



科技创新促进渔业高质量发展

2024中国水产学会**范蠡**学术大会

论文摘要集

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目 录

第一专题 水产绿色健康养殖新技术新模式

不同水草生态环境差异对小龙虾生长性能和肠道食物组成的影响	1
凡纳滨对虾肝胰腺对碳酸盐碱度胁迫分子应答：基于转录组学和代谢组学联合分析的见解	2
碳酸盐碱度胁迫和恢复对凡纳滨对虾鳃组织生理功能的影响	3
核壳型反硝化活性胶囊用于养殖尾水反硝化脱氮	4
不同碳源对生物絮团技术养殖海参水质、生理、生长和肠道菌群的影响	5
氨氮胁迫对低盐和海水养殖凡纳滨对虾鳃组织生理稳态的影响	6
三种常见渔药对河川沙塘鳢幼鱼的急性毒性	7
合成菌群通过调控对虾肠道菌群稳态抵抗弧菌侵染的机制	8
高原环境下不同养殖密度对三倍体虹鳟苗种生长性能及肠道健康的影响	9
浮萍能够加强生物絮团技术并实现以福利为导向的南美白对虾可持续养殖	10
刺参夏眠对海洋底泥组成影响的宏基因组-代谢组联合分析研究	11
一株固碳工程菌的构建及其在暗纹东方鲀养殖中的应用	12
微生物组、转录组和生理学分析揭示了日本对虾 (<i>Penaeus japonicus</i>) 对暴露于氧纳米气泡的反应	13
不同养殖模式下大黄鱼肌肉营养成分比较分析	14
虾夷扇贝繁殖前后相关生理生化指标的比较研究	15
循环水养殖日本对虾对饲料蛋白质需要量的研究	16
水产绿色健康养殖新技术新模式专题摘要	17
饲料粘合剂对循环水养殖刺参粪便及氮磷收支的影响研究	18
横带髭鲷精子超微结构及其生理特征	19
通过几何形态学测定香螺发育过程中形态上的差异	20
基于池塘小网箱养殖马口鱼效果研究	21
稻虾综合种养影响稻田温室气体排放的微生物机理	22
抑制氧化应激水平解救高温诱导黄颡鱼雄性化	23
Ca ²⁺ 、Mg ²⁺ 和 K ⁺ 浓度对中间球海胆 (<i>Strongylocentrotus intermedius</i>) 存活、生长和生理指标的影响	24
光谱及光周期对刺参 (<i>Apostichopus japonicus</i>) 稚参的生长性能、免疫能力及肠道微生物群的影响	25

第二专题 水产生物技术与遗传育种

黑鲷“苏海1号”新品种简介	26
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超雄大口黑鲈创制及全雄苗种规模化繁育	27
综合时间序列转录组学和代谢组学揭示美洲牛蛙 (<i>Aquarana catesbeiana</i>) 对米尔伊 丽莎白菌 (<i>Elizabethkingia miricola</i>) 感染的反应机制	28
小黄鱼生长和抗病性状基因组 选择育种研究	30
雌性三倍体长牡蛎卵细胞发生受阻的分子机制研究	31
日本囊对虾两种头胸甲斑纹类型的分子机制研究	32
基于几何形态测量学的秋刀鱼雌雄个体 形态差异分析和鉴定	33
基于线粒体细胞色素 b 基因的银鲳六个野生群体遗传特征研究	34
控制光周期对中间球海胆生长和 性腺发育的影响	35
河川沙塘鳢的两性异形及繁殖期与 非繁殖期种群形态差异	36
Wnt 信号通路调控长牡蛎黑色素 形成分子机制	37
大黄鱼耐低氧性状的全基因组选择育种研究	38
中华绒螯蟹性别发育研究进展	39
基于罗氏沼虾全长转录本和基因组序列鉴定嗅觉基因家族	40
虹鳟肝脏响应运输胁迫的转录组学分析	41
南美白对虾新型 CHH-like 基因性别差异调控功能的研究	42
小黄鱼肝脏响应盐度胁迫的 转录组比较分析	43
热休克蛋白 20 和血蓝蛋白基因的复制应答中华绒螯蟹干露胁迫	44
17- α 甲基睾酮对暗纹东方鲀性别转化的影响	45
抑肌素调控鱼类肌肉组织脂肪合成的机制研究	46
小黄鱼抗内脏白点病相关功能基因挖掘与鉴定	47
低氧诱导因子 (HIF-1 α) 通过 NF- κ B 调控中华绒螯蟹在低氧胁迫下的免疫应答反应	48
大口黑鲈肝脏线粒体功能和 Ca ²⁺ 交换对急性缺氧的生理反应	49
大黄鱼伪雌鱼诱导技术优化及超雄鱼培育	50
绒螯蟹的杂交和物种形成的基因组学见解	51
非编码 RNA 参与虹鳟热应激的 ceRNA 调控机制作用研究	52
中国鲟鱼产业化发展: 从规模化苗种繁育到育种平台应用	53
基于转录组和代谢组的联合分析揭示中华鳖肤色多样性的形成机制	54
The function of the cytoplasmic dynein light chain PTKM23 in the transport of PTSMAD2 during spermatogenesis in <i>Portunus trituberculatus</i>	55
综合微生物组和代谢组分析揭示了连接肠道微生物和生长的金鲳鱼 (<i>Trachinotus blochii</i>) 的性大小二态性的新见解	56
南美白对虾响应单侧眼柄去除术的内分泌性别差异调控网络研究	57

日本日月贝 (<i>Ylistrum japonicum</i>) 线粒体全基因组及其系统发育分析	58
基因组重测序揭示中国罗氏沼虾群体遗传学现状	59
NLRC3 通过靶向 IRF7 降低草鱼抗病毒先天免疫应答	60
不同浓度的纳米二氧化钛对海湾扇贝产卵及其子代发育的影响	61
三倍体长牡蛎精子生成受阻机制研究	62
比较转录组分析金虎杂交斑 (<i>Epinephelus fuscoguttatus</i> ♀× <i>Epinephelus tukula</i> ♂) 和 虎棕点石斑鱼 (<i>Epinephelus fuscoguttatus</i>) 下丘脑-垂体-性腺轴基因表达	63
高温对翘嘴鳊性别分化和性腺发育的影响	64
17 α -甲基睾酮对罗氏沼虾生长、性别分化、性腺发育及肠道微生物的影响	65
MicroRNAs 调控栉孔扇贝性腺性别发育的分子机制初探	66
黄姑鱼伪雌鱼诱导技术优化及超雄鱼培育的初步研究	67
非编码 RNA 在虾夷扇贝响应高温胁迫中的分子调控机制研究	68
高温胁迫对菲律宾蛤仔影响的初步研究	69
虾夷扇贝耐高温相关 SNP 位点的鉴定及功能分析	70
皱纹盘鲍常温育苗技术优化及其应用研究	71
靶向代谢组学揭示锦鲤体色及色素代谢物的季节可塑性	72
不同溶氧处理对暗纹东方鲀生理生化指标的影响及低氧相关 SNP 位点的开发	73
银鲳耐低温选育及机制研究	74
罗氏沼虾对高温胁迫的行为反应及转录组分析	75
Mn-LIPA 基因在日本沼虾性激素调节和性腺发育中的作用	76
Methyl farnesoate epoxidase (MFE)在日本沼虾卵巢成熟的功能研究	77
基于银鲳基因组揭示银鲳对水母的摄食偏好性及水母毒素的解毒机制	78
美洲鲈响应高温胁迫的分子调控研究	79
团头鲂 bcl2l13 基因在低氧应激及细胞凋亡中的功能研究	80
DNA 甲基化和亚基因组优势揭示脂质代谢在“金虎杂交斑”杂种优势中的作用	81
利用 geNorm、NormFinder 和 BestKeeper 综合评估曼氏无针乌贼 (<i>Sepiella</i> <i>japonica</i>) qRT-PCR 归一化的内参基因稳定性	82
曼氏无针乌贼(<i>Sepiella japonica</i>)的神经肽 F 及其受体基因: 鉴定、特征、表达及其在 摄食调控中的作用	83
东北地区毛蚶池塘养殖试验	84
马口鱼全雄育种技术体系建立与应用	85
全球气候变化下低氧和热暴露对团头鲂抗氧化状态、免疫、凋亡和代谢的影响: 抵 御低氧和热暴露	86
银鲳性别分化过程中幼年雌雄同体的发生及分子机制	87

基于代谢组的不同采收期坛紫菜品质差异分析	88
罗氏沼虾肠道细菌的分离、鉴定与评价	89
鱼类 IL-17 信号通路的人工结构域重排改造及其应用	90
光强对两个坛紫菜品系的生长、碳氮磷元素含量和有机碳释放的影响	91
HGT 调控紫菜适应性进化的基因组特征	92
基于离子组学和代谢组学的坛紫菜产地溯源技术开发与应用	93
脊尾白虾褪黑素昼夜节律变化及眼柄调控作用研究	94
碱胁迫对日本沼虾鳃组织的影响鉴定	95
基于转录组分析的四指马鲛免疫应答机制初探	96
基于全基因组重测序的坛紫菜种藻遗传结构分析	97
基于脂质组学的坛紫菜自由丝状体成熟机制解析	98
碱度暴露对日本沼虾肝胰腺抗氧化状态、代谢功能和免疫反应的影响	99
黄颡鱼耐粗饲性状相关 SNP 及基因鉴定	100
饲料中添加 17 α -甲基睾酮诱导日本沼虾在性分化关键期的性逆转	101
沉水植物在虾蟹淡水养殖中的应用进展	102
罗氏沼虾卵巢再发育规律及启动再次发育的关键基因和信号通路研究	103
中间球海胆不同遗传距离亲本对后代遗传多样性的影响	104
马口鱼 YY 超雄鱼制备研究	105
团头鲂 circRXRBB 通过 miR-155/socs1a 轴调控嗜水气单胞菌感染后的抗菌免疫反 应	106
黑鲷 GSDF 基因的克隆与表达特征	107
通过重测序方法以性别分子标记揭示黑斑原鲑性染色体型	108
扇贝壳闭合力性状的测定与遗传解析	109
胰岛素样雄性腺激素诱导日本沼虾性别逆转和分子途径：对繁殖、生长和性别分化 的启示	110
基于全基因组测序的四指马鲛基因组注释和系统发育分析	111
基于代谢组解析四指马鲛在低温胁迫下的适应机制	112
第三专题 水产养殖动物营养与饲料	
膳食纤维过量摄入对水产动物的致病作用和机制	113
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	114
DHA 强化卤虫无节幼体策略及 DHA 对黄姑鱼 (<i>Nibeal biflora</i>) 仔鱼生长、代谢和 耐低氧能力的影响	115
Mfn2 介导的线粒体融合促进黄颡鱼的脂肪酸 β -氧化	116

维生素 C 通过 TGF- β /Smads 通路介导胶原蛋白合成促进光棘球海胆摄食	117
两种体色日本蟳类胡萝卜素靶向代谢组学 及低温胁迫后抗氧化特性的比较	118
投喂南极磷虾对红螯螯虾幼虾生长、生理生化、免疫及肠道菌群结构的影响	119
基于多组学技术的香螺对不同饵料响应的分子机制	120
裂壶藻作为一种有前景的西藏卤虫无节幼体强化剂在黄姑鱼苗种培育中的应用研究	121
产虾青素马氏副球菌 (<i>Paracoccus marcusii</i>) IHA034 的筛选及其对小黄鱼 (<i>Larimichthys polyactis</i>) 生长性能、抗氧化水平及 肠道屏障的影响研究	122
膳食益生菌对中间球海胆生长、性腺发育与质量、抗氧化能力、肠道健康及 非特异性免疫的影响	123
吊笼养殖附着物替代海泥可以促进刺参 的生长和肠道健康	124
饲料中添加复合乳酸菌对刺参生长、 肠道生理及免疫指标的影响	125
不同脂肪源对大口黑鲈 (<i>Micropterus salmoides</i>) 生长性能、 脂质沉积、 抗氧化 能力和炎性反应的影响	126
亚麻籽油替代鱼油后添加阿卡地新对大黄鱼生长性能和肝脏脂肪沉积的影响	127
双酚 S 诱导淡水小龙虾氧化应激、 脂质代谢紊乱和自噬功能障碍的机制研究	128
不同海带制品对不同规格中间球海胆 的投喂效果研究	129
凝结芽孢杆菌对四指马鲛幼鱼生长性能、 肠道消化酶活性及 肠道菌群的影响	130
两种菜粕营养改进策略对大口黑鲈生长、 代谢、 抗氧化与免疫的影响	131
循环水与流水养殖对光唇鱼肌肉营养成分 的影响	132
饲料中添加植物甾醇可促进高淀粉饲喂下大口黑鲈幼鱼的生长性能、 饲料利用率、 抗氧化能力和葡萄糖代谢功能	133
蚕豆饲料中乳酸菌添加水平对草鱼生长性能和消化机能影响	134
第四专题 水产病害防治与水产品质量安全	
白斑综合征病毒和对虾内参基因双重荧光定量 PCR 检测方法的建立	135
杂交鳢脾脏细胞系的建立及其对杂交鳢弹状病毒敏感性的探究	137
乌梅和黄芩水提物对致病性嗜水气单胞菌的体外抑菌效果及抑菌机理初探	138
虎斑乌贼皮肤溃疡综合征的蛋白质组学分析	139
眼点淀粉卵涡鞭虫感染黄鳍棘鲷致病寄生靶器官确定	140
镀锌材料是一种有效防控鱼类眼点淀粉卵涡鞭虫感染的方法	141
抗簇生蟹奴病的药物筛选和治疗效果研究	142
一种作用于东星斑体表鱼蛭的消除装置	143
草金鱼白点病的诊断和防治方法	144
罗非鱼养殖系统中抗生素的溯源、 传播、 生物累积和关键影响因子研究	145

溶解氧对刺激隐核虫发育规律研究	146
海水中眼点淀粉卵涡鞭虫涡孢子荧光定量 PCR 检测方法的建立	147
密斑刺鲃 (<i>Diodon hystrix</i>) 假交替单胞菌的分离鉴定	148
大口黑鲈源杀鱼爱德华氏菌的生物学特性及其浸泡感染致病性分析	149
斜带石斑鱼白细胞介素 22 基因克隆鉴定 及功能研究	150
大口黑鲈病毒病疫苗研制	151
利用合成生物学在水产中应用乳酸菌	152
抗菌肽 Sparamosin26-54 通过结合脂质介导 病毒裂解对三种水生包膜病毒表现出 抗病毒活性	153
联合 miRNA 与病理学的研究为菲律宾蛤仔抗鳗弧菌的免疫应答提供了新的视角	154
整合转录组学和代谢组学揭示恩诺沙星诱导舒伯特气单胞菌的耐药机制	155
肿瘤坏死因子受体相关因子 6 (TRAF6) 通过 NF- κ B 通路参与调节中华绒螯蟹在蜕 皮 前期的免疫反应	156
黄颡鱼源海豚链球菌的生物学特性、致病性及其全基因组分析	157
一种防控多子小瓜虫病杀虫涂料研发	158
饲料中添加复方中草药对大菱鲃抗杀鲑气单胞菌感染的影响	159
引起日本对虾红体病病原菌分离鉴定及 致病性研究	160
生物絮团中微塑料对罗非鱼的影响	161
中华鲟胸鳍细胞系的建立及其生物学特性	162
大黄鱼中新型抗菌肽 LCAMP 的体外抗菌活性和体内抗河流弧菌感染的作用	163
姜黄提取物对加州鲈生长、抗氧化能力及 抗病力的影响	164
日粮中添加枯草芽孢杆菌对大口黑鲈 生长、免疫以及肠道菌群的影响	165
高温胁迫下 CgmiR307 靶向 CgNrf2 调控长牡蛎氧化应激过程	166
刺激隐核虫 Cathepsin L 基因的克隆及 功能初探	167
西藏特有鱼类黑斑原鲢不同组织微生物群落特征及致病性研究	168
副溶血性弧菌 LF1113 的全基因组测序和 比较基因组学解析	169
达氏鲟幼鲟急性肠炎的病原鉴定及 药敏分析	170
大黄鱼感染盾纤毛虫死亡高峰期的 差异可变剪切和差异表达分析	171
靶向宿主的抗病毒物质在水产养殖中应用 的理论和实践	172
溶藻弧菌富含 sRNA 的外膜囊泡:生物膜被 组装的决定性建造者	173
大口黑鲈微生物群落变化分析	174
高温胁迫下虾夷扇贝糖代谢重编程增强 供能并修复 DNA 损伤	175
副溶血弧菌感染下缢蛏免疫与糖代谢的 权衡策略对其抗病能力影响	176
黄颡鱼细菌病流行病学调查与 药敏快速检测技术研究	177

基于补体 C3 的激活与调节机制探讨大黄鱼和黄姑鱼对刺激隐核虫抗感染差异的分子机理研究	178
鱼类 NLRX1 变体靶向 STING 负调控干扰素抗病毒免疫反应的机制研究	179
许氏平鲷 (<i>Sebastes schlegelii</i>) TRAF 基因的鉴定及其响应杀鱼爱德华氏菌侵染的表达模式研究	180
基于鳊鱼诺卡氏菌感染大黄鱼的头肾转录组学研究	181
加州鲈 pIgR 抗体制备及免疫应答特征研究	182
通过 sRNA15 和 sRNA80 揭示溶藻弧菌生物被膜形成的转录后调控机制	183
虾青素对微囊藻毒素-LR 胁迫下凡纳滨对虾生长性能、肠道结构及肠道微生物的影响	184
曼氏无针乌贼 (<i>Sepiella japonica</i>) IL-17 的分子特征、表达模式及抑菌功能分析	185
抗生素在刺激隐核虫感染大黄鱼过程中的作用研究	186
罗氏沼虾新疾病 (白化病) 的转录组学分析: 对其发病原因和防治方法的初步探究	187
细胞自噬在罗氏沼虾抵御细菌感染中的作用机制研究	188
基于异羟肟酸/紫尿酸铁显色反应和智能手机的牡蛎中弯曲菌现场灵敏比色检测便携生物传感平台	189
尼罗罗非鱼 LCP1 基因的克隆及其在灭活无乳链球菌免疫刺激后的应答	190
斜带石斑鱼对哈维氏弧菌攻毒反应中白细胞介素-15 受体(IL-15R α) α 链的分子和功能研究	191
银鲳对美人鱼发光杆菌的免疫响应及其免疫逃逸机理的初步探究	192
纳米材料介导的海洋弧菌的可视化核酸检测和毒力基因沉默	193
银鲳感染鳊鱼诺卡氏菌不同感染阶段的免疫策略	194
白细胞介素-34 作为肠道屏障功能的正调节因子减轻团头鲂的细菌性肠炎	195
刺激隐核虫表面抗原对大黄鱼免疫保护效果探究	196
第五专题 可持续捕捞	
西北印度洋中尺度涡对鸢乌贼时空分布的影响	197
基于 NODE-GAM 模型和 XGBoost 模型的太平洋大眼金枪鱼渔场预报	198
中西太平洋围网渔业兼捕渔获物组成分布研究	199
基于 Iot 的秋刀鱼渔捞数据收集研究	200
基于耳石微化学技术的秋刀鱼生活史特征的初步研究	201
基于几何形态测量的西北太平洋日本鲭的个体生长规律	202
未来气候情境下中国东海鲑鱼栖息地的时空分布	203
不同空间尺度下秋刀鱼 CPUE 标准化研究	204

南海渔业生态系统结构分析	205
西北太平洋秋刀鱼资源丰度变化与气候—海洋变化的关系	206
东海带鱼延绳钓渔场分布特征	207
西北太平洋远东拟沙丁鱼的摄食策略和营养生态位差异：稳定同位素和脂肪酸分析 的见解	208
打开黑盒模型：热带大西洋海域金枪鱼丰度预测的案例研究	209
热带中西太平洋围网 FSC 和 DFADs 渔获群落多样性分析	210
淀粉基可降解渔具材料的制备与应用研究	211
时空尺度对不同联合物种分布模型的影响：以西北太平洋中上层渔业种类为例 ..	212
西南大西洋阿根廷滑柔鱼栖息地与中尺度涡的关系分析	213
两种鱿鱼的跨太平洋栖息地模式的年代际变化	214
南极磷虾桁杆拖网作业参数调节对网具性能的影响	215
Nordmøre 装置的栅条间距和姿态对拖网网囊稳定性的影响	216
基于结构方程模型的淡水补充对马达加斯加西海岸印度白虾 CPUE 的影响	217
西北太平洋渔业物种的生活史策略研究	218
拖网网囊结构振荡特性对网囊长度的响应变化	219
基于 RF-SHAP 方法的中西太平洋围网鳀资源变动与环境因子关系研究	220
漂流人工集鱼装置影响下的随附金枪鱼类分布建模	221
海豚声波驱赶对罩网捕捞的影响研究	222
渤海湾海域中国毛虾资源开发状态	223
不同规格罩网沉降性能的影响因素分析	224
南海北部张网方形和菱形混合网目网囊的选择性研究	225
黄鳍鲷趋光行为对光照特征响应	226
基于贝叶斯最大熵的中西太平洋鳀资源预测	227
内衬网比例和重锤重量对南极磷虾桁杆拖网水动力性能的影响	228
Super shoot TED 对模拟渔获物入网轨迹的导向试验研究	229
舟山普陀区蚂蚁岛多锚张纲张网渔具渔法调查分析	230
第六专题 水生生物资源养护与水域生态修复	
水文环境塑造了南极布兰斯菲尔德海峡冰鱼（ <i>Chionodraco rastrospinosus</i> ）的遗传种 群结构：线粒体 CO I 和 ND2 基因提供的证据	231
旅顺塔河湾海域浮游动物群落结构及优势种生态位分化研究	232
万宁洲仔岛附近海域游泳生物群落结构及其与环境因子的关系	233
人工繁育中华鲟成体在长江口放流后可以 进行溯河洄游	234
气候变化对浙江近海三种头足类生物潜在生境分布的影响	235

东海不同群体大黄鱼的耳石稳定同位素分析及溯源.....	236
流速对草鱼卵巢发育的影响.....	237
秘鲁外海群茎柔鱼体内汞的生物积累首次评估：群体、性别、摄食生态的影响	238
大连不同群体长牡蛎生殖季节性腺发育对比.....	239
全球灯笼鱼渔业资源研究热点与发展趋势——基于 Citespace 的图谱量化研究 ...	240
基于提升回归树的西白令海峡鳕资源分布环境影响因子分析.....	241
长江口邻近海域渔业群落结构特征与环境因子的关系.....	242
饲用虾青素对青海湖裸鲤生长性能、抗氧化能力、免疫功能及转录水平的影响..	243
新疆特克斯河新疆高原鳅生物学研究.....	244
禁渔期内湘江银鮡个体繁殖力与卵径研究.....	245
以脂肪酸为营养标志物分析阿根廷滑柔鱼卵子发生的营养分配特点.....	246
湘江流域丰水期浮游动物群落结构及其水质评价.....	247
长江口鱼类群落分布对潮沟水文连通性动态变化的响应.....	248
通过生理学、转录组和代谢组的综合分析，揭示了不同体重的三倍体虹鳟鱼脂肪沉积、代谢和免疫的变化.....	249
头足类角质颚形态的生态驱动与功能性演化机制研究.....	250
从系统碳代谢角度探讨缢蛭混养对水产养殖池塘水-气界面 CO ₂ 通量的影响机制	251
大豆低聚糖和蛋白核小球藻对生物絮凝系统水质和微生物群落结构的协同效应..	252
沅江下游大眼鳊仔鱼密度和生长的时空差异性研究.....	253
非经典生物操纵后淡水水库鱼类密度、大小和生物量的水声学评估.....	254
牡蛎养殖对大鹏澳海域氮源影响的研究.....	255
采桑湖浮游动物群落结构及驱动因素.....	256
温度对中华鲟孵化时间和胚胎发育指标的影响.....	257
缢蛭对海水养殖池塘水质改善的潜在作用：综合单因子和水质指数(WQI)评价方法.....	258
长江濒危水生动物亟需重建家园：基于长江鲟自然繁殖行为重塑的实践启示.....	259
稻-罗氏沼虾轮作模式对复垦土壤理化性质及养分供应的影响.....	260
缢蛭养殖对蟹-虾混养系统浮游生物粒径结构及其碳代谢特征的影响.....	261
珠海外伶仃人工鱼礁稳定性研究.....	262
蛋白核小球胞内、外物质对生物絮团培养中水质、絮团形成和微生物组成的影响	263
基于美国哈德逊河条纹鲈的鱼类产卵策略的年代际变化研究.....	264
腊者水电站开发对多依河鱼类多样性和群落组成变化的影响.....	265
第七专题 水产品加工与综合利用	
水产品保鲜和加工技术研究进展.....	266

假单胞菌响应磷虾壳氟胁迫的分子机制解析与代谢工程改造	267
水产品预制菜的研究开发与创新发展	268
利用靶向蛋白质组学和可视化策略研究海参 (<i>Apostichopus japonicus</i>) 体壁中原纤 维蛋白的存在	269
第八专题 休闲渔业与渔文化	
休闲渔业游客感知价值、地点认同与行为意向关系的研究 ——以福建省为例	270
中国快速增长的休闲渔业经济对温室 气体排放的供应链影响	271
中国休闲渔业发展模式略论	272
崇明岛渔文化资源结合新质生产力提质增效的思考	273
望天眼金鱼的血液和玻璃体液生理生化 指标研究	274
第九专题 现代渔业设施装备与信息化	
网衣清洗装置设计及仿真试验研究	275
基于离散延迟涡模型的 PET 网片绕流 特性数值模拟	276
铜合金编织网网片阻力水槽试验研究	277
基于 Tracepro 的秋刀鱼 LED 集鱼灯水下照度研究	278
融合多源框架信息提升渔业机器人 细粒度感知	279
连接方式对金枪鱼延绳钓渔具力学特性研究	280
融合机理模型和机器视觉的斑石鲷生长预测研究	281
基于可解释人工智能理论构建 VGG 模型 金枪鱼识别方法	282
仿生海豚航行器集群水动力研究	283
水生生物健康监测可穿戴传感器研究	284
一种自容式多通道水下照度计的 设计研究	285
重力式深水网箱系统参数化建模及应用	286
基于头足类渔业知识图谱的 智能问答系统研究	287
基于深度学习的金枪鱼延绳钓渔获 图像识别技术分析	288
基于生成对抗网络的鱼类图像识别精度 提升技术研究	289
仿生机器鱼颜色对鲤鱼视觉运动反应的 影响研究	290
基于地理相似性的中西太平洋围网鳀空间 预测与驱动因子研究	291
金鱼不同游泳方式的水动力特性比较研究	292
大洋渔业资源特征原位观测技术研究	293
浙江省设施养殖发展与对策研究	294
第十专题 渔业经济、政策与管理	
日本锦鲤池塘 — 工厂化接力养殖模式经济 效益分析	295

渔业数字化发展对渔民收入影响的时空演变与收敛性分析 296

新质生产力赋能海洋渔业高质量发展的理论逻辑与实践路径探赜——基于马克思主义政治经济学视角的研究 297

不同水草生态环境差异对小龙虾生长性能和肠道食物组成的影响

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摘要: 水草是调控小龙虾养殖生态环境的重要组成部分。为阐明不同类型水草影响小龙虾养殖性能的路径差异, 以水花生和轮叶黑藻为研究对象, 分析了养殖水质指标和水生生物组成对小龙虾养殖性能的影响, 并利用高通量测序技术鉴定了肠道生物饵料的组成。水花生和轮叶黑藻具有较强的水质净化能力, 能够显著提升溶氧含量 ($p < 0.05$), 且显著降低亚硝态氮、氨态氮、硝态氮以及磷酸盐含量 ($p < 0.05$)。水花生组和轮叶黑藻组小龙虾各生长指标显著高于对照组 ($p < 0.05$), 前两者之间无显著性差异 ($p > 0.05$)。温度、溶氧和 pH 是影响水花生组和轮叶黑藻组小龙虾生长发育的主要因素, 对照组为亚硝态氮和氨态氮。对照组浮游生物密度和生物量均显著高于水草组 ($p < 0.05$), 水花生组浮游动植物群落丰度、均匀度及多样性均显著高于对照组 ($p < 0.05$)。冗余分析结果显示, 各组小龙虾肠道食物组成存在极显著性差异 ($p < 0.01$)。

关键词: 关键词: 小龙虾; 水花生; 轮叶黑藻; 浮游生物; 水质指标; 食物组成

Effects of different aquatic environment on growth performance and intestinal natural diet composition of crayfish

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Abstract: Aquatic plant plays a crucial role in controlling the ecological conditions of crayfish aquaculture. *Alternanthera philoxeroides*, and *Elodea nuttallii* were selected as research objects in this paper. In order to clarify the path of different types of aquatic plants affecting crayfish culture performance, the impacts of various aquatic plant habitats on crayfish development performance were examined, and the intestinal natural diet composition was determined using high-throughput sequencing technology. *Alternanthera philoxeroides* and *Elodea nuttallii* exhibited substantial water purifying properties, notably boosting dissolved oxygen ($p < 0.05$), and lowering phosphate content ($p < 0.05$), as well as nitrite, ammonia, and nitrate nitrogen. The growth indicators of the *Alternanthera philoxeroides* and *Elodea nuttallii* groups were significantly greater ($p < 0.05$) than the control, whereas the former two groups showed no significant difference ($p > 0.05$). Temperature, dissolved oxygen, and pH had a greater effect on the growth performance of crayfish in the *Alternanthera philoxeroides* and *Elodea nuttallii* groups, while the nitrite and ammonia nitrogen had a stronger effect in the control group. Plankton in the control group had a significantly higher density and biomass than in the aquatic plant groups ($p < 0.05$), while the water peanut group had a significantly higher abundance, evenness, and diversity of plankton communities than the control group ($p < 0.05$). The results of redundancy analysis revealed that the natural food content in the crayfish intestines varied significantly between the groups ($p < 0.01$). In summary, *Alternanthera philoxeroides* and *Hydrilla verticillata* can improve the aquaculture environment, promote the growth performance of crayfish, and enrich the food composition of crayfish.

Key words: Crayfish; *Alternanthera philoxeroides*; *Elodea nuttallii*; Plankton; Water quality index; Food composition

凡纳滨对虾肝胰腺对碳酸盐碱度胁迫分子的 应答：基于转录组学和代谢组学联合分析 的见解

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摘要：碳酸盐碱度（CA）是影响水生动物生存和生长的环境因子之一。然而，CA胁迫在分子水平上对凡纳滨对虾的毒性效应仍不清晰。本研究通过研究不同浓度CA胁迫下凡纳滨对虾的存活、生长和肝胰腺组织学的变化，并结合转录组学和代谢组学解析肝胰腺的主要功能变化和生物标志物。结果显示，CA胁迫14天后，对虾的存活率和生长速度降低，肝胰腺出现明显的组织学损伤。三个CA胁迫组共有253个基因差异表达，模式识别受体、酚氧化酶系统、解毒代谢等免疫相关基因受到影响；物质转运相关的调节因子和转运蛋白大多下调。此外，CA胁迫还改变了肝胰腺的代谢模式，尤其是氨基酸、花生四烯酸和B族维生素代谢物。差异代谢产物和基因的分析进一步表明，CA胁迫显著改变了ABC转运蛋白、蛋白质消化吸收、氨基酸生物合成和代谢的功能。本研究结果揭示了碳酸盐碱度胁迫诱导凡纳滨对虾免疫、物质转运和氨基酸代谢的变化，并鉴定了与胁迫反应相关的潜在生物标志物。

关键词：对虾; 盐碱水养殖; 基因转录; 代谢物

Molecular response of hepatopancreas of *Litopenaeus vannamei* to carbonate alkalinity stress: Insight from the integration of transcriptomic and metabolomic

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Abstract: Carbonate alkalinity (CA) is one of the environmental factors affecting the survival and growth of aquatic animals. In this study, we investigated the changes of the survival and growth, and hepatopancreas histology of *L. vannamei* under different levels of CA stress, and integrated transcriptomics and metabolomics to explore major functional changes in the hepatopancreas and identify biomarkers. After CA exposure for 14 days, the survival and growth of the shrimp were reduced, and the hepatopancreas showed obvious histological damage. Immune-related genes such as pattern recognition receptors, phenoloxidase system and detoxification metabolism were affected; substance transport-related regulators and transporters were mostly downregulated. Furthermore, amino acids and arachidonic acid metabolism and B-vitamin metabolites was also altered. The integration analysis of differential metabolites and genes further showed that the functions of ABC transporters, protein digestion and absorption, and amino acid biosynthesis and metabolism were highly altered by CA stress.

