.51—4.76。(3)分析显示，地理空间因子(海拔、纬度、岸线发育系数)与理化参数(pH、浊度、水深)共同调控生长特征，且地理空间因子(海拔和岸线发育系数)解释度达 76.4% (P<0.05)，占主导地位。本研究揭示了不同地理群体鲫生长策略及其与环境之间的关系，为进一步探索鲫的生长生态特征和其对环境变化的响应提供了理论依据。

关键词：生长特征；海拔；岸线发育系数；冗余分析；鲫

Growth characteristics and environmental influencing factors of different geographical populations of Carassius auratus

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Abstract: To explore the relationship between the growth characteristics and environmental factors of *Carassius auratus*, this study selected seven lakes with significant geographical differences(Songhua Lake、Wuliangsu Lake、Hengshui Lake、Hongze Lake、Gaoyou Lake、Taihu Lake and Erhai). Based on growth parameters including the length-weight relationship, growth coefficient (k), asymptotic length (L∞), and inflection age (t1), it quantitatively assessed the growth and development of C. auratus in different waters. Furthermore, methods such as Mantel test, Spearman correlation, and redundancy analysis were employed to analyze the impact of environmental factors on their growth. The results showed that: (1) There were significant differences in the average body length and weight among different populations (P<0.05). The growth index b ranged from 2.96 to 3.15, with C. auratus in lakes at lower latitudes exhibited isometric growth, while those in lakes at higher latitudes showing positive allometric growth. (2) All populations demonstrated a fast-growth pattern (k>0.2), with asymptotic length L∞ ranging from 243.50 to 278.25 mm. The inflection age t1 exceeded 2 years in Songhua Lake and Wuliangsuhai Lake populations, while that in the other lakes was around 1 year old. (3) The growth performance index φ′ ranged from 4.51 to 4.76. The analysis revealed that geographical spatial factors (altitude, latitude, and shoreline development coefficient) and physicochemical parameters (pH, turbidity, and water depth) jointly regulated the growth characteristics. Moreover, geographical spatial factors (altitude and shoreline development coefficient) accounted for 76.4% of the variation (P<0.05) and played a dominant role. This study elucidated the growth strategies of C. auratus populations across different geographical regions and their relationship with the environment, providing a theoretical basis for further exploring the growth ecological characteristics of C. auratus and its response to environmental changes.

Key words: Growth parameters; Altitude; Shoreline development index; Redundancy analysis; *Carassius auratus*

龙泉紧水滩倒刺鲃省级水产种质资源保护区水体重金属污染特征及健康风险评价

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摘要：为探明龙泉紧水滩倒刺鲃省级水产种质资源保护区水域的重金属污染程度，评价保护区水域的重金属健康风险，于 2022 年-2023 年分季节采集 5 个站位水质样品，利用 ICP-MS 检测了 11 种重金属元素的含量，运用多元统计方法和健康风险评价模型定量评价了重金属的污染特征和健康风险。结果表明，保护区水域水体中重金属元素的平均质量浓度大小顺序为：Fe>Ni>Mn>Zn>Cu>Cr>As>Se>Pb>Hg>Cd。通过主成分分析得到 4 个主成分，主成分一包括 Mn、As 和 Pb，主成分二包括 Fe 和 Ni，主成分三包括 Cr、Cu 和 Zn，主成分四包括 Cd 和 Hg。健康风险评价表明，饮用水是主要暴露途径，致癌金属元素 Cr、As 和 Cd 引起的年均健康风险数量级为 10-10 a-1-10-6 a-1，非致癌金属元素（Mn、Fe、Ni、Cu、Zn、Hg、Pb、Se）对成人和儿童产生的年均健康风险值远低于 I 级风险水平，属可忽略风险，对保护区范围的暴露人群造成的危害较小。内梅罗综合污染指数显示，冬季污染程度高于其他季节。该研究结果可为保护区水域的水环境管理和保障水库的供水安全提供参考依据。

关键词：水产种质资源保护区；重金属；污染特征；健康风险评价

Characterization of Heavy Metal Contamination in Water and Assessment of Health Risks in the Longquan Jinshuitan Spiny Barbel (*Spinibarbus denticulatus*) Provincial Aquatic Germplasm Resources Reserve

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Abstract: To investigate the heavy metal pollution levels in the aquatic environment of the Longquan Jinshuitan *Spinibarbus denticulatus* Provincial Aquatic Germplasm Resource Conservation Area and assess the health risks associated with heavy metals in the area, water samples were collected seasonally from five monitoring stations between 2022 and 2023. The concentrations of 11 heavy metal elements were measured using ICP-MS, and multivariate statistical methods and health risk assessment models were applied to quantitatively evaluate the pollution characteristics and health risks of heavy metals. The results showed that the average mass concentrations of heavy metal elements in the water of the conservation area followed the order: Fe > Ni > Mn > Zn > Cu > Cr > As > Se > Pb > Hg > Cd. Principal component analysis identified four principal components: the first included Mn, As, and Pb; the second included Fe and Ni; the third included Cr, Cu, and Zn; and the fourth included Cd and Hg. The health risk assessment indicated that drinking water is the primary exposure pathway. The annual average health risks posed by carcinogenic metals (Cr, As, and Cd) ranged from 10^{-10} a^{-1} to 10^{-6} a^{-1}. The annual average health risks from non-carcinogenic metals (Mn, Fe, Ni, Cu, Zn, Hg, Pb, Se) for both adults and children were significantly below the Level I risk threshold, representing negligible risks and posing minimal harm to the exposed population in the conservation area. The Nemerow comprehensive pollution index revealed that pollution levels were higher in winter compared to other seasons. The findings of this study can provide a reference for water environment management in the conservation area and ensure the safety of the reservoir's water supply.

Key words: Aquatic germplasm resource conservation areas; Heavy metals; Pollution characterization; Health risk assessment

探究 2000 年以后中国近海渔业资源评估数据和方法的演变历程

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摘要：中国是全球最大海洋渔业生产国，近海渔业对粮食安全与经济就业至关重要，但面临选择性低、渔业监测体系不完整与专业能力不足等挑战。为推进渔业可持续管理，本文回顾了 2000–2025 年间中国近海 185 篇评估文献，构建物种-数据-方法数据库，系统分析其演变趋势。结果显示：1）近十年相关研究数量迅速增长，2019 年后尤为显著；2）数据类型从数据不足的类型逐步过渡至数据适中的类型，并出现生态系统数据，但始终缺乏数据丰富类型；3）评估方法以调查类和数据有限方法为主，生态系统模型使用渐增；4）评估物种多为底层及小型中上层鱼类，无脊椎动物研究不足；5）各海区科研合作呈多中心格局，但跨海区协作与数据共享仍不足。建议构建统一监测与数据共享体系，提高数据适中类型利用效率，发展适用于本土渔业特征的评估方法，加强无脊椎动物资源研究，并通过模拟研究验证不同方法对生态系统管理的有效性，支撑中国近海渔业的长期可持续利用。

关键词：中国近海；渔业资源评估；混合渔业；生态系统模型；可持续渔业管理

Evolution of Data and Methods in China’s Coastal Fisheries Stock Assessments since 2000

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Abstract： China is the world’s largest marine fishing producer, and its coastal fisheries are crucial to food security, the economy, and employment; however, they face challenges such as low selectivity, an incomplete monitoring system, and limited professional capacity. To advance sustainable management, this study reviews 185 assessment papers on China’s coastal waters from 2000–2025, constructs a species–data–method database, and systematically analyzes temporal trends. The results show: (1) a rapid increase in publications over the past decade, especially after 2019; (2) a shift in data types from predominantly Data-poor to Data-moderate, with the emergence of Eco-data, while Data-rich remains scarce; (3) assessment methods are dominated by survey-based and data-limited approaches, with growing use of ecosystem models; (4) target species are mainly demersal and small pelagic fishes, with insufficient research on invertebrates; and (5) research collaboration forms a multi-center network, yet cross-sea-area cooperation and data sharing remain insufficient.

Key words: China’s coastal fisheries; stock assessment; mixed fisheries; data-limited condition; ecosystem models; sustainable fisheries management

水产常见益生菌的种类、鉴定及应用概述

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摘要：在水产养殖中，益生菌在改善水产动物抗病性、免疫力、健康状况、肠道微生物结构和调控水质方面起着重要作用。益生菌在水产养殖中的应用可以减少抗生素和水产违禁药品等的使用。在水产养殖中推广益生菌有助于促进水产养殖业健康发展并保障人类健康。本文概述了常用益生菌种类、益生菌的鉴定方法和在水产养殖业中的应用，探讨了益生菌在水产养殖领域面临的挑战和未来发展方向，为实现现代水产养殖的绿色可持续发展提供参考。

关键词：益生菌；抗生素；水产养殖；鉴定

Overview of Species, Identification, and Applications of Common Aquatic Probiotics

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Abstract: In aquaculture, probiotics play a crucial role in enhancing the disease resistance, immunity, overall health, gut microbiota structure, and water quality regulation of aquatic animals. The use of probiotics can significantly reduce reliance on antibiotics and banned aquatic drugs. Promoting probiotic applications in aquaculture not only supports the sustainable development of the industry but also safeguards human health. This paper provides an overview of common probiotic types, identification methods, and their applications in aquaculture. It also addresses the challenges faced and future directions for probiotic research, offering insights into achieving green and sustainable modern aquaculture.

Key words: Probiotics; Antibiotics; Aquaculture; Identification

基于肌肉元素指纹图谱分析的鳗鲡地理溯源研究

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摘要：鳗鲡（*Anguilla japonica*）广泛分布于长江及近海水域，是重要洄游型鱼类，然而因过度捕捞与环境污染等问题，鳗鲡的数量日益减少，为了更好鉴别和保护不同水域分布的鳗鲡物种，本研究利用鳗鲡肌肉元素指纹差异对不同来源鳗鲡进行判别和溯源。结果表明，不同来源的鳗鲡具有代表性元素组成，其中宿迁水域（SQ）鳗鲡的特征元素为 Na，其含量显著低于其他水域；崇明水域（CM）鳗鲡的特征元素为 Hg、V，Hg、V 含量显著高于其他水域；嵊泗水域（SS）鳗鲡的特征元素为 Mg、Na，其含量显著高于其他水域。多元分析筛选出鳗鲡肌肉中 V、Hg、Na 3 种判别元素在长江及周边水域具有不同的空间分布模式。将筛选出的特定判别元素通过 LDA 和 OPLS-DA 分析，能够有效区分不同产地的鳗鲡群体，并可对未知来源样本实现快速产地追溯与验证。可见，肌肉元素指纹分析技术可应用于市场监管领域，实现对未知来源样品的有效判别和溯源。

关键词：鳗鲡，元素指纹分析，长江流域，近海，地理溯源

Study on geographical traceability of Anguilla japonica based on muscle elements fingerprint analysis

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Abstract： The Japanese eel (*Anguilla japonica*) is an economically important migratory fish species, with the population declining due to issues such as overfishing and environmental pollution. Therefore, it’s necessary to trace the origin of A. japonica in the Yangtze River Basin and its surrounding waters. This study employs muscle EFA to distinguish and trace different populations of A. japonica. The results indicate that A. japonica from different sources have representative elemental compositions, which from Suqian (SQ), Chongming (CM), Shengsi (SS) are characterized by the element of Na; Hg and V; Mg and Na, respectively. By applying LDA, OPLS-DA to these specific discriminant elements, different geographical populations of A. japonica can be effectively distinguished, enabling rapid origin tracing and verification of unknown samples. Thus, the geographic traceability technology based on A. japonica muscle elemental composition can be applied in market supervision to effectively trace the origin of unknown samples.

Key words: *Anguilla japonica*; elemental fingerprint analysis (EFA), Yangtze River Basin, offshore, geographic traceability

环境因子与适应性分化交互作用下的中华绒螯蟹生态位格局成因

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摘要：全球气候变化正在重塑海洋生物的地理分布与生态位结构。中华绒螯蟹作为我国沿海地区典型的河海洄游型水产经济物种，具有较强的环境适应性与扩散能力，已在欧美等地建立入侵种群。为评估其在未来气候情景下的潜在扩散趋势及生态响应机制，本研究基于 1970 年以来中华绒螯蟹全球分布数据构建了全球分布模型（G-SDM）与亚洲太平洋原生区模型（N-SDM），预测其陆地适生区与海洋繁殖育幼区的潜在变化。结果表明，中华绒螯蟹的潜在适生区呈向高纬度扩张的趋势，高排放情景下分布格局明显北移，阿拉斯加等高纬度地区成为其扩散的热点区域。MESS 与 MoD 分析揭示未来气候异常程度及主导变量存在显著空间异质性。欧洲和北美地区的最不相似变量以年温差和最干季降水等因子为主，亚洲主要受最暖季降水因子驱动。生态位动态分析显示，在高排放情景下中华绒螯蟹的生态位重心北、重叠度下降。但环境适应性整体变化有限，反映出其对气候变化的高响应性。

关键词：气候变化，分布格局，地理分化，物种分布模型，生态位扩展

The pattern of the ecological niche of Eriocheir sinensis is shaped by the interaction of environmental factors and adaptive differentiation

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Abstract：Global climate change is altering the distribution and ecological niches of marine life. The Chinese mitten crab, a migratory species with strong adaptability, has become invasive in Europe and other regions. To predict its potential spread and ecological response under future climate scenarios, this study developed global and regional distribution models using data since 1970. The findings indicate that the crab's suitable habitats are moving towards higher latitudes, with a significant northward shift under high emission scenarios. Alaska and other high-latitude areas are emerging as key expansion zones. Analyses showed notable spatial differences in future climate anomalies and key variables. Ecological niche analysis indicates that under high emission scenarios, the Chinese mitten crab's niche center is shifting northward with decreasing overlap, though its overall environmental adaptability remains largely unchanged, highlighting its strong response to climate change.

Key words: Climate change, distribution pattern, geographical differentiation, species distribution model, ecological niche expansion

珠江口外伶仃海洋牧场及邻近海域游泳动物群落物种及谱系多样性的研究

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摘要：谱系多样性能够在了解群落的进化历史和生态恢复力方面提供独特的视角，但目前谱系多样性在海洋生态领域的研究与实际应用较少。为了解广东外伶仃海洋牧场及其邻近海域游泳动物群落物种及谱系多样性的变化特征及其对环境因子变化的响应，本研究于2020年4月和9月、2021年9月、2023年3月在珠江口外伶仃国家级海洋牧场示范区开展共4个航次的海洋渔业资源和环境因子调查。采用物种多样性指数和谱系多样性指数对游泳动物的群落多样性季节变化及其对环境因子的响应进行了分析。结果表明，pH值、水深和营养盐等环境因子构成了群落结构的基础筛选框架，而季节性演替则主导了群落的周期性波动。RDA分析和Mantel相关性分析结果显示，pH值、化学需氧量和无机氮是影响游泳动物物种多样性的重要环境因子，而谱系多样性受水体透明度和叶绿素a浓度影响的较大。

关键词：游泳动物群落；海洋牧场；谱系多样性；环境因子；珠江口

Study on the species and phylogenetic diversity of nekton community in Wailingding marine ranching and its adjacent waters, Pearl River Estuary

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Abstract： This study addressed the underrepresentation of phylogenetic diversity in marine ecology by comprehensively assessing the nekton community in Wailingding marine ranching. Four voyages between 2020 and 2023 analyzed seasonal nekton diversity and its environmental drivers using both species and phylogenetic diversity indices. Results showed that pH, water depth, and nutrients structured the community, with seasonal changes dictating periodic fluctuations. Species diversity was significantly influenced by pH, chemical oxygen demand, and inorganic nitrogen, while phylogenetic diversity was primarily affected by water transparency and chlorophyll a. The study concluded that nekton species and phylogenetic diversity exhibit distinct temporal and spatial variation patterns. These findings provide crucial scientific references for marine ranching, fishery resource protection, and advancing research on marine organism phylogenetic diversity.