Key words: Shrimp; Saline-alkali; Gene transcription; Metabolites

碳酸盐碱度胁迫和恢复对凡纳滨对虾鳃组织生理功能的影响

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摘要：碳酸盐碱度是对虾盐碱水养殖中影响其存活和生长的主要环境因子。鳃是 CA 对对虾毒性效应的靶器官。本研究将凡纳滨对虾暴露 5 mmol/L CA 胁迫 7 天，然后解除暴露恢复 7 天，探究了鳃组织在 CA 胁迫和恢复中的生理变化特征。结果显示，CA 胁迫导致抗氧化酶 T-AOC、T-SOD、POD 和 CAT 活性上升。此外，抗氧化（*romo1*、*nrf2* 和 *gpx*）、ER 应激（*bip*、*ire1* 和 *xbp1*）、细胞凋亡（*casp-3*）、免疫（*alf*、*crus*、*pen-3*、*lys* 和 *propo*）、解毒（*cyp450* 和 *gst*）和渗透调节（*nka- α* 、*nka- β* 、*ca*、*aqp*、*tip4*、*vatp*、*clc*、*nhe* 和 *ccp*）基因相对表达水平上升，而抗氧化（*sod* 和 *hsp70*）和细胞凋亡（*casp-9*）基因相对表达水平下降。对虾解除胁迫后，部分生理指标变化虽有改善，但未恢复至对照水平。本研究揭示了 CA 胁迫会对对虾鳃的生理稳态造成负面影响。

关键词：对虾；碳酸盐碱度；鳃；生理反应

Changes in the physiological homeostasis of the gills of *Litopenaeus vannamei* under carbonate alkalinity stress and recovery conditions

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Abstract: Carbonate alkalinity is the main environmental factor affecting the survival and growth of shrimp in saline-alkali aquaculture. Gill is the target organ of toxic effect of CA on prawn. In this study, *Litopenaeus vannamei* was exposed to 5 mmol/L CA stress for 7 days, and released for 7 days, and the physiological changes of gill tissue during CA stress and recovery were explored. The results showed that the activities of antioxidant enzymes T-AOC, T-SOD, POD and CAT increased under CA stress. In addition, antioxidation (*romo1*, *nrf2* and *gpx*), ER stress (*bip*, *ire1* and *xbp1*), apoptosis (*casp-3*), immunity (*alf*, *crus*, *pen-3*, *lys* and *propo*), detoxification (*cyp450* and *gst*) and osmotic adjustment (*nka- α* , *nka- β* , *ca*, *aqp*, *tip4*, *vatp*, *clc*, *nhe* and *ccp*) genes were increased, and the relative expression levels of antioxidant (*sod* and *hsp70*) and apoptosis (*casp-9*) genes were decreased. After the CA was relieved, some physiological indexes changed, but they did not return to the control level. This study revealed that CA stress would negatively affect the physiological homeostasis of shrimp gills.

Key words: Shrimp; Carbonate alkalinity; Gills; Physiological response

核壳型反硝化活性胶囊用于 养殖尾水反硝化脱氮

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摘要: 反硝化细菌和有机碳源的缺乏以及 DO 的抑制导致养殖系统反硝化不足, 最终导致养殖尾水中硝酸盐积累。为解决这一问题, 采用封装法制备了一种新型生物活性胶囊, 该胶囊可为水产养殖尾水的反硝化过程提供有机碳源、反硝化细菌和适宜的微环境。独特的成型工艺可缩短封装反硝化菌的恢复时间。胶囊具有核壳型结构, 且表面多孔, 孔径为 150.0 ~ 300.0 nm, 该胶囊具有恢复时间短、脱氮性能好等特点。第一天硝酸盐去除率达到 86.2%, 最终维持在 99.7%。氮在胶囊内的转化途径包括反硝化、硝酸盐同化还原、硝酸盐异化还原和固氮作用。该反硝化胶囊活性恢复时间短, 反硝化性能好, 可用于水产养殖废水或其他低碳氮比废水的反硝化。

关键词: 养殖尾水; 反硝化; 反硝化细菌; 微生物固定化; 封装

Core-Shell Bioactive Capsule for Aquaculture Wastewater Denitrification

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Abstract: Lack of denitrifying bacteria and organic carbon sources, and the inhibition of DO lead to deficient denitrification in aquaculture systems and finally cause nitrate accumulation in aquaculture wastewater. In order to solve this problem, in this paper, encapsulation method is introduced to prepare a novel bioactive capsule, which could provide organic carbon source, denitrifying bacteria, and suitable microenvironment for aquaculture wastewater denitrification. And could reduce the recovery time of the enclosed denitrifying bacteria. The morphology of the capsule and its nitrate removal rate and nitrogen conversion pathway in synthetic aquaculture wastewater were investigated. The capsule had a porous surface and the pore diameter ranged from 150.0 nm to 300.0 nm. The capsule exhibited short recovery time and excellent denitrification performance. The nitrate removal rate reached 86.2% on the first day and finally maintained at 99.7%. The nitrogen conversion pathway in the capsule included denitrification, assimilatory nitrate reduction, dissimilatory nitrate reduction, and nitrogen

Key words: : aquaculture wastewater; denitrification; denitrifying bacteria; immobilized microorganisms; encapsulation

不同碳源对生物絮团技术养殖 海参水质、生理、生长和肠道菌群的影响

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摘要: 本研究探讨了碳酸氢钠和醋酸钠在生物絮团技术(BFT)中作为碳源的潜力, 以改善海参养殖水质。在 64 天试验中, 将海参幼参分为 5 组:S(蔗糖)、SSa(蔗糖+醋酸钠)、SSb(蔗糖+碳酸氢钠)、Nc(无碳源)和 Cg(对照)。结果显示, SSb 组(pH 8.28)水质最优, 氨氮(0.501 mgL⁻¹)和亚硝酸盐(0.031 mgL⁻¹)显著降低, 生物絮团体积(17 mL⁻¹)和增重率(78.5%)均处于最佳水平。超氧化物歧化酶(179 U mL⁻¹)和过氧化物酶(1.59 U mL⁻¹)活性也最高, 肠道益生菌增加, 有害菌减少。研究表明, 碳酸氢钠作为碳源, 能显著优化水质, 促进海参生长, 展现出其在 BFT 系统中的潜力。

关键词: 刺参; 碳源; 生物絮团; 水质; 肠道菌群

Effects of Different Carbon Sources on Water Quality, Physiology, Growth, and Intestinal Microbiota in Cultured Sea Cucumber (*Apostichopus japonicus*) with Biofloc Technology

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Abstract: This study explored the potential of sodium bicarbonate and sodium acetate as carbon sources in biofloc technology (BFT) to improve sea cucumber aquaculture water quality, in a 64-day experiment juvenile sea cucumbers were divided into five groups. S (sucrose), SSa (sucrose + sodium acetate), SSb (sucrose + sodium bicarbonate), Nc (no carbon source), and Cg (control). Results showed that the SSb group (pH 8.28) had the best water quality, with significantly reduced ammonia nitrogen (0.501 mg L⁻¹) and nitrite (0.031 mg L⁻¹) levels. optimal biofloc volume (17 mL⁻¹), and weight gain (78.5%). The SSb group also exhibited the highest activities of superoxide dismutase (179 U mL⁻¹) and peroxidase (1.59 U mL⁻¹), with an increase in beneficial gut bacteria and a reduction in harmful bacteria. The study suggests that sodium bicarbonate as a carbon source can significantly enhance water quality and promote sea cucumber growth, showing potential in BFT systems.

Key words: *Apostichopus japonicus*; carbon; biofloc; water quality; intestinal flora

氨氮胁迫对低盐和海水养殖凡纳滨对虾鳃组织生理稳态的影响

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摘要: 氨氮是影响对虾生存和健康的重要水质因子, 而鳃是氨毒性的主要效应器官。本研究探讨了海水和低盐度条件下氨氮胁迫对凡纳滨对虾鳃生理稳态的毒性作用。结果显示, 氨氮胁迫导致对虾鳃丝收缩严重, 鳃血管变形甚至破裂。氧化应激指标如 LPO 和 MDA 含量以及 T-AOC 和 GST 活性在 SAN 和 LAN 组均升高, 而 CAT 和 POD 活性以及抗氧化相关基因 (nrf2、cat、gpx、hsp70 和 trx) 表达量均降低。此外, 参与内质网应激 (ire1 和 xbp1)、细胞凋亡 (casp-3、casp-9 和 jnk)、解毒代谢 (gst、ugt 和 sult)、糖代谢 (pdh、hk、pk 和 ldh) 和三羧酸循环 (mdh、cs、idh 和 odh) 的基因表达量在 SAN 和 LAN 组均降低。这些结果有助于解析氨氮胁迫对海水和低盐度养殖对虾的毒理机制。

关键词: 对虾; 鳃; 氨氮; 盐度; 生理功能

Toxicity of ammonia stress on the physiological homeostasis in the gills of *Litopenaeus vannamei* under seawater and low-salinity conditions

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Abstract: Ammonia is a major water quality factor influencing the survival and health of shrimp, while the gill is the main effector organ for ammonia toxicity. The toxicity of ammonia stress on gill physiological homeostasis of *Litopenaeus vannamei* under seawater and low salinity conditions was explored. The results show that ammonia stress caused the severe contraction of gill filaments and the deformation or even rupture of gill vessels. Oxidative stress indicators such as LPO and MDA contents, T-AOC and GST activities were increased in the SAN and LAN groups, while CAT and POD activities and the levels of antioxidant-related genes (nrf2, cat, gpx, hsp70 and trx) were decreased. In addition, the levels of the genes involved in ER stress (ire1 and xbp1), apoptosis (casp-3, casp-9 and jnk), detoxification (gst, ugt and sult), glucose metabolism (pdh, hk, pk and ldh) and the tricarboxylic acid cycle (mdh, cs, idh and odh) were decreased in the SAN and LAN groups. These results are helpful to analyze the toxicological mechanism of ammonia stress on the seawater and low salinity cultured shrimp.

Key words: Shrimp; Gills; Ammonia; Salinity; Physiological function

三种常见渔药对河川沙塘鳢幼鱼的急性毒性

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摘要：采用静态急性毒性试验法研究了3种常用水产用药物对河川沙塘鳢（*Odontobutis potamophila*）幼鱼24、48、72 h (t) 半致死质量浓度 ρ (LC50) (95%置信区间)以及安全质量浓度 (SC)。结果表明，聚维酮碘对河川沙塘鳢幼鱼24、48、72 h的半数致死质量浓度 ρ 分别为1 466、1 148、997.6 mg/L，安全浓度为270.0 mg/L；辛硫磷对河川沙塘鳢幼鱼24、48、72 h的半数致死质量浓度 ρ 分别为4.030、1.207、0.409 mg/L，安全浓度为0.108 5 mg/L；高效氯氰菊酯对河川沙塘鳢幼鱼24、48、72 h的半数致死质量浓度 ρ 分别为3.007、2.695、0.9740 mg/L，安全浓度为0.724 6 mg/L。

关键词：高效氯氰菊酯；辛硫磷；聚维酮碘；河川沙塘鳢幼鱼；毒性效应

Acute toxic effects of several common fish drugs on *Odontobutis potamophila* juveniles

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Abstract: In order to study toxic effect of several common fish drugs on *Odontobutis potamophila* juveniles, static bioassays were conducted. Results showed that the 24, 48 and 72 h (t) ρ (LC50) of povidonum-iodum (PVP-I) to the fish with 95% confidence interval was estimated to be 1 466, 1 148, 997.6 mg/L, respectively, with the safe concentration being 270.0 mg/L. Results show that the 24, 48 and 72 h (t) ρ (LC50) of phoxim to the fish with 95% confidence interval was estimated to be 4.030, 1.207, 0.409 mg/L, respectively, with the safe concentration being 0.108 5 mg/L. Results show that the 24, 48 and 72 h (t) ρ (LC50) of Beta-thermometric (beta-CYP) to the fish with 95% confidence interval was estimated to be 3.007, 2.695, 0.974 mg/L, respectively, with the safe concentration being 0.724 6 mg/L.

Key words: Beta-thermometric; phoxim; povidonum-iodum; *Odontobutis potamophila* juveniles; toxic effect

合成菌群通过调控对虾肠道菌群稳态抵抗弧菌感染的机制

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摘要: 宿主肠道共生微生物群是抵御病原体入侵的重要屏障。然而对虾肠道中具体哪些微生物类群在抵抗病原菌感染中起关键作用还有待研究。本研究通过比较弧菌感染后健康、患病和死亡对虾的肠道微生物群落, 筛选并定向分离与弧菌感染抗性相关的关键类群, 构建 4 个合成菌群 (SynComs), 探究 SynComs 提升对虾抗弧菌感染的微生态机制。结果表明: 1) 弧菌感染后保持健康的对虾肠道显著富集某些特异性类群, 从健康对虾肠道分离出 5 株对应的红杆菌, 1 株黏着杆菌和 1 株脱醌杆菌; 2) 构建 4 种 SynComs, 添加后均可提高对虾存活率和弧菌感染抗性; 3) SynComs 添加均显著改变对虾肠道微生物群落组成, 各菌株均能定殖于对虾肠道中, 其相对丰度与对虾弧菌感染抗性呈正相关关系, 尤其是与各菌株丰度之和呈显著正相关; 4) 添加菌株多样性越高对微生物群落结构影响越大, 添加 SynComs 增加了对虾肠道微生物群落共现网络复杂性。

关键词: 南美白对虾; 肠道细菌群落; 合成菌群; 副溶血弧菌抗性; 共现网络

Synthetic bacterial community confers protection against *Vibrio parahaemolyticus* infection via regulating the stability of gut bacterial community in *Penaeus vannamei*

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Abstract: Host gut commensal bacterial community is a crucial barrier against pathogen invasion. However, the specific taxa that play a key role in resisting pathogens is unclear. We compared the gut bacterial communities of healthy, diseased, and moribund shrimp after *Vibrio* infection, and isolated the key taxa from healthy shrimp to construct SynComs. The result indicated that certain taxa belonging to Rhodobacteraceae, Flavobacteriaceae, Demequinaceae were enriched in the healthy shrimp gut. Four SynComs were constructed, and the addition of SynComs considerably changed gut bacterial community composition of shrimp. All strains in SynComs colonized the gut well, and their relative abundances, particularly the total abundances of each strain, were positively correlated with resistance to *Vibrio*. Higher strain diversity had a bigger influence to the bacterial community structure. Meanwhile, the addition of SynComs augmented the complexity of the bacterial community co-occurrence network. Our findings suggested that specific gut bacteria promote the resistance of shrimp against pathogens.

Key words: : *Penaeus vannamei*; Gut bacterial community; Synthetic community; *Vibrio parahaemolyticus* resistance; Co-occurrence network

高原环境下不同养殖密度对三倍体虹鳟苗种生长性能及肠道健康的影响

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摘要: 为探究高原环境下三倍体虹鳟苗种培育的最适养殖密度, 本研究设置了三种不同养殖密度(低密度组(LD) 100尾/桶中密度组(MD) 200尾/桶; 高密度组(HD) 300尾/桶), 开展了为期60d的养殖实验。结果显示, LD组终末体重(Wt)和特定生长率(SGR)显著高于HD组($P < 0.05$); LD组的存活率显著高于HD组($P < 0.05$); 不同养殖密度水体和肠道菌群 α 多样性存在一定差异; PCA结果显示不同养殖密度水体和肠道菌群存在显著差异($P < 0.05$); 水体和肠道菌群中的优势菌门均为变形菌门、厚壁菌门、拟杆菌门; HD和MD假单胞菌属占比显著高于LD; 共现网络分析显示, 在三种不同养殖密度在LD与MD中共现网络显示出较高的平均度, 说明LD与MD肠道菌群与水体菌群环境更为稳定。综上, 高原环境下更适合低密度养殖, 该结果为高原环境下三倍体虹鳟生态高效、健康养殖提供参考。

关键词: 养殖密度; 虹鳟; 生长指标; 水体; 肠道菌群; 共现网络

The effects of different aquaculture densities on the growth performance and intestinal health of triploid rainbow trout seedlings in high-altitude environments

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Abstract: To investigate the optimal breeding density for triploid rainbow trout seedlings in high-altitude environments, this study set three different stocking densities (Low-Density group (LD) 100 fish/barrel, Medium Density group (MD) 200 fish/barrel, High-Density group (HD) 300 fish/barrel) and conducted a 60-day cultivation experiment. The results showed that the final body weight (Wt) and specific growth rate (SGR) of the LD group were significantly higher than those of the HD group ($P < 0.05$). The survival rate of the LD group was significantly higher than that of the HD group ($P < 0.05$). There are certain differences in the Alpha diversity of water bodies and gut microbiota among different aquaculture densities. The PCA results show significant differences ($P < 0.05$) in water and gut microbiomes between different aquaculture densities. The dominant phyla in both aquatic and intestinal microbiomes are Proteobacteria, Firmicutes, and Bacteroidetes. The proportion of Pseudomonas genera in HD and MD is significantly higher than that in LD. The co-occurrence network analysis showed that the co-occurrence

Key words: : Stocking density; Oncorhynchus mykiss; growth indicators; water body; intestinal microbiota; co-occurrence network

浮萍能够加强生物絮团技术并实现以福利为导向的南美白对虾可持续养殖

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摘要: 本研究将浮萍引入到养殖南美白对虾 (*Penaeus vannamei*) 的生物絮团技术 (Biofloc technology, BFT) 中, 命名为浮萍-南美白对虾生物絮团综合养殖组 (DBG), 并与无浮萍的对照组 (CG) 进行比较。实验进行 55 天后, DBG 的硝态氮、总氮、可溶性活性磷酸盐和可溶性有机碳的积累峰值显著降低 ($P < 0.05$)。此外, 南美白对虾肠道和肝胰腺中抗氧化酶和消化酶活性在 DBG 中显著升高 ($P < 0.05$)。DBG 还表现出增重率和特定生长率的显著增加 ($P < 0.05$)。代谢组学和转录组学分析结果表明, 浮萍中的营养物质通过调节肠道中的血清素代谢来增强免疫力并减少炎症。此外, 通过添加浮萍实现的饮食富集也提高了南美白对虾对几丁质、蛋白质和维生素等营养物质的消化和吸收。总之, 将浮萍纳入 BFT 系统有助于更稳定的水产养殖环境并提高养殖福利。

关键词: 生物絮团技术; 浮萍; 南美白对虾; 生态养殖; 动物福利

Duckweed promises to be an important link in promoting biofloc technology for ecological and welfare-oriented *Penaeus vannamei* farming

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Abstract: This experiment explored the integration of duckweed with biofloc technology (BFT) in the culture of *Penaeus vannamei*. A duckweed-biofloc group (DBG) was compared to a control group (CG) without duckweed. After 55 days, DBG showed significant reductions in nitrate nitrogen, total nitrogen, reactive phosphate and dissolved organic carbon ($P < 0.05$). Antioxidant and digestive enzyme activities in the gut and hepatopancreas, weight gain, and specific growth rates in DBG were significantly higher, while feed conversion ratios were lower ($P < 0.05$). Duckweed was observed in the gut, confirming effective feeding and improved gut morphology. Metabolomic and transcriptomic analyses indicated that duckweed's phytochemicals enhanced immunity and reduced inflammation via serotonin metabolism. Nutrient digestion and absorption, including chitin, protein, and vitamins, were improved, correlating with enzyme activity. Overall, duckweed combined with BFT stabilized the aquaculture environment and enhanced shrimp welfare.

Key words: Biofloc technology; Duckweed; *Penaeus vannamei*, ecological culture; Animal welfare

刺参夏眠对海洋底泥组成影响的宏基因组-代谢组联合分析研究

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摘要: 为探索海参夏眠对底泥成分的影响, 运用宏基因组-代谢组关联技术分析同一刺参养殖池塘中的夏眠位点和非夏眠位点的底泥组成。结果显示 (1) 夏眠位点和非夏眠位点的底泥样本在微生物组成上无显著差异, 但在致病菌和腐败菌其相对丰度上有所不同; (2) 夏眠位点和非夏眠位点的底泥样本中抗生素抗性基因的潜在宿主平均相对丰度存在差异; (3) 与非夏眠位点底泥样本相比, 夏眠位点底泥样本中抗生素抗性基因 *tetW* 和 *floR* 的平均绝对丰度下降, 而 *tetM* 的平均绝对丰度上升; (4) 与非夏眠位点的底泥样本相比, 夏眠位点底泥样本中共鉴定到 74 种差异代谢物, 其中 4 种差异代谢物与抗菌活性和细菌生理具有强相关性。本研究结果提示, 抗生素抗性基因 *tetM* 可能是海参夏眠期间养殖底泥中监测和指示抗生素抗性基因转移和底泥状态的关键标记物。综上, 本研究中所获结果不仅揭示了海洋生物生理行为对海洋生态环境系统的影响, 也为水产养殖的管理提供新的参考资料。

关键词: 海洋底泥; 宏基因组; 代谢组; 刺参; 夏眠

Integrated metabolome–metagenome analysis provides new insights into the impacts of sea cucumber (*Apostichopus japonicus*) aestivation on marine sediment composition

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Abstract: To explore the impacts of *Apostichopus japonicus* aestivation on sediment composition, sediments were sampled from aestivation sites (ASs) and non-aestivation sites (NASs) of a pond, and metabolome–metagenome integrated analysis was performed. The results showed that 1) no significant difference in the microbial composition of sediments between ASs and NASs, but the relative abundances of some pathogenic and spoilage species changed; 2) altered average relative abundances of potential host of antibiotic resistance genes (ARGs) were observed; 3) compared with NASs, decreased average absolute abundances of *tetW* and *floR* but the increased abundance of *tetM* were observed in ASs; 4) Four out of 74 significantly differentially expressed metabolites (SDMs) correlated with antibacterial activity and bacterial physiology were identified in ASs compared with NASs. All data indicate that *tetM* might be a key indicator for monitoring ARG transfer or sediment status during aestivation revealing the impacts of the physiological behavior of inhabitants and providing a novel aquaculture management.

Key words: Marine sediment; Metagenome; Metabolome; *Apostichopus japonicus*; Aestivation

一株固碳工程菌的构建及其在暗纹东方鲀养殖中的应用

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摘要: 暗纹东方鲀(*Takifugu fasciatus*)是一种重要的经济鱼类,但其养殖过程中产生的碳排放对环境造成了严重的影响。因此,为了降低暗纹东方鲀养殖过程中的碳排放问题,从淡水池塘养殖水体中筛选出具有固碳功能的菌株,通过16S rDNA基因测序鉴定为深红螺菌(*Rhodospirillum rubrum*),选择表达载体,确定导入载体的目的基因,通过连接转化实验,得到构建的重组质粒,将含有目的基因的质粒载体转化到深红螺菌中,使其获得新的遗传信息。比较了在暗纹东方鲀养殖水体中菌株对碳源的利用情况,设置三个处理组:空白组、深红螺菌组、固碳工程菌组,表明对养殖水体进行10 d处理后,优化后的菌株较未优化的菌株固碳功能明显提高,温室气体CO₂和CH₄减排达到20%以上,利用微生物基因工程技术改造菌株提升固碳能力为今后构建低碳暗纹东方鲀养殖体系、促进暗纹东方鲀产业可持续发展具有重大意义。

关键词: 光合细菌;暗纹东方鲀;工程菌;养殖污水;固碳

Construction of a carbon sequestration engineering bacterium and its application in the breeding of *Takifugu fasciatus*

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Abstract: *Takifugu fasciatus* is an important economic fish, but its carbon emissions during aquaculture have a serious impact on the environment. To reduce carbon emissions in its aquaculture, carbon fixing functional strains were screened from freshwater pond aquaculture water, identified as *R. rubrum* by 16S rDNA, and a recombinant plasmid was constructed by ligation and transformation. The plasmid vector containing the target gene was transformed into *R. rubrum*. Comparing the utilization of carbon sources by bacterial strains in the aquaculture water of *T. fasciatus*, a blank group, a deep red snail bacterial group, and a carbon fixation engineering bacterial group were set up. After 10 days of treatment, the optimized strains showed a significant improvement in carbon fixation function compared to the unoptimized strains, with CO₂ and CH₄ emissions reduced by more than 20%. The use of microbial genetic engineering technology to modify bacterial strains to enhance carbon fixation capacity is of great significance for constructing a low-carbon *T. fasciatus*.

Key words: Photosynthetic bacteria; *Takifugu fasciatus*; Engineering bacteria; Aquaculture wastewater; Carbon fixation

微生物组、转录组和生理学分析揭示了日本对虾（*Penaeus japonicus*）对暴露于氧纳米气泡的反应

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摘要：日本对虾是一种高价值的甲壳类动物，长期低产。氧纳米气泡（NB-O₂）技术的应用有可能解决这个问题。本研究进行 40 天，在两套循环水养殖系统（RAS）中饲养日本对虾幼虾。对照组（LS）的溶氧维持在 7.5 ± 0.5 mg/L，而实验组（HS）补充 NB-O₂，溶氧在 15.0 ± 0.5 mg/L。本研究主要关注 NB-O₂ 对日本血吸虫肠道微生物组、转录组和生理适应的影响。结果表明，肠道微生物组方面，一些益生菌的丰度增加，如乳杆菌和红假单胞菌，同时保持微生物平衡。转录组分析揭示了适应高氧的关键途径，有氨基酸代谢、能量代谢和抗氧化能力等，并在生理实验中得到证实。总之，本研究证实了用 NB-O₂ 技术养殖日本对虾具备可行性。

关键词：日本对虾，氧纳米气泡，溶氧

Microbiome, transcriptome, and physiology analyses revealed the response of kuruma shrimp (*Penaeus japonicus*) to exposure to oxygen nanobubbles

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Abstract : *Penaeus japonicus*, a high-value crustacean, long-term low yields. The application of oxygen nanobubble (NB-O₂) technology has potential to address this issue. This study was conducted for 40 days. Juvenile *P. japonicus* were reared in two recirculating aquaculture systems (RAS). In the control group (LS), the dissolved oxygen was maintained at 7.5 ± 0.5 mg/L, while in the experimental group (HS), the dissolved oxygen was 15.0 ± 0.5 mg/L supplemented with NB-O₂. This study focused on the effects of NB-O₂ on the intestinal microbiome, transcriptome, and physiological adaptation of *S. japonicum*. The results showed that the abundance of some probiotics, such as *Lactobacillus* and *Pseudomonas rubrosa*, was increased in the gut microbiome while maintaining microbial balance. Transcriptome analysis revealed the key pathways of adaptation to hyperoxia, including amino acid metabolism, energy metabolism and antioxidant capacity, which were confirmed by physiological experiments. In conclusion, this study demonstrated the feasibility of using NB-O₂ in shrimp culture.

Key words: : *Penaeus japonicus*, Oxygen nanobubble, Dissolved oxygen

不同养殖模式下大黄鱼肌肉营养成分比较分析

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摘要: 以野生大黄鱼作为对照, 试验分析了池塘内虾池养殖与池塘“跑道”养殖模式下鲜活肌肉的基本营养成分、脂肪酸组成和氨基酸组成等指标。表明: 池塘跑道粗蛋白含量和灰分最高, 池塘虾池粗脂肪含量 3.38% 显著低于为池塘跑道 9.52%; 均检测出 17 种氨基酸, 其中 7 种必需氨基酸; 不同组间氨基酸、必需氨基酸和鲜味氨基酸总量差异不明显; 池塘虾池必需氨基酸指数大于 80%, 是良好蛋白源; EAA/TAA、NEAA/TAA 两者无显著差异; 第一限制氨基酸均为蛋氨酸+胱氨酸; 饱和脂肪酸、单不饱和脂肪酸、多不饱和脂肪酸、EPA+DHA 总量以及 $\Sigma n3PUFA/\Sigma n6PUFA$ 均存在显著差异, 其中多不饱和脂肪酸总量以池塘虾池最高, EPA+DHA 总量为池塘跑道 2.13 倍。综上所述, 池塘虾池养殖模式下的大黄鱼肌肉其营养成分具有高蛋白低脂肪、多不饱和脂肪酸丰富、氨基酸组成平衡的特点, 是值得推广的绿色健康养殖新模式。

关键词: 大黄鱼; 养殖模式; 营养评价; 氨基酸; 脂肪酸

Comparative Analysis of Nutrient Composition in the Muscle of *Larimichthys crocea* in Different Culture Models

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Abstract: To explore the differences in muscle nutritional quality of *Larimichthys crocea* between shrimp pond aquaculture and pond "runway" aquaculture, wild *L. crocea* was used as a control to analyze the basic nutritional components, fatty acids, and amino acids of fresh muscle. Results indicate that pond runways have the highest protein and ash content, while the crude fat content in shrimp ponds is 3.38%, significantly lower than that of pond runways. 17 amino acids were detected, including 7 essential amino acids, with the essential amino acid index of pond shrimp exceeding 80%. No significant differences were found between EAA/TAA and NEAA/TAA ratios, which surpassed the FAO/WHO ideal protein pattern. The first limiting amino acid is methionine+cystine. The total polyunsaturated fatty acids in shrimp ponds are the highest, with EPA+DHA being 2.13 times that of pond runways. In summary, the nutrient composition of *L. crocea* muscle in shrimp culture mode features high protein, low fat, rich polyunsaturated fatty acids, making it a new green and healthy culture mode worthy of promotion.

Key words: *Larimichthys crocea*, culture mode, nutritional evaluation, amino acids; fatty acids

虾夷扇贝繁殖前后相关生理生化指标的比较研究

何萍

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摘要: 为探究虾夷扇贝繁殖后高死亡率问题,本研究采用分子生物学方法,对比分析雌雄虾夷扇贝繁殖前后机体成分、酶活性及代谢组学差异。结果显示:(1)繁殖前虾夷扇贝机体中粗蛋白、粗脂肪和糖原含量均高于繁殖后。其中粗脂肪最显著,雄性下降 28.36%,雌性下降 12%。(2)繁殖后 SOD、CAT、T-AOC 等免疫酶活性均有显著差异。(3)繁殖前后,扇贝肌肉和性腺代谢物差异显著,共鉴定出 1644 种差异代谢物。肌肉中 903 种,主要涉及谷氨酸能突触等通路。性腺中 903 种,主要涉及 2-氧代羧酸、ABC 转运蛋白等通路。由此可见,繁殖行为对于虾夷扇贝是一个及其消耗能量的过程。综上,繁殖行为会对虾夷扇贝营养成分、酶活和肌肉以及性腺代谢等一系列相关生理生化指标产生影响。本研究结果对于虾夷扇贝繁殖后死亡率提高提供了一定的理论参考。

关键词: 虾夷扇贝,生化成分,酶活,代谢组

Comparative study on related physiological and biochemical indexes of scallop before and after reproduction

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Abstract: To investigate the high mortality rates in scallops post-reproduction, this study utilized molecular biology techniques to analyze changes in body composition, enzyme activity, and metabolites in both male and female scallops before and after reproduction. Key findings include: (1) Pre-reproduction scallops had higher levels of crude protein, fat, and glycogen compared to post-reproduction, with the most significant drop in crude fat 28.36% in males, 12% in females. (2) Post-reproduction, there were notable changes in immune enzyme activities such as SOD, CAT, and T-AOC. (3) A total of 1644 distinct metabolites were identified in the muscle and gonads, with 903 linked to neurotransmitter pathways in muscle and the others to energy and transport pathways in gonads. These results indicate that reproduction is energetically costly for scallops, impacting their nutritional status, enzyme activity, and metabolism. The study offers insights into the reasons behind the high mortality rates observed after scallop reproduction.

Key words: *Patinopecten yessoensis*, biochemical components, enzyme activity, metabolome

循环水养殖日本对虾饲料蛋白质需要量的研究

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摘要：近年来使用循环水养殖日本对虾(*Marsupenaeus japonicas*)逐渐兴起，但循环水条件下日本对虾的蛋白质需要量研究仍然欠缺。本研究旨在探索日本对虾在循环水养殖条件下的最适蛋白质需要量。实验配制粗蛋白含量（占干物质%）分别为35%、40%、45%、50%、55%和60% (P35、P40、P45、P50、P55和P60)的6种饲料，分别投喂初始体重为1.86g的日本对虾，试验周期56天。实验结果表明，P45组的增重率和特定生长率显著最高，根据增重率拟合回归方程结果表明，日本对虾的饲料最适蛋白质需要量为46.13%，各组均有较高的成活率。P45组显著提高了消化酶活性、抗氧化指标，改善了肠道形态，P50组肠道微生物群多样性显著最高。综上所述，循环水养殖日本对虾的最佳蛋白质含量为46.13%，但饲料中50%的蛋白蛋白质含量有益于肠道微生物群多样性。

关键词：日本对虾、循环水养殖系统、蛋白质需要量、生长性能

Dietary protein requirements of kuruma shrimp *Marsupenaeus japonicas* in recirculating aquaculture system

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Abstract : The farming of *Marsupenaeus japonicas* in recirculating aquaculture system (RAS) is relatively recent, consequently, knowledge of their dietary protein requirements is still insufficient. This study aimed at assessing the optimal protein requirement of *M. japonicas* in RAS. Six experimental diets were devised to contain 35%, 40%, 45%, 50%, 55%, and 60% crude protein, and were fed in triplicate groups of 20 shrimp (initial body weight 1.86 ± 0.01 g) at a feeding rate of 3.0% body weight per day for 56 days. At the end of the feeding period, the optimal protein requirement was estimated at 46.13% for weight gain rate, and specific growth rate with all groups exhibited high survival rates. The P45 diet increased the digestive enzymes activities, antioxidant indices and improved intestinal morphology, while the P50 diet showed the highest intestinal microbiome diversity. Hence, results from this study suggested that the optimal protein requirement of *M. japonicas* fed in RAS was determined to be 46.13%, but protein levels up to 50% can be beneficial to the intestinal microbiome diversity.

Key words:: *Marsupenaeus japonicas*, Recirculating aquaculture system, Protein requirements, Growth performance

水产绿色健康养殖新技术新模式专题摘要

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摘要：随着全球人口增长和对水产品需求的增加，传统的养殖方式难以长期维持产量和质量，可能导致水体污染、养殖废水排放和水生态系统破坏，而消费者对水产品的质量、健康性和安全性要求越来越高。传统的养殖模式已经无法满足市场的需求和环境的质量。水产绿色健康养殖的新技术和新模式通过生态友好型的手段，提升了水产养殖业的可持续性和生产效率。这些新技术包括水循环养殖系统（RAS）、生物絮团技术（BFT）、智能化养殖管理系统、以及环境友好的饲料和水处理技术等，能够有效降低水体污染、减少药物和化学品的使用。各国对于环境保护和食品安全的法规日益严格，发展绿色养殖是响应这些政策要求的必要举措，也有助于获得政府的支持和资助。因此，发展绿色健康养殖不仅是为了保护环境，更是为了确保水产行业的可持续发展，提高经济效益和水产品的安全性。

关键词：水产养殖；健康养殖；可持续发展

special Abstract on New Technologies and Models for Green and Healthy Aquaculture

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Abstract : With the global population growth and the increasing demand for aquatic products, traditional aquaculture methods are struggling to maintain yield and quality in the long term. This could lead to water pollution, discharge of aquaculture wastewater, and the destruction of aquatic ecosystems. Consumers are increasingly demanding higher quality, health, and safety standards for aquatic products. The traditional aquaculture model can no longer meet market demands and environmental quality standards. New technologies and models for green and healthy aquaculture have enhanced the sustainability and productivity of the aquaculture industry through eco-friendly means. These new technologies include Recirculating Aquaculture Systems (RAS), Biofloc Technology (BFT), intelligent aquaculture management systems, as well as environmentally friendly feed and water treatment technologies, which can effectively reduce water pollution and decrease the use of drugs and chemicals.

Key words: : Aquaculture; Healthy Aquaculture ; Sustainable Development

饲料粘合剂对循环水养殖刺参粪便及氮磷收支的影响研究

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摘要: 刺参循环水养殖中饲料和粪便易溶散的特性, 加剧了养殖水体悬浮固体颗粒物浓度高、尾水氮磷排放超标等问题。本研究设置了饲料中无粘合剂添加的对照组和分别添加 5% 红薯淀粉、黄原胶、瓜尔胶和卡拉胶的处理组, 探究粘合剂对粪便特性及系统氮磷收支的影响, 旨在确定适宜的粘合剂。结果表明, 添加粘合剂可显著提高刺参粪便粒径和粘度, 其中瓜尔胶和黄原胶的提升效果最优。氮磷收支结果表明, 添加红薯淀粉组流向刺参生长的氮、磷最多, 而流向残饵粪便和溶散在水体中的氮、磷相对较少。红薯淀粉的添加显著提高了刺参对氮、磷的利用率。相关性分析显示粪便粒径-粘度-氮磷收支间具有相关性, 其中粪便粒径与残饵粪便中的氮、磷含量呈正相关, 而与水中溶解的氮、磷含量呈负相关。本研究建议采用红薯淀粉作为粘合剂可优化粪便特性, 减少氮磷排放。

关键词: 刺参; 循环水养殖; 粘合剂; 粪便特性; 氮磷收支

Effects of feed binders on feces and nitrogen and phosphorus budgets in recirculating aquaculture system of *Apostichopus japonicus*

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Abstract: This study examined the effect of feed binder on fecal viscosity, particle size, and the nitrogen (N) and phosphorus (P) budget in the recirculating aquaculture system (RAS) for *Apostichopus japonicus*. The goal was to identify a suitable binder for *A. japonicus* RAS. We set up control group without binder and groups with 5% sweet potato starch, xanthan gum, guar gum, and carrageenan, respectively. The binder significantly increased fecal particle size and viscosity. The most N and P flowed to the growth of *A. japonicus* in group with sweet potato starch. There was relatively less N and P flowing towards the residual bait feces and dissolved in the water. Moreover, sweet potato starch improved the utilization of N and P by *A. japonicus*. Correlation analysis revealed an interrelation among fecal particle size-viscosity-N and P budget. Fecal particle size showed positive correlation with N and P in residual bait feces, while negative correlation with dissolved N and P in water. In conclusion, this study suggested that sweet potato starch was a suitable binder for *A. japonicus* RAS.

Key words: *Apostichopus japonicus*, recirculating aquaculture system, binder, Fecal properties, nitrogen and phosphorus budget.

横带髯鲷精子超微结构及其生理特征

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摘要: 为探究横带髯鲷 (*Hapalogenys mucronatus*) 精子形态、生理特性, 以提高人工繁殖的受精率, 利用扫描电镜和透射电镜观察其精子结构, 并设置不同梯度的盐度、pH 和温度, 探讨横带髯鲷精子快速运动时间、寿命与环境因子的关系。结果表明: 横带髯鲷精子由头部、中部和鞭毛三段组成, 精子头部近球形或椭球形, 头部直径为 $(1.56\pm 0.05)\mu\text{m}$, 细胞核中染色质高度浓缩, 核膜紧贴于质膜, 无顶体; 中段主要由袖套腔与中心粒复合体构成; 鞭毛细长有侧鳍, 为典型“9+2”微管结构。横带髯鲷精子的适宜盐度范围为 22~28, 盐度为 26 时精子寿命达到最大值 425 s; 适宜 pH 范围为 7~10, 在 pH 为 7 时, 精子活力最强, 精子寿命达到最大值 430 s; 适宜温度 18°C~26°C, 水温 22°C 时精子寿命最长 427 s。建议横带髯鲷卵子和精子受精时的最佳水环境条件为盐度为 24~26、pH 为 7~8.7、温度为 20~22°C。

关键词: 横带髯鲷; 精子; 超微结构; 环境因子

Ultrastructure and physiological characteristics of sperm in *Hapalogenys mucronatus*

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Abstract: In order to explore the sperm morphology and physiological characteristics of *Hapalogenys mucronatus* and improve the fertilization rate of artificial reproduction, the sperm structure was observed by scanning electron microscopy and transmission electron microscopy, and different gradients of salinity, pH and temperature were set up to explore the relationship between the rapid movement time, life span and environmental factors of *Hapalogenys mucronatus* sperm. The results showed that the sperm of *Hapalogenys mucronatus* consisted of three parts: head, middle part and flagella. The head of sperm was nearly spherical or ellipsoidal, with a diameter of $(1.56\pm 0.05)\mu\text{m}$. The chromatin in the nucleus was highly concentrated, and the nuclear membrane was close to the plasma membrane without acrosome. The middle part is mainly composed of sleeve cavity and centriole complex. The flagellum is slender and has lateral fins, which is a typical “9+2” microtubule structure.

Key words: *Hapalogenys mucronatus*; sperm; ultrastructure; environmental factors

通过几何形态学测定香螺发育过程中形态上的差异

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摘要: 对香螺 (*Neptunea cumingi*) 3、6、9、12月龄4个发育阶段的外壳形态变化采用传统测量学、几何形态学和交叉验证方法进行研究。结果表明: 利用 PAST 对所有香螺壳型进行比较, 表明香螺每个发育阶段都有典型的形态特征, 这些特征的差异主要集中于螺层数目的变化和壳顶形态的改变。香螺壳体大小和壳体形态在定义的空间内表现出具有各自特征性的个体发育轨迹, 因此香螺个体的发育具有异速生长的特点, 因此可以通过香螺壳体形态的变化对黄渤海香螺进行无损年龄鉴定。其次, 对样品进行单因素方差分析, 结果显示各组样本之间存在极显著性差异。通过生长曲线形状得知在 12 月龄以前香螺生长速度逐渐加快。不同月龄香螺的外壳尺寸有明显的差异, 因此可以通过香螺的外壳尺寸对其进行初步的无损年龄鉴定。本文的研究结果可为野外香螺资源管理和水产养殖管理中的香螺生长阶段的确定提供参考。

关键词: 个体发育, 香螺, 几何形态计量学, 异速生长;

Ontogenetic Changes During Development of the Whelk *Neptunea cumingii* Determined Using a Geometric Morphometric Method

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Abstract: In this study, we assessed the morphological changes of whelk (*Neptunea cumingii*) shells at 3, 6, 9, and 12 months of development using traditional measurements and geometric morphometry, and we cross-validated the results using a different sample of whelks. We detected distinct patterns in shell length distribution at each stage, respectively. *N. cumingii* displayed specific morphological characteristics at each stage, primarily in the number of spiral layers and the shape of the shell apex. Individual development exhibited unique growth trajectories in shell size and shape, indicating allometric growth characteristics. One-way analysis of variance demonstrated significant differences among age groups. The growth curve based on shell length revealed an accelerating growth rate of *N. cumingii* before 12 months of age. Our results illustrated the effectiveness of using a non-destructive approach for age identification of *N. cumingii* in China and provided valuable insights for resource management and aquaculture practices.

Key words: geometric morphometry, *Neptunea cumingii*, ontogeny, allometry;

基于池塘小网箱养殖马口鱼效果研究

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摘要: 本试验旨在探究池塘小网箱养殖马口鱼 (*Opsariichthys bidens* Gunther) 的效果。试验将塑胶渔排放置于池塘中部, 使用聚乙烯网箱捆绑于塑胶渔排上, 分三个网箱试验组 (分别编号为 M1、M2 和 M3), 网箱规格为长 2.0 m×宽 2.0 m×深 1.5m。选择初始体重为(13.90±0.55)g 马口鱼幼鱼, 每个网箱平均投放 360 尾左右, 投喂粗蛋白为 41%的膨化配合饲料。通过 66 天的网箱养殖后结果发现, 3 组网箱马口鱼的平均存活率为 (70.88±4.83) %、特定生长率为 (0.97±0.04) %/day、饲料系数为 (2.15±0.15), 体质量增长呈指数函数: $y = 11.563e^{0.2125x}$ ($R^2 = 0.9879$)。本试验还观察到网箱养殖马口鱼的摄食与生长在水温 26~30℃时表现最佳。

关键词: 马口鱼; 池塘小网箱; 生长性能

Effects of small-scale cage aquaculture on *Opsariichthys bidens* Gunther based on pond

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Abstract: To investigate the effect of small-scale cage aquaculture on *Opsariichthys bidens* Gunther in pond, the experiment placed plastic fishing rafts in the middle of the pond and tied cage to the polyethylene. They were divided into 3 groups (numbered M1, M2, and M3), with cage size of 2.0 m in length, 2.0 m in width, and 1.5 m in depth. Each small-scale cage had 360 fish with initial body weight (13.90±0.55) g, and fed with a 41% crude protein puffed formula feed. After 66 days of small-scale cage culture, the results showed that the average survival rate were (70.88±4.83) % of 3 groups, the specific growth rate were (0.97±0.04) %·d⁻¹, and the feed coefficient were (2.15±0.15). The body weight growth showed an exponential function: $y = 11.563e^{0.2125x}$ ($R^2 = 0.9879$). This experiment also observed that the feeding and growth performances of the performed best at water temperatures were 26-30 °C of *Opsariichthys bidens* Gunther.

Key words: : *Opsariichthys bidens* Gunther; smal-scale cage aquaculture in pond; growth performances

稻虾综合种养影响稻田温室气体排放的微生物机理

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摘要: 将传统水稻单作(RM)转换为稻虾(克氏原螯虾)综合种养模式(RCIS)会改变温室气体排放相关的土壤理化性质及微生物。然而, RCIS对稻田温室气体排放及全球增温潜势(GWP)的影响仍不清晰。因此, 本研究于2022年和2023年在江苏省高邮市开展大田试验, 通过设置RM和RCIS2个处理, 研究甲烷(CH₄)和氧化亚氮(N₂O)排放、土壤理化性质及相关的微生物丰度(产甲烷菌、甲烷氧化菌、反硝化细菌和硝化细菌)在RCIS下的变化。结果表明: 与RM相比, RCIS显著增加CH₄排放和降低N₂O排放。RCIS下CH₄排放增加主要是因为其显著提高了土壤mcrA基因丰度和mcrA/pmoA的比例, 而N₂O排放的降低主要是因为其显著提高了土壤nosZ基因丰度和nosZ/(amoA+nirK+nirS)的比例。

关键词: 甲烷; 氧化亚氮; 产甲烷菌; 反硝化细菌; 稻虾综合种养模式

Microbial mechanism of rice-crayfish integrated system affecting greenhouse gas emission from paddy fields

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Abstract: The conversion from rice monoculture (RM) to rice-crayfish integrated system (RCIS) could change soil physicochemical properties and microorganisms related to greenhouse gas (GHG) emissions. Nevertheless, it is still unclear the responses of GHG emissions and global warming potential (GWP) from paddy fields to RCIS. Here, we conducted a field experiment to investigate the changes in the emissions of methane (CH₄) and nitrous oxide (N₂O), GWP, soil physicochemical properties and the associated microbial abundances (methanogen, methanotrophs, denitrifier and nitrifier) under RCIS in Gaoyou City, Jiangsu Province, China from 2022 to 2023. There were three treatments, including RM and RCIS. Compared with RM, RCIS all significantly increased CH₄ emission and decreased N₂O emission. The increased CH₄ emission was due to the significantly higher mcrA gene abundance and ratio of mcrA/pmoA under RCIS. While the significantly higher nosZ gene abundance and ratio of nosZ/(amoA+nirK+nirS) under RCIS were responsible for its reduced N₂O emission. Furthermore, the increases in gene abundances of

Key words: Methane; Nitrous oxide; Methanogen; Denitrifier; Rice-crayfish integrated system

抑制氧化应激水平解救高温诱导 黄颡鱼雄性化

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摘要: 全球变暖下水温升高诱导鱼类雄性化, 导致种群性别比例极不平衡, 性二态型鱼类生长差异巨大、资源分配不均, 从而造成巨大的经济损失。在本研究中, 在黄颡鱼性别分化关键时期 (12-70DPH) 设置 HT (33.5°C)、HE300 (高温和大黄素 300mg/kg) 和 HE1200 (高温和大黄素 1200mg/kg) 组, 对黄颡鱼的性别表型比进行统计。结果显示, HT 处理主要有雌性 (FM)、雄性 (M) 和间性 (IS) 三种性别表型。在 65 和 75DPH 时 HT 组有 28.6% (M 为 10.7%, IS 为 17.9%) 发生雄性化, HE300 和 HE1200 分别仅有 6.3% (IS) 和 8.3% (IS)。在 125DPH 时 HT 组有 10.3% (M 为 7.7%, IS 为 2.6%), 而 HE300 与 HE300 组均为 0。

关键词: 性别分化; 性别控制; 高温; 氧化应激; 雄性化; 大黄素

Inhibition oxidative stress levels rescues high temperature induced masculinization in yellow catfish

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Abstract: Increased water temperature under global warming induces masculinization in fish, resulting in highly unbalanced population sex ratios, huge differences in the growth of sexually dimorphic fish, and unequal distribution of resources, which in turn causes great economic losses. In this study, HT (33.5°C), HE300 (high temperature and emodin 300 mg/kg) and HE1200 (high temperature and emodin 1200 mg/kg) groups were set up during the critical period of sex differentiation of yellow catfish (12-70DPH), and the sex phenotype ratios of yellow catfish were counted. The results showed that HT treatments had three main sex phenotypes: female (FM), male (M) and intersex (IS). Masculinization occurring in 28.6% (10.7% for M and 17.9% for IS) of the HT groups at 65 and 75 DPH, and only 6.3% (IS) and 8.3% (IS) of the HE300 and HE1200, respectively. At 125 DPH there were 10.3% (7.7% for M and 2.6% for IS) in the HT group and 0 in both the HE300 and HE300 groups. Compared with the FM group, CAT, SOD and MDA significantly increased, GSH-Px significantly decreased and oxidative stress level significant

Key words: sex differentiation; sex control; high temperature; oxidative stress; masculinization; emodin

Ca²⁺、Mg²⁺和K⁺浓度对中间球海胆 (*Strongylocentrotus intermedius*) 存活、 生长和生理指标的影响

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摘要: 为探讨 Ca²⁺、Mg²⁺ 和 K⁺ 浓度对中间球海胆 (*Strongylocentrotus intermedius*) 的影响, 分别设置 0.5、1、1.5 和 2 倍正常海水浓度的 Ca²⁺、Mg²⁺ 和 K⁺ 实验组对海胆进行养殖, 并对海胆存活率、特定生长率、性腺指数及部分酶活性进行了检测和分析。结果显示, Ca²⁺、Mg²⁺ 和 K⁺ 浓度的降低会显著降低海胆的存活率 (P<0.05); Mg²⁺ 浓度的升高会显著降低海胆的特定生长率; Ca²⁺ 和 K⁺ 浓度的升高能显著提高海胆的性腺指数, 但 2 倍浓度的 Ca²⁺ 和 K⁺ 会显著降低性腺指数; Ca²⁺ 和 Mg²⁺ 浓度对胃蛋白酶活性影响显著, 随着离子浓度的增加胃蛋白酶活性呈现上升的趋势; 2 倍浓度的 K⁺ 会显著增加酸性磷酸酶活性。研究表明, Ca²⁺、Mg²⁺ 和 K⁺ 对中间球海胆生长、生理功能和酶活性影响较大, 在利用非自然海水养殖时, 应注意检测和调节离子浓度。

关键词: 中间球海胆; Ca²⁺; Mg²⁺; K⁺

Effects of Ca²⁺、Mg²⁺ and K⁺ concentrations on the survival, growth and physiological indexes of *Strongylocentrotus intermedius*.

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Abstract: To investigate the effects of Ca²⁺, Mg²⁺, and K⁺ concentrations on *Strongylocentrotus intermedius*, experimental groups with Ca²⁺, Mg²⁺, and K⁺ concentrations set at 0.5, 1, 1.5, and 2 times those of normal seawater were established for cultivation. The decrease of Ca²⁺, Mg²⁺, and K⁺ concentrations significantly reduced the survival rate of sea urchins (P<0.05); the specific growth rate of sea urchins was decreased with the increase of Mg²⁺ concentration; the increase of Ca²⁺ and K⁺ concentration could significantly increase the gonad index of sea urchin, but Ca²⁺ and K⁺ at twice the concentration could significantly reduce the gonad index; Ca²⁺ and Mg²⁺ concentrations had a significant impact on pepsin activity, which increased as ion concentrations rose; the activity of acid phosphatase was significantly increased by 2 times concentration of K⁺. Ca²⁺, Mg²⁺ and K⁺ had a great influence on the growth, physiological function and enzyme activity of *Strongylocentrotus intermedius*, and the ion concentration should be detected and adjusted when using unnatural seawater aquaculture.

Key words: *Strongylocentrotus intermedius*; Ca²⁺; Mg²⁺; K⁺

光谱及光周期对刺参（*Apostichopus japonicus*）稚参的生长性能、免疫能力及肠道微生物群的影响

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摘要：本研究以刺参(*Apostichopus japonicus*)稚参为实验对象，将其置于三种光周期 0L: 24D (DD)、14L: 10D (LD)、24L: 0D (LL)的全光谱(W)、橙光(O)及红光(R)的环境中进行为期 40d 的养殖实验，分析其生长、基因表达及肠道微生物群的变化。结果表明，W-LD 和 R-LD 组稚参的生长性能显著提高。R-LD 组 *c-myc*、MAPK-7 和 GDF-8 基因表达水平显著提高，R-LD 和 R-LL 组 HSP90 基因的表达水平显著提高，R-LD 组 *Aj-p105* 和 *lys* 的基因表达量显著提高，LL 组 HSP70 和 *Aj-p50* 基因的表达量显著下调。R-LD 组 Rhodobacteraceae 等有益菌的丰度增加，*Vibrio* 等致病菌的丰度减少，并促进与复制修复、细胞信号等相关功能的微生物富集。综上，每日 14h 红光照射能够提高稚参的生长性能及免疫能力，维持肠道微生物群落的健康稳定。

关键词：光环境；刺参；生长；免疫；肠道微生物群

Effects of light spectrum and photoperiod on the growth performance, immune capacity, and gut microbiota of juvenile *Apostichopus japonicus*.

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Dalian Ocean University

Abstract : This study examined the effects of different light conditions on juvenile *Apostichopus japonicus*, which were cultured for 40 days under three photoperiods: 0L:24D (DD), 14L:10D (LD), and 24L:0D (LL) with full-spectrum (W), orange (O), and red (R) light. Growth performance, gene expression, and gut microbiota were analyzed. Results indicated that the W-LD and R-LD groups exhibited significantly improved growth performance. In the R-LD group, the expression of *c-myc*, MAPK-7, and GDF-8, increased significantly, while HSP90 expression was elevated in both the R-LD and R-LL groups. The R-LD group also showed higher expression of *Aj-p105* and *lys*, while the LL group exhibited lower expression of HSP70 and *Aj-p50*. Additionally, beneficial bacteria such as Rhodobacteraceae increased, while harmful bacteria like *Vibrio* decreased in the R-LD group, enriching microbes associated with functions such as replication and cell signaling. Overall, 14 hours of daily red light exposure improved growth performance, boosted immune functions, and supported a healthy gut microbiota in juvenile sea cucumbers.

Key words: : Light environment; Sea cucumber; Growth; Immunity; Gene expression; Intestinal microbiota

黑鲷“苏海 1 号”新品种简介

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

关键词：黑鲷；新品种

brief introduciton on new strain of black porgy "Suhai No.1"

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

Key words:: Black porgy; New strain

超雄大口黑鲈创制及 全雄苗种规模化繁育

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

关键词: 大口黑鲈; 性逆转; YY 超雄鱼; 全雄鱼

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

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

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

综合时间序列转录组学和代谢组学揭示美洲牛蛙（*Aquarana catesbeiana*）对米尔伊丽莎白菌（*Elizabethkingia miricola*）感染的反应机制

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摘要：本研究利用时间序列转录组和代谢组对美国牛蛙响应 *E. miricola* 的应答进行研究。在本研究中，牛蛙肝脏和脾脏在细菌感染后 0、1、2 和 3 天内的转录组中分别发现了 3818 和 4166 个 DEGs，代谢组中分别发现了 518 和 464 个 DAMs。转录组分析揭示了大量的 DEGs 富集于各种免疫反应、信号转导和脂质代谢途径。短时序列表达挖掘器（STEM）分析表明，在细菌感染期间，牛蛙肝脏和脾脏分别出现了 6 和 7 种显著的基因表达变化模式。代谢组分析表明，*E. miricola* 感染分别影响了肝脏和脾脏中的 86 条和 75 条途径，主要涉及脂质代谢、氨基酸代谢、碳水化合物代谢和信号转导。最后，对细菌感染后牛蛙的转录和代谢谱之间的关系进行了相关分析。总之，本研究通过多组学方法阐明了牛蛙对 *E. miricola* 感染的转录和代谢反应机制，为系统表征牛蛙对病原体入侵反应的复杂调控网络提供了参考。

关键词：米尔伊丽莎白菌；时序；转录组；代谢组；牛蛙；肝脏；脾脏

Integrated time-series transcriptome and metabolomics to reveal the response mechanisms of American bullfrogs (*Aquarana catesbeiana*) to *Elizabethkingia miricola* infection

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Abstract: As a zoonotic pathogen, *Elizabethkingia miricola* is ubiquitous in the natural environment and capable of inducing disease in humans and a variety of animals. Therefore, investigating the response mechanism of the host against *E. miricola* invasion can facilitate the development of efficient strategies to control *E. miricola* infection. Herein, this study was undertaken to delineate the temporal influence of *E. miricola* on the American bullfrogs (*Aquarana catesbeiana*), an economically important species, at both the transcriptomic and metabolomic levels. Transcriptome and metabolome were applied to screen the differentially expressed genes (DEGs) and differentially abundant metabolites (DAMs) across a time series. In the present study, a total of 3818 and 4166 DEGs were identified in the transcriptome, alongside 518 and 464 DAMs in the metabolome, across 0, 1, 2, and 3 days after bacterial infection in the liver and spleen of bullfrogs. Transcriptome analysis revealed numerous DEGs enriched in various immune response, signal transduction, and lipid metabolism pathway. Short Time-series Expression Miner (STEM) analysis indicated 6 and 7 significant patterns of gene expression variation in the liver and spleen of bullfrogs during bacterial infection. Additionally, Gene Set Enrichment Analysis (GSEA) demonstrated that a series of immune and lipid metabolism pathways exhibited altered expression patterns at different time points in the liver and spleen during pathogen infection. Metabolomic analysis indicated that *E. miricola* infection affected 86 and 75 pathways in the liver and spleen, respectively, primarily involving lipid metabolism, amino acid metabolism, carbohydrate metabolism, and signal transduction. Both KEGG enrichment analysis and STEM

analysis suggested that glycerophospholipid pathway may play a crucial role in bullfrogs' defense against bacterial infection. Finally, a correlation analysis was conducted to investigate the relationship between the transcriptional and metabolic profiles in both organs post-bacterial infection. In conclusion, this study elucidated the transcriptional and metabolic response mechanism of bullfrogs in response to *E. miricola* infection through a multi-omics approach, providing insight into the systematic characterization of the complex regulatory network underlying the response to pathogen invasion. In general, our findings suggested that the bullfrog exhibits stage-specific immune and metabolic responses as a means to counteract *E. miricola* infection.

Key words: *Elizabethkingia miricola*; *Aquarana catesbeiana*; time-series; transcriptome; metabolomics; bullfrogs; liver; spleen

小黄鱼生长和抗病性状基因组 选择育种研究

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摘要：基于染色体水平小黄鱼基因组，对野生和养殖群体进行重测序筛选 SNP 位点，结合生长、肉质、耐温性等性状相关位点，开发出 100K 的 SNP 芯片，其平均检出率 98.75%，平均一致率 98.53%。利用深度学习和图像识别技术建立了生长表型高通量采集方法；通过测定人工感染病原菌后个体存活时间和存活状态建立抗内脏白点病性状表型测定方法。基于芯片分型获得群体基因型，结合生长、抗病表型，利用 GBLUP、Bayes 和机器学习算法进行性状遗传评估，获得生长和抗病性状遗传力分别为 0.38~0.53 和 0.32~0.34。预测生长性状 GEBV 可靠性为 0.64~0.65，明显高于基于系谱信息预测的 EBV 可靠性（0.55~0.57）。按照约 30% 的留种率筛选优良亲本繁殖的后代，生长速度较家系选育提高约 5%，表明基因组选择育种较家系选育具有明显的优越性，研究结果对于水产种业快速发展具有重要促进作用。

关键词：小黄鱼；基因组；SNP 芯片；生长；抗病；基因组选择育种

无

无
无

Abstract: 无

Key words: 无

雌性三倍体长牡蛎卵细胞发生受阻的 分子机制研究

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摘要: 三倍体动物通常表现为不育, 但是在雌性三倍体长牡蛎中呈现繁殖力差异, 不育的个体被称为雌性 β ; 可育的个体被称为雌性 α 。本研究通过不同倍性的雌性长牡蛎性腺的比较转录组分析, 结果显示 DNA 修复和重组可能是影响雌性三倍体牡蛎育性差异的关键通路。通过进一步验证发现雌性 β 中的 DNA 损伤水平显著高于二倍体和雌性 α 。组织学和超微结构分析显示, 三倍体性腺中存在大量细胞核异常的生殖细胞。CDC42 基因表达与 DNA 损伤增加和基因组稳定性有关, 在雌性三倍体中 CDC42 基因表达异常升高。通过在增殖期和成熟期三倍体中注射 CDC42 特异性抑制剂 (ZCL278) 发现, 雌性三倍体性腺中 DNA 损伤显著减少, 卵母细胞数量增加, 异常生殖细胞减少, 表明抑制 CDC42 蛋白活性促进雌性三倍体长牡蛎配子发生。转录组分析表明, ZCL278 可能通过上调 PI3K-AKT 信号通路激活 DNA 损伤修复, 促进雌性三倍体性腺发育和卵细胞发生。

关键词: 三倍体; 长牡蛎; CDC42; DNA 损伤; 卵细胞发生

Investigating the molecular mechanism of block oogenesis in triploid *Crassostrea gigas*

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Abstract: Triploid Pacific oyster *Crassostrea gigas* exhibits notable differences in fecundity, with the sterile individuals referred to as female β , while the fertile individuals referred to as female α . In the present study, comparative transcriptome analyses of female oyster gonads showed that DNA repair and recombination may be the key pathways affecting fertility differences in female triploid oysters. The further studies showed significantly higher levels of DNA damage in gonadal cells of female β compared to diploids and female α . Histological and ultrastructural analyses revealed great abnormal germ cells present in triploid gonadal follicles. CDC42 has been implicated in processes related to increased DNA damage and genomic instability, while significantly elevated CDC42 expression in triploid gonads compared to the diploids. Inhibition of CDC42 activity in triploids using ZCL278, resulted in a significant reduction in DNA damage, increased oocyte numbers. Transcriptome profiling revealed that CDC42 inhibition upregulated the PI3K-AKT signaling pathway along with DNA repair activation.