Key words: nekton community; marine ranching; phylogenetic diversity; environmental factor; Pearl River Estuary

西北太平洋远东拟沙丁鱼生活史特征及资源状态分析

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摘要：远东拟沙丁鱼（*Sardinops melanostictus*）是我国西北太平洋围网渔业的重要对象。基于2023—2024年“淞航号”调查数据，本研究估算其生长与死亡参数，并利用YPR和LBB模型评估资源状况。结果显示，体长与体重关系为$W=4.59\times10^{-6}L^{3.16}$（$R^2=0.90$）；生长方程参数$L_\infty=21.63$ cm、$k=0.39$、$t_0=-0.77$。总死亡$Z=1.35$，自然死亡$M=0.63$，捕捞死亡$F=0.72$，开捕年龄1.42龄、叉长12.40 cm。YPR结果显示F略高于$F_{0.1}$（0.64），远低于Fmax（3.40）；LBB结果显示B/BMSY=1.58，Lc/Lc_opt=0.82。敏感性分析表明M及先验参数对估计影响较大。总体上，该种群处于健康状态，未过度捕捞，但大个体比例偏低，建议适度提高开捕体长以促进资源可持续利用。

关键词：远洋渔业；中上层种类；生长；死亡；资源评估

Life history traits and Stock status of Japanese sardine(*Sardinops melanostictus*) in the Northwest Pacific Ocean

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Abstract：Japanese sardine (*Sardinops melanostictus*) is an important target species in China’s purse seine fisheries in the Northwest Pacific. Based on survey data from the research vessel Song Hang (2023–2024), this study estimated its growth and mortality parameters and assessed stock status using the Yield Per Recruitment (YPR) and Length-based Bayesian Biomass (LBB) models. The length–weight relationship was $W=4.59\times10^{-6}L^{3.16}$ ($R^2=0.90$). The von Bertalanffy growth parameters were $L_\infty=21.63$ cm, $k=0.39$, and $t_0=-0.77$. Total mortality (Z) was 1.35, with natural mortality (M)=0.63 and fishing mortality (F)=0.72. YPR results showed that F slightly exceeded $F_{0.1}$ (0.64) but was far below Fmax (3.40). LBB results indicated B/BMSY=1.58 and Lc/Lc_opt=0.82. Sensitivity analysis revealed that uncertainty in M and prior parameters (L_∞, M/k) significantly affected estimates. Overall, the stock is healthy and not overfished, though the proportion of large individuals is low. Moderately increasing capture length is recommended to enhance spawning potential and promote sustainable utilization.

Key words: distant-water fishery; pelagic fish; growth; mortality; stock assessment

长江口禁渔前后代表性鱼类生活史特征及资源状况的对比研究

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摘要：为评估长江十年禁渔对河口鱼类资源恢复的生态成效，本研究选取长江口两个代表性鱼类龙头鱼（*Harpadon nehereus*）与刀鲚（*Coilia nasus*），基于 2017-2023 年长江口渔业资源调查数据，综合运用生长方程、死亡系数估算及单位补充量亲体生物量（SSBPR）模型，对比分析了禁渔前后其生活史特征与资源状态的演变。研究结果表明，禁渔措施对两种鱼类的资源恢复产生了显著但差异化的影响。

关键词：长江口；十年禁渔；生活史特征；资源恢复

A Comparative Study on the Life History Traits and Resource Status of Representative Fish Species in the Yangtze River Estuary Before and After the Fishing Ban

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Abstract：To evaluate the ecological effectiveness of the Yangtze River ten-year fishing ban on the restoration of fish resources in the estuary, this study selected two representative fish species in the Yangtze River Estuary—Bombay duck (**Harpadon nehereus**) and tapertail anchovy (**Coilia nasus**). Based on fishery resource survey data from the Yangtze River Estuary between 2017 and 2023, we conducted a comprehensive analysis by integrating growth equations, mortality coefficient estimations, and the spawning stock biomass per recruit (SSBPR) model to compare the temporal variations in their life history traits and resource status before and after the implementation of the fishing ban. The results demonstrate that the fishing ban has had a significant, although divergent, impact on the resource recovery of the two species.

Key words: Yangtze River Estuary; Ten-year fishing ban; Life history traits; Resource recovery

未来气候变化下的南极磷虾与纽鳃樽生态位与栖息地利用：进一步重叠，还是分离?

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摘要：南极磷虾（*Euphausia superba*）和纽鳃樽（*Salpa thompsoni*）是南大洋生态系统中重要的大型浮游动物类群。然而，气候变化对它们栖息地的影响仍不明确，尤其是随着纽鳃樽栖息地向南扩张，磷虾栖息地可能发生空间位移的潜在影响尚不清楚。因此，理解这两种关键物种在南大洋生态系统中的相互作用至关重要。本研究利用生态位模型预测了 1996－2015 年期间及未来（2050 年代和 2100 年代）南大洋磷虾与纽鳃樽的栖息地分布及生态位特征。结果显示，磷虾主要分布于陆架区域，而纽鳃樽更常见于相对较北的海域。此外，两者在南极半岛西部、凯尔盖朗群岛和罗斯海等地存在一定的分布重叠。在未来情景下，磷虾和纽鳃樽的高适宜栖息地均呈减少趋势，空间和生态重叠程度下降。本研究强调了磷虾与纽鳃樽在南大洋生态系统中的相互作用的重要性，为南大洋生态系统的保护与管理提供关键信息。

关键词：南极磷虾，纽鳃樽，气候变化，栖息地适宜性，生态位模型

Progress in the application of submerged plants in shrimp and crab freshwater aquaculture

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Abstract：Antarctic krill (*Euphausia superba*) and salps (*Salpa thompsoni*) are vital and important macrozooplankton grazers in the Southern Ocean ecosystem. However, the impact of climate change on their habitats remains unclear, particularly regarding the potential spatial displacement of krill habitats due to the southward expansion of salps. Understanding the interactions between these two key species in the Southern Ocean ecosystem is therefore crucial. This study used ecological niche modeling to predict the austral summer and autumn habitat distribution and ecological niches of krill and salps during the period (1996−2015) and under future scenarios (2050s and 2100s). The results showed that krill are mainly distributed in shelf regions, while salps are more prevalent in open ocean areas farther north compared to krill, such as the Lazarev Sea. Additionally, some overlap in their distributions is observed in the Western Antarctic Peninsula, the Kerguelen Islands and the Ross Sea. Under future scenarios, both krill and salps are projected to experience a reduction in their high-potential habitats, with decreasing spatial and ecological overlap. This study emphasizes the significance of krill and salps interactions in the Southern Ocean ecosystem. The findings provide valuable information for the conservation and management of the Southern Ocean ecosystem.

Key words: Antarctic krill, Salps, climate change, habitat suitability, Ecological niche model

耳石年轮在青海湖裸鲤群体鉴别中的应用及增殖放流效果评估

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摘要：青海湖裸鲤的增殖放流是资源恢复的关键措施，科学评估其贡献率对保护工作至关重要。本研究通过对比野生群体与增殖放流个体的耳石微结构特征，建立了一种有效的贡献率评估方法。研究发现，增殖放流个体与野生个体的耳石第一年轮尺寸存在显著差异。由于人工养殖环境下条件优越（如恒温饲料充足），增殖放流群体在 1 龄时生长速率更快，导致耳石沉积速率加快，第一年轮明显大于野生群体。本研究以耳石第一轮径作为关键指标，采用 K-均值聚类分析对河道采集的样本进行分类。结果显示，河道群体中 18.33%（n=22）的个体被划分到以增殖放流个体为主的聚类 1 中，据此可明确识别为人工放流来源。捕获的河道群体年龄为 5-9 龄，这一聚类结果反映了 2015-2019 年间增殖放流对当前繁殖群体资源量的贡献程度。耳石微结构分析为量化增殖放流在青海湖裸鲤资源恢复中的作用提供了可靠技术支撑，证实人工放流是弥补自然种群不足的有效手段。

关键词：青海湖裸鲤；耳石年轮；群体鉴别；增殖放流效果评估

APPLICATION OF OTOLITH MICROSTRUCTURE IN POPULATION IDENTIFICATION OF GYMNOCYPRIS PRZEWALSKIIAND AND EVALUATION OF STOCK ENHANCEMENT EFFECTS

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Abstract：The stock enhancement of Gymnocypris przewalskii is crucial for its resource recovery in Qinghai Lake, necessitating a scientific evaluation of its contribution. This study developed an assessment method by comparing otolith microstructure between wild and stocked fish. A significant difference was found in the first annulus size, with stocked fish showing faster growth and larger first annuli due to superior artificial conditions (e.g., constant temperature, ample food). Using the first annulus diameter as a key indicator, K-means clustering analysis classified river-collected samples. Results showed that 18.33% (n=22) of the river population, aged 5-9 years, were identified as artificially released, reflecting the contribution of stock enhancement from 2015-2019. This otolith-based approach provides a reliable technique to quantify the role of stock enhancement, confirming its effectiveness in supplementing the natural population.

Key words: Gymnocypris przewalskii; otolith microstructure ; population identification; stock enhancement effectiveness assessment

刺参的逃逸、吸附与假死应激反应模式研究

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摘要：生物调动应激反应来应对压力源。本研究识别了刺参的三种应激反应模式，分别为逃逸、黏附与假死。在逃逸模式中，刺参首次蠕动时间显著缩短、运动速度加快，同时去甲肾上腺素、皮质醇水平和葡萄糖激酶活性显著上升，这些反应有助其快速远离同类尸体。处于黏附模式时，刺参的吸附指数与运动随机性显著增强，伴随去甲肾上腺素和皮质醇水平显著升高以及γ-氨基丁酸含量显著下降，这些反应体利于其探索更广泛的区域。在假死模式中，其表现为首次爬行时间显著延长、蜷缩指数增高、爬行频率降低，同时肾上腺素水平显著下降。这些反应有利于其通过抑制移动和蜷缩身体来减轻机械损伤。

关键词：海参，逃逸，黏附，假死，行为反应，生理反应

Stress response patterns of fleeing, adhesion and thanatosis in the sea cucumber *Apostichopus japonicus*

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Abstract： Organisms mobilize stress responses to counteract stressors. The present study identifies three stress response patterns in *Apostichopus japonicus*: fleeing, adhesion, and thanatosis. In fleeing pattern, they showed significantly shorter time of the first crawl and higher movement speed, accompanied by significantly rising levels of norepinephrine, cortisol, and glucokinase activity. These responses enable them to move away from conspecific carcasses more rapidly. In adhesion pattern, they showed significantly higher adhesion index and movement randomness, accompanied by significantly rising levels of norepinephrine and cortisol, and reduced level of gamma-aminobutyric acid. These responses enable them to explore more areas. In thanatosis pattern, they showed significantly longer time of the first crawl, higher curling index, and lower crawling frequency, accompanied by significantly reduced level of epinephrine. These responses enable them to mitigate the mechanical damages through inhibiting movement and curling their bodies.

Key words: sea cucumber, fleeing, adhesion, thanatosis, behavioral response, physiological response

气候变化下西北太平洋生态系统结构和功能的演变

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摘要：全球范围的海洋生态系统的变化受到包括气候变化在内的多种因素的影响。本研究根据上海海洋大学“淞航”号科考船的实地调查数据，基于已构建的Ecopath模型，运用Ecosim模拟不同碳排放情景下气候变化对西北太平洋生态系统资源量和影响结构的影响，预测未来的动态变化。结果表明，西北太平洋各功能群生物量和捕捞量普遍受海洋变暖的影响。从本世纪中后期来看，鲨鱼、剑鱼、金枪鱼等顶级捕食者和沙丁鱼、秋刀鱼、灯笼鱼等小型鱼类的变化幅度较大，而甲壳类、浮游生物、碎屑等受影响较小，生物量保持稳定。鲐鱼的生物量和捕捞量均在高排放情景中呈现出剧烈上升的乐观趋势。在高碳排放情景中，总生物量在本世纪中后期下降了近50%。主要是因为大部分功能群的适温范围较窄且偏好温度较低，其生物量在海表温度剧烈变化后受到强烈影响。本研究结果可以为区域性渔业管理组织制定预防性养护管理措施，以及基于生态系统的渔业管理提供技术支撑和数据参考。

关键词：EBFM；Ecopath with Ecosim；西北太平洋；全球变暖；生态系统模型

Evolution of Structure and Function in the Northwest Pacific Ecosystem under Climate Change

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Abstract：Global changes in marine ecosystems are influenced by multiple factors, including climate change. Based on field survey data from the research vessel Songhang of Shanghai Ocean University and utilizing the established Ecopath model, this study employs Ecosim to simulate dynamic changes in biomass and structure of the pelagic ecosystem in the northwest Pacific under future ocean warming scenarios. Model projections indicate that biomass across functional groups in the northwest Pacific is generally impacted by ocean warming. By the mid-to-late 21st century, top predators and small pelagic fishes exhibit relatively significant change, while plankton, cephalopoda, and pacific saury show lesser impacts with relatively stable biomass. In the high-emission scenario, total biomass decreased by nearly half in the mid-to-late 21st century, primarily due to most functional groups having narrow temperature tolerance ranges and preferring lower temperatures, which rendered their biomass strongly vulnerable to abrupt changes in sea surface temperature.

Key words: climate change; EBFM; Ecopath with Ecosim; ecosystem model; global warming; the Northwest Pacific

贝类筏式养殖对附近海域大型底栖动物时空分布及底栖生态健康状态的影响

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摘要：为评估贝类筏式养殖对底栖生态系统的影响，本研究对比分析了枸杞岛贻贝养殖区及外围区域的大型底栖动物群落结构特征及底栖生态健康状态。结果显示，养殖区内丰度和生物量存在显著性季节差异，且外围区域丰度和生物量在冬季均显著高于养殖区。PERMANOVA 及 RDA 分析结果显示，养殖区外围环境因子对群落结构影响显著，而养殖区内不显著，环境因子对群落结构的解释率为 18–29%。正内聚力结果显示，两区域正内聚力均高于负内聚力。AMBI 显示，养殖区内外大型底栖动物群落多样性指数均处于较高水平，受轻微干扰，且生态质量均为良好。M-AMBI 进一步分析显示两区域生态状态均为极佳。综上，枸杞岛贻贝筏式养殖对大型底栖动物群落结构产生了一定影响，但并未损害底栖生态系统健康，研究结果可为近海贝类健康养殖提供理论支撑。

关键词：贝类筏式养殖、大型底栖动物、群落结构、环境因子、底栖生态健康状况

Effects of raft shellfish farming on the spatial and temporal distribution of macrobenthos and benthic ecological health status in nearby waters

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Abstract： To assess the impact of raft-style bivalve farming on benthic ecosystems, this study compared the community structure and ecological health of large benthic animals in the mussel farming area of Gouqi Island and its surroundings. Results showed significant seasonal variations in abundance and biomass within the farming area, while the surrounding region had notably higher values in winter. PERMANOVA and RDA analyses indicated that environmental factors in the surrounding area significantly influenced community structure (explanatory rate of 18–29%), whereas those within the farming area did not. Both regions exhibited high positive cohesion, and AMBI analysis revealed high diversity indices, indicating minor disturbance and good ecological quality. M-AMBI confirmed excellent ecological status in both regions. Thus, while mussel farming affected benthic community structure, it did not compromise ecosystem health, supporting sustainable offshore bivalve farming.

Key words: Raft shellfish farming; Macrobenthos; Community structure; Environmental factors; Benthic ecological health status

胃含物分析揭示了黄花鱼（*Larimichthys polyactis*）在变化环境中的适应能力

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摘要：小黄鱼（Larimichthys polyactis）是亚洲水域重要的渔业资源。尽管有记录显示其种群数量下降，但过去二十年间其在东海的年捕获量始终保持稳定。理解该物种如何适应海洋生态系统动态变化，对生态研究和渔业管理均具有重要意义。本研究调查了东海小黄鱼食性十年间的变化趋势。2022-2023 年浙江南部近海 487 个样本的分析鉴定出 40 种饵料，其中鱼类和虾类为主要饵料。结果表明不同个体发育阶段的摄食习性存在差异：大个体较小个体摄食更多的鱼和更少的虾。典型对应分析（CCA）结果表明，水深和纬度与小黄鱼食物组成呈高度相关性。历史数据对比显示，近二十年小黄鱼食性发生显著转变：甲壳类比例明显下降而小鱼类（如七星底灯鱼）占比上升至 17.6%。这种转变可能是小黄鱼对全球变暖下七星底灯鱼种群北移的适应性反应。该发现深化了我们对小黄鱼在环境变化中的适应性的认识。

关键词：摄食生态；食物组成；食性转变；小黄鱼；胃含物分析

Stomach content analysis highlights the adaptive capacity of yellow croaker (*Larimichthys polyactis*) in changing environment

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Abstract： The yellow croaker (Larimichthys polyactis) is a critically important fishery resource in Asian waters. The study investigated decadal changes in the feeding habits of yellow croaker in the East China Sea. Analysis of 487 individuals in southern Zhejiang coastal waters (2022–2023) identified 40 prey items, with fish and shrimp as the dominant groups. Obviously ontogenetic variation in the feeding habit were found, larger individuals consumed more fish and fewer shrimp than smaller size individuals. The result of the canonical correspondence analysis (CCA) indicated that depth and latitude exhibited high correlations with the food composition of yellow croaker. Historical comparisons revealed a marked dietary shift of yellow croaker in the last two decades. The proportion of crustaceans were declined obviously, while that of small fish, such as B. pterotum, increased to 17.6 %. This shift is likely an adaptive response of yellow croaker to the northward expansion of B. pterotum populations under global warming.

Key words: Feeding ecology; food composition; dietary shift; yellow croaker; stomach content analysis.