Key words: Triploid; *Crassostrea gigas*; CDC42; DNA damage; Oogenesis

日本囊对虾两种头胸甲斑纹类型的 分子机制研究

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摘要: 日本囊对虾(*Marsupenaeus japonicus*)隶属甲壳纲、十足目、对虾科, 俗称斑节虾、竹节虾、花虾, 是我国对虾养殖的重要的经济品种。日本囊对虾有两种外观表型, 差异主要体现在头胸甲的斑纹上, 然而我们对其头胸甲斑纹形成的分子机制尚不清楚。类型 I 群体主要分布于我国南海北部、东海和日本海域, 类型 II 分布于我国南海、东南亚和澳大利亚海域。本研究首先检测了虾甲壳中的虾青素含量, 用显微镜观察了虾表皮色素细胞的组成, 通过转录组测序分析两种虾的差异 mRNA 和 miRNA, 并从中筛选出了一些可能与体色相关的基因, 包括 CRCN-A2、CRCN-C1 和 Apo-D 等, 这些差异基因的氨基酸组成和二级结构存在显著差异, 并对这些基因的功能进行了深入研究; 同时鉴别到了 18 个差异 miRNA, 其中 14 个上调, 4 个下调。研究结果有助于阐明日本囊对虾体色形成的分子机制, 旨在为探索甲壳动物的体色和花纹形成提供参考。

关键词: 日本囊对虾; 体色; 差异表达基因; 转录组测序

Molecular Mechanisms of Two Types of Head and Chest Armor Patterns in *Marsupenaeus japonicus*

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Abstract: The Japanese shrimp (*Marsupenaeus japonicus*) belongs to the Crustacea, Decapoda, and Penidae families, commonly known as spotted shrimp, bamboo shrimp, and flower shrimp. It is an important economic variety in shrimp farming in China. There are two appearance phenotypes of Japanese shrimp, mainly reflected in the markings of their head and chest armor. However, the molecular mechanism of the formation of these markings is still unclear. Type I population is mainly distributed in the northern South China Sea, East China Sea, and Japanese waters, while Type II is distributed in the South China Sea, Southeast Asia, and Australian waters. This study first detected the astaxanthin content in shrimp shells, observed the composition of shrimp epidermal pigment cells under a microscope, analyzed the differential mRNA and miRNA between the two shrimp species through transcriptome sequencing, and screened out some genes that may be related to body color, including CRCN-A2, CRCN-C1, Apo-D, etc. The amino acid composition and secondary structure of these differential genes showed significant dif

Key words: *Marsupenaeus japonicus*; Body color; Differentially expressed genes; Transcriptome sequencing

基于几何形态测量学的秋刀鱼雌雄个体 形态差异分析和鉴定

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摘要: 秋刀鱼(*Cololabis saira*)是西北太平洋海域的重要渔业资源。为了研究其雌雄间的形态差异并开发性别鉴定新方法,本研究基于2022年5月至11月期间从该区域收集的150尾样本,采用几何形态测量学中的地标点法进行分析,并通过判别分析构建了性别鉴别模型。样本分为两组:一组包含107尾用于建立模型;另一组43尾用于测试模型实际应用。结果显示:(1)在相对扭曲主成分分析中,第1和第2主成分分别解释了63.43%和11.79%的总变异,表明降维以及区分效果均较好,其中I型和II型地标点对性别区分较为重要,累积贡献率分别为57.94%和41.83%,而III型地标点的作用较小。(2)薄板样条分析显示,性别间的主要形态差异出现在眼部、躯干前部及尾部。(3)利用第一组数据建立的模型在判别分析与交叉验证中达到91.6%和88.8%的准确率,应用于第二组时也达到了88.45%的准确度。

关键词: 秋刀鱼;几何形态测量学;地标点;雌雄鉴定

Analysis of morphological differences and discrimination between female and male Pacific saury based on Geometric Morphometrics

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Abstract: Pacific saury (*Cololabis saira*) is an important fishery resource in the Northwest Pacific Ocean. To study morphological differences between sexes and to develop a new method for sex identification, this research analyzed 150 samples collected from the region between May and November 2022 using geometric morphometrics with landmark point analysis, and constructed a sex identification model through discriminant analysis. The samples were divided into two groups: one group of 107 individuals was used to build the model, while another group of 43 individuals was used to test the practical application of the model. The results showed that:(1) In the relative warps principal component analysis, the first and second principal components explained 63.43% and 11.79% of the total variation, respectively, indicating good dimensionality reduction and differentiation effects. Type I and Type II landmarks were more significant for sex differentiation, with cumulative contribution rates of 57.94% and 41.83%, respectively, whereas the role of Type III landmarks was minor.

Key words:: Pacific saury;Geometric Morphometrics;Landmark;sex differentiation

基于线粒体细胞色素 b 基因的银鲳六个野生群体遗传特征研究

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摘要: 银鲳 (*Pampus argenteus*) 是我国重要的经济海水鱼类, 但过度捕捞导致其野生资源减少。本研究利用线粒体细胞色素 b (Cytb) 基因标记, 对我国黄海、东海及南海的 6 个银鲳野生群体进行了遗传多样性和遗传分化分析。研究结果显示, 银鲳群体总体遗传多样性指数为 0.611, 核苷酸多样性为 0.07026, 表明银鲳具有较好的遗传多样性。然而, 部分群体如如东、象山、台州、海口和广西的遗传多样性较低, 暗示可能存在近亲繁殖问题。遗传分化分析表明, 黄海和东海的银鲳群体与南海群体之间的遗传距离在 0.18856~0.19217 之间, FST 值为 0.99106, 表明存在显著的遗传分化, 这可能与地理隔离有关。此外, 研究发现霞浦群体可能经历过历史扩张, 而其他群体则相对稳定。本研究为银鲳的资源保护和人工繁殖提供了重要的遗传学依据。

关键词: 遗传距离, 群体, 扩张, Cytb;

Genetic Characteristics of Six Wild Populations of Silver Pomfret (*Pampus argenteus*) Based on Cytb Gene

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Abstract: *Pampus argenteus* is an important economic marine fish in China; however, overfishing has led to a decline in its wild resources. This study utilized the mitochondrial cytochrome b (Cytb) gene marker to analyze the genetic diversity and differentiation of six wild populations of *P. argenteus* in the Yellow Sea, East China Sea, and South China Sea of China. The results revealed an overall genetic diversity index of 0.611 and nucleotide diversity of 0.07026 for *P. argenteus*, indicating good genetic diversity. However, some populations such as Rudong, Xiangshan, Taizhou, Haikou, and Guangxi showed lower genetic diversity, suggesting possible inbreeding issues. Genetic differentiation analysis indicated a genetic distance of 0.18856~0.19217 and an FST value of 0.99106* between the Yellow Sea and East China Sea populations and those from the South China Sea, demonstrating significant genetic differentiation, likely related to geographical isolation. Additionally, the study found that the Xiapu population may have experienced historical expansion, while other populations remained relatively

Key words: Genetic distance, population, expansion, Cytb

控制光周期对中间球海胆生长和性腺发育的影响

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摘要: 提高海胆养殖过程中的性腺产量是非常重要的。本文研究了中间球海胆在 5 种不同的光周期（光暗比为 0L: 24D、8L:16D、12L:12D、16L:8D、24L:0D）下照射一年多的体重生长和性腺发育情况。结果表明：一天中光照时间越多，海胆壳径越小、体重越低。0L 完全黑暗条件下海胆生长更快，表现出更大的壳径和体重，但是性腺重量却没有优势，至实验结束时，16L 组性腺重最大（ $6.90\pm 0.63\text{g}$ ），性腺指数最高（ $12.77\pm 0.85\%$ ）。性腺分析表明，在黑暗条件下海胆性腺红度值和黄度值低于其他光照条件下，而亮度值却没有显著差异（ $P > 0.05$ ），与标准色相比，没有光照射的海胆色差较大，外观颜色偏白色暗淡。性腺组织学显示光照时间越长，海胆性腺出现成熟期的比例越大。本研究结果可为陆地海胆养殖提高产量提供新的参考。

关键词: 中间球海胆；光周期；生长；性腺发育

Effects of manipulate photoperiod on growth and gonadal development of sea urchin *Strongylocentrotus intermedius*

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Abstract: This paper presents a study of the body weight growth and gonadal development of the sea urchin *Strongylocentrotus intermedius* under five different photoperiod regimes: 0 h light:24 h dark (0L), 8 h light:16 h dark (8L), 12 h light:12 h dark (12L), 16 h light:8 h dark (16L), 24 h light:0 h dark (24L) for more than one year were studied. The results show that increased light exposure duration reduces test diameter and body weight in sea urchins. The sea urchin exhibited accelerated growth under 0L dark conditions, displaying larger test diameter and body weight. However, no discernible advantage was observed in gonad weight. After the experiment, the gonad weight ($6.90\pm 0.63\text{g}$) of the 16L group was the greatest and the gonad index ($12.77\pm 0.85\%$) was the highest. The results of the gonadal histology demonstrated that the proportion of mature gonads in sea urchins increased with prolonged exposure time. The results obtained can serve as a valuable reference point for the improvement of sea urchins cultivation yields.

Key words: *Strongylocentrotus intermedius*; photoperiod; growth; gonadal development

河川沙塘鳢的两性异形及繁殖期与非繁殖期种群形态差异

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摘要: 河川沙塘鳢 (*Odontobutis potamophilus*) 为东亚特有小型淡水底栖肉食性鱼类。近年来, 已发展成为一个非常具有潜力的水产养殖品种。本研究利用传统形态性状测量及框架性状分析方法研究了江苏省河川沙塘鳢的两性异形及繁殖期与非繁殖期种群形态差异。结果显示, 在两性特征中, 河川沙塘鳢个体大小异形表现明显, 两性异形指数为-0.013, 表明雄鱼大于雌鱼。雄性在尾柄高、尾鳍长等方面显著大于雌性, 以此来增加竞争能力以及对后代的保护能力。雌性个体具有较大的腹腔容量, 增加了繁殖输出, 提高繁殖适合度。另外, 河川沙塘鳢存在形态特征的季节差异, 生活史不同时期物质和能量分配不同, 繁殖期会投入更多的能量用于繁殖, 而非繁殖期则是将更多能量用于与繁殖无直接关系的器官的生长。繁殖期个体拥有相对较大的眼径、眼间距, 推测与食物资源的季节性变化有关; 背鳍前距和胸鳍基长较长, 可能因性腺发育饱满导致该时期个体腹腔容积变大。

关键词: 河川沙塘鳢, 两性异形, 繁殖期与非繁殖期, 形态差异

Sex dimorphism of *Odontobutis potamophilus* and morphological difference during reproduction and non-reproduction period

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Abstract: *Odontobutis potamophila* is a demersal piscivore endemic to East Asia, was selected as a potential aquaculture target. Sex dimorphism of *O.potamophilus* and morphological difference during reproduction and non-reproduction period were investigated using traditional morphological character measurement and truss method. The results showed the sexual dimorphism index was -0.013, indicating a significant sexual dimorphism in body size. Males have larger caudal peduncle depth and caudal fin length than females, which could be advantageous in competition for spouses and protection of offspring. Females increase individual fecundity by increasing the capacity of abdominal cavity. Furthermore, results indicated that a distinct seasonal variation occurred in *O.potamophilus*. Individuals had larger eye diameter and interorbital width during reproduction period, which might be related to food resource availability. Individuals also had larger pre-dorsal length and pectoral fin base length, likely associated with the increasing capacity of abdominal cavity as a result of gonadal maturity.

Key words: *Odontobutis potamophilus*; sex dimorphism; reproduction and non-reproduction period; morphological difference;

Wnt 信号通路调控长牡蛎黑色素形成分子机制

闵悦

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摘要: 长牡蛎 (*Crassostrea gigas*) 是全球分布最广、产量最大的海洋贝类, 其壳色对市场价值和育种选择具有重要影响。黑色素合成的分子机制是贝类壳色研究的重点。本研究基于壳黑和壳白长牡蛎外套膜转录组数据, 鉴定了 CgWnt1 和 CgWnt2b-a 基因, 发现其在壳黑外套膜外褶区域高表达。RNA 干扰和抑制实验表明, 抑制 Wnt 信号通路会削弱黑色素生成, 降低酪氨酸酶活性, 并导致黑色素小体沉积异常。此外, 研究显示 CgMITF 通过其 bHLH 结构域与转录辅助因子 p300 协同作用, 激活下游靶基因转录。CgMITF 的 bHLH 结构域在物种间高度保守, 且含有关键赖氨酸残基 K6 和 K43, 能够与下游靶基因的 E-box 基序相互作用, 激活基因表达。结果表明, Wnt/ β -catenin 信号通路通过 MITF 调控黑色素合成, 揭示了长牡蛎中黑色素生成的关键机制。

关键词: Wnt/ β -catenin, MITF, 黑色素, 长牡蛎

Wnt/ β -catenin pathway mediates melanogenesis process in the *Crassostrea gigas*

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Abstract: The Pacific oyster (*Crassostrea gigas*) is a widely distributed marine bivalve, with shell color being a key trait influencing market value and breeding. This study focused on the molecular mechanisms of melanin synthesis. We identified CgWnt1 and CgWnt2b-a from the transcriptomes of black- and white-shelled oysters, showing higher expression in the outer fold of black mantle tissues. RNA interference and inhibitor experiments demonstrated that Wnt pathway inhibition reduces melanin production, lowers tyrosinase activity, and leads to uneven melanosome deposition. Further research revealed that CgMITF, through its conserved bHLH domain, works with transcriptional cofactor p300 to activate downstream gene transcription. The CgMITF-bHLH domain is highly conserved across species and includes key lysine residues (K6, K43), which interact with the E-box motif of target genes to promote transcription. These findings suggest that the Wnt/ β -catenin pathway regulates MITF and melanin synthesis in *Crassostrea gigas*.

Key words: Wnt/ β -catenin, MITF, melanin, *Crassostrea gigas*

大黄鱼耐低氧性状的全基因组选择育种研究

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摘要: 大黄鱼是我国养殖产量最高的海水鱼类, 产业经济价值巨大。然而, 低氧胁迫在养殖过程中频繁发生, 给大黄鱼养殖业带来了严重损失。鉴于此, 本研究利用全基因组选择的方法, 进行大黄鱼耐低氧品系选育的初步探究。利用 SNP 芯片和 dd-RAD 两种基因分型方法分别进行大黄鱼耐低氧性状的全基因组选择育种, 基于不同参数对基因组预测准确性的探究结果显示, 对于 SNP 芯片, GBLUP 是最佳的 GS 模型, 而基于 GWAS 策略选出的 2,500 个 SNP 与全部 38,472 个 SNP 的基因组预测准确性基本接近; 对于 dd-RAD, Bayes B 是最佳的 GS 模型, 而选择全部 17,934 个 SNP 时基因组预测准确性最高。基于建立的最佳 GS 策略, 分别对相应的候选群体进行耐低氧育种值估计和繁育, 与对照组相比, 子代的半致死溶氧浓度分别降低了 6.43% 和 13.45%。这表明, 对于大黄鱼耐低氧性状的选育, GS 是一种有效的选育方法。

关键词: 大黄鱼; 低氧; 基因组育种; 遗传力

Genomic selection for hypoxia tolerance in large yellow croaker

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Abstract: Two genotyping methods, SNP-chips and dd-RAD, were utilized for breeding *L. crocea* for hypoxia tolerance trait by GS, respectively. The results of the exploration of genome prediction accuracy based on different parameters showed that, for SNP-chips, GBLUP was the best GS model, and the genome prediction accuracy of 2,500 SNPs selected based on the GWAS strategy was basically close to that of all 38,472 SNPs; for dd-RAD, the accuracy of genome prediction was basically close to that of the whole genome selection method. accuracy was basically close; for dd-RAD, Bayes B was the best GS model, while the genomic prediction accuracy was highest when all 17,934 SNPs were selected. Based on the established optimal GS strategy, the hypoxia-tolerant breeding values were estimated and bred for the corresponding candidate populations, respectively, and median lethal concentration of the offspring were reduced by 6.43% and 13.45%, respectively, compared with the control group. This suggests that GS is an effective selection method for the hypoxia tolerance trait in *L. crocea*.

Key words: *Larimichthys crocea*; Hypoxia; Genomic selection; Heritability

中华绒螯蟹性别发育研究进展

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摘要: 本课题组筛选出河蟹性别特异性分子标记, 解决了发育早期的性别鉴定问题。将该标记应用于早期发育阶段的性别研究中, 如雄性激素 IAG 及其转录因子 iDMY 基因的幼体和卵裂期胚胎的雌雄差异表达。不同的遗传材料对解析和揭示遗传发育机制起到不可替代的作用。本课题组利用同时具有促雄腺和卵巢的间性蟹材料开展了性别关键基因和转录组学的研究。经性别特异性分子标记检测, 所用样品为遗传雌性。对眼柄、卵巢、促雄腺转录组数据的分析揭示, 与正常雌蟹和雄蟹相比, 间性蟹眼柄中乙酰胆碱受体的表达显著上调, 雌性激素 CFSH 显著下调而 IAG 略有上调; 乙酰化过程中的组蛋白发生显著变化, 提示间性蟹的形成与组蛋白的乙酰化关联。对河蟹性别关键基因的进一步分析显示, 发育至溞状幼体 IV 期后, 雄性个体中 IAG 的表达量快速增加, CFSH 表达量急剧下降; 雌性个体则相反。上述研究结果为深入解析中华绒螯蟹性别发育机制、从而建立性别调控技术提供重要参考。

关键词: 特异性分子标记; 关键基因; 间性蟹; 中华绒螯蟹; 性别发育

Research progress on sex development of *Eriocheir sinensis*

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Abstract: We identified sex-specific molecular markers in Chinese mitten crabs to improve sex identification during early development. These markers facilitated the analysis of differential expression of the male hormone IAG and its transcription factor iDMY in larvae and cleavage-stage embryos. Using intersex crabs, which exhibit both masculinizing and ovarian traits, we studied key sex genes and transcriptomics. Molecular marker confirmed that they are genetically female. Transcriptomic analysis showed that in intersex crabs, acetylcholine receptor expression was significantly upregulated in the eyestalks, while CFSH was downregulated and IAG slightly upregulated. Significant changes in histone acetylation were also observed, linking it to intersex development. After reaching the IV nauplius stage, IAG expression increased rapidly in males while CFSH expression sharply decreased; the pattern was reversed in female individuals. These findings enhance our understanding of sex development mechanisms in Chinese mitten crabs and support the establishment of sex regulation techniques.

Key words: Sex molecular markers; Key genes; Intersex crab; *Eriocheir sinensis*; Sex development

基于罗氏沼虾全长转录本和基因组序列 鉴定嗅觉基因家族

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摘要: 嗅觉基因家族包括气味结合蛋白 (OBPs)、化学感觉蛋白 (CSPs)、嗅觉受体 (ORs)、离子受体 (IRs) 和味觉受体 (GRs)。本研究对罗氏沼虾进行 PacBio 测序获得 38,955 个全长转录本, N50 为 3383 bp。通过对全长转录本和全基因组序列的注释, 发现 18 个 MrORs、16 个 MrIRs、151 个 MrIGluRs (离子型谷氨酸受体)、2 个 MrVIGluRs (变异型离子型谷氨酸受体) 和 3 个 MrCRs (化学感受受体)。CRs 是最早在虾类中发现的。利用日本沼虾现有的全基因组序列, 发现 4 个 MnORs、21 个 MnIRs、79 个 MnIGluRs、5 个 MnVIGluRs、1 个 MnGR 和 1 个 MnOBP。通过扫描显微镜发现罗氏沼虾第一触角存在羽状刚毛 (PS)、硬刺刚毛 (HTS)、竹笋刚毛 (BSS)、软刺刚毛 (STS) 和化感刚毛 (AE), 第二触角存在 HTS 和 BSS, 步足存在 PS。

关键词: 罗氏沼虾; 全长转录本; 嗅觉受体; 离子型受体; 离子型谷氨酸受体

Identification and characterization of olfactory gene families in *Macrobrachium rosenbergii* based on full-length transcripts and genome sequences

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Abstract: The olfactory gene families include odorant binding proteins (OBPs), chemosensory proteins (CSPs), olfactory receptors (ORs), ionotropic receptors (IRs) and gustatory receptors (GRs). A total of 38,955 full-length transcripts with an N50 length of 3383 bp were obtained through PacBio sequencing in *Macrobrachium rosenbergii*. Through the annotation of full-length transcripts and whole-genome sequences, 18 MrORs, 16 MrIRs, 151 MrIGluRs (ionotropic glutamate receptors), 2 MrVIGluRs (variant ionotropic glutamate receptors) and 3 MrCRs (chemosensory receptors) were identified. The CRs were first identified in prawns and shrimps. The olfactory gene families in *M. nipponense* were identified, comprising 4 MnORs, 21 MnIRs, 79 MnIGluRs, 5 MnVIGluRs, 1 MnGR and 1 MnOBP, using the available whole-genome sequences. Meanwhile, the presence of plumose setae (PS), hard thorn setae (HTS), bamboo shoot setae (BSS), soft thorn setae (STS) and aesthetascs (AE) on the antennules, HTS and BSS on the second antennae, and PS on the pereopods of *M. rosenbergii* were observed by scanning electron microscope.

Key words: *Macrobrachium rosenbergii*; Full-length transcripts; Olfactory receptor; Ionotropic receptor; Ionotropic glutamate receptor

虹鳟肝脏响应运输胁迫的转录组学分析

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摘要: 为探究虹鳟响应运输胁迫的生理机制, 本研究以虹鳟为研究对象, 通过模拟活鱼运输, 进行了运输胁迫试验, 之后分别采集对照组(运输 0 h 组) 和处理组(运输 8 h 组) 虹鳟肝脏组织进行转录组分析。差异表达基因 (DEGs) 分析结果显示, 与对照组相比, 处理组共鉴定出 4389 个 DEGs, 其中上调 2526 个, 下调 1863 个。GO 功能注释结果表明, DEGs 主要与转移酶活动、催化活动等分子功能相关, 主要富集在细胞代谢过程、胞内受体信号通路等生物学过程条目。KEGG 富集分析发现, DEGs 显著富集在能量代谢和免疫相关通路中。为了验证转录组数据的可靠性, 利用 qRT-PCR 技术检测相关通路中 7 个候选基因的表达量变化情况, 其结果与转录组结果一致。

关键词: 虹鳟; 转录组; 运输胁迫; 糖脂代谢; 细胞凋亡

Transcriptomic Analysis of Rainbow Trout Liver Response to Transport Stress

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Abstract: To explore the physiological mechanism of rainbow trout response to transportation stress,, a transport stress test was conducted by simulating the transport of live fish in this study. Afterwards, liver tissue samples of rainbow trout were collected from the control group (transported for 0 h) and the treatment group (transported for 8 h) for transcriptome analysis. A total of 4389 differentially DEGs were identified between the two groups, of which 2526 DEGs were upregulated and 1863 DEGs were downregulated. GO enrichment revealed that DEGs were mainly associated with transferase activity and catalytic activity, and were significantly enriched in cell metabolism process and intracellular receptor signaling pathways. Based on KEGG enrichment analysis, we found that energy metabolism- and immune-related pathways were markedly enriched by DEGs. In addition, reliability verification of the transcriptome results was performed by qRT-PCR to detect the expression level changes of 7 candidate genes, and the results were consistent with the transcriptome results.

Key words:: Rainbow trout; Transcriptome; Transport stress; Glycolipid metabolism; Apoptosis

南美白对虾新型 CHH-like 基因性别差异 调控功能的研究

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摘要: 甲壳动物高血糖激素(Crustacean hyperglycemic hormone, CHH)家族是一类重要的神经内分泌激素, 在能量代谢、生长蜕皮、发育繁殖等多方面发挥作用。南美白对虾(*Penaeus vannamei*)是重要的养殖虾类且在生长性状中表现出性别二态性。然而, 目前对于 CHH 家族在对虾生长性别二态性形成中的具体功能知之甚少。本研究利用转录组与基因组数据综合分析了南美白对虾中 CHHs 的表达模式, 并鉴定出一个新型 CHH-like 基因。我们通过原位杂交及 qPCR 验证了其时空表达特征, 并开展了体内 RNAi 敲降及重组蛋白处理以揭示 CHH-like 基因在雌雄南美白对虾中的功能作用。研究结果显示南美白对虾 CHH-like 基因具有雄性偏向表达特征且在雌雄个体生长方面发挥相反的作用, 表明 CHH-like 具有性别差异调控功能。本研究为理解南美白对虾生长性别二态性的形成机制提供了新的理解与证据。

关键词: 南美白对虾;CHH;雌雄差异

Sex-biased regulatory functions of a novel CHH-like gene in *Penaeus vannamei*

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Abstract: The crustacean hyperglycemic hormone (CHH) family is a group of neuroendocrine hormones that play important roles in growth, molting and reproduction. *Penaeus vannamei* is the most dominant farmed shrimp and exhibits sexual dimorphism in growth. However, little is known about the function of the CHH family in the formation of sexual dimorphism in shrimp growth. In this study, we first analyzed the expression pattern of CHHs in *P. vannamei* using transcriptomic and genomic data, and identified a novel CHH-like gene. The spatiotemporal expression patterns of CHH-like were verified by in situ hybridization and qPCR. Moreover, in vivo RNAi knockdown and recombinant CHH-like treatments were carried out to analyze the functional roles of CHH-like in both male and female *P. vannamei*. Our results showed that the CHH-like gene of *P. vannamei* is male-biased and plays opposite roles in the growth of males and females, suggesting that CHH-like has a sex-biased regulatory function. This study provides new evidence for the formation of sexual dimorphism in the growth of *P. vannamei*.

Key words: *Penaeus vannamei*;CHH;male-female difference

小黄鱼肝脏响应盐度胁迫的 转录组比较分析

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摘要: 为探究小黄鱼肝脏响应盐度胁迫的分子机制, 对高盐(盐度 35, HS)、低盐(盐度 5, LS) 和正常海水(盐度 25, CS) 处理 6h 后的肝脏进行比较转录组分析。结果显示, 在 HSvs.CS 中共筛选到 DEGs 和差异表达 lncRNA 分别为 1229 和 292 个; LSvs.CS 中筛选到 945 和 184 个; HSvs.LS 中筛选到 745 和 254 个。功能富集分析发现, HSvs.CS 和 LSvs.CS 中的 DEGs 均显著富集于代谢、凋亡及免疫相关通路, 表明盐度胁迫条件下, 小黄鱼肝脏中多个类型通路参与机体调节。比较发现, 相较于低盐度, 高盐下小黄鱼体内的响应过程更多元。此外, HSvs.LS 中 DEGs 与 HSvs.CS 和 LSvs.CS 富集的通路存在不同, 表明小黄鱼响应不同的盐度胁迫机制存在差异。本研究探讨了盐度胁迫条件下, 小黄鱼肝脏在基因水平的响应调节机制, 为解析小黄鱼响应盐度变化的分子机制提供理论支撑。

关键词: 小黄鱼, 肝脏, 盐度胁迫, 转录组, 差异表达基因

Comparative transcriptome analysis of liver response to salinity stress in *Larimichthys polyactis*

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Abstract: To explore the molecular mechanism of liver response to salinity stress in *Larimichthys polyactis*, comparative transcriptome analysis on liver treated with high salt (salinity 35, HS), low salt (salinity 5, LS) and normal seawater (salinity 25, CS) for 6h. Results showed that a total of 1229 DEGs and 292 differentially expressed lncRNAs were detected in HSvs.CS. 945 and 184 were screened in LSvs.CS. 745 and 254 are filtered in HSvs.LS. Functional enrichment analysis showed that DEGs in HSvs.CS and LSvs.CS were significantly enriched in metabolism, apoptosis and immune-related pathways, indicating that several types of pathways in the liver were involved in body regulation under salinity stress. Compared with low salinity, the response processes in high salinity were more diverse. The pathways enriched by DEGs in HSvs.LS were different from those in HSvs.CS and LSvs.CS, indicating that there were differences in the response mechanisms to different salinity stress. This study providing theoretical support for the analysis of the molecular mechanism of *L. polyactis* response to salinity changes.

Key words: *Larimichthys polyactis*, liver, salinity stress, transcriptome, differentially expressed genes

热休克蛋白 20 和血蓝蛋白基因的 复制应答中华绒螯蟹干露胁迫

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摘要: 基因复制是基因组进化的主要驱动力之一, 在提高生物环境适应方面发挥着关键作用。中华绒螯蟹基因组以及干露转录组数据揭示了两类存在基因复制现象并响应干露胁迫的基因家族—热休克蛋白 20 和血蓝蛋白。在中华绒螯蟹基因组中, 共鉴定了 14 个 HSP20 基因和 41 个 HMC 基因。在 HSP20 基因家族中, 存在 1 个假基因; 其余 13 个基因均有不同程度的组织表达并响应干露胁迫。其中, 5 个 HSP20 存在串联重复, 3 个存在近端重复, 不同的重复类型具有不同的表达模式。这 8 个 HSP20 基因的内含子和外显子的数量不同, 其在干露胁迫下鳃中的表达也不同。在 HMC 基因家族中, 39 个 HMC 基因分别位于四条染色体上, 并存在串联重复现象。这些基因内含子和外显子数量的差异, 也伴随着组织分布的不同, 其中的大部分基因 (35 个) 响应了干露胁迫。位于不同染色体上的 HMC 对干露胁迫的响应不同, 转录调控分析揭示了低氧诱导因子在这些 HMC 上的结合位点不同。

关键词: 复制基因; 小热休克蛋白; 血蓝蛋白; 中华绒螯蟹; 干露胁迫

The replications of heat shock protein 20 and hemocyanin resistance to air exposure stress in *Eriocheir sinensis*

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Abstract: Utilizing the genomic data of *Eriocheir sinensis* and the transcriptome data of air exposure stress, it was found that two gene families exhibit gene duplication and respond stress: heat shock protein 20 (HSP20) and hemocyanin (HMC) families. In the genome, 14 HSP20 genes and 41 HMC genes was identified. In HSP20 gene family, 1 gene was identified as a pseudogene. The remaining genes exhibited varying degrees of tissue expression and responded to air exposure stress. Among these, 5 genes contained tandem duplications and 3 genes exhibited proximal duplications, with distinct expression patterns. The number of introns and exons of HSP20 led to differences in the expression under stress. In HMC gene family, 39 genes were located on four chromosomes and formed tandem duplications. The differences in the number of introns and exons in these genes were varied in tissue distribution, with the majority (35 genes) responding to air exposure stress. Variations in the binding sites of hypoxia inducible factor influenced the different responses of different replications to air exposure stress.

Key words: Gene duplication; Small heat shock proteins; Hemocyanin; *Eriocheir sinensis*; Air exposure stress

17- α 甲基睾酮对暗纹东方鲀性别转化的影响

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摘要: 为探究 17 α -甲基睾酮对暗纹东方鲀 (*Takifugu fasciatus*) 性逆转的作用及其潜在的分子机制, 对 11 ~ 150 dph 幼鱼投喂添加 30 mg / kg (MT30) 和 60 mg / kg (MT60) 浓度 MT 的饲料。MT 处理成功生产了雄性群体, 但抑制了性腺指数 (GSI) 和血清性类固醇激素 (T 和 E2) 水平。在转录组分析中, MT30 和 MT60 与 XX 雌性对照的比较中分别鉴定到 3079 和 4051 个差异表达基因。PI3K-Akt 信号通路 (PI3K-Akt signaling pathway) 为 MT 暴露后显著富集通路。从转录组数据中鉴定得 *Foxh1*, 推测其为暗纹东方鲀性逆转相关的潜在关键基因。克隆 *foxh1* 的 cDNA 全长序列。*foxh1* 在肝脏和卵巢中显著高表达, MT 处理后在精巢中表达显著降低。本研究为暗纹东方鲀的单性育种提供了依据。

关键词: 17 α -MT, 暗纹东方鲀, 性逆转, 转录组, *foxh1*

The effect of 17 α -methyltestosterone-induced sex reversal of *Takifugu fasciatus*

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Abstract: This study was aimed to investigate the effect of 17 α -methyltestosterone (MT) induced sex reversal in *Takifugu fasciatus* and its potential molecular mechanism. The fish were fed 30 mg/kg (MT30) and 60 mg/kg (MT60) diets supplemented with MT from 11 to 150 dph. MT treatment was successfully produced all male population but suppressed gonadosomatic index (GSI) and serum sex steroid hormones (T and E2) levels. In the transcriptome analysis, 3,079 and 4,051 differentially expressed genes (DEGs) were identified in the comparison groups of MT30 vs. female control and MT60 vs. female control, respectively. PI3K-Akt signaling pathway was the highly enriched biological pathways after MT exposure. *foxh1* was identified from the transcriptome data and suggested to be the potential critical gene related to sex reversal. The full cDNA of *foxh1* was cloned. *foxh1* was significantly highly expressed in liver and ovary. After MT treatment, the expression of *foxh1* in testis was significantly decreased ($p < 0.05$). This study provides a basis for the mono-sex breeding of *T. fasciatus*.