从转录组测序揭示青蛤（*Cyclina sinensis*）在梯度极低频电磁场（ELF-EMF，50 Hz）暴露下的生物效应

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摘要：随着风电场的规模化建设，水生生物持续暴露于极低频电磁场（ELF-EMF）的情况日益凸显。本研究探讨了 50 Hz 极低频电磁场（5 μT 与 15 μT）对双壳贝类青蛤（Cyclina sinensis）的 14 天持续暴露影响。结果表明，高强度电磁场暴露会显著降低青蛤存活率并诱发氧化应激。转录组分析显示，低强度与高强度暴露组分别鉴定出 1509 和 4936 个差异表达基因，且呈现剂量效应关系。KEGG 通路富集分析表明，高强度极低频电磁场主要影响内质网蛋白质加工与氧化磷酸化通路：上调基因（ATF6B、DNAJC3）提示内质网应激激活，而下调基因（ND2、ND4、CYTB、COX3）则表明线粒体能量合成功能受损。这些发现揭示高强度极低频电磁场可能通过破坏蛋白质稳态与 ATP 合成途径引发机体生理应激。本研究为解析极低频电磁场的生态风险提供了分子层面的理论依据，对制定可持续可再生能源开发生物安全准则具有支撑意义。

关键词：极低频电磁场；青蛤；生物效应；从头转录组分析；氧化磷酸化

Transcriptomic analysis reveals the density-dependent molecular basis of Extremely Low-Frequency Electromagnetic Fields (ELF-EMF, 50 Hz) exposure in the clam (*Cyclina sinensis*)

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Abstract： With the expansion of wind farms, aquatic organisms are increasingly exposed to extremely low-frequency electromagnetic fields (ELF-EMF). This study investigated the 14-day impact of 50 Hz ELF-EMF (5 and 15 μT) on the bivalve Cyclina sinensis. High-intensity exposure significantly reduced survival and induced oxidative stress. Transcriptome analysis revealed 1,509 and 4,936 differentially expressed genes at low and high intensities, respectively, showing a dose-response. KEGG enrichment indicated high-intensity ELF-EMF affected endoplasmic reticulum protein processing and oxidative phosphorylation. Up-regulated genes (ATF6B, DNAJC3) indicated ER stress, while down-regulated genes (ND2, ND4, CYTB, COX3) suggested impaired mitochondrial energy production. These results show high-intensity ELF-EMF may disrupt proteostasis and ATP synthesis, causing physiological stress. This work provides molecular insights into ELF-EMF ecological risks and supports biosafety guidelines for sustainable renewable energy.

Key words: Extremely Low-Frequency Electromagnetic Fields (ELF-EMF); Cyclina sinensis; Bioeffects; De novo transcriptome profiling; Oxidative phosphorylation

基于生态通道模型象山港铁港生态系统结构与功能

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摘要：基于 Ecopath 模型，对象山港铁港生态系统研究表明，铁港港湾生态系统能量流动以浮游植物→浮游动物→鱼类的牧食链为主，有机碎屑→底栖生物→鱼类的碎屑链起到辅助作用。营养级能量转化效率整体低于林德曼效率，其中营养级Ⅰ到营养级Ⅱ的能量转化效率仅为 7.33%，营养级Ⅲ到营养级Ⅳ能量转化效率最高为 8.6%。系统总流量 2020 年最高为 20624 $t\cdot km^{-2}\cdot a^{-1}$，2021 年受环境扰动影响下降至 9464 $t\cdot km^{-2}\cdot a^{-1}$，2023 年恢复至 21817 $t\cdot km^{-2}\cdot a^{-1}$。总初级生产量/总呼吸量（TPP/TR）为 2.10，连接指数（CI）与杂食指数（SOI）较低，分别为 0.42 和 0.22，表明生态系统成熟度较低并处于发育初期，其食物网结构简单且稳定性不足。秋季 TPP/TR 为 1.59 较春季 2.56 更接近 1，CI 和 SOI 分别为 0.44 和 0.29 较春季 0.16 和 0.45 高，秋季生态系统稳定性高于春季。

关键词：象山港铁港；生态系统；Ecopath；营养级；能量流动

Structure and Function of the Xiangshan Bay Tiegang Bay Ecosystem Based on Ecopath Model

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Abstract： Tiegang Bay is located at the bottom of Xiangshan Bay, Zhejing Province. Based on the Ecopath model, research of the Tiegang Bay ecosystem revealed that the energy flow in the bay ecosystem primarily followed the grazing chain of phytoplankton → zooplankton → fish, with the detrital chain of organic detritus → benthic organisms → fish playing a supplementary role. The overall energy conversion efficiency across trophic levels was lower than Lindeman's efficiency, with the conversion efficiency from trophic level I to II being only 7.33%, and the highest efficiency from trophic level III to IV reaching 8.6%. The total system throughput peaked at 20,624 $t\cdot km^{-2}\cdot a^{-1}$ in 2020 but declined to 9,464 $t\cdot km^{-2}\cdot a^{-1}$ in 2021 due to environment disturbances, then recovered to 21,817 $t\cdot km^{-2}\cdot a^{-1}$ in 2023. The Total Primary Production (TPP) to Total Respiration (TR) ratio was 2.10, while the Connection Index (CI) and Omnivorous Index (SOI) were relatively low at 0.42 and 0.22, respectively, indicating a less mature ecosystem in its developmental stage.

Key words: Tiegang Bay; ecosystem; ecopath;trophic level;energy flow

湘江细鳞鲴群体遗传多样性及种群历史动态研究

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摘要：湘江永州段、衡阳段、东江湖段、茶陵段和浏阳段的细鳞鲴共检测出变异位点 37 个，单倍型 24 个，单倍型多样性（Hd）、核苷酸多样性（Pi）和群体间遗传距离变化范围分别为 0.755 ~ 0.911，0.00277 ~ 0.00556 和 0.00467 ~ 0.00658。UPGMA 聚类树显示，HY 与 LY 聚为一支，YZ 与 CL 聚为一支。基于 Fst 指数的计算表明，HY 与 DJH 和 CL 存在低等程度的遗传分化，DJH 与 YZ 和 CL，LY 与其他四个群体均存在中等程度的遗传分化，而 YZ 与 CL 和 HY 均不存在分化。24 个单倍型中仅 Hap1 为 5 个群体的共享单倍型，单倍型间未形成与地理位置相对应的进化支聚类关系。Mantel test 分析发现湘江细鳞鲴群体遗传差异与地理距离间不存在显著关系。5 个群体的遗传变异主要来源于群体内部。湘江细鳞鲴种群维持了较高的遗传多样性，且处于长期稳定或者存在遗传亚结构分化的状态。

关键词：湘江，细鳞鲴，遗传多样性，D-loop，单倍型

Study on Genetic Diversity and Population Historical Dynamics of the Xenocypris microlepis Population in the Xiangjiang River

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Abstract： This study collected Xenocypris microlepis from five geographic populations the Xiang River. Haplotype diversity (Hd), nucleotide diversity (Pi), and inter-population genetic distance ranged from 0.755 to 0.911, 0.00277 to 0.00556, and 0.00467 to 0.00658, respectively. The UPGMA clustering tree showed that HY and LY clustered together, while YZ and CL formed another cluster. Low-level genetic differentiation occured between HY and both DJH and CL. Moderate differentiation existed between DJH and YZ/CLand between LY and the other four populations. Among the 24 haplotypes, only Hap1 was shared across all five populations. No evolutionary clade clustering corresponding to geographic locations emerged among haplotypes. Mantel test analysis revealed no significant relationship between genetic differentiation and geographic distance. Genetic variation within the five populations accounted for 90.48% of total variation. This study demonstrates that Xiangjiang populations maintain high genetic diversity and are in a state of long-term stability or genetic substructure differentiation.

Key words: Xiangjiang River; Xenocypris microlepis; genetic diversity; D-loop; haplotype

关于促进葛洲坝下中华鲟繁殖群体恢复的遗传干预构想：一个非共识的探讨

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摘要：葛洲坝截流后，中华鲟种群陷入螺旋衰退，受后续涉水工程等的进一步影响，中华鲟种群快速衰减，并于 2013 年首次出现自然繁殖中断，亟需采取措施恢复中华鲟自然可持续种群。通过文献梳理和理论借用，分析了中华鲟自然群体演变困境，显示中华鲟自然群体深陷困境的关键可能在于其未能及时适应葛洲坝截流后的洄游繁殖条件变化。从恢复中华鲟野外可持续种群的目标出发，提出促进中华鲟适应葛洲坝截流后洄游繁殖条件的需求，然后从种群遗传的生态学适应角度分析中华鲟繁殖群体适应葛洲坝截流后洄游繁殖条件的可能性，探讨了通过遗传干预促进中华鲟葛洲坝下繁殖群体恢复的可能性，并梳理了通过遗传干预促进中华鲟葛洲坝下繁殖群体恢复的具体困难及未来构想。

关键词：中华鲟；洄游节律；遗传结构；等位基因；基因频率；遗传管理；适应；种群恢复

Conception for promoting the recovery of the Chinese sturgeon (*Acipenser sinensis*) natural reproductive population below the Gezhouba Dam through genetic intervention: A non-consensus discussion

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Abstract：As a flagship species in the Yangtze River, Chinese sturgeon (*Acipenser sinensis*) fell into a spiral population decline after the Gezhou Dam. Then, its natural reproduction was interrupted in 2013. The key problem in this tragedy is that the Chinese sturgeon failed to adapt to the changes in migration and breeding conditions caused by the Gezhou Dam. Aimed the goal of restoring self-sustaining populations of wild-spawning Chinese sturgeon, the current manuscript 1) raised the demand of promoting the adaptation of Chinese sturgeon to the new migration and breeding conditions; 2) explained the possibility of Chinese sturgeon adapting to the new migration and breeding conditions in the perspective of population genetics; 3) discussed the practical possibility of promoting the adaptation of Chinese sturgeon to the new migration and breeding conditions; 4) finally, delineated the operational difficulties and future expectations of promoting the adaptation of Chinese sturgeon to the new migration and reproduction conditions.

Key words: Chinese sturgeon; migration rhythm; genetic structure; allele; allele frequency; genetic management; adaptation; population restoration

湘江水系蛇鮈的生长和年龄

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摘要：为了了解湘江水系蛇鮈的生长和年龄结构，本研究于 2023 和 2024 年 5 月、9 月、10 月于湘江水系 6 个河段采集 1358 尾蛇鮈样本，通过生物学测量与鳞片以及耳石微结构分析其生长参数及年龄组成。结果显示，样本体长范围为 4.4～21.7cm，体重范围为 0.9～110.4g，体长—体重呈幂函数指数关系：W=0.01L 3.0065(r 2 =0.9589)，属于匀速生长类型。样本年龄结构由 0-3 龄组成，其中 1 龄组为优势组，占总体的 43.08%，最大年龄为 3 龄。von Bertalanffy 生长模型拟合形式，体长生长方程为：Lt =23.133[1- e-0.423(t+0.602)]，体重生长方程：Wt=126.35[1-e-0.423(t+0.602)]3.0065，生长拐点年龄为 2.0003 龄。研究表明，湘江水系蛇鮈呈现生长快速、年龄结构简单、世代交替快等特征。

关键词：蛇鮈；年龄结构；生长特性；湘江水系；资源管理

Growth and Age of Saurogobio dabryi in the Xiangjiang River System

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Abstract：To understand the growth and age structure of Saurogobio dabryi in the Xiangjiang River system, this study collected 1,358 specimens from six river sections during May, September, and October of 2023 and 2024. Growth parameters and age composition were analyzed through biological measurements, scale observation, and otolith microstructure analysis. Results showed that the body length of the samples ranged from 4.4 to 21.7 cm, and the body weight ranged from 0.9 to 110.4 g. The relationship between body length and body weight followed a power function: W = 0.01L^3.0065, indicating isometric growth. The age structure of the samples consisted of individuals from 0 to 3 years old, with the 1-year-old group being the dominant cohort and the maximum age being 3 years. The body length growth equation was: Lt = 23.133[1 - e^(-0.423(t + 0.602))], and the body weight growth equation was: Wt = 126.35[1 - e^(-0.423(t + 0.602))]^3.0065. The study indicates that Saurogobio dabryi in the Xiangjiang River system exhibits rapid growth, a simple age structure, and fast generational turnover.

Key words: Saurogobio dabryi; Age structure; Growth characteristics; Xiangjiang River System; Resource management

湘江中下游不同江段银鮈种群结构、生长和繁殖特征的差异

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摘要：鱼类的结构、生长和繁殖随着环境条件而发生改变，湘江干流中下游的 8 个梯级电站将影响着鱼类。本研究于 2023 年和 2024 年在湘江中下游永州段和衡阳段、株洲段和长沙段采集银鮈 920 尾，体长和体重范围分别为 46.9−146.9cm 和 1.47−62.1g。长沙段个体显著小于其它三个江段 ($P<0.05$)，衡阳段生长指数显著低于永州和长沙段($P<0.05/6$)；年龄范围为 1-5 龄，永州段和衡阳段以 2 龄为主，株洲和长沙段以 2 龄和 1 龄为主。株洲段生长率快于衡阳段和长沙段 ($P < 0.05/6$)。永州段和长沙段的绝对繁殖力、体长相对繁殖力显著大于衡阳段和株洲段 ($P<0.05$)；卵径大小从永州段至长沙段一直下降，呈现显著的差异($P<0.05$)。这些表明永州段种群受到电站影响最小；衡阳段个体大，株洲段和长沙段种群个体小，衡阳段至长沙段繁殖力增高，卵径降低，衡阳段受到电站的影响最大，随着下游受到的影响逐渐降低。

关键词：洞庭湖，年龄，繁殖，银鮈

Longitdudinal variations in population structure, growth, and reproductive characteristics of a widely distributed fish, Squalidus argentatus in Xiangjiang–a main heavily dammed tributary of Dongting Lake.

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Abstract： A total of 920 Squalidus argentatus were collected in the middle and lower reaches of the Xiangjiang River, where dam cacades were erected. Standard length and body weight ranged from 46.9 to 146.9cm and 1.47 to 62.1g. Body size was significantly smaller at Changsha than at the other sites ($P<0.05$). Allometric growth index was significantly higher at Yongzhou and Changsha than Hengyang ($P<0.05$). Age ranged from 1 to 5 year, with the dominant class of age 2 at Yongzhou and Hengyang and ages 2 and 1 at Zhuzhou and Changsha. Fish grew significantly faster at Zhuzhou than at Hengyang and Changsha ($P < 0.05/6$). Absolute fecundity and relative fecundity were significantly more at Yongzhou and Changsha than at Hengyang and Zhuzhou ($P<0.05$). Egg diameter decreased in the downstream direction, with significant difference between each two sites ($P<0.05$). These results revealed that dam cacades showed little impact at Yongzhou and had heavy effect on growth and fecundity of Squalidus argentatu at Hengyang, and the effect level decreased in the downstream.

Key words: Dongting Lake, age, fecundity, Squalidus argentatus

微塑料和氟化物对辽河流域浮游动物完整性的影响

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摘要：本研究对辽河流域春、夏、秋季的浮游动物采样结果显示，共鉴定出浮游动物 4 类 42 种，轮虫 26 种，原生动物 10 种，桡足类 4 种，枝角类仅 2 种。辽河水体共检测出微塑料 13 种，全氟化合物 14 种，各环境因子在采样点间差异极显著（P<0.01）；确定 9 个参照点和 15 个受损点，共选取 24 个候选生物指标，构建辽河流域浮游动物完整性指数，核心指标由总分类单元数、枝角类分类单元数、枝角类生物量%、Margalef 丰富度指数和中型浮游动物捕食者%组成。采用比值法对 0~2.82 分布范围数值进行 3 等分，建立辽河流域湿地浮游动物完整性指数健康评价标准：0~0.94，重度干扰；0.94~1.88，中度干扰；1.88~2.82，轻度干扰；>2.82，无干扰。结果表明，辽河流域 87.5%受到不同程度的干扰，12.5%无干扰。

关键词：辽河流域，新污染物，浮游动物，完整性

Impact of microplastics and fluorides on the integrity of zooplankton in the Liaohe River Basin

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Abstract: The sampling results of zooplankton in spring, summer, and autumn in the Liaohe River Basin showed that a total of 42 species of zooplankton, 26 species of rotifers, 10 species of protozoa, four species of copepods, and only two species of cladocera were identified. We found 13 types of microplastics and 14 types of perfluorinated compounds in the Liaohe River water body, and the differences in various environmental factors between sampling points were extremely significant (P<0.01). There are nine reference points and 15 damaged points were identified, and a total of 24 candidate biological indicators were selected to construct the integrity index of zooplankton in the Liaohe River Basin. The core indicators consist of the number of total taxonomic units, the number of cladistic taxonomic units, the biomass% of cladistic organisms, the Margalef richness index, and the percentage of medium-sized zooplankton predators. Using the ratio method to divide the distribution range of 0-2.82 into three equal parts, establish a health evaluation standard for the integrity index of zooplankton in wetlands of the Liaohe River Basin: 0-0.94, severe interference; 0.94-1.88, moderate interference; 1.88-2.82, mild interference; >2.82, no interference. The results showed that 87.5% of the Liaohe River Basin was affected to varying degrees of interference, while 12.5% had no interference.

Keywords: Liaohe River Basin, new pollutants, zooplankton, integrity

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第七专题 水产品加工与综合利用

大黄鱼单体运输过程中空间应激与低温缓解机制研究

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摘要：我国作为全球最大的水产品生产国和消费国，年水产品总产量达 6800 万吨，连续 33 年保持世界首位。大黄鱼是我国四大海产之首，素有“国鱼”之美誉。秉性“天生胆小”，抗逆性差、应激性极强，在养殖和运输途中极易死亡。相较于市场上常见的冰鲜大黄鱼，鲜活大黄鱼肉质细嫩、鲜味浓郁，同规格价格约为冰鲜冷藏品的 2-3 倍。鲜活鱼品相较于冰鲜、冷冻产品，因其食品安全性高且能最大限度保留原有肉质风味与营养价值而更受消费者青睐。单体包装鲜活鱼品物流运输具有肉质鲜美、运输灵活的特点，可缩短运输环节、提高存活率及促进地方性鱼品销售。本研究利用有限空间限制大黄鱼活动来减少其应激，但狭小空间也是大黄鱼的应激来源，可通过低温来缓解大黄鱼的空间应激。通过研究大黄鱼单体运输过程中空间应激与低温缓解机制来减低大黄鱼活体运输中的应激，提高大黄鱼运输存活率，以期为大黄鱼电商物流提供智能化运输装备，助力新鲜大黄鱼“邮”得更远。

关键词：大黄鱼；活体运输；应激机制

Study on spatial stress and hypothermic mitigation mechanism during individual transportation of *Pseudosciaena croaker*

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Abstract： Large yellow croaker, known as the "national fish" due to its prominent status among China's four major marine products, is inherently timid, with poor stress resistance and strong irritability, making it highly susceptible to death during breeding and transportation. This study utilizes limited space to restrict the movement of large yellow croaker to reduce its stress, but the confined space also serves as a source of stress for the fish. Low temperature can alleviate the spatial stress of large yellow croaker. By studying the mechanisms of spatial stress and low-temperature alleviation during the individual transportation of large yellow croaker, we aim to reduce stress during live transportation, improve survival rates, and provide intelligent transportation equipment for e-commerce logistics of large yellow croaker, thereby enabling fresh large yellow croaker to be "mailed" farther.

Key words: Live transport; large yellow croaker; stress;

热加工和贮藏对绿盘鲍干鲍理化特性及挥发性风味物质的影响

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摘要：研究以热风干燥的绿盘鲍 (*Haliotis discus hannai*♀× *H. fulgens*♂) 为对象，探究 80℃、95℃热加工及室温、冷冻储存对其理化特性与挥发性风味物质的影响，理化评价含常规营养、氨基酸、脂肪酸等指标。结果显示，95℃处理显著提升甘氨酸、脯氨酸及单不饱和脂肪酸，降低胶原蛋白；80℃处理显著提高黏附性。冷冻贮藏降胆固醇，室温贮藏降饱和脂肪酸但增硬度、咀嚼性且破坏肌纤维。电子鼻与 HS-SPME/GC-MS 分析发现组间风味差异显著，鉴定 24 种挥发性化合物（含 7 种醛类、5 醇类等），高温加工增醇、醛、酮类，室温贮藏增醛类，冷冻贮藏降烷烃类。OAV 分析表明壬醛、1 - 辛烯 - 3 - 醇、辛醛为关键风味物。综上，95℃加热表现最佳，室温贮藏促风味积累，研究为干鲍鱼加工提供数据支持。

关键词：干鲍；加工温度；贮藏条件；理化特性；挥发性风味物质

Effects of thermal processing and storage on physicochemical properties and volatile flavor compounds of dried abalone (*Haliotis discus hannai*♀×*H. fulgens*♂)

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Abstract： This study focused on hot-air-dried abalone (*Haliotis discus hannai* ♀ × *H. fulgens* ♂), investigating effects of thermal processing (80 ℃, 95 ℃) and storage (room temperature, frozen) on its physicochemical properties and volatile flavor compounds, with evaluations covering proximate composition, amino acids, fatty acids, rehydration ratio, histological structure, and texture. Results showed 95 ℃ significantly increased Gly, Pro, monounsaturated fatty acids and reduced collagen; 80 ℃ notably enhanced adhesiveness; frozen storage decreased cholesterol, while room-temperature storage reduced saturated fatty acids but increased hardness, chewiness and damaged muscle fibers. Electronic nose and HS-SPME/GC-MS revealed distinct flavor differences among groups, identifying 24 volatile compounds. High temperature increased alcohols, aldehydes, ketones; room-temperature storage elevated aldehydes; frozen storage reduced alkanes. OAV analysis indicated nonanal, 1-octen-3-ol, octanal as key flavor compounds. In conclusion, 95 ℃ heating performed best, room-temperature storage promoted flavor.

Key words: Dried abalone, Heating temperature, Storage condition, Physicochemical property, Volatile flavor compound

年龄和性别对中华鳖黄河品系裙边营养价值的影响

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摘要：为探究年龄与性别对中华鳖裙边营养价值的影响，本研究以 2~6 龄黄河鳖为对象，比较了雌雄个体裙边的组织形态、营养成分、氨基酸组成及胶原纤维密度等方面的差异。结果显示：（1）性别显著影响裙边宽/背甲宽、裙边厚/体高、裙边重/体重（$P<0.05$）；年龄显著影响后两项指标；两者交互作用影响裙边重/体重。（2）裙边水分、灰分和粗蛋白含量在性别间差异显著，粗脂肪则无；年龄仅显著影响粗脂肪；年龄与性别对水分、灰分和粗蛋白存在交互影响。（3）氨基酸总量在性别间差异显著，年龄影响不显著。（4）雌鳖的必需氨基酸、半必需氨基酸、非必需氨基酸及呈味氨基酸总量均显著高于雄鳖。（5）年龄显著影响呈味氨基酸含量，但不影响必需氨基酸总量。（6）性别与年龄均显著影响胶原纤维密度，雄性高于雌性，2 龄个体最低。综上，年龄和性别是影响黄河鳖裙边营养价值的关键因素。

关键词：中华鳖；黄河品系；裙边；营养价值

The influence of age and gender on the calipash nutritional value of the Yellow River strain of Chinese Soft-Shelled turtle

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Abstract：This study investigated the effects of age and gender on the nutritional value of the calipash in the Yellow River strain of *Pelodiscus sinensis*. Results showed: Gender significantly influenced the ratios of calipash width/carapace width, calipash thickness/body height, and calipash weight/body weight . Age significantly affected the latter two ratios, and their interaction influenced calipash weight/body weight. Moisture, ash, and crude protein content differed significantly between genders, while crude fat did not. Age only significantly affected crude fat content, and the interaction of age and gender influenced moisture, ash, and crude protein. Total amino acid showed significant gender-based differences but no age-related variation. Females had significantly higher contents of total essential (ΣEAA), semi-essential, non-essential, and delicious amino acids (ΣDAA) than males. Age significantly influenced ΣDAA but not ΣEAA. Gender and age significantly affected collagen fiber density, with males and older turtles having higher density.

Key words: *Pelodiscus sinensis*; Yellow River strain; Calipash; Nutritional value

明胶与不同多糖复合膜的制备及对冷藏虹鳟脂质氧化的影响

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摘要：寻找天然大分子化合物制备可食用可降解食品包装材料已成为研究热点。以明胶为基质材料制备可食性保鲜膜，并分别复合壳聚糖、果胶及海藻酸钠三种多糖，研究多糖的添加对明胶膜物理性质、微观结构及对冷藏虹鳟脂质氧化情况的影响。膜的微观结构表明多糖与明胶之间形成了均一稳定的结构，红外光谱显示添加多糖影响了 O-H 键的弯曲和伸缩振动，从而影响了氢键的形成。果胶和海藻酸钠的添加将膜的水蒸气透过性提高，同时壳聚糖将明胶膜的透光率至多降低 30%。虹鳟冷藏研究结果表明，复合膜处理的虹鳟将菌落总数可接受限值从 9 天延长至 12 天左右，同时 TBARs 值也有类似结果，脂肪酸构成表明复合膜处理延缓了不饱和脂肪酸的氧化。说明明胶经多糖复合后形成的活性包装材料具有优越的阻隔性能和良好的应用前景。

关键词： 明胶，壳聚糖，果胶，海藻酸钠，复合膜，虹鳟

Preparation of composite films of gelatin and polysaccharides and effect on lipid oxidation of rainbow trout during cold storage

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Abstract： The search for natural macromolecular compounds to prepare edible and degradable food packaging materials has become a research hotspot. Edible preservation film was prepared by using gelatin as matrix material, and chitosan, pectin and sodium alginate were compounded separately. The research was aimed to study the effects of the addition of polysaccharide in gelatin film on the physical properties, microstructure and lipid oxidation of rainbow trout in cold storage. The microstructure of the films showed that a homogeneous and stable structure was formed between the polysaccharide and gelatin. The infrared spectrum showed that the addition of polysaccharide affected the bending and stretching vibration of O-H bond, thus affecting the formation of hydrogen bond. The addition of pectin and sodium alginate significantly improved the water vapor permeability of the film, while chitosan reduced the light transmittance of the gelatin film by up to 30%. The acceptable limit of total viable counts of rainbow trout treated with composite film was extended from 9 days to about 12 days, and the thiobarbituric acid reactive substance(TBARs) value had similar results. The fatty acid composition showed that the oxidation of unsaturated fatty acid was delayed by the treatment of composite film. In conclusion, the active packaging material formed by the compound of gelatin and polysaccharide has a good application prospect.

Key words: gelatin, chitosan, pectin, sodium alginate, composite film, rainbow trout

第八专题 休闲渔业与渔文化

中国渔文化价值的量化分析与传承初探

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摘要：中国渔文化作为中华文明的重要载体，承载着千年历史记忆与民族智慧结晶，在当代社会转型中展现出独特的再生价值。针对渔业经济结构性调整带来的渔文化传承危机，文章通过多维度解构渔文化核心内涵、资源谱系与外延，首次提出渔文化丰度量化指标。基于倾向得分匹配法的量化研究表明，渔文化对休闲渔业发展具有显著正向影响，产生年均 44.6 亿元的经济增益效应，有力印证了其在产业升级与区域经济中的赋能价值。通过系统梳理当前渔文化的研究和传承现状以及面临的困境，提出提升价值认知、强化资源调查、开展区域试点传承、拓展宣传普及渠道、深化转化应用、推进可持续研究以及加强国际合作等针对性发展建议，为完善文化保护传承体系提供理论框架与实践方案，助推渔文化实现创造性转化与创新性发展，为建设文化强国与海洋强国贡献独特力量。

关键词：渔文化；鱼文化；量化分析；保护与传承；倾向得分匹配法

Research on the Value and Inheritance of Chinese Fishery Culture

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Abstract： As an important carrier of Chinese civilization, fishery culture has not only precipitated thousands of years of historical memory, but also renewed its value in contemporary society. This paper focuses on Chinese fishery culture, systematically analyzes its connotation value, resource distribution and extension, and for the first time proposes a quantitative indicator of fishery culture abundance, and uses the propensity matching score method to explore its contribution to the development of leisure fishery. The study shows that the abundance of fishery culture has a significant positive impact on the output value of leisure fishery, with an average quality improvement effect of 4.46 billion yuan, which highlights the value of fishery culture in empowering aquatic industry and promoting local economic growth. The paper also comprehensively examines the current situation of research and inheritance of Chinese fishery culture and the development dilemmas it faces, including the change of inheritance subjects, the impact of urbanization, uneven development and lack of professional tale.

Key words: fishery culture; fish culture; quantitative analysis; protection and inheritance; propensity score matching method

枯草芽孢杆菌胞内提取物促进锦鲤（*Cyprinus carpio var. koi*）免疫力及肠道菌群

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摘要：本研究系统评估了三种枯草芽孢杆菌菌株（F18、PC4、LS16）胞内提取物对锦鲤免疫反应、抗氧化能力及肠道菌群的影响。试验将400尾健康锦鲤随机分为五组，分别投喂添加F18、PC4、LS16胞内提取物、三者混合物及空白对照的饲料，养殖周期9周。结果表明，虽然各提取物均有效改善了血清免疫与抗氧化指标。其中，LS16提取物表现出显著调控免疫相关基因表达的能力，可下调肝脏tnf-α基因同时上调肠道occ基因。通过微生物群落分析发现，LS16处理能显著提高肠道中金黄杆菌属的相对丰度，同时降低气单胞菌属比例。日粮中添加枯草芽孢杆菌胞内提取物显著增强了对维氏气单胞菌的抗病力。代谢组学分析显示，LS16组以硬脂酰胺等脂类为主，PC4组富含油酰胺和核苷类物质，F18组则主要积累苯丙氨酸等多种氨基酸及其衍生物。综合研究结果，枯草芽孢杆菌LS16的胞内提取物能够改善锦鲤的免疫力和肠道菌群。

关键词：益生菌；枯草芽孢杆菌；胞内提取物；细菌群落；代谢物

Bacillus subtilis intracellular extracts promote immunity and intestinal microbiota in Koi Carp (*Cyprinus carpio var. koi*)

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Abstract：This study evaluated the effects of intracellular extracts from three Bacillus subtilis strains (F18, PC4, and LS16) on immunity, antioxidant status, and intestinal microbiota in koi carp. Four hundred healthy fish were divided into five groups and fed diets with phosphate-buffered saline (control), F18, PC4, LS16, or a mixture of the three extracts for nine weeks. Serum immune parameters, immune-related gene expression, microbial diversity, and resistance to A. veronii were assessed. Supplementation with B. subtilis extracts enhanced immune and antioxidant indices. LS16 notably downregulated hepatic tnf-α and upregulated intestinal occ. Lefse analysis showed increased Chryseobacterium and reduced Aeromonas in the LS16 group. Fish fed extracts also displayed significantly higher resistance to A. veronii. Metabolomics revealed distinct profiles: LS16 enriched in lipids (e.g., stearamide), PC4 in oleamide and nucleosides, and F18 in amino acids such as phenylalanine. Overall, LS16 intracellular extract shows strong potential to improve koi immunity and gut health.

Key words: probiotics; Bacillus subtilis; intracellular extracts; bacterial community; metabolites

獐子岛休闲海钓者垂钓动机及行为差异

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摘要：獐子岛凭借独特的海洋资源成为我国北方著名的休闲海钓圣地。精准识别海钓者垂钓动机与行为差异，对优化海钓产业管理与发展具有重要意义。本研究以獐子岛休闲海钓者为对象，852份有效问卷，运用因子分析、聚类分析及方差分析等方法，探究海钓者休闲动机及群体行为差异。结果表明：（1）海钓者以男性（86.6%）中青年(26-59岁)（85.7%）专科或本科（46.6%）月收入超10000元（55.7%）为主，游客主要来源辽宁省内（50%）（2）主成分分析将休闲动机归纳为“解压求逸、学习与自我成长、社交休闲、社群逐趣”四类，除社群逐群外其他三种动机在性别、年龄、学历、月收入存在显著差异（P<0.05）；海钓年频率、年花销、渔具投入等行为与学习与自我成长动机呈显著正相关（P<0.05）；（3）聚类分析可将海钓者划为“放松休闲型、技能提升型、社交需求型、自主体验型”四类群体，其中自主体验型群体的渔获放生比例最高。

关键词：獐子岛，休闲海钓，休闲动机，休闲行为

Fishing Motivations and Behavioral Differences of Recreational Marine Anglers in Zhangzi Island

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Abstract: Based on 852 valid questionnaires from recreational anglers on Zhangzi Island, this study examines their motivations and behavioral patterns using factor, cluster, and variance analysis. Key findings reveal: (1) Participants are predominantly male (86.6%), aged 26–59 (85.7%), highly educated (46.6% college or above), and with monthly incomes over ¥10,000 (55.7%); half are from Liaoning Province. (2) Motivations are categorized into four types: stress relief and relaxation, learning and self-growth, social leisure, and community-driven interest. Except for community interest, the other three show significant differences ($p < 0.05$) across demographics. Behaviors such as annual fishing frequency, expenditure, and gear investment are significantly correlated with learning and self-growth motivation ($p < 0.05$). (3) K-means clustering identified four angler segments: relaxation-oriented, skill enhancement-oriented, social needs-oriented, and self-experience-oriented—the last showing the highest catch-and-release rate.

Key words: Zhangzi Island; Recreational Marine Fishing; Leisure Motivation; Leisure Behavior

第九专题 现代渔业设施装备与信息化

基于知识蒸馏的无人机航拍图像金枪鱼围网捕捞目标检测与识别方法研究

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摘要：侦察具有捕捞价值的金枪鱼自由鱼群或人工漂流集鱼装置随附鱼群是提高金枪鱼围网船捕捞效率的重要环节。传统方法依赖鸟类活动等视觉线索，而直升机与雷达等现代技术提升了搜索能力。然而，受高成本与安全性问题制约，以无人机代替直升机完成鱼群搜索已成为行业发展趋势。本研究提出一种基于知识蒸馏与模型压缩的优化 YOLOv6 深度学习模型，用于实时海洋目标检测。评估了四种 YOLOv6 变体（YOLOv6l/m/s/t），其中 YOLOv6t-学生/蒸馏模型（模型 13）以仅 24.89 GFLOPs 的计算量实现了 0.722 mAP0.5 的最佳平衡。太平洋实地测试显示，其对 FAD 的检测准确率达 94.81%，该框架为替代直升机提供了经济高效的无人机智能搜索方案，并支持未来集成雷达、声纳等传感器以拓展海洋监测侦察应用。

关键词：无人机图像；深度学习；目标检测；知识蒸馏

Research on tuna purse seine fishing target detection and recognition method for Unmanned Aerial Vehicle aerial images based on knowledge distillation

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Abstract： Tuna purse seine fleets face high costs in locating fish aggregations, whether free-swimming or around fish aggregating devices (FADs), therefore efficient detection is crucial. While traditional methods relied on visual cues like bird activity, modern technologies such as helicopters and radar have improved search capacity. However, due to high costs and safety concerns, the industry is shifting toward unmanned aerial vehicles (UAVs). This study proposes an optimized YOLOv6-based deep learning model for real-time marine object detection, using model compression and knowledge distillation. Four YOLOv6 variants (YOLOv6l/m/s/t) were evaluated, with YOLOv6t-student/distillation (Model 13) achieving the best balance—0.722 mAP0.5 at just 24.89 GFLOPs. Field tests in the Pacific Ocean showed 94.81% FAD detection accuracy. This framework offers a cost-effective UAV alternative to helicopters and supports future integration of additional sensors (e.g., radar, sonar) for broader marine monitoring.