Key words: 17 α -methyltestosterone; *Takifugu fasciatus*; Sex reversal; Transcriptome; *foxh1*

抑肌素调控鱼类肌肉组织脂肪合成的 机制研究

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摘要: 抑肌素是 TGF β 超家族的一员, 主要在肌肉组织表达, 是肌肉细胞增殖和肌肉生长的负调控因子, 哺乳类和鱼类敲除抑肌素基因促进肌肉组织生长, 前期研究表明, 鱼类敲除抑肌素不仅可以显著增加肌肉细胞增殖, 肌肉组织的脂肪合成和积累也显著增强, 这可能是提升鱼类肌肉品质的新思路和新途径。经检测我们发现, 抑肌素敲除可以显著提高肌肉组织合成代谢信号通路, 餐后 mTOR 信号通路显著增强, 利用 PI3K 抑制剂可以显著抑制肌肉组织 mTOR 信号通路的活性, 在饥饿状态下, 敲除抑肌素显著抑制 mTOR 信号通路活性。敲除抑肌素可以显著提高脂类合成代谢和分解代谢, 敲除抑肌素斑马鱼和鳊鱼的肌肉脂肪含量都显著上升, 肌肉中胰岛素信号通路活性显著上升, 胰岛素、胰岛素受体底物转录水平显著升高; 肌肉对葡萄糖的吸收水平显著增加。胰岛素启动子的开放程度显著变化, 进一步说明了抑肌素敲除可以实现胰岛素异位表达, 从而促进肌肉糖脂转换, 增加肌肉脂肪含量。

关键词: 胰岛素, mTOR 信号, 肌肉组织, 脂类合成, 葡萄糖吸收

The mechanisms of myostatin regulating fat synthesis in fish muscle tissue

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Abstract: Previous studies have shown that myostatin knockout in fish cannot only significantly increase muscle cell proliferation, but also significantly enhance fat synthesis and accumulation. This may be a new approach to improve the quality of fish muscle. We found that myostatin knockout can significantly improve the anabolic signaling pathway of muscle tissue, and the mTOR signaling pathway is significantly enhanced after meals. This suggests that myostatin knockout can significantly enhance the assimilation of nutrients in food by fish. Myostatin knockout can significantly improve lipid anabolism and catabolism, and the muscle fat content of both zebrafish and Mandarin fish after myostatin knockout is significantly increased. Our further detection found that the activity of insulin signaling pathway in muscle is significantly increased. The Chromatin accessibility of insulin promoter changed significantly which further indicated that myostatin knockout could induced insulin ectopic expression, thereby promoting muscle glucose lipid conversion and increasing muscle TG content.

Key words: insulin, mTOR signal, muscle tissue, lipid synthesis, glucose absorption

小黄鱼抗内脏白点病相关功能基因挖掘 与鉴定

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摘要: 小黄鱼作为新兴的海水养殖对象, 内脏白点病问题日益凸显。挖掘抗病相关基因是利用分子育种技术培育抗病新品种的重要前提。本研究利用 GWAS 方法成功挖掘抗病相关 SNP 位点 22 个, 注释相关功能基因 60 个, 主要富集在 Ubiquitin mediated proteolysis, Cytosolic DNA-sensing pathway 等通路; 对抗性组、敏感组和对照组肝脏进行比较转录组分析, 发现大部分差异表达基因显著富集在 Necroptosis, NOD-like receptor signaling pathway 等通路。GWAS 与转录组联合分析发现 *sting1* 是抗病关键基因, 其介导的 NOD-like receptor signaling pathway 的激活可能在小黄鱼抗内脏白点病中起着关键作用。研究结果进一步加深了小黄鱼抗病相关研究, 为小黄鱼抗病良种选育奠定了重要基础。

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

Exploring of candidate genes related to visceral white-nodules disease resistance in *Larimichthys polyactis*

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Abstract: As an emerging marine aquaculture object, visceral white-nodules disease (VWND) problem of *Larimichthys polyactis* has become increasingly prominent. Scanning disease-resistance related genes is a vital prerequisite for breeding new disease-resistance varieties using molecular breeding techniques. In this study, we successfully excavated 22 disease-resistance related SNPs by GWAS, and annotated 60 functional related genes, which were mainly enriched in Ubiquitin mediated proteolysis, Cytosolic DNA-sensing pathway. Based on transcriptome analysis of the livers of the resistant, sensitive and control groups, we found most of the differentially expressed genes (DEGs) were significantly enriched in pathways of Necroptosis, and NOD-like receptor signaling pathway. The integration of GWAS and transcriptome analysis revealed that *sting1* is a key gene for disease resistance, and the activation of *sting1*-mediated NOD-like receptor signaling pathway may play a crucial role in VWND resistance of *L. polyactis*. The results further deepen the research on disease resistance of *L. polyactis*.

Key words: *Larimichthys polyactis*, Visceral white-nodules disease, GWAS, Transcriptome, *sting1*

低氧诱导因子 (HIF-1 α) 通过 NF- κ B 调控中华绒螯蟹在低氧胁迫下的免疫应答反应

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摘要: 氧是生物赖以生存的首要条件, 缺氧严重影响水产甲壳动物的免疫防御能力。低氧诱导因子 (HIF-1 α) 是参与缺氧反应的重要因子, 具有免疫调节功能, 但其是否参与调控甲壳动物低氧胁迫下的免疫应答尚不清楚。本研究对处于低氧胁迫下的中华绒螯蟹进行嗜水气单胞菌刺激, 结果显示, 菌刺激后 HIF-1 α 和抗脂多糖因子 (ALFs) 的表达量均显著降低。此外, 在低氧胁迫下抑制或激活 HIF-1 α 后再进行病原刺激, 发现抑制 HIF-1 α 显著下调 ALFs 的表达, 而激活 HIF-1 α 则显著上调 ALFs 的表达。进一步研究发现, HIF-1 α 正向调控 Relish 表达量及 NF- κ B 的磷酸化水平, 且血淋巴的细菌清除能力在 HIF-1 α 激活组显著强于抑制组和对照组。综上所述, 在低氧胁迫下, 病原菌抑制 HIF-1 α 和 ALFs 的表达量, HIF-1 α 能够通过 NF- κ B 正向调控 ALFs 的表达。本研究为探究甲壳动物在低氧胁迫下的免疫应答机制提供依据。

关键词: 低氧诱导因子(HIF-1 α); 抗脂多糖因子; 低氧胁迫; 免疫应答; 中华绒螯蟹

Hypoxia-inducible factor-1 α (HIF-1 α) regulates the immune response via NF- κ B under hypoxia stress in Chinese mitten crab (*Eriocheir sinensis*)

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Abstract: Oxygen is vital for organism survival. Hypoxia impairs the immune defense of aquatic crustaceans. Hypoxia-inducible factor-1 α (HIF-1 α) is crucial in the hypoxia response with immunomodulatory function. This study investigates its role in the immune response of *Eriocheir sinensis* under hypoxic conditions (DO<2 mg/L) followed by *Aeromonas hydrophila* injection. Results revealed significant reductions in the expression levels of HIF-1 α and anti-lipopolysaccharide factors (ALFs) in hemolymph. Inhibition of HIF-1 α under hypoxia stress led to down-regulated ALFs expression, while activation resulted in up-regulation. HIF-1 α also positively regulated Relish expression and NF- κ B phosphorylation. The bacterial clearance ability of hemolymph in HIF-1 α activation group was significantly higher than that in HIF-1 α inhibition and hypoxia groups. Thus, under hypoxia stress and pathogen stimulation, the expression levels of HIF-1 α and ALFs decreased significantly, and HIF-1 α regulated the expression of ALFs via NF- κ B, contributing to understanding crustacean immune responses under hypoxia stress.

Key words: HIF-1 α ; Anti-lipopolysaccharide factors; Hypoxia stress; Immune response; *Eriocheir sinensis*

大口黑鲈肝脏线粒体功能和 Ca^{2+} 交换对急性缺氧的生理反应

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摘要: 氧对水生动物来说是一个关键因素。高密度水产养殖和环境退化将不可避免地导致大口黑鲈(*Micropterus salmoides*)等鱼类的缺氧应激。本研究旨在研究缺氧条件下大口黑鲈线粒体功能和 Ca^{2+} 交换以确定其对缺氧的反应。对大口黑鲈进行缺氧($1.2 \pm 0.2 \text{ mg/L}$)处理 24 h, 分析其肝脏线粒体和内质网(ER)参数。缺氧条件下, 观察了大口黑鲈原代肝细胞 Ca^{2+} 浓度的变化。结果表明, 缺氧下自噬增强伴随活性氧(ROS)的生成和电子传递链(ETC)活性发生改变。其次, 缺氧增强了缺氧应激早期(8 h 前)线粒体的融合、裂变及生物合成和 ER 质量控制。第三, 缺氧调节了三羧酸(tricarboxylic acid, TCA)循环通量, 导致 TCA 中间代谢物(柠檬酸和氧戊二酸)的积累。此外, 观察到内质网 Ca^{2+} 外排。 Ca^{2+} 转运体基因表达显著变化。这些结果为缺氧条件下大口黑鲈的生理和代谢变化提供了新的见解。

关键词: 大口黑鲈; 低氧暴露; 线粒体; 内质网; Ca^{2+} 稳态

Physiological responses to acute hypoxia in the liver of largemouth bass by alteration of mitochondrial function and Ca^{2+} exchange

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Abstract: Oxygen is a critical factor for aquatic organisms. High-density aquaculture and environmental degradation can induce hypoxic stress in fish species, such as the largemouth bass. This study aims to investigate the response of mitochondrial function and Ca^{2+} exchange in largemouth bass under hypoxic conditions. Following 24 hours of hypoxic exposure, we analyzed the parameters of liver mitochondria and endoplasmic reticulum in largemouth bass. We observed changes in intracellular Ca^{2+} concentration within primary liver cells of largemouth bass subjected to hypoxia. The results indicate enhanced autophagy along with alterations in reactive oxygen species generation and electron transport chain activity during hypoxia. Additionally, hypoxia promotes early-stage mitochondrial fusion, fission, biosynthesis, and endoplasmic reticulum quality control processes. Furthermore, it regulates the tricarboxylic acid cycle, resulting in the accumulation of intermediate metabolites. Notably, we also observed changes in ER Ca^{2+} efflux and gene expression related to Ca^{2+} transporters.

Key words: Largemouth bass; Hypoxia exposure; Mitochondria; ER; Ca^{2+} homeostasis

大黄鱼伪雌鱼诱导技术优化及超雄鱼培育

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摘要: 3. 雄性大黄鱼因体型修长受青睐, 具有生产优势, 全雄苗种是高品质养殖的迫切需求。性逆转伪雌鱼和培育超雄鱼是大黄鱼 XY 型性别决定系统中建立全雄性种群的常规方法。本研究在 45-125 日龄间投喂含不同浓度 (0、0.2、1 和 5 mg/kg) E2 的饲料诱导伪雌鱼, 并分析了生长、存活、抗氧化能力、性腺发育和性别基因表达。结果显示, E2 会抑制生长, 降低存活率, 提高抗氧化酶活性, 且 5 mg/kg E2 组生长和存活率显著低于其他组。处理组性别逆转率分别是 67%, 100% 和 100%, 所以 1 mg/kg E2 为本研究最佳诱导剂量。6 月龄伪雌鱼卵巢组织形态学与对照组无差异, 而 9 月龄后卵巢发育滞后。伪雌鱼同雌鱼仅表达雌性特异性基因 *cyp19a1a*, 不表达雄性特异性基因 *dmrt1*。通过分子鉴定和组织学观察, 证实了伪雌鱼与雄鱼交配能产生超雄鱼。本研究建立了诱导大黄鱼伪雌鱼和培育超雄鱼的有效方法, 为全雄大黄鱼生产奠定了基础。

关键词: 大黄鱼; 性逆转; 伪雌鱼; 超雄鱼

Optimization of neo-female induction technology and breeding of super-male fish in large yellow croaker (*Larimichthys crocea*)

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Abstract: Male large yellow croaker, favored for their slender build, can improve breeding economic benefits with all-male cultivation. Sex reversal to produce neo-female and supermale fish is method for all-male populations within the XY sex system. The study induced neo-female fish by feeding diets with E2 concentrations (0, 0.2, 1, 5 mg/kg) to large yellow croaker. E2 was found to inhibit growth, lower survival, and boost antioxidant enzyme activity, showing a dose-dependent effect. Sex reversal rates were 67%, 100%, and 100% in respective treatment groups, making 1 mg/kg E2 the best induction dose. At six months, neo-female fish ovaries were histologically similar to controls, but development lagged after nine months. These fish, like females, expressed only the female gene *cyp19a1a*, not the male gene *dmrt1*. Molecular and histological confirmation showed neo-female fish could produce supermales when mated with males. The study established effective methods for inducing neo-female and cultivating supermale large yellow croaker, supporting all-male production with theory and tech know-how.

Key words: Large Yellow Croaker; Sex Reversal; Neo-Female Fish; Supermale Fish

绒螯蟹的杂交和物种形成的基因组学见解

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摘要: 杂交是一种常见的自然现象, 对适应性演化、物种分布和生物多样性具有重要的影响。然而, 杂交如何影响基因组结构并促进适应性演化的遗传基础仍然没有充分解析。本研究通过分析来自不同地理区域的7个绒螯蟹种群的全基因组数据, 揭示中国和日本绒螯蟹之间存在复杂的杂交历史, 并且两者的杂交产生了两个不同的生态种群: 合浦和俄罗斯绒螯蟹, 它们具有独特的基因组结构和生态适应性。与繁殖、发育和温度适应相关的基因表现出强烈的选择信号, 可能有助于它们的表型多样性塑造和生态适应。同时, 与繁殖相关的基因, 如 *Birc6*、*Bap31* 和 *Poxn*, 在合浦绒螯蟹中显示出强烈的选择清除信号。此外, 研究结果证实合浦绒螯蟹是一种同倍体体杂交物种, 起源于一个古老的杂交事件, 解决了关于其长期的分类争议。本研究揭示了绒螯蟹的演化历史, 并强调了杂交在推动物种适应性、范围扩张和物种多样性方面的关键作用。

关键词: 杂交, 生殖隔离, 生态分布, 适应性演化

Genomic Insights into Hybridization and Speciation of Mitten Crabs in the *Eriocheir* Genus

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Abstract: Hybridization is a prominent and influential phenomenon with significant implications for adaptive evolution, species distribution and biodiversity. However, the intricacies of how hybridization influences genomic structure and facilitates adaptive evolution still elude our full understanding. Analyzing whole genome data from seven *Eriocheir* genus populations across diverse regions, we have validated a complex hybridization history between Chinese and Japanese mitten crabs. This hybridization gave rise to two distinct ecological species: Hepu and Russian mitten crabs with unique genomic architectures and adaptations. Genes related to reproduction, development, and temperature adaptation exhibit strong selection signals, potentially contributing to their phenotypic diversity and ecological niches. Genes associated with reproduction, namely *Birc6*, *Bap31*, and *Poxn*, displayed evidence of selective sweeps in Hepu mitten crabs. Furthermore, Hepu mitten crab is a homoploid hybrid species that originated from an ancient hybridization event, resolving its longstanding taxonomic controversy.

Key words: Hybrid speciation; Reproductive isolation; Ecological distribution; Adaptative radiation

非编码 RNA 参与虹鳟热应激的 ceRNA 调控机制作用研究

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摘要: 虹鳟是一种典型的冷水性鱼类, 夏季高温是其养殖过程中的最大威胁。研究发现非编码 RNA 介导的竞争性内源 RNA (ceRNA) 调控可能是虹鳟应对热刺激和增强适应性的主要策略。在本研究中我们发现将外源性 novel-m0007-5p mimics 和 inhibitor 转染至原代虹鳟肝细胞, 可靶向结合并抑制靶基因 hsp90ab1 和 LOC110485411, 且对肝细胞活力、增殖和凋亡无显著影响。novel-m0007-5p 过表达对热应激条件下 hsp90ab1 和 LOC110485411 的抑制作用具有时效性。同样, siRNA 通过沉默 LOC110485411 的表达来影响 hsp90ab1 的表达。在虹鳟中, LOC110485411 和 hsp90ab1 可通过“海绵吸附”与 novel-m0007-5p 竞争性结合, 干扰 LOC110485411 可影响 hsp90ab1 的表达。这些结果为虹鳟抗应激药物的筛选提供了可能。

关键词: 虹鳟, 热应激, ceRNA, 非编码 RNA, 调控机制

Role of non-coding RNAs involved in the ceRNA regulatory mechanism of heat stress in rainbow trout (*Oncorhynchus mykiss*)

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Abstract: Rainbow trout (*Oncorhynchus mykiss*) is a typical cold-water fish species. With the advent of global warming and an increase in extreme high-temperature events, summer heat poses the greatest threat to rainbow trout aquaculture. In response to thermal stress, rainbow trout initiate stress defense mechanisms, and it has been suggested that non-coding RNA (miRNAs, lncRNAs)-mediated competitive endogenous RNA (ceRNA) regulation of target genes (mRNAs) may be a primary strategy for coping with thermal stress and enhancing adaptability in this species. In this study, we employed high-throughput sequencing to identify the LOC110485411-novel-m0007-5p-hsp90ab1 ceRNA interaction network that influences thermal stress in rainbow trout, and we validated their targeting relationships and functions. These findings provide a basis for the screening of stress-resistance drugs in rainbow trout.

Key words: Rainbow trout, heat stress, ceRNA, non-coding RNA, regulatory mechanism

中国鲟鱼产业化发展：从规模化苗种繁育到育种平台应用

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摘要: 鲟鱼是全球化的养殖鱼类, 在世界四十多个国家都有养殖历史。鲟鱼养殖已有 150 余年的发展历程, 中国的商品化鲟鱼养殖始于上世纪 90 年代中期, 并在短时间内取得了快速发展。根据 2009 年 FAO 的统计数据, 中国的鲟鱼养殖产量已占全球总产量的 80%。目前, 我国的鲟鱼苗种已经实现了全年四季“订单式”生产。在实现鲟鱼规模化人工繁殖的技术突破后, 产业重点逐渐从苗种数量扩展到质量提升。为此, 陆续建立了包括杂交育种、家系选育、雌核发育、性逆转诱导、基因编辑和全基因组选择等在内的多种育种技术, 培育出了通过全国水产原良种审定的新品种“鲟龙 1 号”和“京龙 1 号”。根据 CITES 对鲟鱼贸易种质背景的要求, 相关分子标记也已被开发用于鲟鱼种质鉴定。此外, 中国的鲟鱼鱼子酱产量已占全球总产量的 50% 以上。多种育种技术的开发与集成应用为缩短鲟鱼育种世代、加速新品种的培育提供了广阔的可能性。

关键词: 鲟鱼, 苗种繁育, 育种技术

The Industrialization of Sturgeon in China: From Large-Scale Seed Production to the Construction and Application of Breeding Platform

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Abstract: Sturgeon is a globally cultivated species, farmed in over 40 countries worldwide. With a history of more than 150 years in aquaculture, China's commercial sturgeon farming began in the mid-1990s and has experienced rapid growth. According to FAO statistics from 2009, China's sturgeon production accounts for 80% of the global output. Currently, China has achieved year-round, on-demand production of sturgeon fry. Following breakthroughs in large-scale artificial breeding, the focus of fry breeding has shifted from quantity to quality improvement. As a result, China has gradually established a range of breeding technologies, including hybrid breeding, family selection, gynogenesis, sex reversal induction, gene editing, and whole-genome selection. These efforts have led to the development of new breeds, such as "Xunlong No. 1" and "Jinglong No. 1". In line with CITES requirements for the genetic background of sturgeon in trade, molecular markers for sturgeon germplasm identification have also been developed.

Key words: sturgeon, seed production, breeding technology

基于转录组和代谢组的联合分析揭示中华鳖 肤色多样性的形成机制

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摘要: 中华鳖(*Pelodiscus sinensis*)是东亚和东南亚重要的淡水养殖种。不同品系之间最大的外部差异是肤色和斑点, 但其形成机制尚不清楚。为探讨华鳖肤色多样性的机制, 选择3种不同表型的华鳖(金色鳖、中华鳖日本品系和清溪乌鳖)对其色素细胞进行观察, 并进行皮肤转录组和代谢组比较分析。结果表明, 三种中华鳖的皮肤中均存在黑色素细胞、黄色素细胞和虹彩细胞。然而, 在色素细胞的组成和细胞器方面存在差异。黄金鳖中的基因 *asip* 的上调和谷胱甘肽和半胱氨酸的积累导致了褐黑色素的产生, 导致了皮肤呈现黄色。清溪乌鳖的 *dct* 基因表达上调和吲哚-5,6-醌积累, 导致其产生真黑色素, 使皮肤呈现黑棕色。日本菌株产生真黑素和泛黑素, 但黑素体的存在导致皮肤变深, 呈现墨绿色。黄金鳖和日本鳖通过增加虹膜细胞的产生形成白色斑点, 清溪乌鳖通过诱导虹膜细胞内黑色素细胞的迁移和凋亡形成黑色斑点。

关键词: 中华鳖, 肤色多样性, 色素细胞, 转录组, 代谢组

Transcriptome and Metabolome Provide Insight into the Formation Mechanism of Skin Pigmentation Diversity in Chinese soft-shelled turtle (*Pelodiscus sinensis*)

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Abstract: Chinese soft-shelled turtle (*Pelodiscus sinensis*) is an important freshwater breeding species in East and Southeast Asia. The most external differences among different strains are skin pigmentation and blotches, but the mechanism of their formation is unknown. To investigate the mechanism of skin pigmentation diversity in Chinese soft-shelled turtle, three unique phenotypes (Golden strain, Japanese strain and Qingxi black strain) were selected to observe the chromatophores, and the transcriptome and metabolome were compared. The results showed the presence of melanophores, xanthophores and iridophores in the skin of all three strains. However, there were differences in the composition and organelles of chromatophores. The upregulation of gene *asip* and elevated accumulation of glutathione and cysteine in Golden strain resulted in the production of pheomelanin, leading to yellow pigmentation in the skin. The upregulation of gene *dct* and elevated accumulation of indole-5,6-quinone in Qingxi black strain resulted in the production of eumelanin, which made the skin appear black-brown. Ja

Key words: *Pelodiscus sinensis*, Pigmentation diversity, Chromatophore, Transcriptome, Metabolome.

无

无
无

摘要：无

关键词：无

The function of the cytoplasmic dynein light chain PTKM23 in the transport of PTSMAD2 during spermatogenesis in *Portunus trituberculatus*

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Abstract: Cytoplasmic dynein participates in transport functions and is essential in spermatogenesis. KM23 belongs to the dynein light chain family. The TGF β signaling pathway is indispensable in spermatogenesis, and Smad2 is an important member of this pathway. We cloned PTKM23 and PTSMAD2 from *Portunus trituberculatus* and measured their expression during spermatogenesis. Then, we assessed the localization of PTKM23 with PTDHC and α -Tubulin, and the results suggested that PTKM23 functions in intracellular transport during spermatogenesis. We knocked down PTKM23 in vivo, the localization of PTDIC with α -Tubulin and that of PTSMAD2 with PTDHC changed after PTKM23 knockdown. We transfected PTKM23 and PTSMAD2 into HEK-293T cells and verified their colocalization. These results indicate that PTKM23 is involved in the assembly of cytoplasmic dynein and microtubules during spermatogenesis and that PTKM23 mediates the participation of cytoplasmic dynein in the transport of PTSMAD2 during spermatogenesis. This study provides a theoretical molecular biological basis for breeding of *P. trituberculatus*.

Key words: *Portunus trituberculatus*, KM23, SMAD2, spermatogenesis, RNAi

综合微生物组和代谢组分析揭示了连接肠道微生物和生长的金鲳鱼 (*Trachinotus blochii*) 的性大小二态性的新见解

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摘要: 布氏鲳鲈的生长模式是性二态性的, 这表现为雌性更好的生长表现。研究金鲳鱼的性二态性, 以及分析肠道微生物群和代谢物对这些差异的影响, 将有助于揭示其生长二态性的调节机制。在本研究中, 将布氏鲳鲈 (平均体重 = 44.34 ± 2.36 g) 随机分为三组 (雄性、雌性和混合), 每组 3 个重复, 进行为期 8 周的培养实验。布氏鲳鲈肠道的微生物群落表现出性别特异性, 雌性具有更高的多样性和丰度。值得注意的是, *Holosporaceae* 在雌性中显著富集, 表明它在促进生长方面起着重要作用。此外, 代谢组学分析揭示了肠道代谢的差异, 雌鱼的脂质代谢增强, 尤其是甘油磷脂代谢途径。甘油磷酸胆碱与肠道菌群的变化呈显著正相关, 表明其与微生物的相互作用在维持肠道稳态中起着重要作用。总之, 富含 *Holosporaceae* 和甘油磷酸胆碱的水平有利于布氏鲳鲈的生长。本研究结果将有助于揭示金鲳鱼生长二态性的调控机制。

关键词: *Trachinotus blochii*; 生长表现; 肠道微生物组学; 代谢组学

Integrative microbiome and metabolome analysis reveals novel insights into sexual size dimorphism in golden pompano (*Trachinotus blochii*) linking gut microbiota and growth

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Abstract: Growth patterns in *Trachinotus blochii* are sexually dimorphic, which is manifested by better growth performance in females. Studying the sexual dimorphism of gold pompano, along with analyzing the effects of intestinal microbiota and metabolites on these differences, will help to reveal the regulatory mechanisms underlying their growth dimorphism. The microbial communities of male and female *T. blochii* intestines exhibited sex-specificity, with the females having higher diversity and abundance. Notably, *Holosporaceae* was significantly enriched in females, suggesting it plays an important role in promoting growth. Furthermore, the metabolomic analysis revealed an enhancement in lipid metabolism in females, particularly in the glycerophospholipid metabolism pathway. Glycerophosphocholine was significantly positively correlated with changes in intestinal microbiota, indicating that its interaction with microorganisms played an important role in maintaining intestinal homeostasis. In conclusion, the enriched levels of *Holosporaceae* and glycerophosphocholine benefited *T. blochii* growth.

Key words: *Trachinotus blochii*; Growth performance; Intestinal microbiomics; Metabolomics

南美白对虾响应单侧眼柄去除术的 内分泌性别差异调控网络研究

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摘要: 十足类物种常在生长和发育等方面表现出性别差异, 然而广泛应用于生产促熟的眼柄去除术所引发的内分泌性别差异调控仍不清晰。因此, 我们对十足类重要养殖种南美白对虾眼柄去除后的眼柄及肝胰腺开展了多重 RNA-seq 分析以系统揭示其内分泌性二态基因调控网络。其中转录组差异分析表明, 雌性在能量代谢调控方面偏好储存而雄性则倾向于消耗。同时, 我们深入分析基因及转录本水平表达差异, 以揭示转录变体及同源异构体的调控机制。结果显示, 超过 26% 的差异转录本由选择性剪切产生且其差异类型表现出组织偏好性; 而多聚腺苷酸化占差异的约 7%, 其引发的 3'UTR 变化具有性别偏好, 雌性显著增长而雄性则缩短。经过共表达网络构建及对蜕皮及倍半萜激素通路系统分析, 筛选出 Trypsin、Chit1 等关键基因的性别特异转录本, 同时阐明 miR-750/2788/ 281 等枢纽 miRNA 的重要调控作用, 为后续分子手段助力生产提供可能。

关键词: 南美白对虾, 眼柄去除术, 选择性剪切, 多聚腺苷酸化, 激素调控, MicroRNA, 性别偏好

Deciphering the sexually dimorphic endocrine regulatory network of *Penaeus vannamei* after unilateral eyestalk ablation

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Abstract: Sexual dimorphism in growth and development is commonly observed in decapods, but the sex-biased endocrine regulation induced by eyestalk ablation is still unclear. Therefore, we conducted a comprehensive transcriptomic study on the hepatopancreas and eyestalks of both female and male *Penaeus vannamei*. Overall, females prioritized energy storage, while males tended to consumption. Additionally, we conducted an in-depth analysis of both genes and transcripts to elucidate the mechanisms of transcript isoforms and variants. It showed that AS explained over 26% of the expression differences, with differential types exhibiting tissue preference. APA accounted for approximately 7% in each group, and the length diversity of 3'UTR exhibited gender specificity. Specifically, the 3'UTR of female became significantly longer, while it became shorter in males. Through co-expression network and hormone pathway analysis, specific transcripts of key genes were identified. The regulatory roles of pivotal miRNAs were elucidated, providing potential molecular tools to support production in the future.

Key words: *Penaeus vannamei*, Eyestalk ablation, Alternative splicing, Polyadenylation, Hormonal regulation, MicroRNA, Sex bias

日本日月贝(*Ylistrum japonicum*) 线粒体全基因组及其系统发育分析

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摘要: 日本日月贝(*Ylistrum japonicum*)是一种极具商业价值的扇贝, 因其长距离游泳的能力著称。尽管日本日月贝有着重要的经济价值, 但该物种遗传和基因组层面的研究却十分有限。本研究首次报道了日本日月贝线粒体全基因组。其线粒体基因组全长 19,475 bp, 包含 13 个蛋白编码基因、3 个核糖体 RNA 和 23 个转运 RNA。使用了两种不同的系统发育分析方法, 探索了该物种在扇贝科家族中的系统发育位置。基于线粒体基因组对 15 个扇贝科物种及外类群进行的系统发育分析, 以及通过 16S rRNA 进行的单基因系统发育分析, 构建了两个系统发育树, 以更清晰的认识日本日月贝在的进化位置。本研究对日本日月贝的遗传构成与进化历史提供了重要的见解, 增强对这一重要经济物种的认识。

关键词: 碟形扇贝; 线粒体基因组; 分类学

The Mitochondrial Genome of *Ylistrum japonicum* (*Bivalvia*, *Pectinidae*) and Its Phylogenetic Analysis

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Abstract: The *Ylistrum japonicum* is a commercially valuable scallop known for its long-distance swimming abilities. Despite its economic importance, genetic and genomic research on this species is limited. This study presents the first complete mitochondrial genome of *Y. japonicum*. The mitochondrial genome is 19,475 bp long and encompasses 13 protein-coding genes, three ribosomal RNA genes, and 23 transfer RNA genes. Two distinct phylogenetic analyses were used to explore the phylogenetic position of the *Y. japonicum* within the family Pectinidae. Based on one mitochondrial phylogenetic analysis by selecting 15 Pectinidae species and additional outgroup taxa and one single gene phylogenetic analysis by 16S rRNA, two phylogenetic trees were constructed to provide clearer insights into the evolutionary placement of *Y. japonicum* within the family Pectinidae. This study offers critical insights into the genetic makeup and evolutionary history of *Y. japonicum*, enhancing our knowledge of this economically vital species.

Key words: saucer scallop; mitogenome; taxonomy

基因组重测序揭示中国罗氏沼虾群体遗传学现状

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摘要: 从 10 个种群中选取 189 个个体, 包括从国外引进的原始种群或中国驯化种群, 即佛罗里达 (FD)、“南太湖 2 号” (NT)、越南 (YN)、斯里兰卡 (SK)、孟加拉 (ML)、泰国 (TG)、台湾 (TW)、“数丰 1 号” (SF)、正大 (ZD) 和新缅甸 (NMD)。根据 300,828 个全基因组 SNP 位点分析这些种群的遗传多样性和种群结构。种群结构分析和系统发育树显示, 10 个种群共有 4 个祖先, 国内种群 (即 SF、ZD、TW 和 NT) 具有相同的祖先。此外, 采用固定指数估计 (Fst) 和核苷酸多样性 (Pi) 对代表性群体 (即 ML 和 SF) 进行选择扫描分析, 鉴定出 7 个阳性选择的基因, 包括 Prox1、Foxl1、TLK2、Gna14、Ust、Mnt 和 Ipo9。这些发现有助于阐明引进群体的育种潜力, 并为深入了解我国国内罗氏沼虾选用品系的遗传状况提供参考。

关键词: 罗氏沼虾; 遗传多样性; 群体结构; 正选择基因

Genome resequencing reveals genetic status of *Macrobrachium rosenbergii* populations in China

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Abstract: 189 individuals were sampled from 10 populations, including original populations introduced from abroad or domesticated populations in China, i.e., Florida (FD), "Nantaihu No.2" (NT), Vietnam (YN), Sri Lanka (SK), Bangladesh (ML), Thailand (TG), Taiwan (TW), "Shufeng No.1" (SF), Zhengda (ZD) and New Myanmar (NMD). The genetic diversity and population structure of these populations were analyzed based on 300,828 genome-wide SNP loci. Population structure analysis and the phylogenetic tree showed that the 10 populations shared 4 ancestors, and the domestic populations (i.e., SF, ZD, TW and NT) had the same ancestor. In addition, Estimation of Fixation index (Fst) and nucleotide diversity (Pi) estimations were used to perform selective sweep analysis with the representative populations (i.e., ML and SF), and 7 positively selected genes were identified, including Prospero Homeobox 1 (Prox1), Forkhead Box L1 (Foxl1), Trousled Like Kinase 2 (TLK2), G Protein Subunit Alpha 14 (Gna14), Uronyl 2-sulfotransferase (Ust), MAX Network Transcriptional Repressor (Mnt) and Importin-9 (Ipo9).