Key words: UAV images, deep learning, target detection, knowledge distillation

基于高频窄波束宽带声学系统的鱼体目标强度测量研究

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摘要：鱼体目标强度(TS)的精准测量是准确评估养殖场景鱼类生物量的关键。本研究设计并搭建了一套中心频率 700kHz、带宽 100kHz、波束开角 1°(水平)×20°(垂直)的声学测量系统，通过脉冲压缩技术提升时域分辨率，结合主瓣检测与重采样算法，实现了对部分鱼体回波主瓣的准确提取与能量计算。采用标准球校准法对系统进行 TS 标定，进而精确计算鱼体的 TS。以鳜鱼为测量对象，实验结果显示，鳜鱼鱼体 TS 具有方向依赖性，不同声波入射角下(0°~90°)TS 范围为-53.18~-43.66dB，声波垂直入射鱼体时鱼体体侧向与头尾向目标强度相差 8.39dB。鱼体不同部位的 TS 值存在差异性，含鱼鳔的腹部区域 TS 值（-49.80dB）较不含鱼鳔的头部（-59.13dB）和尾部（-59.09dB）平均高出 9.31dB，表明鱼鳔是主要散射源。研究可为养殖鱼类生物量声学监测提供关键基础参数，有助于优化声学监测算法。

关键词：目标强度；后向散射；高频窄波束宽带声学；脉冲压缩；养殖鱼类

Study on Fish Target Strength Measurement Based on High-Frequency Narrow-Beam Broadband Acoustic System

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Abstract： Precise measurement of fish target strength (TS) is essential for biomass assessment in aquaculture. We designed an acoustic measurement system with a center frequency of 700 kHz, a bandwidth of 100 kHz, and a beam angle of 1° × 20° . By employing pulse compression and integrating main lobe detection with resampling algorithms, the system enables extraction the main lobe of echoes from fish bodies. The system was calibrated using the standard sphere. Siniperca chuats was selected as the experimental subject. Results demonstrated that fish TS exhibits directional dependence, with values ranging from -53.18 to -43.66 dB under varying incident angles (0°–90°). The TS of the lateral body was 8.39 dB higher than that of the head and tail regions. Significant differences in TS were observed among anatomical regions, with the swimbladder-containing abdominal area (-49.80 dB) averaging 9.31 dB higher than the head (-59.13 dB) and tail (-59.09 dB) regions, indicating that the swimbladder is the principal scattering source.

Key words: Target strength; Backscattering; High-frequency narrow-beam broadband acoustics; Pulse compression; Cultured fish

波流作用下深海坐底式网箱的耦合动力响应研究

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摘要：在海水养殖产业中，坐底式网箱常布置于近海区域，用于鱼类的养殖。坐底式网箱通常由大型钢制桁架结构构成，在其外围环绕大面积柔性网衣。坐底式网箱处于海床之上，长期承受波浪和海流作用而发生振动。本研究采用欧拉-伯努利梁理论对网箱框架结构的振动进行模拟，利用集中质量法模拟大面积柔性网衣的三维振动。基于势流理论刻画波浪和海流的联合作用，利用 Morison 方程计算作用于网箱框架和网衣上的水动力载荷。建立波流联合作用下坐底式网箱的三维耦合动力响应理论模型，采用数值方法对此动力响应方程进行求解。通过试验结果和有限元模拟结果的对比验证了该模型的有效性，进一步探究波流作用下坐底式网箱的耦合振动特性。研究结果表明：在波浪和流场的共同作用下，网箱桁架结构与网衣之间存在着复杂的动力耦合作用，将会导致网线张力增大，更容易发生网衣破坏。

关键词：坐底式网箱，波流作用，动力响应，网线张力

Three-dimensional vibrations of a bottom-set net cage subjected to waves and currents

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Abstract： Bottom-set net cages have been deployed in offshore areas for fish culture. These cages usually consist of large steel truss-type frames surrounded by numerous flexible fishing nets. Positioned on the seabed, the bottom-set net cages are exposed to waves and currents, which induce vibrations over time. In this study, the frame of a bottom-set net cage, usually constructed from pipes, is modeled using the Euler-Bernoulli beam theory. The flexible fishing nets, composed of millions of net twines, are simulated using the lumped-mass method. The combined wave-current flows are described based on the potential flow theory. Hydrodynamic forces acting on the frame and nets are calculated using the Morison equation. Subsequently, a dynamic model is developed to simulate the three-dimensional vibrations of a bottom-set net cage subjected to combined waves and currents. After validating the present model, the vibration characteristics of the bottom-set net cage are analyzed in detail. The results demonstrate that the dynamic interactions between the cage frame and flexible nets are complex.

Key words: Bottom-set net cage, Waves and currents, Dynamic responses, Net tensions.

重力式升降网箱设计及动力响应特性试验研究

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摘要：重力式深水网箱在未来相当长时间内仍然是发展深远海养殖的重要设施。针对传统重力式深水网箱台风等极端环境下安全性仍存不足问题，本研究提出一种新型重力式升降网箱，通过改进桁架系统、系泊系统及增设升降控制部件，提高网箱结构强度及稳定性。为评估新型升降网箱的水动力特性，开展了网箱漂浮和下潜状态下的物理模型试验，试验结果表明：新型重力式升降网箱下潜后，网箱结构的安全性和稳定性显著提高：总系泊力最大减少约 63.22%；迎浪侧系泊力最大减少 66.54%；前侧面系泊力最大减少 60.55%；后侧面系泊力最大减少 64.97%；背浪面系泊力最大减少 58.39%；网箱纵摇幅值最大减少 58.41%；网箱升沉最大减少 48.50%。本研究验证了所设计的新型重力式升降网箱极端海况下适用性，为深远海养殖发展提供一种新型设施选择，且可为该新型重力式升降网箱后续进一步优化提供数据支撑。

关键词：重力式网箱，升降网箱，模型试验，系泊力，运动响应

Research on Design and Hydrodynamic Response of a Gravity-type Liftable Cage

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Abstract： This study presented a novel kind of gravity-type liftable net cage. And the physical model test in floating and submerged state was conducted to assess the hydrodynamic properties of the novel kind of liftable cage. The results showed that the new cage can effectively reduce the structural safety and stability after submersion by diving into water. Under test conditions, the total mooring force reduction is more than 20%, the maximum reduction is approximately 63.22%, the maximum reduction of the wave side mooring force reaches 66.54%, the maximum reduction of the front side mooring force reaches 60.55%, the maximum reduction of the rear side mooring force reaches 64.97%, and the maximum reduction of the back wave side mooring force reaches 58.39%. This study confirmed that the new gravity liftable cage presented in this paper can be used in extreme sea conditions and also can provide key data to support the new gravity liftable cage's further optimization.

Key words: Gravity-type Cage、Liftable Cage、Model Test、Mooring Force、Motion Response

新型吸鱼泵关键技术研发及产业化

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摘要：在渔业生产中，渔获的提升与输送至关重要。随着渔业现代化技术的不断进步，吸鱼泵在这一环节的应用日益广泛。针对传统真空式、离心式和射流式吸鱼泵存在成本高、能耗高、鱼类损伤等方面的问题，团队改进工艺、设备组成、关键设备结构、自动控制，研发出具有自主知识产权的导流式吸鱼泵、真空引水式吸鱼泵、螺旋管式吸鱼泵 3 种新型吸鱼泵。与传统吸鱼泵相比，新型吸鱼泵对鱼类无损伤，且在成本、能耗方面更具优势。团队为 15 万吨级智慧渔业大型养殖工船“国信 1 号 2-1”和“国信 1 号 2-2”设计了 12 台真空引水式吸鱼泵，已于 2024 年 5 月交付。与“国信 1 号”上的真空式吸鱼泵相比，真空引水式吸鱼泵对鱼类无损伤，且输送量提高 33%，能耗降低 80%，成本降低 30%。未来，团队将继续优化新型吸鱼泵的工艺流程和关键设备结构，推动新型吸鱼泵在渔获提升与输送领域的广泛应用。

关键词：新型吸鱼泵；鱼类损伤；养殖工船；真空引水式吸鱼泵；导流式吸鱼泵；螺旋管式吸鱼泵

The key technology development and industrialization of novel fish pumps

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Abstract： The fish catches and transportation is crucial in fishery production. With the development of modern fishery technologies, the application of fish pumps has become increasingly widespread. Aiming at the problems of high cost, high energy consumption and fish damage in traditional fish pumps, which were vacuum fish pumps, centrifugal fish pumps and jet fish pumps, the team improved the process, equipment composition, key equipment structure and automatic control and developed three new types of fish pumps, which were flow-guiding fish pumps, vacuum water diversion fish pumps, and spiral tube fish pumps. The three new types of fish pumps had the independent intellectual property rights. Compared with traditional fish pumps, the new types of fish pumps have significant advantages in terms of cost and energy consumption and cause no damage to fish. In the future, our team will further optimize the process flow and key equipment structure of the new fish pumps and promote their wide application in the field of fish catches and transportation.

Key words: novel fish pump; fish damage; aquaculture vessel; vacuum water diversion fish pump; flow-guiding fish pump; spiral tube fish pump

离心水泵式负压吸鱼系统的设计与多相流模拟

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摘要：针对深远海大型设施养殖平台单体产量突破百吨级后面临的活鱼高效起捕难题，设计了一种利用离心水泵驱动形成稳定负压的大流量吸鱼系统。基于理想气体状态方程得出液位变化仅为集鱼箱容积总高度的 10.3%以内就能形成适于吸鱼的工作压力，据此设计了集鱼箱装置的关键尺寸，并利用多孔介质模型构建拦鱼格栅模型，基于 VOF 与 CFD-DEM 耦合方法对吸鱼过程进行三维瞬态数值分析。结果表明：吸鱼过程液位保持基本恒定，压力波动范围在-37.5~-26.5 kPa 之间，最大压力变化率为 0.037 kPa/s，远低于鱼类损伤阈值，工作压力相对初始值-35 kPa 的变化不到 7%；集鱼箱内鱼群分布随着流量增大呈现显著差异：流量升高会增加堵塞风险，需要通过弧形格栅设计、扩大开口尺寸及增设导鱼通道优化拦鱼格栅结构以降低堵塞风险，进一步提升吸捕量。

关键词：吸捕装置；三相流；离散元模型；压力波动；堵塞预测

Design and Multiphase Flow Simulation of a Centrifugal Pump Negative-Pressure Fish Suction System

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Abstract： To address the challenge of efficiently harvesting live fish from large-scale aquaculture platforms in deep sea, where the yield per individual platform has exceeded 100 tons, a high-capacity fish suction system utilizing a centrifugal water pump to create a stable negative pressure was designed. Based on the ideal gas state equation, it was found that a pressure suitable for fish suction could be formed when the liquid level change was within 10.3% of the total height of the fish collection tank. The key dimensions of the fish collection tank device were designed accordingly. A fish barrier grid model was constructed using a porous medium model, and a three-dimensional transient numerical analysis of the fish suction process was performed based on the coupled VOF and CFD-DEM method. The numerical results showed that the liquid level remained basically constant during the fish suction process, with pressure fluctuations ranging from -37.5 to -26.5 kPa, and the maximum pressure change rate was 0.037 kPa/s, which was far below the fish damage threshold.

Key words: fish suction device; three-phase flow; discrete element model; pressure fluctuation; clogging prediction

中高强聚乙烯纤维的研发及在重力式网箱的示范应用

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摘要：随着水产养殖从近岸传统模式向深海转型，传统的聚乙烯（HDPE）有结网难以满足现代水产养殖快速发展的需求。而聚乙烯（HDPE）有结网的机械性能与聚乙烯单丝的强度密切相关，因此对聚乙烯单丝的力学性能提出了更高的要求，尤其在结节强度方面。基于前期基础，本文研究了热塑性弹性体（TPE）增韧改性对超高分子量聚乙烯（UHMWPE）纤维结构和性能的影响。结果表明，TPE 相均匀分散在连续的 UHMWPE 基体中，形成典型的海岛结构。TPE 的加入提高了共混纤维的结节强度，同时两组分间的分子间作用力减弱，使 UPE 纤维更容易沿拉伸方向排列，促进晶体取向。TPE 的加入导致共混纤维的表观结晶度降低，相反，提高了共混纤维的结节强度。我们成功开发出断裂强度≥10 cN/dtex，结节强度≥5 cN/dtex 的增强增韧聚乙烯单丝，且在重力式网箱（温州）外网上实现了示范应用。

关键词：增强增韧聚乙烯纤维；结节强度，重力式网箱

Medium high strength polyethylene fiber; knot strength, gravity cage

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Abstract： With aquaculture transitioning from nearshore to offshore and deep-water environments, high-strength and tough polyethylene fishing monofilaments have been developed to satisfy the operational requirements of modern fisheries. This article studied the effect of thermoplastic elastomer (TPE) toughening modification on the structure and properties of ultra-high molecular weight polyethylene (UHMWPE) fibers. The results indicate that TPE phase is uniformly dispersed in the continuous UHMWPE matrix, forming a typical island structure. The addition of TPE improves the knot strength of the blended fibers, while reducing the intermolecular forces between the two components, making it easier for UPE fibers to align along the stretching direction and promoting crystal orientation. We have successfully developed reinforced and toughened polyethylene monofilaments with a fracture strength of ≥ 10 cN/dtex and a knot strength of ≥ 5 cN/dtex, and demonstrated their application on a gravity cage.

Key words: reinforced and toughened polyethylene monofilaments ; knot strength;gravity cage

新型潜降式网箱在不同水深条件下受规则波作用的动力响应和系泊响应实验研究

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摘要：为研究波浪波高、周期和锚链拖地长度对新型潜降式网箱水动力响应特性的影响，提高其稳定性。本文通过物理模型实验方法，基于弗劳德相似准则构建 1:40 缩尺模型，设置漂浮、悬浮和坐底三种作业工况，结合波高（5~15 cm）、波浪周期（0.801~1.289 s）及锚链拖地长度（17~37 cm）多参数进行试验。结果显示：网箱的垂荡、纵荡和纵摇均与波高呈显著正相关关系；漂浮工况下网箱的垂荡和纵荡与周期呈正相关，纵摇则随周期的增加呈减小趋势；悬浮工况下网箱垂荡响应与周期无明显关系，纵荡和纵摇与周期呈正相关；网箱所受系泊力在漂浮工况下与波高和周期均呈显著正相关，在悬浮工况下与二者无显著关系；网箱从漂浮工况下潜至悬浮工况后的垂荡、纵荡和纵摇值平均减幅分别达到 66.05%、28.67%、72.93%，表明网箱具有良好的潜降抗风浪特性。

关键词：潜降式网箱；水动力特性；物理模型实验；规则波

Experimental investigation into the dynamic and mooring response of a novel submersible cage to regular waves at various depths

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Abstract: This study examines the effects of wave height, period, and anchor chain drag length on the hydrodynamic response of a novel submersible net cage to improve stability. Physical model tests using a 1:40 scale model based on Froude similarity were conducted under floating, suspended, and bottom-seated conditions. Tests covered wave heights of 5–15 cm, periods of 0.801–1.289 s, and chain drag lengths of 17–37 cm. Results show that vertical and longitudinal oscillations and heave motion increase with wave height. Under floating conditions, oscillations correlate positively with period, while heave decreases as period increases. Under suspended conditions, vertical oscillation is insensitive to period, whereas longitudinal oscillation and heave increase with it. Mooring forces correlate positively with wave height and period in the floating state but not in the suspended state. Transitioning from floating to suspended reduces vertical oscillation, longitudinal oscillation, and heave by 66.05%, 28.67%, and 72.93%, indicating excellent wave resistance during submergence.

Key words: submersible net cage; hydrodynamic characteristics; physical modeling experiment; regular waves

渔业机器人对空间深度信息的数据挖掘进展

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摘要：渔业机器人正成为提升海洋渔业智能化水平的核心装备，其对水下空间深度数据信息的挖掘能力至关重要。传统上，依赖于陆地激光雷达的测距原理与水下声呐的主动探测技术，虽能获取精确点云，但存在成本高、分辨率有限等瓶颈。近年来，基于视觉的深度估计方法取得显著进展：水下单目深度估计模型通过学习大量数据，可从单张图像预测深度信息，极大降低了硬件依赖；而神经辐射场与3D高斯溅射等新型隐式表征技术，则能从稀疏图像序列中高质量地重建水下三维场景，实现逼真的新视角合成。此外，扩散模型在生成高质量训练数据和增强深度估计鲁棒性方面展现出巨大潜力。未来，融合多模态传感器与先进人工智能算法的渔业机器人，将在水产养殖监测、资源评估与自主作业等方面实现更深远的数据挖掘与应用。

关键词：渔业机器人，深度数据挖掘，水下三维重建，神经辐射场

Advances in the Extraction of Spatial Depth Information for Fishery Robots

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Abstract： Fishery robots are emerging as core equipment for enhancing the intelligence of marine fisheries, with their capability to mine spatial depth data being of paramount importance. Traditionally, reliance on ranging principles derived from terrestrial LiDAR and active detection technologies like underwater sonar can acquire precise point clouds but faces bottlenecks such as high cost and limited resolution. Recent years have witnessed significant progress in vision-based depth estimation methods: underwater monocular depth estimation models can predict depth information from single images by learning from vast datasets, significantly reducing hardware dependency. Novel implicit representation techniques, such as Neural Radiance Fields (NeRF) and 3D Gaussian Splatting, can reconstruct high-quality 3D underwater scenes from sparse image sequences, enabling realistic novel view synthesis. Furthermore, Diffusion models show great potential in generating high-quality training data and enhancing the robustness of depth estimation. In the future, fishery robots integrating multi-modal sensors.

Key words: Fishery Robots，Depth Data Mining，Underwater 3D Reconstruction，Neural Radiance Fields

基于集污性能的圆形养殖池进水模式评估

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摘要：循环水养殖是目前工厂化养殖的主流，其循环过程主要依靠水泵供能，并且极易发生污物堆积现象。本研究引入入口冲力（Fi）、速度均匀系数（UC50）、池内平均速度（Vavg）、进水角度（0~90°）、进水位置（d=r、1/2r、1/4r）和高度（接近水面、中层水面、接近池底）综合评价了两种进水模式（竖直射流、水平射流）下养殖池内的水动力特性，期望能在水泵能耗尽可能小的同时保证池内污物的清除。研究表明：两种射流状态下，入口冲力皆和池内流场强度呈正相关，入口冲力越大池内流场强度越高；进水角度方面，竖直射流模型下流场性能排序为：0°＞15°＞30°＞45°＞60°＞75°＞90°，水平射流模型下流场性能排序为：15°＞0°＞30°＞45°＞60°＞75°＞90°；改变进水位置，其他参数不变，竖直射流和水平射流模型均为 d=r 处流场性能最佳；进水高度不同时，两种模式皆为中层进水流场性能最佳。

关键词：循环水养殖 水动力特性 速度均匀系数 污物清除

Evaluation of Hydrodynamic Characteristics in Circular Aquaculture Tanks Based on Waste Removal

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Abstract: Recirculating aquaculture (RAS) is the mainstream of industrial aquaculture. Its circulation mainly relies on water pumps for energy and is highly prone to pollutant accumulation. This study introduced inlet impulse (Fi), velocity uniformity coefficient (UC50), average in-tank velocity (Vavg), inlet angle (0~90°), inlet position (d=r, 1/2r, 1/4r) and inlet height (near surface, mid-water, near tank bottom) to evaluate aquaculture tank hydrodynamic characteristics under two inlet modes (vertical jet, horizontal jet), aiming to ensure pollutant removal while minimizing pump energy consumption. Results showed that under both jets, inlet impulse correlated positively with in-tank flow field intensity—the greater the impulse, the higher the intensity. For inlet angles: vertical jet performance order was 0°＞15°＞30°＞45°＞60°＞75°＞90°; horizontal jet order was 15°＞0°＞30°＞45°＞60°＞75°＞90°. When inlet position changed (other parameters unchanged), both models had optimal performance at d=r. For heights, mid-water inlet worked best in both modes.

Key words: Recirculating Aquaculture，Inlet Modes，Inlet Impulse，velocity Uniformity Coefficient，Pollutant Removal

基于 Tracepro 的灯光围网集鱼灯优化配置研究

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摘要：集鱼灯是光诱捕捞生产作业中一种重要的辅助装备。为了高效利用集鱼灯灯光，本文基于 Tracepro 光学仿真软件对集鱼灯配置进行优化研究。通过利用 Tracepro 建立理论照度模型，比较 Tracepro 计算值与实测值发现，Tracepro 计算值与实测值的拟合决定系数接近于 1，表明理论照度模型符合实际发光情况。通过模型计算了集鱼灯不同安装角度下（20°、40°、60°）的有效水体面积、体积以及深度。根据有效水体体积和有效水体深度，得到集鱼灯最佳安装角度在 60°-70°之间。

关键词：集鱼灯；照度计算；Tracepro；灯光围网

Optimization of lighting lamps allocation based on tracepro in light purse seine

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Abstract： The lighting lamps are crucial equipment for light attracting fishery targeting species.In order to efficiently utilize the light from the lighting lamps,this paper conducts an optimization study on the lighting lamps allocationbased on the Tracepro. By establishing a theoretical illumination model using Tracepro,a comparison between the calculated values and the measured values reveals that the determination coefficient of the fit between the two is close to 1.It indicates that the theoretical illumination model conforms to the actual lighting conditions。The model calculates the effective water area, volume, and depth under different installation angles (20°, 40°, 60°) of the lighting lamps.Based on the effective water volume and effective water depth, it is found that the optimal installation angle of the lighting lamps falls between 60° and 70°.

Key words: The lighting lamps；illumination calculation；Tracepro；light purse seine

FishFeedingNetLite:用于鱼类摄食行为实时识别的轻量级混合网络

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摘要：在高密度与工厂化养殖环境下，准确量化与识别鱼群摄食行为仍具挑战。为实现实时、精确的摄食识别，本文提出一种新颖的平滑摄食指数(flsmoothed)，通过自适应融合多维运动一空间特征对摄食状态进行动态划分;并设计了一种轻量化网络 FishFeedingNetLte(FFNL)，将高效卷积、多尺度特征融合与轻量化注意力相结合，模型在仅包含 0.42M 参数、0.72G FLOPs 的情况下，实现了 97.70%的平均准确率，大量实验证明，FFNL 在与现有主流轻量模型比较中具有更优的分类性能和更快的推理速度，具备在边缘设备中部署的潜力。所提出的 Fismoothed 与 FFNL 协同方法，为低成本、可靠的智能投喂监测与决策支持提供了可行路径，有望推动水产养殖的科学化、精细化管理。

关键词：鱼类摄食行为，行为量化，轻量级神经网络，实时识别

FishFeedingNetLite (FFNL): A Lightweight Hybrid Network for Real-Time Fish Feeding Behavior Recognition

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Abstract： In aquaculture, accurate quantification and recognition of fish-school feeding behaviour under real-world, high-density conditions remains challenging. To enable real-time, precise feeding-state analysis, we introduce a novel Smoothed Feeding Index (FIsmoothed) that adaptively categorises feeding states by fusing multi-dimensional motion–spatial features. We also propose FishFeedingNetLite (FFNL), a lightweight neural network that combines efficient convolutions, multi-scale feature fusion, and lightweight attention. FFNL requires only 0.42M parameters and 0.72G FLOPs, yet achieves a robust average classification accuracy of 97.7%. Extensive experiments show that FFNL outperforms state-of-the-art lightweight models and is well suited for edge deployment. Together, FIsmoothed and FFNL provide a reliable, low-cost solution for real-time feeding-state identification and decision support in intelligent aquaculture feeding systems.

Key words: Fish feeding behaviour, Behaviour quantification, Lightweight neural network, Real time recognition

基于声学技术的水下生物监测、预警与定位遥测关键技术及应用

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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，为海洋生态保护和资源管理提供了有力技术支持。

关键词：渔业信息；声学技术；SV 声呐；生物遥测

Key Technologies and Applications of Underwater Biological Monitoring, Early Warning, and Telemetry Based on Acoustic Technology

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Abstract：Focusing on the advantages of acoustic technology in underwater environments, this study integrates three key technologies—NEO-SV sonar, a dedicated data processing unit, and ultrasonic telemetry—to achieve marine organism monitoring, early warning, and positioning. The sonar, serving as the fundamental sensing component, detects and captures raw underwater target information. The data processing unit efficiently analyzes sonar echoes to accurately identify target features and locations. Ultrasonic telemetry leverages the propagation characteristics of sound in water to enable reliable positioning, tracking, and remote data transmission. Together, these three technologies form a complete chain from data acquisition and analysis to application and transmission, significantly enhancing the precision and real-time performance of underwater biological monitoring systems and providing robust technical support for marine ecological protection and resource management.

Key words: fisheries information；acoustic technology; SV-sonar; biotelemetry

养殖网笼清洗装置设计与试验研究

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摘要：针对吊笼养殖网笼易被藻类、贝类附着影响养殖效益的问题，本文设计了一种结合螺旋输送毛刷辊与空化射流的机械化清洗装置。通过测量网笼及紫贻贝的力学特性，为结构设计提供依据；利用 Ansys-Fluent 软件分析空化喷嘴结构对气相体积分数的影响，确定最优角型喷嘴参数为喉管长度 6.1 mm、喉管直径 1.42 mm、扩散角 30.7°，对应气相体积分数达 0.998。通过空蚀试验开展喷嘴作业参数优化，得出最优组合为泵压 24.3 MPa、靶距 15.1 mm、夹角 8.4°，此时空蚀体积为 0.0223 cm^3。基于仿真与试验结果试制样机并进行性能测试，结果显示该装置对紫贻贝的平均清洗效率为 5 笼/min，清洗率达 88.8%。本研究为网笼附着物清洗提供了高效可靠的机械化解决方案，具备良好推广应用价值。

关键词：网笼清洗；附着物；角型喷嘴；空化射流；机械化清洗

Design and experimental study of raft type shellfish breeding cage net cleaning device

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Abstract：To tackle biofouling on aquaculture cage nets, this study developed a mechanized cleaner combining a helical brush roller and a cavitating jet. The mechanical properties of nets and Mytilus edulis were measured to inform the design. Numerical simulation optimized the angular nozzle's geometry, achieving a gas phase volume fraction of 0.998. Cavitation erosion tests further optimized operational parameters, yielding a maximum erosion volume of 0.0223 cm^3. Prototype tests demonstrated a cleaning efficiency of 5 cages/min and an 88.8% removal rate for Mytilus edulis, confirming the solution's effectiveness and application potential.

Key words: Cage net cleaning; Fouling organisms; Angular nozzle; Cavitating jet; Mechanized cleaning

菲律宾蛤仔苗离散元仿真参数标定与播苗试验

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摘要：为提高菲律宾蛤仔播苗过程离散元仿真精度、优化播苗部件，本研究测量了贝苗本征参数，采用 Hertz-Mindlin 无滑移接触模型建立仿真模型，并通过自由落体碰撞、斜面滑动与滚动试验，标定了贝苗与 304 不锈钢、EVA 发泡材料和 FKM23 橡胶间的接触参数。结果显示，贝苗与上述材料的碰撞恢复系数分别为 0.332、0.298、0.459，静摩擦因数分别为 0.390、0.561、0.488，滚动摩擦因数分别为 0.444、0.585、0.520。以堆积角相对误差为指标，经最陡爬坡与正交旋转组合试验优化，得到贝苗间接触参数为：碰撞恢复系数 0.4、静摩擦因数 0.409、滚动摩擦因数 0.438。验证试验表明，堆积角仿真与实测值最大相对误差小于 4%，播苗分布变异系数仿真与台架试验最大相对误差小于 5%，证实参数可靠。本研究可为贝类精准播苗装置设计与仿真优化提供参考。

关键词：菲律宾蛤仔苗；离散元法；参数标定；贝类播苗；接触参数

Calibration of discrete element simulation parameters and seeding experiment of *Ruditapes philippinarum*

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Abstract： To improve the simulation accuracy of Philippine clam seedling sowing, this study determined intrinsic parameters of seedlings and established a DEM model using the Hertz-Mindlin no-slip contact model. Contact parameters with 304 stainless steel, EVA foam, and FKM23 rubber were calibrated via free-fall, inclined-sliding, and rolling tests, yielding collision recovery coefficients of 0.332, 0.298, and 0.459; static friction coefficients of 0.390, 0.561, and 0.488; and rolling friction coefficients of 0.444, 0.585, and 0.520, respectively. Inter-seedling parameters were optimized to 0.4, 0.409, and 0.438 via stacking angle tests. Validation showed less than 4% error in stacking angle and under 5% in distribution variation coefficient, confirming reliability for optimizing shellfish seeding devices.

Key words: Philippine clam seedlings; Discrete Element Method;Parameter calibration;Shellfish seeding; Contact parameter

机液耦合网箱装置设计及试验

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摘要：针对海水养殖网箱易被紫贻贝等生物附着的问题，本文基于空化射流与机械打击原理，设计了一种机液耦合式网箱清洗装置。通过万能试验台开展刀片破贝力学试验，确定了适用刀片类型；进一步利用LS-Dyna软件模拟破贝过程，以紫贻贝所受合力为指标，优化得出刀片最优结构参数组合为切角54°、厚度2.7 mm、刀刃角10.5°，此时贝体受力达245.24N。随后以塑性应变能为评价指标，优化得到刀片安装参数为刀倾角18°、刀间距19.3 mm、水平安装角–19°，对应塑性应变能为1219.09 J，破碎效果最优。整机试验表明，该装置清洗效率为330 m²/h，清洗效率为89.7%。本研究可为网箱高效清洗装备研发与养殖机械化升级提供技术支持。

关键词：网箱清洗；机液耦合；刀片结构；安装方式

Design and test of mechanical and hydraulic combined net cage cleaning device

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Abstract： Biofouling by Mytilus galloprovincialis threatens aquaculture net integrity and economic returns. This study presents a mechano-hydraulic cleaning device integrating cavitating jets with mechanical impact. Mechanical crushing tests identified suitable blades, while LS-Dyna simulations optimized structural parameters. With resultant force as the index, the optimal blade configuration was: cutting angle 54°, thickness 2.7 mm, edge angle 10.5°, achieving 245.24 N force. Installation parameters optimized via plastic strain energy yielded: inclination 18°, spacing 19.3 mm, horizontal angle -19°, reaching 1219.09 J strain energy. Full-scale tests demonstrated 89.7% cleaning efficiency at 330 m²/h, supporting mechanized aquaculture development.

Key words: Cage Net Cleaning ;Hydromechanical Coupling; Blade Structure; Mounting Method

基于 yolov8 的拖网网具图纸数字化研究

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摘要：针对拖网网具图纸大多为手工绘制或者电子图像，不利于网具的自动化设计，数字化拖网网具图纸有着显著的优势。通过收集获取 171 张拖网网具图纸，对其中的文本（text）、网衣展开图主体（PDD）、符号（symbol）和其余部件（other）四个类别进行标注，采用目标检测模型 YOLOv8s 进行目标检测研究。结果表明：总体精确率达 83.9%，召回率为 54.4%，mAP50 为 63.6%，mAP50-95 为 49.4%，其中对总体指标影响较大的为文本和符号的召回率，分别为 49.3%和 16.4%。研究结果验证了 YOLOv8s 模型在当前目标检测任务上的有效性，同时也揭示了对于文本和符号等小目标召回率相对较低的性能瓶颈。本研究对拖网网具内容检测精度达 83.9%，可以为拖网网具图纸的数字化提供数据支持，为拖网网具的创新设计提供原始数据积累。

关键词：拖网网具，数字化，yolov8s

Research on Digitalization of Trawl Gear Drawings Based on YOLOv8

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Abstract: Most existing trawl drawings are hand-drawn or raster images, hindering automated design. This study digitized 171 trawl drawings, annotating text, planar development drawings (PDD), symbols, and other components. The YOLOv8s model achieved 83.9% precision, 54.4% recall, and 63.6% mAP50. However, low recall for text (49.3%) and symbols (16.4%) remains a challenge. The results demonstrate YOLOv8s' effectiveness for drawing digitization while highlighting the small target detection bottleneck. This research provides valuable data support for automated trawl design innovation.