Key words: *Macrobrachium rosenbergii*; Genetic diversity; Population structure; Positively selected genes

NLRC3 通过靶向 IRF7 降低草鱼抗病毒先天免疫应答

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摘要: NLRC3 属于 nod 样受体家族, 被认为是先天免疫机制的调节剂。在本研究中, 我们首次报道了草鱼 NLRC3 (CiNLRC3) 在抗病毒免疫应答中起负调控作用。功能分析显示, 过表达 CiNLRC3 显著降低 IFN 启动子活性, 阻碍细胞抗病毒反应, 从而促进病毒复制。相反, 通过 siRNA 沉默 CiNLRC3 可以增强这些抗病毒活性, 证实它是一个负调控因子。此外, 研究表明, CiNLRC3 可以抑制鱼类视黄酸诱导基因 I (RIG-I) 样受体 (RLR) 介导的 IFN 反应。对过表达 CiNLRC3 的毛囊肾 (CIK) 细胞的转录组学分析显示, *irf7* 转录物水平显著降低, 提示可能的机制途径。进一步的分子研究表明 CiNLRC3 在细胞质中与 CiIRF7 共定位, 并通过与 IRF7 蛋白相互作用并促进其降解, 从而减弱抗病毒免疫, 从而对 I 型 IFN 的产生产生负面影响, 总之, 这些发现强调了硬骨鱼 NLRC3 在抗病毒先天免疫反应中的关键抑制作用。

关键词: 草鱼、NLRC3、IFN 反应、IRF7、抗病毒免疫, 负调节

NLRC3 attenuates antiviral innate immune response by targeting IRF7 in grass carp (*Ctenopharyngodon idelus*)

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Abstract: NLRC3 belongs to the NOD-like receptor family and is recognized as a modulator of innate immune mechanisms. In this study, we firstly report that *Ctenopharyngodon idelus* NLRC3 (CiNLRC3) acts as a negative regulator in the antiviral immune response. In vivo, CiNLRC3 is ubiquitously expressed across tested tissues, displaying particularly high expression in the heart and spleen. Notably, CiNLRC3 expression is markedly upregulated following grass carp reovirus (GCRV) infection both in vivo and in vitro. Functional assays revealed that overexpression of CiNLRC3 substantially diminishes IFN promoter activity and hampers cellular antiviral responses, thereby facilitating viral replication. Conversely, silencing of CiNLRC3 through siRNA transfection enhances these antiviral activities, confirming it is a negative regulator. Additionally, our research demonstrates that CiNLRC3 impedes the retinoic acid-inducible gene I (RIG-I)-like receptor (RLR)-mediated IFN response in fish. Transcriptomic analysis of *Ctenopharyngodon idelus* kidney (CIK) cells overexpressing CiNLRC3 highlighted a significant

Key words: *Ctenopharyngodon idella*, NLRC3, IFN response, IRF7, antiviral immunity, negative regulator.

不同浓度的纳米二氧化钛对海湾扇贝产卵及其子代发育的影响

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摘要: 为探究不同浓度纳米二氧化钛 (n-TiO₂) 对海湾扇贝产卵及其子代发育的影响, 本研究对利用不同浓度纳米二氧化钛对海湾扇贝进行诱导产卵, 并对其子代生长发育进行记录。实验结果表明: 实验组扇贝排卵时间缩短, 比对照组提前一小时; 随着 n-TiO₂ 浓度增加, 卵的变态时间缩短, 但在 D 形幼虫时期变态时间恢复一致。在多细胞时期和囊胚期, 实验组卵径显著大于对照组 ($P < 0.05$), 且差距随浓度增加而加大。D 形幼虫时期及之后, 实验组壳长壳高显著小于对照组 ($P < 0.05$), 并随 n-TiO₂ 浓度提高而减小, 影响持续至成贝阶段。成贝的壳长、壳宽和壳高随 n-TiO₂ 浓度提高而减小, 与对照组存在显著差异 ($P < 0.05$), 但两实验组间无显著差异 ($P > 0.05$)。研究提供了实验室和海区实验数据, 为评估 n-TiO₂ 等新型纳米材料对扇贝等经济贝类养殖的影响提供了参考资料。

关键词: 海湾扇贝, 纳米二氧化钛, 不同浓度, 产卵, 子代发育

Effects of different concentrations of nano-titanium dioxide on spawning and progeny development of *Argopecten irradians*

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Abstract: In order to investigate the effects of different concentrations of nano titanium dioxide (n-TiO₂) on the spawning of *Argopecten irradians* and the development of their offspring, the present study was carried out to induce the spawning of *Argopecten irradians* by using different concentrations of n-TiO₂, and the growth and development of their offspring were recorded. The experimental results showed that: the oviposition time of scallops in the experimental group was shortened, one hour earlier than that of the control group; the metamorphosis time of eggs was shortened with the increase of n-TiO₂ concentration, but the metamorphosis time was restored to be consistent in the period of D-shape larvae. During the multicellular and bastula stages, the egg diameter of the experimental group was significantly larger than that of the control group ($P < 0.05$), and the difference increased with the increase of n-TiO₂ concentration. The shell length and height of the experimental group were significantly smaller than those of the control group during the D-shape larvae stage and beyond ($P < 0.05$), but there was no significant difference between the two experimental groups ($P > 0.05$).

Key words: *Argopecten irradians*, nano titanium dioxide, different concentrations, spawning, zygote development

三倍体长牡蛎精子生成受阻机制研究

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摘要：精子发生是极其复杂的细胞发育过程，在三倍体动物中，第三组同源染色体的存在使得减数分裂过程中同源染色体配对更为困难，导致精子生成受阻。本研究通过石蜡切片 HE 染色和冷冻切片免疫荧光，判定三倍体雄性长牡蛎性腺中成熟精子量显著低于正常的二倍体，表明三倍体长牡蛎精子发生严重受阻。利用透射电镜和细胞凋亡检测，证明三倍体雄性长牡蛎在性腺发育早期的精原细胞有丝分裂正常进行。通过磷酸化组蛋白 H2AX 免疫荧光实验，证实三倍体雄性长牡蛎初级精母细胞在减数分裂过程中无法完成从偶线期向粗线期的转变，导致减数分裂停滞。细胞周期异常停滞的结果通常是启动细胞程序性凋亡，TUNEL 实验证明三倍体雄性长牡蛎性腺中凋亡细胞数量显著增多。此外，三倍体长牡蛎所产生的少量精子，其头部和尾部显著增大，DNA 含量为二倍体牡蛎精子的 1.5 倍。该研究为三倍体牡蛎精子发生受阻提供了新的见解，强调了其在水产养殖中的重要性。

关键词：长牡蛎；三倍体；雄性不育；减数分裂受阻

Studies on the mechanism of spermatogenesis arrest in triploid Pacific oysters

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Abstract: Spermatogenesis is a complex development process. Meiosis in diploid animals is already an intricate process. The challenges intensify in triploid cells. In this study, histological analysis and immunostaining revealed a markedly low abundance of mature spermatozoa in triploids, indicating a severe blockade in spermatogenesis. Ultrastructural analysis and apoptosis analysis demonstrated that triploid males underwent normal spermatogonial mitosis. Analysis of phosphorylated histone H2AX (γ -H2AX) displayed numerous γ -H2AX staining in developed triploid gonads, with a significantly higher number of apoptotic cells confirmed by the TUNEL assay. These findings suggest a potential arrest at the zygotene stage, leading to cell apoptosis. Flow cytometry confirmed spermatozoa from triploids containing approximately 1.5 times the DNA content of spermatozoa from diploids. The sperm head size and flagella length in triploids surpassed those in diploids. This study provides novel insights into the blocked spermatogenesis in triploid oysters, emphasizing the importance of sterility in aquaculture.

Key words: Crassostrea gigas; triploid; male; sterility; meiotic arrest

比较转录组分析金虎杂交斑 (*Epinephelus fuscoguttatus* ♀ × *Epinephelus tukula* ♂) 和虎棕点石斑鱼 (*Epinephelus fuscoguttatus*) 下丘脑-垂体-性腺轴基因表达

邱弈树, 段鹏飞, 丁小雨, 李振通, 王心怡, 黎琳琳, 刘阳, 王林娜, 田永胜*
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摘要: 无

关键词: 无

Comparative Transcriptome Analysis of the Hypothalamic–Pituitary–Gonadal Axis of Jinhu Grouper (*Epinephelus fuscoguttatus* ♀ × *Epinephelus tukula* ♂) and Tiger Grouper (*Epinephelus fuscoguttatus*)

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Abstract

Abstract: Jinhu groupers, the hybrid offspring of tiger groupers (*Epinephelus fuscoguttatus*) and potato groupers (*Epinephelus tukula*), have excellent heterosis in fast growth and strong stress resistance. However, compared with the maternal tiger grouper, Jinhu groupers show delayed gonadal development. To explore the interspecific difference in gonadal development, we compared the transcriptomes of brain, pituitary, and gonadal tissues between Jinhu groupers and tiger groupers at 24-months old. In total, 3034 differentially expressed genes (DEGs) were obtained. KEGG (Kyoto Encyclopedia of Genes and Genomes) enrichment analyses showed that the osteoclast differentiation, oocyte meiosis, and ovarian steroidogenesis may be involved in the difference in gonadal development. Trend analysis showed that the DEGs were mainly related to signal transduction and cell growth and death. Additionally, differences in expression levels of *nr4a1*, *pgr*, *dmrt2*, *tbx19*, and *cyp19a1* may be related to gonadal retardation in Jinhu groupers. A weighted gene co-expression network analysis revealed

Key words:

Jinhu grouper (*Epinephelus fuscoguttatus* ♀ × *Epinephelus tukula* ♂); *Epinephelus fuscoguttatus*; gonadal development; transcriptome

高温对翘嘴鲌性别分化和性腺发育的影响

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摘要：高温会引起鱼类如异育银鲫、罗非等鱼类性腺分化障碍，促进雄性化。本研究开展了鳊幼鱼（20dph）高温（35℃和36℃）处理实验，结果显示，经过60天高温处理，通过性别标记区分对XX和XY染色体型的个体，检测和分析每个个体的性腺形态，表明高温对性别分化没有显著影响。进一步检测了80日龄高温处理个体的血清激素，雌二醇和11-KT水平比对照组（25℃）显著升高，性腺组织foxl2和cyp19a1a基因表达量显著升高。KDM6bb基因的可变剪接被认为和罗非高温诱导转性正相关，通过检测鳊KDM6bb基因第五内含子的剪接水平，发现高温处理对KDM6bb的可变剪接没有显著影响。综上分析，鳊鱼可能不具有高温转性的机制，本研究为性别分化和环境互作提供了优良材料和优秀案例，为鱼类性别分化的进化机制提供了新的见解。

关键词：鳊；高温处理；性别分化；Kdm6bb基因

The effect of high temperature on the sex differentiation and gonad development in mandarin fish

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Abstract: High temperature can cause the barrier of gonadal differentiation of fish such as *Carassius auratus* and *tilapia* and promote masculinity. In this study, high temperature (35℃ and 36℃) treatment experiment was carried out on juvenile mandarin fish (20dph). None significant phenotypes were distinguished after 60 days of high temperature treatment based on the analysis of the gonad morphology of each individual. High temperature had no significant effect on sex differentiation. Further, the levels of serum hormones, estradiol and 11-KT in 80-day-old individuals treated with high temperature were significantly higher than those in the normal temperature (25℃) control group, and the expression levels of foxl2 and cyp19a1a genes in gonad tissue were significantly increased. The variable splicing of KDM6bb gene is believed to be positively correlated with the high temperature induced conversion of *tilapia*. We detected the splicing level of the fifth intron of KDM6bb gene in *Siniperca chuatsi* and found that high temperature treatment has no significant effect on the variable splicing of KDM6bb.

Key words: *Siniperca chuatsi*, sex differentiation, high temperature treatment, KDM6bb gene

17 α -甲基睾酮对罗氏沼虾生长、性别分化、性腺发育及肠道微生物的影响

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

关键词: 罗氏沼虾; 甲基睾酮; 性别分化; 肠道微生物

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

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Abstract: The function of 17 alpha-methyltestosterone (MT) includes inhibiting ovarian development and inducing spermatogenesis, making it widely used for artificial sexual reversal in fish. However, its role in crustacean sex development remains understudied. In this study, we evaluated the effects of MT on growth, sex differentiation, and gonadal development in *Macrobrachium rosenbergii* by incorporating different concentrations of MT into feed. This was combined with assessments of sex ratio, histological observation, qPCR analysis, and intestinal microbial diversity analysis. The results demonstrated that a concentration of 1500 mg/kg MT promoted the growth of *macrobrachium rosenbergii*; however, various concentrations only significantly inhibited male growth. These findings provide important theoretical foundations and references for optimizing gender control strategies within aquaculture practices as well as establishing healthy aquaculture models.

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

MicroRNAs 调控栉孔扇贝性腺性别发育的分子机制初探

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摘要: 动物性腺性别发育包括性别决定和性别分化两个古老且高度保守的生物学过程, 其受到复杂的基因网络调控。MicroRNA (miRNAs) 作为重要的基因表达调控因子, 在生物性别发育中扮演了举足轻重的角色, 然而在非模式生物特别是双壳贝类中, 相关的研究还相对薄弱。本研究以海洋经济贝类栉孔扇贝 (*Chlamys farreri*) 为研究对象, 利用高通量测序技术, 在其性别起始分化阶段壳高 5.0 mm 幼贝雌雄性腺中筛选获得 11 个性别偏好性 miRNAs, miRNA-mRNA 联合分析并结合体外和体内验证实验, 发现其中 1 个尚未报道的新 miRNA 可靶向雌性性别决定基因 *Foxl2*, 参与卵巢形成和卵子发生, 另外还确定了 1 个 miRNA 可以靶向雄性性别分化基因 *Dmrt1*, 介导精子发生和精巢功能维持。本研究初步构建了一个 miRNAs 调控栉孔扇贝性腺性别发育的分子调控网络, 研究结果为贝类性控育种技术的开发提供了重要的理论基础。

关键词: microRNA; 性腺性别; 栉孔扇贝; *Foxl2*; *Dmrt1*

A preliminary exploration of the molecular mechanisms of microRNAs regulating the sexual development of scallop gonads

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Abstract: Gonadal sex development involves two highly conserved biological processes, sex determination and sex differentiation, which are regulated by complex genetic networks. MiRNAs play pivotal roles in the determination and differentiation of sex in animals. However, researches in non-model organisms, especially bivalves, remains scarce. This study focused on the identification of sexually dimorphic miRNAs at the initial period of sex differentiation in *Chlamys farreri*, a commercially important marine bivalve. Eleven sex-biased miRNAs exhibiting sex-biased expression were screened out, and a novel miRNA was found to target the female sex-determining gene *Foxl2* and participated in the formation of ovaries and oogenesis. Another miRNA was identified as targeting the male sex-differentiation gene *Dmrt1*, mediating the spermatogenesis and testis functional maintenance. This study established a molecular regulatory network of miRNAs regulating the gonadal sex development of *Chlamys farreri*, and laid a theoretical basis for the development of mollusk sex control breeding technology.

Key words: microRNA; Gonadal sex; *Chlamys farreri*; *Foxl2*; *Dmrt1*

黄姑鱼伪雌鱼诱导技术优化及超雄鱼培育的初步研究

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摘要: 黄姑鱼 (*Nibea albiflora*) 是我国重要的海水经济鱼类, 性控育种对于丰富育种资源、改良种质特性以及提升产量等方面具有重要作用。本研究使用含不同浓度 (1、5 和 10 mg/kg) 的 17 β -雌二醇 (E2) 的饲料投喂黄姑鱼幼苗, 以建立雄鱼性逆转为伪雌鱼 (XY ♀) 的诱导技术, 并探究 E2 对试验鱼生长、性腺发育及性别相关基因表达等方面的影响。研究结果发现 5 mg/kg 和 10 mg/kg 的 E2 处理组逆转率均为 100%, 而 10 mg/kg E2 处理对黄姑鱼的生长有显著的抑制, 表明 5 mg/kg E2 为诱导最佳剂量; 性腺组织学结果表明, 90 dph 前伪雌鱼性腺与对照雌鱼无显著差异, 而 180 dph 以后伪雌鱼性腺发育相对滞后。将二龄性成熟伪雌鱼与普通雄鱼交配, 采用性别分子特异标记和组织学检测表明成功获得了超雄鱼 (YY ♂)。本研究为黄姑鱼性别决定机制解析及全雄群体的规模化培育建立了理论依据和技术支撑。

关键词: 黄姑鱼; 性逆转; 伪雌鱼; 超雄鱼

Optimization of neo-female induction technology and preliminary study on super-male production in yellow drum (*Nibea albiflora*)

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Abstract: The yellow drum (*Nibea albiflora*) is a significant economic fish species in China. Sex control breeding can enhance breeding resources, improve germplasm traits, and boost production. In this study, yellow drum larvae were fed pellets with 1, 5, and 10 mg/kg of 17 β -estradiol (E2) to induce sex reversal from males to neo-females and study E2's effects on growth, gonadal development, and sex-related gene expression. The sex-reversal ratios of 5 and 10 mg/kg E2-treated groups both reached 100%, but the 10 mg/kg group significantly inhibited the growth of the yellow drum, indicating that 5 mg/kg of E2 is the optimal dose for inducing neo-females. Histological observations of the gonads showed no differences between neo-females and control females before 90 dph, but delayed development in neo-females after 180 dph. Two-year-old sexually mature neo-females were mated with normal males, and super-males (YY ♂) were detected in the offspring through sex molecular specific markers and histological examination.

Key words: *Nibea albiflora*; sex reversal; neo-female; super-male

非编码 RNA 在虾夷扇贝响应高温胁迫中的分子调控机制研究

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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调控机制, 本研究利用全转录组学技术进行了不同高温胁迫下虾夷扇贝鳃丝非编码 RNA 表达谱变化分析。高温胁迫后, 分别获得差异表达 mRNA、miRNA、lncRNA 和 circRNA 各 2017、120、1477 和 1722 个。构建了虾夷扇贝响应高温胁迫的 lncRNA/circRNA-miRNA-mRNA ceRNA 调控网络。对网络靶基因功能分析发现, 内质网应激、HSP 结合、纤毛运动和细胞凋亡等过程显著富集, 很可能表明虾夷扇贝通过激活内质网应激和细胞凋亡、抑制纤毛活动等过程来适应高温环境, 而以上过程均受到非编码 RNA 调控。进一步分析发现内质网应激通路关键基因, 如 GRP78、HSP90、Hsp70, 同时受到 lncRNA 和 circRNA 与 miRNA 的竞争性调控。本研究探讨了非编码 RNA 在虾夷扇贝响应高温胁迫中的调控机制。

关键词: 虾夷扇贝, 高温胁迫, 全转录组, 非编码 RNA, ceRNA

Molecular regulatory mechanism of non-coding RNA in *Patinopecten yessoensis* in response to heat stress

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Abstract: *Patinopecten yessoensis*, a vital aquaculture species in North China, has recently suffered massive deaths in summer. In this study, whole transcriptome sequencing was used to analyse expression changes of non-coding RNAs in gills of *P. yessoensis* under different heat stress. There were 2017, 120, 1477 and 1722 mRNAs, miRNAs, lncRNAs and circRNAs differentially expressed after heat stress. The lncRNA/circRNA-miRNA-mRNA ceRNA networks were constructed. Functional analysis revealed processes of ER stress, HSP binding, ciliary activity and apoptosis significantly enriched, indicating *P. yessoensis* probably activated ER stress and apoptosis, and suppressed ciliary activity to adapt to high temperature, and the above processes were regulated by non-coding RNA. Further, key genes of ER stress, e.g., GRP78, HSP90, Hsp70, were competitively regulated by lncRNA/circRNA with miRNA. The study explored the regulatory mechanism of non-coding RNA in response to heat stress in *P. yessoensis*.

Key words: *Patinopecten yessoensis*; heat stress; whole transcriptome sequencing; non-coding RNA; ceRNA

高温胁迫对菲律宾蛤仔影响的初步研究

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摘要: 为了探究蛤仔在长期高温胁迫下的分子机制, 本研究首先通过长期高温养殖实验测定菲律宾蛤仔的存活情况和能量代谢基本数据, 随后选取了经历长期高温胁迫的菲律宾蛤仔鳃组织为样本, 运用转录组测序技术, 通过差异基因分析、基因集富集分析、WGCNA 共表达网络构建、Mufzz 时序性分析等多种方法对菲律宾蛤仔应对长期高温胁迫的机制进行了初步讨论。通过对高温胁迫下蛤仔转录组的分析, 对蛤仔应对高温胁迫的差异基因表达规律有了一定的理解, 从分子内部揭示蛤仔对温度变化的响应机制, 开展了基因与不同胁迫时间节点的关联分析, 初步筛选了与高温相关的核心基因, 为蛤仔耐高温品系的改良提供基础数据支持。

关键词: 菲律宾蛤仔、高温、鳃组织、呼吸代谢、转录组

A preliminary study on the effects of high temperature stress on the population of *Ruditapes philippinarum*

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Abstract: Due to its simple breeding method, low investment cost, rich nutrition, and delicious taste, it has a broad market. But with the expansion of aquaculture scale and the impact of global warming, high water temperature has become an important factor restricting the development of the industry. In order to explore the molecular mechanism of the long-term high temperature stress on the *Ruditapes philippinarum*, this study first determined the survival status and basic energy metabolism data of *Ruditapes philippinarum* through long-term high temperature cultivation experiments. Subsequently, the gill tissues of *Ruditapes philippinarum* that had experienced long-term high temperature stress were selected as samples, and transcriptome sequencing technology was used to conduct preliminary discussions on the mechanism of *Ruditapes philippinarum*'s response to long-term high temperature stress through differential gene analysis, gene set enrichment analysis, WGCNA co-expression network construction, and Mufzz temporal analysis. By analyzing the transcriptome of clams under high temperature stress,

Key words: *Ruditapes philippinarum*; high temperature; gill tissue; respiratory metabolism; transcriptome

虾夷扇贝耐高温相关 SNP 位点的鉴定及功能分析

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摘要: 虾夷扇贝是我国北方重要的养殖贝类, 近些年随着海水温度上升, 其生长发育受到严重影响。为筛选虾夷扇贝耐高温相关 SNP 位点, 本研究对 1000 只虾夷扇贝进行了长期的热胁迫实验, 分别筛选出热敏感群体和耐热群体, 并对两群体各 100 个个体进行了全基因组重测序。测序共获得 2585.5 Gb 数据, 平均测序深度高于 10×, 检测共获得 14,769,450 个 SNP。利用全基因组关联分析鉴定获得 16 个耐高温相关 SNP。在这些 SNP 位点上下游 100kb 范围内共鉴定到 56 个候选基因。候选基因的功能富集分析显示脂肪酸代谢、纤毛活动、神经调控、线粒体和细胞膜等过程显著富集。与转录组关联分析表明, 脂肪酸代谢基因 *mecr*、*HACD2* 及纤毛活动基因 *BBS4*、*Rtnn*、*SPAG17* 在高温胁迫后均发生显著差异表达, 推测脂肪酸代谢和纤毛活动等过程在虾夷扇贝耐受高温过程中发挥重要作用。本研究为耐高温虾夷扇贝分子育种工作提供了候选位点。

关键词: 虾夷扇贝, 高温, SNP, 全基因组关联分析

Identification and Functional Analysis of SNPs Related to Heat Tolerance in the Yesso scallop (*Patinopecten yessoensis*)

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Abstract: Yesso scallop is an important aquaculture molluscs in North China. To screen heat-tolerant SNPs in Yesso scallops, the study conducted a long-term heat stress experiment on a population with 1000 individuals. Heat-sensitive and heat-tolerant groups were selected. Whole-genome resequencing was performed on 100 scallops from each group. Totally, 2585.5 Gb sequencing data was obtained with an average depth over 10×. A total of 14,769,450 SNPs were detected, and 16 SNPs were identified related to heat tolerance by GWAS. 56 candidate genes were identified around these SNPs. Enrichment analysis showed the genes mainly involved in fatty acid metabolism, ciliary activity, neuromodulation, mitochondria and cell membrane. Association analysis with the transcriptome indicated fatty acid metabolism genes *mecr*, *HACD2*, and ciliary activity genes *BBS4*, *Rtnn*, *SPAG17* were differentially expressed after heat stress, indicating fatty acid metabolism and ciliary activity probably play key roles in heat tolerance for Yesso scallops. This study supplies candidate sites for molecular breeding of heat-tolerant scallops.

Key words: Yesso scallop, High temperature, SNP, Genome-wide association study

皱纹盘鲍常温育苗技术优化及其应用研究

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摘要：皱纹盘鲍是一类重要的经济贝类，其育苗技术对于养殖产业的发展至关重要。本研究以长岛种群、山东养殖种群、人工选育种群为养殖对象采用性腺发育规律及营养强化技术对性腺发育的影响，并筛选适合夏季高温期使用的底栖硅藻作为稚鲍饵料。结果表明，长岛种群亲鲍的性腺发育显著滞后于养殖等亲本群体，但采用中投生物生产的底栖硅藻藻粉进行营养强化后，其性腺发育水平得到显著提高。此外，研究对比了卵形藻、双眉藻以及常规使用的舟形藻作为稚鲍饵料的效果，结果表明，夏季高温期间卵形藻和双眉藻因其强附着力度和高温耐受性，可提供充足饵料供稚鲍采食，并且稚鲍生长显著优于对照组。然而，中投生物藻粉组由于高温期发生酸臭腐败现象，需进一步研究其应用效果。综上，通过选择强附着力度的卵形藻和高温耐受性强的双眉藻作为底栖硅藻来源，可以有效克服常规技术中因藻类在高温期脱落而造成的稚鲍死亡和掉板问题。

关键词：皱纹盘鲍、常温育苗、性腺发育、营养强化

Optimization and Application Study of Temperature-controlled Larval Rearing Techniques for *Haliotis discus hannai*

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Abstract: *Haliotis discus hannai* is an important economic shellfish, and its larval rearing technology is crucial for the development of the aquaculture industry. This study focused on three populations: the Changdao population, the Shandong farmed population, and the artificially selected population. The study examined the effects of gonadal development patterns and nutritional enhancement techniques on gonadal development, and screened suitable benthic diatoms as feed for juvenile abalones during the high-temperature summer period. The results showed that the gonadal development of parent abalones from the Changdao population was significantly delayed compared to those from farmed populations. However, after using benthic diatom powder produced by Zhongtuo Bio for nutritional enhancement, the gonadal development levels were significantly improved. Additionally, the study compared the effects of *Chaetoceros* (ovoid diatoms), *Skeletonema* (browsleeve diatoms), and the commonly used *Navicula* (navicula diatoms) as feed for juvenile abalones. The results indicated that during the high-temperature

Key words: *Haliotis discus hannai* 、 Temperature-controlled larval rearing 、 Gonadal development 、 Nutritional enhancement

靶向代谢组学揭示锦鲤体色及色素代谢物的季节可塑性

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摘要: 锦鲤体色主要由遗传决定, 同时受温度、水质、光照等养殖环境的剧烈影响。研究锦鲤体色变化规律, 阐明锦鲤体色调控的分子机制, 有助于为提高我国锦鲤产业国际竞争力提供理论基础和技术支撑。连续追踪 4 个不品系、6 种表型的德系锦鲤在不同季节的体色变化, 发现锦鲤白色皮肤的黄度在不同季节发生剧烈变化。德系昭和锦鲤与九纹龙锦鲤的皮肤在冬季常现蓝色(隐墨), 夏秋季节蓝色皮肤亮度下降, 皮肤逐渐变为黑色。红色皮肤的稳定性具有品系差异, 仅在德系昭和锦鲤的红色皮肤中观察到黄度的季节性变化。

基于自主构建的锦鲤体色相关代谢物靶向代谢组学检测流程, 开展不同季节德系锦鲤血清样本的靶向代谢物组学分析, 发现季节变化通过肾上腺素-cAMP 途径调控锦鲤白色皮肤黄度变化, 褪黑素可能同时参与黑色和红色皮肤的季节变化。德系红白锦鲤的红色皮肤与血清类胡萝卜素代谢物不随季节变化, 具有高度稳定性。研究结果将为锦鲤体色调控和个性化养殖提供理论支撑。

关键词: 体色, 季节可塑性, 肾上腺素, 褪黑素, 类胡萝卜素

Targeted metabolomics revealed the seasonal plasticity of skin color and pigment metabolites in ornamental koi carp

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Abstract: The skin color of koi carp is mainly determined by genetics, and is also greatly influenced by the environment factors. Studying the changing patterns of koi color will promote the market competitiveness of China's koi carp industry. Tracking the skin color changes of scaleless koi in different seasons, we found that the yellowness of the white skin of all koi changed dramatically in different seasons. The skin of scaleless Showa and Nigen-ryu koi often appeared cyan in winter, while the lightness of the cyan skin decreased in summer and autumn, and the skin gradually turned black. The stability of red skin showed breed-specific differences. Only yellowness of red skin was observed seasonal changes in Showa koi.

Based on our detection workflow targeting koi skin color-related metabolites, we conducted targeted metabolomics analyses of serum samples from scaleless koi in different seasons. The results revealed seasonal changes in yellowness of white skin in koi carp through the epinephrine-cAMP pathway. The melatonin might also be involved in the seasonal changes of black and red s

Key words: Skin color; Seasonal Plasticity; Epinephrine; Melatonin; Carotenoids

不同溶氧处理对暗纹东方鲀生理生化指标的影响及低氧相关 SNP 位点的开发

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摘要：水体溶氧是影响鱼类的重要环境因子，本研究检测不同溶氧处理（ $7.1\pm 0.5\text{mg/L}$ ， $5.7\pm 0.5\text{mg/L}$ ， $4.0\pm 0.5\text{mg/L}$ ）对暗纹东方鲀生理生化影响和肝组织转录组测序的比较分析。结果显示：溶氧越低，暗纹东方鲀生长越受抑制。随着溶氧降低，全长、体重、肝体比、肥满度呈明显下降趋势，摄食反应时间明显增加。用 qPCR 检测 CAT、SOD、GSH-PX 基因在肝肠组织中的表达分布，随着溶氧降低，呈上调趋势。此外， α -淀粉酶、脂肪酶均随溶氧降低而降低，胰蛋白酶无明显趋势。同时通过转录组学分析不同溶氧对暗纹东方鲀肝组织代谢的影响，在此基础上开发出低氧相关的 SNP 位点。这些结果有望为暗纹东方鲀适应溶氧波动、分子辅助育种提供一定理论依据，也为该鱼良种选育提供基础资料。

关键词：暗纹东方鲀；生理生化指标；转录组；低氧；SNP

Effects of different dissolved oxygen on the physiological and biochemical indexes of *Takifugu obscurus*, excavating of hypoxia-related gene SNPs

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Abstract : Dissolved oxygen (DO) in water is an important environment factor for fish. The physiological and biochemical indexes and transcriptome analysis of *Takifugu obscurus* were analyzed under different levels of dissolved oxygen. The results showed that the growth of *Takifugu obscurus* was suppressed. With the decrease of dissolved oxygen, the total length, body weight, hepatic steatosis index (HSI), and condition factor showed a significant downward trend, and the feeding response time increased significantly. The CAT, SOD activities, and GSH-PX content showed an upward trend in liver and intestinal tissue with qPCR. In addition, the α -Amylase, lipase activities decreased with decreasing DO, but trypsin content had no obvious trend. At the same time, the effects of dissolved oxygen on liver metabolism of *T. fasciatus* were analyzed by transcriptomics. The physiological and biochemical index, the transcriptome and hypoxia-related SNPs were seriously studied, which has laid a theoretical foundation for adapting to DO fluctuations and molecular assisted breeding of *T. fasciatus*.