Key words: Trawl gear, Digitalization, YOLOv8s

基于 MRFA 改进 STGCN 的
深远海网箱溶解氧预测方法

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摘要：深远海网箱养殖兼具生态效益、产品品质与养殖产量优势，是水产养殖业可持续发展的关键。溶解氧作为核心环境因子，直接影响养殖生物生长代谢，其实时监测与多步精准预测是保障生产安全、规避经济损失的重要支撑。多因素水质参数变化过程中存在时空耦合作用，呈现非线性、动态性与复杂性特征，溶解氧参数易受其他水质因子的影响，特别是在开放复杂养殖海域，仅由溶解氧单因素预测缺乏准确性。为此，本文提出一种新型时序预测模型 M-STGCN，该模型基于时空图卷积网络（STGCN）进行优化，通过图神经网络捕捉多水质参数的互相关性，借助多感受野聚合（MRFA）模块提取多尺度时序特征，解码器引入多注意力机制实现跨水层信息融合，并融合并行映射解码器对不同水层进行联合预测。实验验证表明，该模型对未来多步溶解氧预测表现优异，相较于原始 STGCN 性能提升 14%~37%，可精准捕捉溶解氧动态变化，为智能养殖监测预警提供可靠技术支持。

关键词：深远海养殖；时序预测；溶解氧；时空图卷积网络；多感受野聚合；

A Dissolved Oxygen Prediction Method for Offshore Aquaculture Cages Based on STGCN Improved by MRFA

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Abstract：Offshore cage aquaculture, with ecological benefits, quality and yield advantages, is crucial for aquaculture sustainability. Dissolved oxygen (DO), a core environmental factor, directly affects cultured organisms' growth and metabolism. Its real-time monitoring and accurate multi-step prediction are vital for production safety and loss avoidance. Water quality parameters exhibit spatiotemporal coupling, nonlinear, dynamic and complex traits. DO is susceptible to other factors, making single-factor prediction inaccurate in open complex sea areas. To address this, we propose M-STGCN, optimized from STGCN. It captures multi-parameter intercorrelations via graph neural networks, extracts multi-scale temporal features through MRFA, integrates multi-attention for cross-water-layer fusion, and uses parallel decoders for joint prediction. Experiments show the model achieves excellent MAE in multi-step DO prediction, with 14%~37% improvement over original STGCN. It accurately captures dynamic DO changes, supporting intelligent aquaculture monitoring and early warning.

Key words: Offshore aquaculture; Time series prediction; Dissolved Oxygen; Spatial-Temporal Graph Convolutional Network; Multi-Receptive-Field-Aggregation

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，为海洋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：Focusing on the advantages of acoustic technology in underwater environments, this study integrates three key technologies—NEO-SV sonar, a dedicated data processing unit, and ultrasonic telemetry—to achieve marine organism monitoring, early warning, and positioning. The sonar, serving as the fundamental sensing component, detects and captures raw underwater target information. The data processing unit efficiently analyzes sonar echoes to accurately identify target features and locations. Ultrasonic telemetry leverages the propagation characteristics of sound in water to enable reliable positioning, tracking, and remote data transmission. Together, these three technologies form a complete chain from data acquisition and analysis to application and transmission, significantly enhancing the precision and real-time performance of underwater biological monitoring systems and providing robust technical support for marine ecological protection and resource management.

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

基于计算机视觉的大黄鱼长度提取和质量估算方法

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摘要：随着水产养殖业的迅猛发展，精准水产养殖作为优化养殖管理和提升经济效益的关键手段，已成为研究领域的热点之一。本研究提出了一种创新的鱼类形态计量分析与质量估算方法。实验结果表明，该模型在 Pbox、Pmask、Rbox、Rmask、mAP50box、mAP50mask、Params、FLOPs 等指标上分别达到了 94.8%、99.8%、99.6%、99.7%、98.8%、98.9%、2.38 M、8.5 G。该模型能够更有效地捕捉缺陷区域的判别性特征，对形态与尺度变化更为敏感，从而显著提升了检测与分割的精度。此外，本文还建立了大黄鱼长度-体重的函数关系模型（n=30）：W = 0.0138 × L^3.1877（R² = 0.8976）。利用该模型对大黄鱼的体重进行估算，结果显示模型预测性能优良，平均相对误差为 2.88%，均方根误差为 12.26 g，表明该模型适用于大黄鱼的质量估算。

关键词：大黄鱼；YOLO v13；长度提取；质量估算

A Computer Vision Approach for Body Length Measurement and Weight Prediction in Large Yellow Croaker

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Abstract: With the rapid development of the aquaculture industry, precision aquaculture has emerged as a key approach for optimizing farming management and enhancing economic efficiency, becoming a research hotspot. This study proposes an innovative method for fish morphometric analysis and mass estimation. Experimental results demonstrate that the model achieved 94.8%, 99.8%, 99.6%, 99.7%, 98.8%, 98.9%, 2.38 M, and 8.5 G in Pbox, Pmask, Rbox, Rmask, mAP50box, mAP50mask, Params, and FLOPs, respectively. The model can more effectively capture discriminative features of target regions and exhibits greater sensitivity to morphological and scale variations, thereby significantly improving detection and segmentation accuracy. Furthermore, we established a length-weight relationship model for large yellow croaker (n=30): W = 0.0138 × L^3.1877 (R² = 0.8976). Validation results show excellent prediction performance with a mean relative error of 2.88% and root mean square error of 12.26 g, indicating the model's suitability for mass estimation of large yellow croaker.

Key words: Large Yellow Croaker; YOLOv13; Morphometric Analysis; Mass Estimation; Instance Segmentation

第十专题 渔业经济、政策与管理

水产品贸易对渔民增收的影响研究——基于 2012–2022 年省级面板数据的分析

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摘要：基于 2012-2022 年中国部分省级行政单位的面板数据，以各省份每年人均渔民收入水平作为研究对象，探究水产品贸易对渔民收入增长的影响机制。首先构建双固定效应模型验证水产品贸易对渔民收入的直接影响，并进行稳健性检验，再从地理位置、经济发展水平与政府干预程度三个角度探讨水产品贸易影响渔民收入的异质性，然后揭示了劳动生产率在水产品贸易提升渔民收入过程中的中介作用。结果显示：水产品贸易对渔民收入水平的影响显著为正，这种作用在沿海地区、经济发展水平高的地区以及政府干预程度高的地区更加显著；并且水产品贸易一定程度上可以通过提高渔民的劳动生产率进而提升其收入水平。未来，政府应该重视水产品贸易的积极作用，针对不同地区的地理特征、经济发展水平和政府干预程度等制定差异化的政策措施，通过提升渔业技术水平、优化渔业产业结构、加强市场监管等促进渔民增收。

关键词：水产品贸易；渔民收入；劳动生产率；政府干预

Research on the Impact of Aquatic Product Trade on Fishermen's Income Increase ——An Analysis Based on Provincial Panel Data from 2012 to 2022

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Abstract： Using panel data of some Chinese provincial administrative units (2012-2022) and focusing on provincial annual per capita fishermen's income, this study explores how aquatic product trade affects fishermen's income growth. A two-way fixed effects model (with robustness test) verified the trade's direct impact; heterogeneity was analyzed from geography, economic development and government intervention; labor productivity's mediating role was also revealed. The results show that aquatic product trade positively impacts fishermen's income (more significantly in coastal, high economic development and high intervention areas) and boosts income via improving labor productivity. In the future, the government should highlight the trade's role, make region specific policies and promote fishermen's income by advancing fishery technology, optimizing industrial structure and strengthening market supervision.

Key words: Aquatic product trade; Fishermen's income; Labour productivity; Government intervention

“十四五”时期我国特色淡水鱼产业全要素生产率测算及影响因素研究

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摘要：为探究“十四五”时期我国特色淡水鱼产业高质量发展路径，本文测度了产业全要素生产率（TFP）的演变特征，并识别了其关键驱动因素。研究采用 DEA-Malmquist 指数与面板回归模型，基于 2020—2025 年调研面板数据，测度并分解产业 TFP，进而实证检验了人力资本、组织模式等因素的影响。结果显示：产业 TFP 年均增长 3.75%，但增长模式失衡，主要由规模效率驱动，技术进步贡献有限；产业内部分化为“均衡高增长”“效率追赶”与“瓶颈停滞”三种模式；回归分析表明，人力资本与合作社是驱动 TFP 增长的关键正向因素，而技术培训呈显著负向效应，规模与资本投入影响不显著。结论认为，产业正处由规模驱动向创新与管理驱动转型的关键期。展望“十五五”，亟需通过强化技术创新与优化社会化服务体系，激活技术进步与纯技术效率，推动产业高质量发展。

关键词：特色淡水鱼；全要素生产率；Malmquist 指数；影响因素；“十五五”展望

Study on the calculation and influencing factors of total factor productivity of my country's characteristic freshwater fish industry during the "14th Five-Year Plan" period

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Abstract： This study investigates the total factor productivity (TFP) of China's specialty freshwater fish industry from 2020–2025 to identify its growth drivers and development path. Using panel data from 1,038 farms, we employ a two-stage model, first using the DEA-Malmquist index to measure TFP and then a panel regression to identify its determinants. Results show that TFP grew 3.75% annually, but the growth was imbalanced, driven by scale efficiency while technological progress (TC) stagnated. We identify three distinct growth patterns among species. The regression reveals that human capital and cooperatives are key positive drivers, while technical training has a significant negative effect. We conclude the industry is in a critical transition from scale- to innovation-driven growth. For the 15th Five-Year Plan, activating TC and pure technical efficiency through technological innovation and optimizing social service systems is crucial for high-quality development.

Key words: Special freshwater fish; total factor productivity; Malmquist index; influencing factors; outlook for the 15th Five-Year Plan

基于物质平衡模型的浙江南部近海生态系统碳流通特征与渔业扰动分析

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摘要：本研究基于 2023 年在浙江南部近海进行的渔业资源综合调查资料和文献信息，应用 Ecopath 模型构建了碳单位的浙江南部近海生态系统模型，以评估碳在该海域高营养级生物之间的流通特征。研究结果表明，浙南海生态系统的总碳流量为 588.619gC/m2/year。系统的净系统生产力（NSP）作为生态系统封存外部二氧化碳净值的指标，在本研究中 NSP 为 54.741gC/m2/year，相较于物理层面的东海海-气碳通量而言，本研究的碳汇结果与其处于一个量级但稍高，可能是因为考虑了细菌的呼吸作用。进一步地，为量化捕捞活动对浙南海碳汇功能的影响，在静态模型研究的基础上，应用 Ecosim 模型模拟了从禁捕到增加捕捞强度的碳汇功能变化。结果表明，以 NSP 作为海洋生态系统碳汇指标来看，实施不同的捕捞策略下，浙南海生态系统的碳汇功能并没有显著改变，各情景间 NSP 变化幅度为 52.47~53.50 gC/m2/year。

关键词：生态系统模拟；浙江南部近海；食物网；细菌；捕捞策略；碳汇；碳循环

Characteristics of carbon flow and fishery disturbance in the southern coastal area of Zhejiang ecosystem based on a material balance model

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Abstract： This study is based on the survey data of the southern coastal area of Zhejiang in 2023, using a combination of EwE model to assess the flow of carbon at higher trophic levels from a static structure perspective, and dynamically simulate the impact of fishing intensity (from no fishing to increased fishing) on carbon sink function.The results indicated that the total carbon flow of the SCZ ecosystem was 588.619 g/m2/year. The net system production (NSP) of the system serves as an indicator of the net value of external CO2 sequestered by the ecosystem，, and in this study, the NSP was 54.741 g/m2/year. In comparison to the physical air-sea carbon flux in the East China Sea, the carbon sink results obtained in this study were of a similar magnitude but were slightly elevated, likely attributable to the inclusion of bacterial respiration.Using NSP as a proxy for the marine carbon sink, the carbon sequestration capacity of the ecosystem did not differ significantly across fishing scenarios, with NSP varying between 52.47 and 53.50 g/m2/year.

Key words: ecosystem modeling; southern coastal area of Zhejiang; Food webs; bacteria; fishing scenarios; carbon sink; carbon cycle

基于 GNNWR 的太平洋黄鳍金枪鱼资源的环境驱动机制研究

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摘要：黄鳍金枪鱼（*Thunnusalbacares*）是金枪鱼渔业的主要捕捞对象之一，在世界远洋渔业的发展中具有重要地位，广泛分布于太平洋、印度洋、大西洋的热带、亚热带及温带海域，其中，太平洋是世界黄鳍金枪鱼捕捞的主要作业海域。研究黄鳍金枪鱼的渔场分布对于渔业资源的可持续利用、渔业管理和海洋生态系统的保护具有重要意义。本文总结了黄鳍金枪鱼渔业资源状况、生物学特征、渔场分布和环境因子之间的关系，分析了国内外学者在研究渔场资源丰度时所采取的方法，分析了目前研究存在的缺陷及问题。进一步，本文引入 Liang-Kleeman 信息流（IF）和地理加权回归神经网络（GNNWR）和两种创新方法，前者基于信息流理论识别环境因子与渔业资源间的因果关系，克服传统相关分析的局限；后者通过融合神经网络非线性能力与空间局部建模优势，显著提升了复杂海洋环境中资源预测的精度与适应性。

关键词：渔业资源；黄鳍金枪鱼环境因子；Liang-Kleeman 信息流；GNNWR

Research on the Environmental Driving Mechanisms of Pacific Yellowfin Tuna Resources Based on GNNWR

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Abstract: Yellowfin tuna (*Thunnus albacares*) is one of the primary target species in the global tuna fishery and holds significant importance in the development of distant-water fisheries. It is widely distributed across tropical, subtropical, and temperate waters of the Pacific, Indian, and Atlantic Oceans, with the Pacific Ocean being the main fishing ground for global yellowfin tuna. Studying the distribution of yellowfin tuna fishing grounds is of great significance for the sustainable utilization of fishery resources, fisheries management, and the conservation of marine ecosystems. This paper summarizes the status of yellowfin tuna fishery resources, biological characteristics, the relationship between fishing ground distribution and environmental factors, and analyzes the methods employed by domestic and international researchers in assessing the abundance of fishery resources, as well as the limitations and challenges in current research. Furthermore, this study introduces two innovative approaches: the Liang-Kleeman Information Flow (IF) and the Geographically Weighted Neural Network Regression (GNNWR). The former identifies causal relationships between environmental factors and fishery resources based on information flow theory, overcoming the limitations of traditional correlation analysis. The latter enhances the accuracy and adaptability of resource prediction in complex marine environments by integrating the nonlinear capabilities of neural networks with the advantages of localized spatial modeling.

Key words: Fishery Resources; Yellowfin tuna; Environmental factors; Liang-Kleeman information flow; GNNWR

气候变化下太平洋北极区域渔业资源再分配及管理策略研究

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摘要：气候变暖与海冰退缩正加速太平洋北极地区鱼类的北向扩张，并重塑区域渔业资源格局。本研究基于动态生物气候包络模型（DBEM），在不同气候情景（SSP1-2.6 与 SSP5-8.5）及鱼类对海洋酸化的不同响应下，模拟评估了太平洋北极区域主要经济鱼类的生产力变化、空间分布迁移及最优渔业管理策略。结果显示，南部大海洋生态系统（东白令海、西白令海、阿留申群岛）种群丰度与最大捕捞潜力呈持续下降趋势，而北白令海则显著增加，如纳入鱼类对酸化的响应将进一步扩大区域差异并削弱总体生产力。各物种丰度纬度质心均表现出北向迁移趋势，平均速率约 4.9 km/年，表明渔业生产力预计由东白令海渔场向极地高纬陆架转移。最小遗憾准则分析结果表明，预防型捕捞策略（F = 0.8–0.9 FMSY）可在气候变暖与酸化响应双重不确定条件下最小化长期经济损失。本研究可以为快速变化的太平洋北极区域构建前瞻性的渔业管理框架提供科学依据。

关键词：气候变化；北极；太平洋北极通道；渔业资源；适应性渔业管理

Pacific Arctic Region Under Climate Change: Fish Species Redistribution and Alternative Management

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Abstract： Ocean warming and sea-ice retreat are accelerating northward expansion of fish in the Pacific Arctic, reshaping regional fisheries. Using the Dynamic Bioclimate Envelope Model (DBEM), we projected changes in productivity, distribution, and management strategies for major commercial species under SSP1-2.6 and SSP5-8.5, accounting for varying responses to ocean acidification. Abundance and maximum catch potential decline in southern LMEs (Eastern and Western Bering Sea, Aleutians) but increase in the Northern Bering Sea; acidification amplifies these contrasts. Species abundance centroids shift northward at 4.9 km per year, indicating redistribution toward high-latitude shelves. Minimax regret analysis shows precautionary harvest rates (F = 0.8–0.9 FMSY) minimize long-term economic loss under climate and acidification uncertainty. This study links environmental drivers with biological responses, supporting adaptive, forward-looking fisheries management in the Pacific Arctic.

Key words: climate change; Arctic; Pacific Arctic Region; fishery resources; adaptive fisheries management

中国对 RCEP 成员国水产品出口贸易效率研究：基于贸易便利化视角

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摘要：RCEP 的签署将东亚区域经济一体化和农产品贸易自由化提升到新的高度。本文综合评价了 RCEP 成员国的贸易便利化水平，并将贸易便利化作为贸易非效率项引入随机前沿引力模型，测算中国水产品出口贸易效率，得出以下结论：RCEP 成员国贸易便利化属于一般便利水平；进口国的经济规模、两国水产品贸易的互补性和共同语言能够显著促进中国水产品出口，中国经济规模和距离对中国水产品出口具有阻碍作用；中国水产品出口 RCEP 成员国的平均效率约为 0.55，还有很大的出口潜力和提升空间；未来贸易效率提升的关键在于改善贸易便利化水平。

关键词：RCEP；出口贸易效率；贸易便利化

Research on the Trade Efficiency of China's Aquatic Products Exports to RCEP Member Countries: From the Perspective of Trade Facilitation

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Abstract： The signing of RCEP elevates East Asian regional economic integration and agricultural trade liberalization to new heights .This paper comprehensively evaluates the trade facilitation levels of RCEP member states. By incorporating trade facilitation as a term of trade inefficiency into a random frontier gravity model, it measures the efficiency of China's aquatic product exports and concludes that: The economic scale of importing countries, the complementarity of bilateral aquatic products trade, and shared languages significantly promote China's aquatic products exports, while China's economic scale and distance act as barriers to such exports; The average efficiency of China's aquatic products exports to RCEP member countries is approximately 0.55, indicating substantial untapped export potential and room for improvement; Enhancing trade facilitation levels is key to boosting future trade efficiency.