Key words: : *Takifugu obscurus*; Physiological and biochemical indexes; Transcriptome; Hypoxia; SNP

银鲳耐低温选育及机制研究

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摘要：温度是影响鱼类生长、发育、新陈代谢和生理的重要环境因素，鱼类应对低温刺激的分子机制各不相同。银鲳 (*Pampus argenteus*) 是我国重要的海水经济鱼类，在解决人工繁育问题的基础上开展产业化推广，推广过程中发现，水温成为限制养殖地区和养殖方式的重要因素。当水温低于 13℃，银鲳食欲下降，行为学变化明显。而银鲳应对低温的生理极限和响应机制尚不清楚。本研究通过群体选育获得 F4 代银鲳耐低温品系，选育过程中通过转录组筛选关键基因及通路，对银鲳低温适应过程中的脂代谢；MAPK 通路中的 *dusp1/5* 基因调控机制进行了相关研究并获得初步结果。

关键词：银鲳；耐低温；SCD1；DUSP 家族

Breeding and mechanism research of silver pomfret resistant to low temperature

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Abstract : Temperature is a critical environmental factor influencing the growth, development, metabolism, and physiology of fish. The molecular mechanisms through which fish respond to low temperatures vary significantly. *Pampus argenteus* is a key marine economic species in China, and its aquaculture promotion has been undertaken following the resolution of artificial breeding challenges. Throughout this promotional process, it became evident that water temperature serves as a significant limiting factor for both cultivation areas and methods. When water temperatures fall below 13°C, the appetite of *P. argenteus* diminishes markedly, accompanied by noticeable behavioral changes. Nevertheless, the physiological limits and response mechanisms of *P. argenteus* to low temperatures remain poorly understood. This study successfully developed a low-temperature tolerant strain of *P. argenteus* through selective breeding and identified key genes and pathways via transcriptome analysis during this selection process. Additionally, the research explored lipid metabolism along with the regulatory mechanisms o

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

罗氏沼虾对高温胁迫的行为反应及转录组分析

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摘要: 随着全球气候变暖和极端天气增多, 夏季持续高温影响罗氏沼虾的生理活动。为探究罗氏沼虾对高温胁迫的行为反应及基因表达情况, 以罗氏沼虾虾苗为研究对象, 从 29°C 以 1°C/4 h 的速率进行升温, 直至虾苗全部死亡, 采集早死、半死、最后死亡及对照组样本进行转录组测序。结果显示, 水温 30°C~36°C, 虾苗游泳速度和摄食率增加; 37°C 时活动减少且停止摄食, 死亡率上升; 38°C~39°C 出现大量死亡, 死亡个体肌肉发白。转录组测序共获得 83.66 Gb 数据, 注释到 185231 个 Unigenes, 识别 11879 个差异表达基因; KEGG 富集和蛋白质互作网络分析显示, 抗原加工与呈递、内质网蛋白质加工信号通路中的热休克蛋白家族基因尤其 Hsp70 显著上调, 推测高温会影响罗氏沼虾的免疫系统及细胞内蛋白质合成, HSPs 可能在维持细胞稳态、增强耐高温中起关键作用。本研究为研究罗氏沼虾的高温胁迫响应机制和抗逆品种培育提供参考依据。

关键词: 罗氏沼虾; 高温胁迫; 转录组测序; 差异表达基因

Behavioral response and transcriptome analysis of *Macrobrachium rosenbergii* to high temperature stress

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Abstract: Global warming and extreme weather have made *Macrobrachium rosenbergii* vulnerable to high summer temperatures. In this study, post-larvae exposed to increasing temperatures were monitored for behavioral and gene expression changes. Results showed that at 30°C-36°C prawns' swimming speed and feeding rate increased, but at 37°C activity declined and feeding stopped; massive deaths with muscle whitening occurred at 38°C-39°C. Transcriptome sequencing (83.66 Gb) annotated 185,231 Unigenes and identified 11,879 differentially expressed genes. KEGG and PPI network analyses showed significant up-regulation of heat shock proteins (HSPs), especially Hsp70 in antigen processing and endoplasmic reticulum protein synthesis pathways. These results suggested high temperatures affect the immune system and protein synthesis, with HSPs playing a key role in enhancing thermal tolerance, which provides insights into heat stress response mechanisms in *M. rosenbergii*, aiding the development of heat-resistant strains.

Key words: *Macrobrachium rosenbergii*; high-temperature stress; transcriptome sequencing; differentially expressed genes

Mn-LIPA 基因在日本沼虾性激素调节和性腺发育中的作用

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摘要: 本研究探讨了溶酶体酸性脂肪酶 A (LIPA) 在日本沼虾性激素调节和性腺发育中的作用。通过克隆全长 Mn-LIPA 的 cDNA 序列, 利用实时荧光定量 PCR (quantitative real-time PCR, qPCR) 分析其不同组织和发育阶段的表达模式, 发现该基因在日本沼虾肝胰腺、脑神经节和精巢中有较高的表达水平, 表明其可能参与性别分化和性腺发育。原位杂交显示, 在沼虾的精囊和肝胰脏中存在强烈的 Mn-LIPA 信号, 这表明该基因在类固醇合成和精子成熟中有重要作用。LIPA 敲降后, 雄虾的雄性特异性基因如 IAG, GS 和 Dmrt11E 的表达水平显著提升, 且在组织学上能够观察到精子发育和成熟被抑制。另外, 通过向雄虾注射性激素, 本研究还探究了 Mn-LIPA 与性腺发育相关基因 (IAG、SG 和 Dmrt11E) 以及激素 (17 β -雌二醇和 17 α -甲基睾酮) 的关系。

关键词: 日本沼虾; 溶酶体酸性脂肪酶 A; 性激素; 性腺发育; 生殖; RNA 干扰

Role of Mn-LIPA in Sex Hormone Regulation and Gonadal Development in the Oriental River Prawn, *Macrobrachium nipponense*

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Abstract: This study investigates the role of lysosomal acid lipase (LIPA) in sex hormone regulation and gonadal development in *Macrobrachium nipponense*. The full length Mn-LIPA cDNA was cloned, and its expression patterns were analyzed using quantitative real-time PCR (qPCR) in various tissues and developmental stages. Higher expression levels were observed in the hepatopancreas, cerebral ganglion, and testis, indicating the potential involvement of Mn-LIPA in sex differentiation and gonadal development. In situ hybridization experiments revealed strong Mn-LIPA signaling in the spermatheca and hepatopancreas, suggesting a potential role in steroid synthesis and sperm maturation. Increased expression levels of male-specific genes, such as IAG, SG and Dmrt11E, were observed after dsMn-LIPA injection, and significant inhibition of sperm development and maturation was observed histologically. Additionally, the relationship between Mn-LIPA and sex-related genes (IAG, SG, and Dmrt11E) and hormones (17 β -estradiol and 17 α -methyltestosterone) was explored by administering sex hormones to male prawns.

Key words: *Macrobrachium nipponense*, Mn-LIPA, sex hormone, gonadal development, reproduction, RNAi.

Methyl farnesoate epoxidase (MFE)在日本沼虾卵巢成熟的功能研究

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摘要：法尼索酸甲酯环氧化酶（MFE）是一种编码与幼虫激素合成相关的酶的基因。该基因cDNA总长1695bp,开放阅读框长度为1482bp,编码493个氨基酸。Mn-MFE在肝胰腺中表达量最高，其次为卵巢和鳃，在心脏和肌肉组织中表达较弱，在眼柄和颅神经节中表达较少。在幼虫期Mn-MFE表达保持稳定。卵巢表达与卵巢发育呈正相关，肝胰脏表达与卵巢发育呈负相关。原位杂交结果显示，该信号在卵母细胞、细胞核、细胞膜和卵泡细胞中均有表达，且在O-IV期表达强度最强。与对照组相比，沉默该基因导致性腺指数和卵巢过O-III期百分比显著降低。然而，实验组和对照组之间蜕皮的累计频率没有差异。此各组之间在发育速度上存在差异，但在亚细胞结构上没有差异。综上所述，Mn-MFE对日本沼虾成体卵巢发育有促进作用，但对蜕皮无影响。

关键词：日本沼虾；法尼索酸甲酯环氧化酶；卵巢成熟；RNA干扰

Functional study of the role of the methyl farnesoate epoxidase gene in ovarian development of *Macrobrachium nipponense*

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Abstract： Methyl farnesoate epoxidase (MFE) is a gene encoding an enzyme related to juvenile hormone biosynthesis. Its cDNA has a total length of 1695 bp and the open reading frame length of 1482 bp, encoding 493 amino acids. It was highly expressed in the hepatopancreas, followed by the ovary and gill, weakly expressed in heart and muscle tissue, and barely expressed in the eyestalk and cranial ganglion, remaining stable during the larval period. Ovarian development was positively correlated with its expression and negatively correlated with hepatopancreatic expression. In situ hybridization showed that the signal was expressed in the oocyte, nucleus, cell membrane and follicular cells, expressing at stage O-IV was strongest. The knockdown of Mn-MFE resulted in a greatly lower gonadosomatic index and percentage of ovaries past stage O-III compared to the control group. But it's similar in the cumulative frequency of molting. Besides, it isn't same in speed but not in subcellular structure. Totally, Mn-MFE promoted ovarian development of *Macrobrachium nipponense* adults, but had no effect on molting.

Key words: *Macrobrachium nipponense*; Methyl farnesoate epoxidase; ovarian development; RNAi

基于银鲳基因组揭示银鲳对水母的摄食偏好性及水母毒素的解毒机制

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摘要: 银鲳对水母有着强烈的摄食偏好性。为解释这种奇特摄食行为, 我们对银鲳进行基因组测序: 雌鱼基因组大小为 536.33Mb, 雄鱼为 553.79Mb, 其中 550.82 Mb 被锚定在 24 条 gap-free 染色体上。基于比较基因组发现, 银鲳与蓝鳍金枪鱼进化关系较近。投喂银鲳水母后对其嗅囊、舌、脑及肠道微生物进行转录组或 16S 测序, 发现水母投喂提高了嗅觉和味觉及食欲正调控相关基因的表达及 *Lactococcus* 等五种益生菌在肠道中的丰度。PLA2 是水母毒素的主要毒性蛋白。在银鲳基因组中鉴定到一个 PLA2 inhibitor (PLI), 互作模拟后发现与水母 PLA2 存在多个互作位点; 通过 CO-IP 发现其与两个水母 PLA2 确实存在互作关系。在细胞中过表达和干扰该基因后进行毒素攻毒, 检测细胞活性、凋亡及相关调控基因发现, 银鲳 PLI 对水母毒素有明显的抑制作用。综上, 本文初步解析了银鲳进化地位及其摄食水母的原因。

关键词: 银鲳; 基因组; 水母; 摄食;

Revealing the Feeding Preferences of Silver Pomfret for Jellyfish and the Detoxification Mechanisms Against Jellyfish Toxins Based on the Genome of Silver Pomfret

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Abstract: We sequenced the genomes of silver pomfret: the genome size of the female fish was 536.33 Mb, and that of the male fish was 553.79 Mb, with 550.82 Mb anchored on 24 gap-free chromosomes. After feeding silver pomfret with jellyfish, we transcribed or 16S sequenced the olfactory sac, tongue, brain, and intestinal microbiota to find that jellyfish feeding increased the expression of odor and taste receptor-related genes and appetite-regulating genes, as well as the abundance of five probiotic bacteria, *Lactococcus*, in the intestine. PLA2 is the main toxic protein in jellyfish venom. We identified a PLA2 inhibitor (PLI) in the silver pomfret genome, and simulation of protein-protein interactions revealed multiple interaction sites between PLI and jellyfish PLA2. CO-IP also showed that PLI interacts with two jellyfish PLA2 proteins. When we overexpressed and knocked down this gene in cells and tested the toxicity of jellyfish venom, we found that silver pomfret PLI had a significant inhibitory effect on jellyfish toxin.

Key words: Silver pomfret; genome; jellyfish; feeding;

美洲鲟响应高温胁迫的分子调控研究

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摘要: 基于高通量测序平台, 分析了美洲鲟鳃和肝脏组织在 24℃ (低温组)、27℃ (中温组) 和 30℃ (高温组) 不同养殖温度下的转录组和 miRNA 信息及蛋白质和代谢物的表达图谱。高温应激显著提高了美洲鲟 SOD、CAT 和皮质醇的活性; 组学研究结果表明, 抗氧化及热休克蛋白家族基因或蛋白的水平显著上调。DEGs 主要富集于内质网的蛋白质折叠、加工和输出途径, DEMs 的靶基因主要富集于粘着斑通路; 关键基因主要富集于代谢途径、氧化磷酸化和糖酵解/糖异生过程相关的通路。联合分析显示, 包括核苷二磷酸激酶 2、腺苷脱氨酶等在内的几种关键酶发生显著改变, 从而影响了鸟苷、鸟嘌呤和肌苷的代谢; L-丝氨酸、L-异亮氨酸、L-胱氨酸、胆碱和甜菜碱等几种重要氨基酸和化合物的含量发生了显著变化, DL-精氨酸和 L-组氨酸的水平也显著降低, 而皮质酮的水平却显著升高, 暗示美洲鲟在高温应激时体内可能更依赖氨基酸而非葡萄糖和脂肪酸来获取能量。

关键词: 美洲鲟; 高温应激; 转录组; 蛋白组; 代谢组

N/A

N/A
N/A

Abstract: N/A

Key words: N/A

团头鲂 *bcl2l13* 基因在低氧应激及细胞凋亡中的功能研究

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摘要: Bcl2l13 (B-cell lymphoma-2 like 13) 作为 Bcl2 家族的一成员, 在哺乳动物细胞凋亡和线粒体自噬中发挥重要功能, 为了解该基因在鱼类低氧应激中的作用, 本研究对团头鲂 *bcl2l13* 基因的序列及表达进行分析, 发现该基因编码的蛋白包含四个 BH 结构域, 一个 BHNo 和一个 TM 跨膜结构域。其编码蛋白主要位于线粒体, 删除 TM 结构域会改变其细胞定位。低氧处理后团头鲂肝脏线粒体受损, *bcl2l13* mRNA 和蛋白水平显著上升。双荧光素酶活性分析进一步显示 Hif-1 α 可与 *bcl2l13* 启动子结合, 调节其转录。将缺失不同结构域的突变载体转染细胞后, 发现过表达 *bcl2l13* 会抑制细胞增殖、促进细胞凋亡, 但缺少 TM、No 结构域后, 细胞增殖显著升高, 凋亡相关因子 caspase 3 的表达显著下调, 说明 *bcl2l13* 基因可促进细胞凋亡, 并且 TM 和 No 结构域在细胞凋亡和增殖中发挥重要作用。

关键词: 团头鲂; *bcl2l13* 基因; 低氧; 细胞凋亡

The role of *Megalobrama amblycephala bcl2l13* gene in hypoxia response and apoptosis

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Abstract: Bcl-2-like protein 13 (Bcl2l13), as a member of the Bcl2 family, plays an important role in cell apoptosis and mitochondrial autophagy of mammals. In order to investigate roles of the *bcl2l13* gene in fish, in this study, sequence and expression of *Megalobrama amblycephala bcl2l13* were analyzed, and showed that Bcl2l13 protein contained four BH domains, one BHNo domain and one TM domain. Bcl2l13 was mainly located in the mitochondria, while deletion of the TM domain changed its localization. After hypoxia treatment, the mitochondria damage of liver was observed, and the mRNA and protein levels of the *bcl2l13* and autophagy-related genes were significantly up-regulated. Luciferase reporter assays confirmed that the *bcl2l13* transcription was regulated by Hif-1 α mediated pathway. Overexpression of *bcl2l13* significantly inhibited cell proliferation and increased the apoptosis rate, while the trend towards with increased apoptosis was attenuated upon deletion of the TM and BHNo domains, especially the TM domain, indicating that the TM and BHNo domains of Bcl2l13 are necessary in apoptosis.

Key words: *Megalobrama amblycephala*; *bcl2l13* gene; Hypoxia; Apoptosis

DNA 甲基化和亚基因组优势揭示脂质代谢在“金虎杂交斑”杂种优势中的作用

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摘要: 新培育的“金虎杂交斑”新品种表现出偏父遗传的生长优势, 为研究杂种优势的潜在调控机制提供了良好模型。整合转录组、DNA 甲基化组和等位基因特异性表达 (ASE) 分析, 揭示了杂交种转录表达、表观修饰和亚基因组优势的调控规律。发现杂交种基因组 DNA 甲基化水平低于纯种亲本。ASE 分析支持父本亚基因组优势调节杂交种偏父遗传的生长优势, 在肌肉组织中, 父本偏移的差异基因全部上调表达。多组学结果强调了脂质代谢通路, 特别是“脂肪酸合成”、“EPA 生物合成”和“信号脂质”在金虎杂交斑杂种优势形成中的重要作用。金虎杂交斑 EPA 测定含量显著高于母本棕点石斑鱼 (8.46% vs 7.46%)。构建了金虎杂交斑杂种优势形成的潜在分子调控网络。其中, *fasn*、*pparg*、*dgat1*、*igf1*、*pomca*、*fgf8a*、*fgfr4* 被鉴定为关键基因。本研究结果解析了金虎杂交斑偏父遗传生长优势形成的分子遗传机制。

关键词: 杂交优势; 遗传效应; 生长; 表观遗传学; 调控机制

DNA methylation and subgenome dominance reveal the role of lipid metabolism in Jinhu grouper heterosis

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Abstract: Nowadays, a new germplasm of hybrid Jinhu grouper, exhibiting paternal-biased growth heterosis, has provided an excellent model for investigating the potential regulatory mechanisms of heterosis. We integrated transcriptome and methylome to unravel the changes of gene expression, epigenetic modification, and subgenome dominance in EFT compared with maternal *E. fuscoguttatus*. Integration analyses showed that the heterotic hybrids showed lower genomic DNA methylation levels than the purebred parent. Furthermore, allele-specific expression (ASE) detected paternal subgenome dominance-regulated paternal-biased heterosis. Multi-omics results highlighted the role of lipid metabolism, particularly “Fatty acid synthesis”, “EPA biosynthesis”, and “Signaling lipids”, in EFT heterosis formation. Coherently, our studies have proved that the eicosapentaenoic acid (EPA) of EFT was greater than that of maternal *E. fuscoguttatus* (8.46% vs. 7.46%). Finally, we constructed a potential regulatory network for control of the heterosis formation in EFT.

Key words: Heterosis; Genetic effect; Growth; Epigenetics; Regulatory mechanism

利用 geNorm、NormFinder 和 BestKeeper 综合评估曼氏无针乌贼 (*Sepiella japonica*) qRT-PCR 归一化的内参基因稳定性

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摘要: 曼氏无针乌贼 (*Sepiella japonica*) 是中国东海重要的经济头足类物种。近年来, 该物种的生物学研究尤其是基因表达分析逐渐增多。实时荧光定量 PCR (qRT-PCR) 的准确性依赖于内参基因标准化, 但目前尚无该物种的内参基因筛选研究。本研究评估了六种候选内参基因 (EF-1 γ 、EF-1 α 、GAPDH、 β -actin、18S rRNA、Tubulin) 在不同组织中的稳定性。结果表明, 各基因在不同组织中的 Ct 值有所差异, EF-1 α 和 EF-1 γ 的 Ct 值变化较小, 表达较为稳定。此外, 在相同的雌雄组织中, 除 Tubulin 外, 其他基因的 Ct 值波动显著不同。通过 geNorm、NormFinder、BestKeeper 和 Delta-Ct 四种算法评估, 研究发现, 雄性和雌性乌贼的基因排名具有组织特异性。同时, 综合排名的结果均表明 EF-1 γ 和 EF-1 α 在雄性和雌性中均为最稳定的内参基因, 其次为 GAPDH。

关键词: 曼氏无针乌贼; 实时荧光定量 PCR; 内参基因

Comprehensive evaluation the stability of internal control genes for qRT-PCR normalization in cuttlefish *Sepiella japonica* using geNorm, NormFinder, and BestKeeper

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Abstract: *Sepiella japonica* is an economically important cephalopod species in the East China Sea. Recent research, especially on gene expression, has increased. Quantitative real-time PCR (qRT-PCR) is widely used for such studies relying on selecting proper reference genes for accuracy. Yet no studies have screened reference genes in *S. japonica*. To ensure reliable qPCR results, six reference genes were assessed in male and female cuttlefish tissues: EF-1 γ , EF-1 α , GAPDH, β -actin, 18S rRNA, and Tubulin. Results showed that EF-1 α and EF-1 γ had the narrowest Ct ranges, indicating stable expression. Significant Ct differences for six genes were found except Tubulin in a few tissues of males and females, implying they may not be suitable for cross-gender comparisons. RefFinder, which contains geNorm, NormFinder, BestKeeper, and Delta-Ct, evaluated gene stability. The findings showed tissue-specific rankings for both male and female cuttlefish. Besides, four algorithms and comprehensive ranking predicted that the two most recommended genes in both genders were EF-1 γ and EF-1 α , followed by GAPDH.

Key words: *Sepiella japonica*, qRT-PCR, reference genes

曼氏无针乌贼(*Sepiella japonica*)的神经肽 F 及其受体基因: 鉴定、特征、表达及其在摄食调控中的作用

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摘要: 神经肽 F (NPF)是脊椎动物神经肽 Y (NPY)的同源物, 能与 G 蛋白偶联受体 NPFR 相互作用。NPF/NPFR 的分子结构、分布模式以及生物学功能已经在部分无脊椎动物的研究中被鉴定, 但是关于软体动物的报道较为缺乏。本研究在曼氏无针乌贼(*Sepiella japonica*)中鉴定和表征出 S_jNPF 以及 S_jNPFR, 多重比对和系统发育分析的证据表明 S_jNPF 与玄妙微鳍乌贼(*Idiosepius paradoxus*)具有很高同源性, S_jNPFR 与虎斑乌贼(*Sepia pharaonis*)有很高同源性。原位杂交和 RT-PCR 数据揭示了两者在乌贼大脑多个功能叶和以及其他组织中的时空表达模式。此外饥饿与再投喂实验表明基因表达水平、胃蛋白酶活性和肠道组织学与饥饿正相关, 与再投喂负相关, 这表明它们对抵抗饥饿和促进进食等行为具有促进作用。本研究目的在于探究 NPF/NPFR 分子特征和功能, 为后续研究提供支持。

关键词: NPF; NPFR; 分子克隆; 投喂调节; 饥饿胁迫

Neuropeptide F and its receptor genes in the cephalopod *Sepiella japonica*: identification, characterization, expression and possible role in starvation resistance and food intake promotion

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Abstract: Neuropeptide F (NPF) is a homolog of vertebrate neuropeptide Y (NPY) and interacts with the G protein-coupled receptor-NPFR, but there are few reports about mollusks. In this study, the NPF and NPFR genes were identified and characterized in *Sepiella japonica*, hereafter called S_jNPF and S_jNPFR, respectively. Evidences from multiple alignments and phylogenetic analysis indicate that S_jNPF exhibits a high degree of homology with the NPF of *Idiosepius paradoxus*, and S_jNPFR demonstrates a high degree of homology with the NPFR of *Sepia pharaonis*. In situ hybridization and RT-PCR data reveal the spatiotemporal expression patterns of both genes in various functional lobes of the brain and other tissues. Furthermore, starvation stress experiments show that the gene expression levels, gastric protease activity, and intestinal histology are positively correlated with starvation and negatively correlated with refeeding, suggesting their potential role in hunger resistance and the promotion of food intake.

Key words: Neuropeptide F; Neuropeptide F receptor; Molecular cloning; Feeding regulation; Hunger stress

东北地区毛蚶池塘养殖试验

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摘要: 为探究在东北地区进行毛蚶池塘养殖的可行性, 本课题组开展了不同规格毛蚶苗种的室外池塘人工养殖试验, 试验期间, 每三个月对苗种的壳长、壳高、壳厚和质量分别进行测量和记录, 并对所得数据统一进行整理和分析。分析结果表明, 在稳定的水体环境中, 经过 9 个月的养殖, 毛蚶大、小规格苗种的生长指标均出现了显著性的增长, 且小规格苗种的生长速度、生长幅度、成活率等均大于大规格苗种, 说明在东北地区可以进行毛蚶的人工池塘养殖工作, 且在同等环境条件下, 投放较小规格苗种, 更有利于毛蚶的快速生长, 以及保持更高的成活率。本研究结果可为毛蚶在东北地区的推广养殖提供一定的技术支持。

关键词: 毛蚶, 不同规格苗种, 池塘养殖, 生长指标

Cockle pond culture experiment in Northeast China

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Abstract: In order to explore the feasibility of pond breeding in northeast China, the experiment of different specifications. During the experiment, the shell length, height, thickness and quality of the seedlings were measured and recorded every three months, and sorted and analyzed the data obtained. The analysis results show that in the stable water environment, after nine months of breeding, the growth index of large, small size seedlings are significant growth, and small size seedlings growth rate, growth, survival rate are greater than the large size seedlings, can be in northeast China, and under the same environmental conditions, on the smaller size seedlings, more conducive to the rapid growth of the cockles, and maintain a higher survival rate. The results of this study can provide some technical support for the promotion of cockca breeding in northeast China.

Key words: Cockles, seedlings of different sizes, pond culture, growth indicators

马口鱼全雄育种技术体系建立与应用

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摘要：性别控制育种不仅是鱼类新种质创制的重要方法，也是种质控制的重要手段。马口鱼，是分布极为广泛的小型肉食性鱼类，其多不饱和脂肪酸（DHA 和 EPA）丰富，熟后肌间刺软化，鳞片薄且软，不用打鳞，出肉率高，是最优质的水产品之一。马口鱼雄鱼体色鲜艳，达上市规格时较雌鱼大 70% 以上，因此全雄马口鱼培育与推广对产业高质量发展具有重要意义。团队通过性别控制育种技术，确定了马口鱼性别分化的关键时间、雌性化诱导的窗口期与浓度、开发了鉴定 XX/XY/YY 基因型的分子标记，成功培育了 XY 伪雌鱼、YY 超雄鱼、YY 伪雌鱼，生产出 2 万尾 YY 超雄鱼群体，建立了马口鱼全雄育种技术体系。该体系的建立与应用，为马口鱼新品种培育提供了重要技术支撑，有效保障了优异种质控制，为马口鱼产业高质量发展提供了重要动力。

关键词：性别控制；性别分化；分子标记；全雄；性逆转

Establishment and application of all-male breeding technology system for horsemouth carp *Opsariichthys bidens*

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Abstract: Sex control breeding is not only an important method for creating new genetic stocks of fish, but also an important means of controlling genetic material. Horsemouth carp, a small predatory fish with a wide distribution, has rich polyunsaturated fatty acids (DHA and EPA). Furthermore, the muscular bone are softened after cooking, there is no need to scale due to the thin and soft scales, the meat yield is high, making it one of the best aquatic products. Male horsemouth carp have bright coloration, and are 70% larger than female fish when they reach market size, making all-male common carp breeding and promotion important for the high-quality development of the industry. Our team used sex control breeding technology to determine the key time for sex differentiation in horsemouth carp, the window period and concentration for feminization induction, developed molecular markers for identifying XX/XY/YY genotypes, successfully bred XY pseudo-female fish, YY super-male fish, and YY pseudo-female fish, and produced a population of 20,000 YY super-male fish, establishing a breeding technolo

Key words: sex control, sex differentiation, molecular marker, all-male, sex reversal

全球气候变化下低氧和热暴露对团头鲂抗氧化状态、免疫、凋亡和代谢的影响：抵御低氧和热暴露

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摘要：团头鲂是我国经济效益显著的主要草食性鱼类，但由于全球变暖和集约化养殖等因素导致的缺氧和高温，使其生存和生长面临严重挑战。为了评估这些应激源的联合效应，我们采用双因素交叉试验，评估同时暴露于低氧（2 mg/L）和热（35°C）对团头鲂氧化应激、免疫、凋亡和代谢的影响。结果表明，缺氧和热暴露引起鱼类氧化应激和 MDA 积累，导致免疫抑制和细胞凋亡。值得注意的是，联合应激源比暴露于单一应激源对生物体的负面影响更大。基于 GC-MS 分析，LO、HT 和 HL 组分别发现 100、108 和 108 个差异代谢物。3 组共有 58 个差异代谢物，其中 16 个上调，10 个下调。同时发现肝脏中氨基酸、核苷酸、脂肪酸等代谢产物异常。此外，无氧代谢生物标志物的积累标志着无氧代谢的开始，甘油磷脂的积累可能维持细胞膜稳定性。这些结果将有助于理解鱼类的缺氧和热应激机制，并为水产养殖管理提供理论依据。

关键词：团头鲂，低氧，高温，氧化状态，免疫反应，细胞凋亡，代谢

Impact of heat and hypoxia stresses on the antioxidant status, immunity, apoptosis and metabolism of *Megalobrama amblycephala* under global climate changes: defense against heat and hypoxia stresses

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Abstract: *Megalobrama amblycephala*, a major herbivorous fish in China, faces challenges due to global warming and intensive farming, leading to hypoxia and heat. A two-factor cross experiment assessed the combined effects of hypoxia (2 mg/L) and heat (35°C) on *M. amblycephala*, revealing increased oxidative stress, MDA accumulation, immunosuppression, and apoptosis in fish. The combined stress had a greater negative impact than single stressors. GC-MS analysis identified 100, 108, and 108 differential metabolites in LO, HT, and HL groups, respectively, with 58 common metabolites, 16 upregulated, and 10 downregulated. Abnormalities in liver amino acids, nucleotides, and fatty acids were observed. Anaerobic metabolism biomarkers indicated the start of anaerobic metabolism, and glycerophospholipids may stabilize cell membranes. These findings aid in understanding fish stress mechanisms under hypoxia and heat, providing a theoretical basis for aquaculture management.

Key words: *Megalobrama megalobrama*, hypoxia, heat, oxidation state, immune response, apoptosis, metabolism

银鲳性别分化过程中幼年雌雄同体的发生及分子机制

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摘要：银鲳 (*Pampus argenteus*) 是海洋经济鱼类中市场价格较高的鱼类之一，具有性别大小二态性，雌鱼的生长速度快于雄鱼，但是该物种的性别分化过程尚未得到研究。组织学研究显示，在性别分化初期全部个体分化出卵母细胞，随后部分个体发生 PN 卵泡的凋亡过程，分化为精巢，此时会出现罕见的幼年雌雄同体期。我们根据 PN 期卵泡和性腺中凋亡小体的比例，将银鲳的性腺发育进一步分为三种不同的类型：A、B、C 型。A 型个体的卵母细胞稳定发育，而 B 型和 C 型个体则经历全部或部分卵母细胞的凋亡，最后发育出精小囊。转录组分析揭示精巢中卵母细胞的凋亡受到凋亡信号的调控，卵巢和精巢分化相关基因同时高表达是出现幼年雌雄同体的原因之一。此外，我们发现性别大小二态性出现于性别分化之前，进一步证据表明，性别分化关键时期雌鱼的性腺和血清中的脂含量显著高于雄鱼，说明银鲳的性别分化可能受到代谢的影响。

关键词：幼年雌雄同体，性腺分化；脂代谢；银鲳

The occurrence and molecular mechanism of juvenile hermaphroditism during the sex differentiation process in silver pomfret.