Key words: RCEP; Export Trade Efficiency; Trade Facilitation

基于统计数据的东海渔业资源开发与经济发展关系研究

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摘要：东海作为我国重要近岸渔场，长期支撑水产品供给和渔业经济发展。随着人口增长、技术进步及资源开发强度提升，捕捞压力加大，经济发展与资源承载协调面临挑战。基于 2003–2024 年《中国渔业统计年鉴》上海、浙江、福建三地数据，构建涵盖捕捞、养殖及经济发展三维指标体系，采用结构方程模型量化捕与养殖效率对产值、贸易、加工及就业影响，评估各指标对整体渔业经济的贡献。结果显示东海渔业呈“捕捞先行、养殖兴起”的阶段性特征，养殖在弥补捕捞减产和支撑经济增长中发挥关键作用。分析表明，捕捞效率与产值、贸易及加工关系复杂，而养殖效率对产值增长和就业稳定具有正向作用，两者在渔业发展中呈互补性。研究表明，东海渔业可持续发展需科学调控捕捞、养殖效率、优化渔具，并结合环境变化与市场条件推动产业结构优化。该研究量化了捕捞与养殖效率对经济各环节的作用路径，揭示资源开发与经济增长关系，为渔业管理、资源保护及产业优化提供科学依据。

关键词：东海；渔业资源开发；经济发展；结构方程模型；渔业效率

The relationship between fisheries resource exploitation and economic development in the East China Sea based on statistical data

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Abstract： The East China Sea is a major nearshore fishing ground in China, supporting seafood supply and fisheries-related economic activities. Population growth, technological advances, and intensified resource use have increased fishing pressure, challenging the balance between economic development and sustainability. Using fisheries data from Shanghai, Zhejiang, and Fujian provinces (2003–2024), this study builds an indicator system covering capture fisheries, mariculture, and economic development. Structural equation modeling (SEM) examines how capture efficiency and aquaculture efficiency affect output, trade, processing, and employment. Results show a “capture-first, aquaculture-rise” pattern, with aquaculture offsetting declining catches and supporting growth. SEM indicates capture efficiency has complex effects, while aquaculture efficiency directly boosts output and stabilizes employment, highlighting their complementary roles. Sustainable management requires regulating capture, improving aquaculture practices, and adapting industry structures to environmental and market change.

Key words: East China Sea; Fisheries development; Economic growth; SEM; Fisheries efficiency

基于 MaxEnt 模型分西北太平洋秋刀鱼潜在栖息地的中长期时空变化

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摘要：本文旨在通过模拟不同气候情景（SSP1-2.6、SSP2-4.5、SSP5-8.5）下的环境变化，评估未来气候变化情境下秋刀鱼栖息地的变化趋势。本研究整合中国大陆秋刀鱼渔船 2013-2023 年的渔业统计资料与当前及未来气候情景（2030-2100 年期间）下的环境数据，利用 MaxEnt 模型预测秋刀鱼栖息地时空变化。所使用的气候情景模拟数据均来自 CMIP6 系列，涵盖海表温度、叶绿素 a 浓度、盐度、混合层深度等七个环境因子。结果发现：1 温度升高，对秋刀鱼栖息地分布的影响最为显著，其次为盐度。2.三种气候情景下，秋刀鱼适生区均有不同程度扩张且都表现出明显的北移趋势。3. 高排放情景下（SSP5-8.5），栖息地空间变化明显，适生区显著增加。说明气候变化将深刻影响秋刀鱼的栖息地分布，特别是在高温室气体排放情景下，栖息地可能发生北移和范围扩张。

关键词：秋刀鱼；MAXENT 模型；潜在栖息地；气候变化；环境因子

Spatiotemporal Variations in the Potential Habitat of Pacific Saury (*Cololabis saira*) in the Northwest Pacific Based on the MaxEnt Model over the Medium and Long Term

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Abstract： This study aims to assess the future habitat changes of Pacific saury (*Cololabis saira*) under different climate change scenarios (SSP1-2.6, SSP2-4.5, SSP5-8.5) by simulating environmental variations. It integrates fishery statistics of Pacific saury from Chinese mainland fishing vessels (2013–2023) with current and projected environmental data (2030–2100) to predict the spatiotemporal changes in potential habitats using the MaxEnt model. The climate scenario simulation data are derived from the CMIP6 series and include seven key environmental factors such as sea surface temperature, chlorophyll-a concentration, salinity, and mixed layer depth. The results show that: (1) rising temperature has the most significant impact on habitat distribution, followed by salinity; (2) under all three climate scenarios, the suitable habitat areas expand to varying degrees and exhibit a clear northward shift; and (3) in the high-emission scenario (SSP5-8.5), spatial changes in habitat are more pronounced, with a substantial increase in suitable areas.

Key words: Pacific saury; MAXENT model; potential habitat; climate change; environmental factors

摸着石头过河：中国捕捞限额制度试点的启示

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摘要：本研究批判性审视了中国将总可捕量（TAC）制度作为其渔业管理体系核心要素的试验。基于政策梳理、案例比较、专家问卷与利益相关者访谈，本文追溯了自 2017 年以来，政策、试点与利益相关者参与如何实现 TAC 的实施。试点表明，在数据有限、以努力量控制为基础的体制下，TAC 制度具有可行性。研究指出，试点项目可作为向科学化和基于权利的管理过渡的载体，但其经验教训必须通过法律、政策与实践予以制度化。若缺乏清晰的路径——应植根于科学决策、监控与合规体系以及基于权利和激励的治理这三大相互支撑的支柱——中国可能将固守于行政便利但生态效益有限的管理实践。对其它发展中国家而言，中国的经验表明，当试点策略与制度巩固和长期治理改革相结合时，能够有效降低早期风险并培育管理能力。

关键词：捕捞配额、中国渔业、制度演变、多物种渔业、科学政策衔接、可持续渔业管理、基于权力的管理

Crossing the River by Feeling the Stones: Institutional Lessons from China’s Total Allowable Catch Pilots

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Abstract：This study critically examines China’s experimentation with Total Allowable Catches as a core element of its evolving fisheries management system. Based on policy review, cross-case analysis, expert surveys, and stakeholder interviews, we trace how political commitment, institutional trials, and stakeholder engagement have shaped TAC implementation since 2017. Our findings suggest that pilots can serve as transitional vehicles toward science-based and rights-based management, but only if their lessons are institutionalized through law, policy, and practice. We highlight that without clear graduation pathways - anchored in three mutually reinforcing pillars of science-based decision-making, integrated monitoring and compliance systems, and rights- and incentive-based governance - China risks locking in administratively convenient but ecologically limited practices. For other developing countries, China’s experience shows that pilot strategies can reduce early risks and build capacity when linked to institutional consolidation and long-term governance reform.

Key words: Catch shares; Chinese fisheries; institutional evolution; multi-species fisheries; science-policy interface; sustainable fisheries management; rights-based management

生鲜电商时代下水产行业的创新发展探究——基于辽宁海参产业转型剖析

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摘要：在电商时代发展的大趋势下，生鲜电商逐渐崭露头角，水产行业正处于史无前例的变革之中。本文以辽宁海参为例，从产地资源和养殖经验等方面分析了辽宁海参产业发展生鲜电商的优势以及面临的机遇与挑战。针对目前辽宁海参行业发展生鲜电商过程中存在的主要问题，提出一系列的创新发展策略，包括优化物流配送、开展线上营销活动、建设自有平台等，以期为推动辽宁海参乃至整个水产行业在生鲜电商时代下的高质量可持续发展提供一定的参考资料。

关键词：海参；生鲜电商；营销模式；创新发展

Research on the innovation and development of aquaculture industry in the era of fresh e-commerce: case study of Liaoning sea cucumber industry

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Abstract：Under the general trend of the development of digital economy, the development wave of the e-commerce era is unstoppable, making the aquaculture industry in the midst of unprecedented change. In this study, the “Liaoning” sea cucumber, a representative aquatic product, was selected as a subject to analyze the advantages, opportunities and challenges of the development of fresh e-commerce from the aspects of origin resources and breeding experience. According to main concerns of the development of Liaoning sea cucumber fresh e-commerce, a series of targeted innovative development strategies were proposed, including optimizing logistics distribution, actively carrying out online marketing activities, building its own platform, using new media and other channels to enhance brand influence, etc. All data of this study will provide a powerful reference for promoting the Liaoning sea cucumber industry and even the whole fishery industry in the era of fresh electricity supplier of high-quality sustainable development.

Key words: Sea cucumber; Fresh electricity supplier; Marketing model; Innovative development

基于多模型比较与环境因子筛选的太平洋黄鳍金枪鱼渔获量与栖息地预测研究

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摘要：黄鳍金枪鱼(*Thunnus albacares*)广泛分布于太平洋、印度洋和大西洋，是一种高度洄游、具有重要经济价值的大洋性鱼类，也是我国远洋渔业重点开发对象。过度捕捞与栖息地退化等因素威胁其资源状况，而环境因子对其分布亦具有显著影响。本文综述了太平洋黄鳍金枪鱼的渔业现状、关键环境因子（温度、盐度、叶绿素、净初级生产力）对其分布的影响机制，以及空间预测模型的应用进展。研究表明，传统统计模型（如 GAM、HSI）因全局拟合的局限性难以有效捕捉海洋环境的空间异质性；相比之下，基于环境相似性原理的地理最佳相似性模型（GOS），通过局部样本的动态筛选与加权预测，显著提升了渔场分布预测精度，并同步输出不确定性空间图谱。GOS 模型为太平洋黄鳍金枪鱼资源保护与适应性管理提供了新视角。未来研究需融合多尺度环境动态与渔业政策，以优化资源的可持续利用策略。因此，采用适宜的方法对太平洋黄鳍金枪鱼的资源开发、利用与保护至关重要。

关键词：黄鳍金枪鱼；环境特征；地理最佳相似性；空间预测；

A Study on Pacific Yellowfin Tuna Catch and Habitat Predictions Based on Multi-Model Comparisons and Environmental Factor Selection

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Abstract： Yellowfin tuna (*Thunnus albacares*) is widely distributed in the Pacific, Indian and Atlantic Oceans, and is a highly migratory oceanic fish with important economic value, and is also a key development object of China's distant-water fishery. Factors such as overfishing and habitat degradation threaten the status of its resources, while environmental factors also have a significant impact on its distribution. In this paper, we reviewed the fishery status of Pacific yellowfin tuna, the influencing mechanism of key environmental factors (temperature, salinity, chlorophyll, net primary productivity) on its distribution, and the application progress of spatial prediction models. The results show that traditional statistical models (such as GAM and HSI) are difficult to effectively capture the spatial heterogeneity of the marine environment due to the limitations of global fitting. In contrast, the Geographic Best Similarity Model (GOS) based on the principle of environmental similarity significantly improves the accuracy of fishery distribution prediction through dynamic screening and weighted prediction of local samples, and simultaneously outputs the uncertainty spatial map. The GOS model provides a new perspective for the conservation and adaptive management of Pacific yellowfin tuna resources. Future research needs to integrate multi-scale environmental dynamics and fishery policies to optimize sustainable resource use strategies. Therefore, the use of appropriate methods is essential for the resource development, utilization and conservation of Pacific yellowfin tuna.

Key words: yellowfin tuna; environmental factors; geographical similarity; Spatial prediction

金枪鱼延绳钓渔业中蓝色饵料对海鸟兼捕的有效性分析

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摘要：本文通过对金枪鱼延绳钓渔业中海鸟兼捕措施成效性分析，梳理主要区域性渔业管理组织（IATTC、WCPFC、IOTC、ICCAT）与国际协定（ACAP）在技术规范与管理措施上的演进，并汇总近年关键缓解技术的试验与应用成效。文章首先概述延绳钓作业机制，指出以收钩数据为主的监测方法普遍低估兼捕事件并存在时间与空间覆盖缺口；并通过分析对比不同区域渔业组织中的兼捕数据，进行定量的文献搜集检索，之后统计分析，通过分析结果来对比不同措施在减少海鸟兼捕的有效性，并得出结果：（1）蓝色染色饵料有效性效果不突出，并且成本较高，对比其他主要核心措施的有效性较低，不足以作为单一措施进行实施，建议与其他措施协同。（2）推广高覆盖率的电子监测（EM）与AI自动识别以填补数据缺口并支持基于证据的动态管理。

关键词：金枪鱼延绳钓；海鸟兼捕；蓝色染色饵料；区域渔业组织

Analysis of the Effectiveness of Blue-Dyed Bait in Reducing Seabird Bycatch in Tuna Longline Fisheries

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Abstract：This study analyzes the effectiveness of mitigation measures for seabird bycatch in tuna longline fisheries, reviewing the evolution of technical regulations and management measures established by major Regional Fisheries Management Organizations (IATTC, WCPFC, IOTC, ICCAT) and the international agreement ACAP. It further summarizes recent experimental results and practical applications of key mitigation technologies. The article first outlines the operational mechanisms of longline fishing, pointing out that monitoring methods primarily based on haul data tend to underestimate bycatch events and exhibit temporal and spatial coverage gaps. Through a quantitative review and comparative analysis of bycatch data reported by different regional fisheries organizations, relevant literature was systematically collected and analyzed. The results indicate that: (1) blue-dyed bait shows limited effectiveness and relatively high costs; compared with other major mitigation measures, its performance is less significant and insufficient for independent implementation, suggesting it should be used in combination with other measures; and (2) expanding the use of high-coverage Electronic Monitoring (EM) systems and AI-based automatic recognition is recommended to address data gaps and support evidence-based dynamic management.

Key words: Tuna longline fishery; seabird bycatch; blue-dyed bait; regional fisheries organization

印度洋黄鳍金枪渔业资源及其与环境关系研究进展

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摘要：黄鳍金枪鱼（*Thunnus albacares*）是印度洋重要的经济鱼种，其资源分布和丰度受海洋环境因素的显著影响。近年来，随着机器学习模型在鱼类生态学研究中的广泛应用，其在关键环境变量筛选和资源丰度预测方面的性能已显著超越传统统计方法，为理解黄鳍金枪鱼与环境因子的复杂关系提供了新的研究范式。本文综述了印度洋黄鳍金枪鱼渔业资源研究的最新进展，重点关注环境驱动机制及其与资源变动的关联。研究表明，海表温度（SST）、叶绿素浓度（Chl-a）、海洋环流及气候指数（如ENSO和IOD）是影响其分布的关键因子，而机器学习方法（如随机森林、最大熵模型和神经网络）能够更高效地识别关键变量并优化预测精度。此外，过度捕捞和气候变化对资源可持续性构成挑战，促使区域渔业管理组织（如IOTC）探索基于生态模型的管理策略。未来研究应进一步结合机器学习与遥感大数据，提升资源评估的动态预测能力，并推动适应性管理框架的发展，以实现印度洋黄鳍金枪鱼渔业的科学管理和长期可持续利用。

关键词：印度洋、黄鳍金枪鱼、渔业资源、气候因子

Research Progress on Yellowfin Tuna Fishery Resources and Their Relationship with Environmental Factors in the Indian Ocean

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Abstract：Yellowfin tuna (*Thunnus albacares*) is an economically important fish species in the Indian Ocean, with its distribution and abundance significantly influenced by marine environmental factors. In recent years, the widespread application of machine learning models in fish ecology research has demonstrated superior performance over traditional statistical methods in key environmental variable selection and resource abundance prediction, providing a new research paradigm for understanding the complex relationship between yellowfin tuna and environmental factors. This review synthesizes the latest advances in the study of yellowfin tuna fishery resources in the Indian Ocean, with a focus on environmental drivers and their association with resource fluctuations. Research indicates that sea surface temperature (SST), chlorophyll-a concentration (Chl-a), ocean currents, and climate indices (e.g., ENSO and IOD) are key factors influencing their distribution. Machine learning methods (e.g., random forest, MaxEnt, and neural networks) have proven more efficient in identifying critical variables and optimizing prediction accuracy. Additionally, overfishing and climate change pose challenges to resource sustainability, prompting regional fisheries management organizations (e.g., IOTC) to explore ecosystem-based management strategies. Future research should further integrate machine learning with remote sensing big data to enhance dynamic forecasting capabilities for resource assessment and promote the development of adaptive management frameworks to ensure the scientific management and long-term sustainable utilization of yellowfin tuna fisheries in the Indian Ocean.

Key words: Indian Ocean, yellowfin tuna, fishery resources, climatic factors

中国水产学会 China Society of Fisheries 1963

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