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Abstract: The silver pomfret (*Pampus argenteus*) is one of the most economically valuable marine fish, characterized by its high market price. This species exhibits sexual size dimorphism, with females growing faster than males. However, the process of sexual differentiation in silver pomfret remains under-researched. Histological studies indicate that during the early stages of sexual differentiation, all individuals develop oocytes. Subsequently, some individuals undergo apoptosis of the primary oocytes, transitioning into testes, which is accompanied by a rare juvenile hermaphroditic phase. We classified the gonadal development of silver pomfret into three distinct types—A, B, and C—based on the proportion of primary oocytes and apoptotic bodies in the gonads. Type A individuals show stable oocyte development, while types B and C experience complete or partial oocyte apoptosis, ultimately resulting in testicular structures. Transcriptomic analysis reveals that oocyte apoptosis in the testes is regulated by apoptotic signals, and the simultaneous high expression of genes associated with ovari

Key words: juvenile hermaphroditism, gonadal differentiation; lipid metabolism; *Pampus argenteus*

基于代谢组的不同采收期坛紫菜 品质差异分析

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摘要: 坛紫菜是我国最重要的大型经济海藻之一, 味道鲜美, 营养丰富, 深受人们喜爱。为了阐明不同采收水次坛紫菜藻体品质发生差异的规律, 本研究采用广靶代谢组和靶向代谢组技术对六个产地的四个采收时期坛紫菜藻体的口感品质、色泽品质和风味品质相关的代谢物进行了鉴定, 结果显示: 1.随着采收次数递增, 纤维素、半纤维素和琼胶等细胞壁组分的积累使坛紫菜藻体变厚, 使坛紫菜的硬度和咀嚼性逐步增大, 从而使得坛紫菜的口感品质变差。2.随着采收次数递增, 叶绿素 A 和藻红蛋白含量显著下降, 藻体色泽由乌黑变浅绿色。3.坛紫菜鲜味的主要贡献者谷氨酸与采收次数呈显著的负相关关系, 同时, 缬氨酸、精氨酸、甲硫氨酸和苯丙氨酸等苦味呈味氨基酸在部分产地第四次收获期时超过风味阈值, 这表明采收次数增加后, 鲜味氨基酸含量的下降以及苦味呈味氨基酸含量的增加共同调控着坛紫菜的风味品质。综上, 本研究结果为不同采收期坛紫菜的品质差异机制解析提供了关键代谢物。

关键词: 坛紫菜; 采收次数; 风味品质; 口感品质; 色泽品质

Analysis of quality difference of *Pyropia haitanensis* at different harvest period based on metabolome

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Abstract: *Pyropia haitanensis* is one of the most important large-scale economic seaweeds in China. In order to elucidate the quality differences of *Pyropia haitanensis* at different harvest periods, this study used broad-target metabolomics and targeted metabolomics techniques to analyze the taste, color and flavor quality at four harvest periods in six production areas. The results showed: 1. The accumulation of cell wall components such as cellulose and agar makes the algal body thicker. The hardness and chewiness gradually increase, thus making the taste quality deteriorate. 2. The content of chlorophyll A and phycoerythrin, PE decreases significantly, and the color of the algae changes from black to green. 3. With the harvest periods increases, the decrease in the content of umami amino acids and the increase in the content of bitter-flavor amino acids jointly regulate the flavor quality of *Pyropia haitanensis*. In summary, the results of this study provide key metabolites for the analysis of the quality difference mechanism of *Pyropia haitanensis* at different harvest periods.

Key words: *Pyropia haitanensis*; harvest periods; flavor quality; taste quality; color quality

罗氏沼虾肠道细菌的分离、鉴定与评价

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摘要：益生菌是一种活的微生物食品补充剂，已被证明对动物健康具有有益的影响。长期以来，内源性益生菌因其具有促进健康的特性而被广泛使用，并已成为水产养殖中生长改善的研究热点。为探究罗氏沼虾和(巨型河虾)肠道内源性益生菌的益生潜力，从罗氏沼虾和(巨型河虾)肠道中共分离出 367 株菌株罗氏沼虾。经 16S rDNA 序列分析，234 株分离菌被鉴定为格氏乳球菌，占可培养肠道细菌总数的 63.76%，提示该菌为菌群的主要成分。为了揭示 *L. garvieae* 的益生特性，对该分离菌株进行了形态学、生理学和生物化学表征。对其产酶能力、抑菌活性、耐酸性、耐高温性和耐 pH 性进行了评估。体外实验表明，*L. garvieae* (No. C6a2) 生长速度较快，迅速进入对数期。此外，该菌株还具有产酸、耐酸、产酶等特性，对致病性金黄色葡萄球菌、嗜水气单胞菌和维氏气单胞菌具有较强的抑菌活性，但是，它缺乏耐高温的能力。

关键词：罗氏沼虾；肠道细菌；益生菌；格氏乳球菌

Isolation, identification, and evaluation of intestinal bacteria in *Macrobrachium rosenbergii*

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Abstract: Probiotics are live microbial food supplements that have been shown to have beneficial effects on animal health. Endogenous probiotic bacteria have long been used for their proposed healthpromoting properties and have become a hot research topic in growth improvement in aquaculture. The endogenous probiotic bacteria from intestines of *Macrobrachium rosenbergii* (giant river prawn) was explored for their probiotic potential, from which 367 bacterial strains were isolated from the intestine of *M. rosenbergii*. After 16S rDNA sequence analysis, 234 isolates were identified as *Lactococcus garvieae*, which accounted for 63.76% of the total number of culturable intestinal bacteria, suggesting that this bacterium was the main component of the microbiota. Furthermore, to reveal the probiotic properties of *L. garvieae*, this isolated bacterial strain was characterized morphologically, physiologically, and biochemically. Its enzyme production capacity, bacteriostatic activity, and resistance to acid, high temperature, and pH, were assessed. In vitro experiments showed that the *L. garvieae*

Key words: *Macrobrachium rosenbergii*; intestinal bacteria; probiotic; *Lactococcus garvieae*

鱼类 IL-17 信号通路的人工结构域重排改造及其应用

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摘要: 微生物的合成生物学开展得火热, 动物的通路改造却相对滞后: 主要依赖基因敲除获得功能缺失表型, 或者通过点突变改变基因活性和表达, 而外源基因转入被视为是危险技术。其实自然界还有另外一种重要机制——结构域重排, 能够有效重构通路并产生新功能。IL-17 通路主导黏膜修复, 被誉为免疫的主指挥, 但在水产动物中研究较少。本研究分析结构域重排如何塑造 IL-17 通路, 并从中挖掘潜在的改造靶点。我们发现, IL-17 通路是由神经营养因子通路和 TLR/IL-1R 通路通过结构域重排形成的嵌合通路, 并在后续演化中多次结构域重排, 导致该通路在不同动物中展现出不同的功能模式。其中, 鱼类 IL-17 通路丢失了死亡结构域, 使其激活能力降到不足原先百分之一。我们通过人工重排恢复了斑马鱼 IL-17 通路的死亡结构域, 发现这一改造不仅恢复了通路的激活性能, 还提升了仔鱼的抗菌能力。该研究为开发基于人工结构域重排鱼类育种技术提供了理论基础。

关键词: IL-17; 黏膜稳态; 通路改造; 结构域重排

Artificial Domain Rearrangement of Fish IL-17 Signaling Pathway and Its Application

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Abstract: While synthetic biology in microorganisms has advanced rapidly, animal pathway modification has lagged behind, relying mostly on gene knockouts or point mutations. Exogenous gene transfer is often seen as risky, but domain rearrangement, a natural mechanism, can effectively remodel pathways to generate new functions. The IL-17 signaling pathway, crucial for mucosal repair and the immune response, is less studied in aquatic animals. This study explored how domain shuffling shapes the IL-17 pathway and identified modification targets. We found that the IL-17 pathway is a chimeric system formed by domain shuffling between the neurotrophin and TLR/IL-1R pathways, with several evolutionary rearrangements leading to diverse functions. In fish, the loss of the death domain reduced activation capacity by over 99%. Artificially restoring this domain in zebrafish IL-17 improved both pathway activation and antibacterial capabilities, providing a foundation for fish breeding technologies using artificial domain rearrangement.

Key words: IL-17, mucosal Homeostasis, pathway engineering, domain shuffling

光强对两个坛紫菜品系的生长、碳氮磷元素含量和有机碳释放的影响

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摘要：本研究分析四个光强（5、50、200 和 500 $\mu\text{mol m}^{-2} \text{s}^{-1}$ ）对坛紫菜品系（W28, WO15-4）的生长速率、组织 CNP 元素含量影响。结果表明，随光强增加两个品系的生长速率呈现先增后降的趋势，在 200 $\mu\text{mol m}^{-2} \text{s}^{-1}$ 最高。组织 C 含量随光强增加呈上升趋势，而组织 NP 含量则呈现下降趋势。这也导致 C:N 和 C:P 比值增加，表明高光抑制了 NP 的吸收。两个品系释放的有机碳占总碳比例随光强增加而上升，且 W28 的增幅明显高于 WO15-4。具体而言，两个品系在有机碳释放方面表现出显著差异，W28 的溶解有机碳（DOC）释放速率随光强增加而增加，而 WO15-4 的 DOC 释放速率不受光强影响。此外，两个品系的颗粒有机碳（POC）释放速率在高光条件下均有所上升，且 W28 的增幅大于 WO15-4。研究表明坛紫菜有机碳释放速率对 4 个光强的应答存在品系特异性，这种差异可能源自两个品系的光合生理和遗传差异。

关键词：光照强度；坛紫菜；碳代谢；溶解有机碳；颗粒有机碳

Effects of light intensity on growth, carbon, nitrogen and phosphorus content and organic carbon release of two *Pyropia haitanensis* strains

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Abstract: The results showed that the growth rate of the two strains increased and then decreased with increasing light intensity, and was highest at 200 $\mu\text{mol m}^{-2} \text{s}^{-1}$. Tissue C content showed an increasing trend with increasing light intensity, while tissue NP content showed a decreasing trend. This also led to an increase in the C:N and C:P ratios, indicating that high light inhibited NP uptake. The proportion of organic carbon to total carbon released by the two strains increased with increasing light intensity, and the increase was significantly higher in W28 than in WO15-4. Specifically, the two strains showed significant differences in organic carbon release, with the rate of dissolved organic carbon (DOC) release from W28 increasing with increasing light intensity, whereas the rate of DOC release from WO15-4 was not affected by light intensity. In addition, the release rate of particulate organic carbon (POC) increased under high light conditions in both strains, and the increase in W28 was greater than that in WO15-4.

Key words: Light intensity; *Pyropia haitanensis*; Carbon metabolism; Dissolved organic carbon; Particulate organic carbon

HGT 调控紫菜适应性进化的 基因组特征

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

关键词: 坛紫菜; 基因组; 共生微生物; 水平基因转移

Genomic characteristics of HGT-mediated adaptive evolution in *Pyropia/Porphyra*

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Abstract:

Intertidal algae may adapt to environmental challenges by acquiring genes from other organisms and relying on symbiotic microorganisms. Here, we obtained a symbiont-free and chromosome-level genome of *Pyropia haitanensis* (47.2 Mb), a type of intertidal algae, by using multiple symbiont screening methods. We identified 286 horizontal gene transfer (HGT) genes, 251 of which harbored transposable elements (TEs), reflecting the importance of TEs for facilitating the transfer of genes into *P. haitanensis*. Notably, the bulked segregant analysis revealed that two HGT genes, sirohydrochlorin ferrochelataase and peptide-methionine (R)-S-oxide reductase, play a significant role in the adaptation of *P. haitanensis* to heat stress. Besides, we found *Pseudomonas*, *Actinobacteria*, and *Bacteroidetes* are the major taxa among the symbiotic bacteria of *P. haitanensis* (nearly 50% of the HGT gene donors). Among of them, a heat-tolerant actinobacterial strain (*Saccharothrix* sp.) was isolated and revealed to be associated with the heat tolerance of *P. haitanensis* through its regulatory effects on the genes

Key words: *Pyropia haitanensis*; genome; symbiotic microorganism; horizontal gene transf

基于离子组学和代谢组学的坛紫菜产地溯源 技术开发与应用

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摘要：坛紫菜广泛栽培于我国南北方沿海，具有很高的营养价值。不同地理来源的坛紫菜的口感、风味，售价差异较大，建立溯源技术对坛紫菜市场的规范化发展具有重要意义。本研究共采集了5个主产区（山东省青岛市、江苏省连云港市、浙江省象山市、福建省福州市和广东省汕头市）4个水次的藻体样品，并测定了相关海水环境因子。通过电感耦合等离子体质谱和广泛靶向代谢组学检测技术在紫菜样品中检测矿质元素及代谢物含量，使用OPLS-DA成功地对不同产地的坛紫菜进行了分类，预测模型显示出良好的拟合度和可预测性。冗余分析结果表明，硝酸盐、溶解氧、海水盐度、总磷对坛紫菜品质的影响最为显著（ $P < 0.05$ ），是影响五个产地坛紫菜品质指标的主要环境因子。本研究通过离子组学和代谢组学方法结合化学计量学成功建立了坛紫菜产地溯源技术，并确定了影响的坛紫菜品质的主要环境因素，有助规范坛紫菜市场，保障产品质量和消费者权益。

关键词：坛紫菜 产地判别 矿质元素 代谢物 化学计量学 环境因素

Development and application of origin traceability technology of *Pyropia haitanensis* based on ionomics and metabolomics.

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Abstract : *Pyropia haitanensis* is widely cultivated along the coasts of northern and southern my country. The taste, flavor, and selling price of *P.haitanensis* from different geographical sources vary greatly. The establishment of traceability technology is of great significance to the standardized development of the *P.haitanensis* market. This study collected algae samples from 5 main producing areas and measured the relevant seawater environmental factors. The content of mineral elements and metabolites in *P.haitanensis* samples was detected using inductively coupled plasma mass spectrometry and broadly targeted metabolomics detection technology. OPLS-DA was used to successfully classify *P.haitanensis* from different origins, shows good fit and predictability. The results of redundancy analysis showed that nitrate, dissolved oxygen, seawater salinity, and total phosphorus had the most significant impact on the quality of *P.haitanensis* ($P < 0.05$), and were the main environmental factors affecting the quality indicators of *P.haitanensis* from the five producing areas.

Key words:: *Pyropia haitanensis*, origin identification, mineral elements, metabolites, stoichiometry, environmental factors

脊尾白虾褪黑素昼夜节律变化及 眼柄调控作用研究

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摘要: 本研究旨在探究褪黑素 (MT, Melatonin) 在脊尾白虾 (*Exopalaemon carinicauda*) 体内的合成机制、分子调控机制。本实验在自然光照条件下取不同时间点 (CZ 为 8:00、AX 为 16:00、BW 为 24:00) 脊尾白虾的血淋巴和眼柄组织, 利用酶标仪测出 MT 的含量; 取眼柄组织, 利用 Illumina HiSeq X-ten™4000 平台进行转录组测序分析。研究结果表明脊尾白虾血淋巴和眼柄组织中 MT 含量存在的昼夜节律, 具有同步性, 且光照会抑制 MT 的合成; 转录组测序结果显示, 共筛选出 1957 个差异基因, KEGG 通路富集分析显示基因显著富集 ($p < 0.01$) 在昼夜节律, 光传导, 糖胺/其他聚糖降解, 糖鞘脂生物合成, 蛋白质消化吸收, 溶酶体, 胆固醇代谢等相关通路上, 说明眼柄调控对昼夜节律、光传到、能量代谢显著影响。本研究为今后了解 MT 在脊尾白虾体内的功能调控提供参考。

关键词: 脊尾白虾; 褪黑素; 昼夜节律; 转录组测序

Study on circadian rhythm change of melatonin and regulation of eye stalk in *Exopalaemon carinicauda*

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Abstract: This study aims to explore the synthesis mechanism and molecular regulation mechanism of melatonin (MT) in the *exopalaemon carinicauda*. In this experiment, the hemolymph and eye handle tissue of the *exopalaemon carinicauda* were taken at different time points (8:00 for CZ, 16:00 for AX and 24:00 for BW), and the content of MT was measured using a microplate reader; Transcriptome sequencing analysis was performed using the Illumina HiSeq X-ten™4000 platform. The results indicate the circadian rhythm of MT content in the hemolymph and eye stalk tissue of *exopalaemon carinicauda*. It has synchronization property, and light will inhibit MT synthesis; Transcriptome sequencing revealed that a total of 1957 differential genes were screened, KEGG pathway enrichment analysis revealed a significant enrichment of genes ($p < 0.01$) in the circadian rhythm, Phototransduction, Glycosaminoglycan/Other glycan degradation, Various types of N-glycan biosynthesis, Protein digestion and absorption, Lysosome, Cholesterol metabolism and other related channels. This indicates that eye stalk regulation has sign

Key words: *Exopalaemon carinicauda*; Melatonin; Circadian rhythm; Transcriptome sequencing

碱胁迫对日本沼虾鳃组织的影响鉴定

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摘要：日本沼虾是中国一种重要淡水经济生物，但日本沼虾耐碱力较弱，不能在中国大多数盐碱水体中进行养殖，因此我们需要对该物种进行耐碱能力的遗传改良。本研究旨在通过组织学观察、抗氧化酶测定、代谢分析和转录组分析来探究不同碱度胁迫 96h 后对日本沼虾鳃组织的影响。本研究结果显示，碱度胁迫影响日本沼虾鳃组织中丙二醛、谷胱甘肽和谷胱甘肽过氧化物酶含量，表明这些抗氧化酶在保护机体免受碱胁迫的机制过程中起到重要作用；代谢途径、次生代谢物的生物合成、植物次生代谢物的生物合成、不同环境下的微生物代谢和氨基酸的生物合成是差异表达代谢物的主要富集代谢途径；水体碱度为 12mmol/L 时对基因表达的影响最大；吞噬体、溶酶体、糖酵解、嘌呤代谢、氨基糖和核苷酸糖代谢和内含作用是主要富集代谢途径因此推测这些代谢途径可能参与日本沼虾应对碱胁迫的机制过程。本研究探究碱度胁迫对日本沼虾鳃组织的影响，为日本沼虾耐碱性的遗传育种提供依据。

关键词：日本沼虾，碱度胁迫，鳃，代谢分析，转录组分析

Identiffication of the effects of alkalinity exposure on the gills of oriental river prawns, *Macrobrachium nipponense*

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Abstract: *Macrobrachium nipponense* is a commercial freshwater species in China. But its alkali tolerance ability is unable to support ti be cultured in most saline-alkali source in China. Thus, it's needed to perform the genetic improvement of alkali tolerance. In the present study, we aimed to analyse the effects of alkali treatment on gills after 96h alkalinity exposure under the different alkali concentrations through performing the histological observations, measurement of antioxidant enzymes and metabolic proffling analysis. The results of the present study revealed that alkali treatment stimulated the contents of malondialdehyde, glutathione, glutathione peroxidase in gills. Metabolic pathways, Biosynthesis of secondary metabolites, Biosynthesis of plant secondary metabolites, Microbial metabolism in diverse environments, Biosynthesis of amino acids were the main enriched metabolic pathways of differentially expressed metabolites. The present study identiffied the effects of alkali treatment on gills, providing evidences for the genetic improvement of alkali tolerance in *M. nipponense*.

Key words: *Macrobrachium nipponense*, Alkalinity exposure, Gill, Metabolic proffling analysis, Transcriptome proffling analysis

基于转录组分析的四指马鲛免疫应答 机制初探

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摘要: 本研究利用 Illumina 高通量测序平台, 对四指马鲛 (*Eleutheronema tetradactylum*) 感染哈维氏弧菌 (*Vibrio harveyi*) 前后的肠道 (Cg-IN-VS-Ig-IN) 和肝脏 (Cg-LI-VS-Ig-LI) 进行了转录组测序分析。结果显示, 四个组共 12 个样本过滤低质量数据后, 最后得到高质量的 reads 分别为 127500428 条、120460136 条、116489562 条、118590388 条。所有样本高质量的 reads 占原始序列的占比范围在 99.61%-99.71%。测序碱基质量值达到 Q20 以上水平的碱基数目及占 Clean Data 的百分比在 97.81%-98.48%之间, Q30 比例在 93.74%-95.46%之间, 各样品 GC 含量在 46.81%-48.47%之间。

关键词: 四指马鲛; 哈维氏弧菌; RNA-Seq; 转录组; 免疫应答;

无

无
无

Abstract: 无

Key words: 无

基于全基因组重测序的坛紫菜种藻遗传结构分析

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摘要：本研究采集了13个坛紫菜主产区育苗场的种藻，利用全基因组重测序技术对种藻群体进行了遗传多样性和遗传结构分析。结果显示，坛紫菜种藻群体的期望杂合度 H_e 为 0.34-0.35，观测杂合度 H_o 为 0.08-0.13，多态信息含量 PIC 为 0.27，香农信息指数 I 为 0.72-0.74，核苷酸多样性 P_i 为 0.0014-0.0018，其遗传多样性处于中等水平。系统发育、主成分分析和群体结构分析表明，坛紫菜种藻群体分为两大分支，按照地理位置表现出明显的聚类关系。整体上，福建北方种藻群体与福建南方种藻群体 F_{st} 值为 0.066，呈中等分化水平，可能是种藻来源不同且相对单一，同时地理距离较远，基因交流较少所致；但是福州桂湾、平潭以及浙江台州市三门县的种藻样品分散在两个分支中，暗示上述地区可能存在人为跨区域引种以及混合不同来源种藻采果孢子苗的现象。本研究结果为准确评估坛紫菜种藻资源遗传多样性奠定了理论基础。

关键词：坛紫菜，种藻，群体结构，全基因组重测序

Revealing genetic population structure of the *Pyropia haitanensis* seed populations by whole-genome resequencing

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Abstract : In this study, we collected the seed populations of *Pyropia haitanensis* from 13 nurseries, and analysed the genetic diversity and genetic structure by using whole-genome resequencing. The results demonstrated that the genetic diversity was at a moderate level. The results of phylogenetic, principal component and population structure analysis revealed that the populations can be divided into two major branches, which exhibited distinct clustering relationships according to geographic locations. The F_{st} value between the northern Fujian and southern Fujian populations indicated a moderate level of differentiation, probably due to the different and homogeneous sources, as well as the long geographical distance and the less gene flow. However, the samples from Guiwan, Pingtan and Sanmen, were scattered in two branches, suggesting that there may be artificial introduction of species across regions and mixing of seed populations from different sources in these areas. The findings established a theoretical foundation for the precise assessment of the genetic diversity of *P. haitanensis*.

Key words: : *Pyropia haitanensis*, the seed populations, population structure, whole-genome resequencing

基于脂质组学的坛紫菜自由丝状体成熟机制解析

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摘要: 丝状体发育不同步限制了紫菜良种的规模化推广。脂质作为植物细胞的重要成分, 不但为各种新陈代谢提供能量, 对于丝状体成熟发育也至关重要, 然而其在调控丝状体成熟过程中的具体机制尚不清楚。因此, 本研究利用脂质代谢组和转录组相结合的方法, 对促熟不同时间后, 丝状体成熟度存在差异的两个坛紫菜品系进行分析, 以探究丝状体成熟的分子机制。结果显示, 甘油磷脂代谢通路是促熟过程中的重要代谢通路, 其中易成熟品系 (S1) 比不易成熟品系 (S2) 的丝状体更早开启甘油磷脂代谢中 PC 的合成和代谢, 更快的产生花生四烯酸, α -亚麻酸, 亚油酸等脂质物质来提高膜的流动性以及增强抗氧化能力。同时, 两个品系在促熟前期都会产生大量的三酰甘油, 降低膜脂的不饱和程度, 以应对成熟过程中的高温影响, 但 S1 比 S2 更快地将三酰甘油代谢利用, 提供能量和维持脂质稳态, 从而更快的促进丝状体的成熟和发育。

关键词: 坛紫菜, 丝状体成熟, 脂质代谢

Lipidomics-based analysis of the maturation mechanism of free conchocelis in *Pyropia haitanensis*

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Abstract : We used a combination of lipid metabolomics and transcriptomics to analyze the conchocelis of two *P. haitanensis* strains with differences in maturity at different time after promotion of ripening to investigate the molecular mechanism of conchocelis maturation. Studies have revealed that the glycerophospholipid metabolic pathway is an important metabolic pathway in the process of ripening. The conchocelis of the early-maturing strain (S1) started the synthesis and metabolism of PC in glycerophospholipid metabolism earlier than those of the slowly-maturing strain (S2), and produced lipids, such as arachidonic acid, α -linolenic acid, and linoleic acid, to improve the fluidity of the membranes and to enhance antioxidant capacity more quickly. Both strains produced large amounts of triacylglycerols to reduce the unsaturation of membrane lipids to cope with the effects of high temperatures during the ripening process, but S1 metabolised triacylglycerols faster than S2 to provide energy and maintain lipid homeostasis, thus promoting conchocelis maturation and development more quickly.

Key words:: *Pyropia haitanensis*, conchocelis maturation, lipid metabolomic

碱度暴露对日本沼虾肝胰腺抗氧化状态、 代谢功能和免疫反应的影响

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摘要: 日本沼虾 (*Macrobrachium nipponense*) 是中国重要的淡水经济物种。本研究通过组织学观察、抗氧化酶活测定和转录组图谱分析测定在碱度为 0 (对照组)、4、8 和 12mmol/L, 暴露时间为 96h 的条件下碱应激对日本沼虾肝胰腺的影响。研究发现, 高碱处理 (>8mmol/L) 会破坏肝胰腺管腔和液泡的正常结构, 并显著刺激超氧化物歧化酶、过氧化氢酶的活性以及总抗氧化能力的水平。代谢图谱分析表明, 本研究中差异表达代谢物的主要富集代谢途径与植物和其他水生动物因环境胁迫引起的代谢途径一致。在转录组图谱分析中, 通过 0mmol/L 与 12mmol/L 的比较筛选出了主要的富集代谢途径和一些显著上调的基因, 预测这些代谢途径和基因参与了日本沼虾对碱应激的适应过程。

关键词: 日本沼虾; 肝胰腺; 碱处理; 代谢图谱分析; 转录组图谱分析

Effects of Alkalinity Exposure on Antioxidant Status, Metabolic Function, and Immune Response in the Hepatopancreas of *Macrobrachium nipponense*

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Abstract: *Macrobrachium nipponense* is an important freshwater economic species in China. In this study, the effects of alkalinity exposure on the hepatopancreas of *M. nipponense* were measured under the alkali concentrations of 0 (control), 4, 8, and 12mmol/L with the exposure time of 96h through histological observations, measurement of antioxidant enzymes and transcriptome profiling analysis. The present study identified that the high-alkali treatment (>8mmol/L) damaged the normal structures of the lumen and vacuoles and significantly stimulated the levels of SOD, CAT, and T-AOC. Metabolic profiling analysis revealed that the main enriched metabolic pathways of differentially expressed metabolites in the present study were consistent with the metabolic pathways caused by environmental stress in plants and other aquatic animals. In the transcriptome profiling analysis, the main enriched metabolic pathways and some significantly up-regulated genes were selected by comparing 0 mmol/L vs. 12 mmol/L, which were predicted to be involved in the adaptation process to alkali treatment in *M. nipponense*.

Key words: *Macrobrachium nipponense*; hepatopancreas; alkali treatment; metabolic profiling analysis; transcriptome profiling analysis

黄颡鱼耐粗饲性状相关 SNP 及基因鉴定

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摘要: 鱼粉、豆粕等水产饲料主要蛋白原料的短缺和价格剧烈波动, 给水产养殖的可持续发展带来了严重的负面影响。本研究以全雌黄颡鱼 (*Tachysurus fulvidraco*) 为研究对象, 探索耐粗饲性状选育的可行性, 以降低养殖成本, 提高养殖可控性。实验设置商业饲料组 (CD, 蛋白含量 39.78%, 鱼粉含量 23.67%)、低鱼粉粗饲组 (LFD, 蛋白含量 35.11%, 鱼粉含量 9.66%) 和无鱼粉粗饲组 (NFD, 蛋白含量 38.42%)。其生长及生理指标结果验证了耐粗饲全雌黄颡鱼选育的可行性。接着, 对雌性黄颡鱼个体进行全基因组关联分析 (GWAS), 结合转录组结果, 鉴定出 *phka1b*、*pex10*、*ormdl2*、*mbd1a*、*mapk12a* 和 *miox* 基因。这些结果为黄颡鱼分子标记辅助育种提供有力支持, 推动黄颡鱼养殖业可持续发展。

关键词: 黄颡鱼; 全雌种群; 粗饲料; 无鱼粉; 候选基因; 遗传育种

Identification of SNP and genes related to roughage-tolerant in yellow catfish (*Tachysurus fulvidraco*)

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Abstract: The shortage and drastic price fluctuations of key protein sources for aquafeeds, such as fish meal and soybean meal, have severely impacted the sustainable development of aquaculture. This study focused on all-female yellow catfish (*Tachysurus fulvidraco*) to explore the feasibility of breeding traits for roughage-tolerant, aiming to reduce costs and enhance farming controllability. Three dietary groups were established: a commercial diet (CD) with 39.78% protein and 23.67% fish meal, a low-fishmeal roughage (LFD) with 35.11% protein and 9.66% fish meal, and a no-fishmeal roughage (NFD) with 38.42% protein. Growth and physiological indicators validated the feasibility of breeding roughage-tolerant all-female yellow catfish. Then, a genome-wide association analysis (GWAS) was conducted on female yellow catfish individuals, combined with transcriptome, *phka1b*, *pex10*, *ormdl2*, *mbd1a*, *mapk12a* and *miox* genes were identified. These findings provide support for molecular marker-assisted selection breeding of yellow catfish, promoting the sustainable development of the industry.

Key words: yellow catfish (*Tachysurus fulvidraco*); all-female populations; roughage; no-fishmeal; candidate gene; genetic breeding

饲料中添加 17 α -甲基睾酮诱导日本沼虾在性分化关键期的性逆转

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摘要: 类固醇 17 α -甲基睾酮 (MT) 具有抑制卵巢的功能。本研究通过在饲料中添加不同浓度的 MT, 研究其对性别比例、生长和性腺发育的影响。40 天后, 各实验组中的雌雄比例有着不同程度的升高, 50mg/kg MT (1.36: 1), 100mg/kg MT (1.57: 1), 200mg/kg MT (2.61: 1); 在添加 200mg/kg MT 组中出现了精巢与卵巢共存的性逆转雄性, 50 和 100 mg/kg MT 可诱导雌性性逆转为雄性。组织学上, 实验组精巢发育较慢, 卵巢发育速度与对照组相近。在添加 200 mg/kg MT 组雄性的 DMRT11E、Foxl2 和 SoxE1 的表达量分别是对照组的 8.65 倍、3.75 倍和 3.45 倍。性逆转雄性的精巢由外源激素所维持, 过度依赖外源激素导致其精巢生长缓慢, 体型小, 生长速度低, 但仍能产生精子。而在雌虾中, MT 具有抑制卵巢发育, 促进生长的作用。

关键词: 17 α -甲基睾酮, 性腺发育, 组织学观察, 日本沼虾, 性别比例, 性逆转

Sex Reversal Induced by Dietary Supplementation with 17 α -Methyltestosterone during the Critical Period of Sex Differentiation in Oriental River Prawn (*Macrobrachium nipponense*)

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Abstract: The steroid 17 α -methyltestosterone (MT) inhibits ovarian function. In the present study, different concentrations of MT were added as dietary supplementation, and the effects on sex ratio, growth, and gonadal development were examined. After 40 days, the sex ratio (male:female) in each group increased at different degrees with 50 (1.36:1), 100 (1.57:1), and 200 (2.61:1) mg/kg MT, and neo-males with testis-ovary coexistence were observed in the 200 mg/kg MT group. Histologically, the development of the testes in experimental groups was slower, but the ovaries of the experimental and control groups had similar developmental rates. The expression levels of DMRT11E, Foxl2, and SoxE1 in males at 200 mg/kg MT were 8.65-, 3.75-, and 3.45-fold greater than those of the control group. Neo-males (sex-reversed female prawns) were maintained by exogenous androgen, and over-reliance led to slow testis growth, small body size, and low growth rate, but sperm was still produced. In female prawns, MT inhibited ovary development and promoted growth.

Key words: 17 α -methyltestosterone; gonadal development; histological observations; *Macrobrachium nipponense*; sex ratio; sex reversal

沉水植物在虾蟹淡水养殖中的应用进展

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摘要: 沉水植物作为水生态系统的初级生产者和重要调节者, 不仅在自然水体修复方面有着巨大的作用, 在养殖水体同样如此。虾蟹淡水养殖中, 沉水植物可以净化水体、提供天然饵料与遮蔽物、降低应激反应、提高免疫力、减少病害发生, 提高生产性能, 提升产出品质, 从而大幅提升了虾蟹的养殖效益。目前已有的相关文献, 其研究重心大多在于沉水植物的水体修复功能, 对水生生物生产指标关注较少, 且目前可以了解到的相关研究成果大部分都是成功的案例, 失败的案例鲜有涉及, 这其实不利于水产行业产业化经验的总结。尤其是在针对某一具体养殖品种的适应性水草方面, 如何在种植技术、品种选择搭配及与其他技术结合等方面进行技术突破, 从而克服项目自身的限制因素, 使沉水植物在促进养殖品种生长方面得到更广泛应用是一个非常具有实际意义的课题。

关键词: 沉水植物; 虾蟹; 生长

Progress in the application of submerged plants in shrimp and crab freshwater aquaculture

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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: submerged plants; shrimps and crabs; growth

罗氏沼虾卵巢再发育规律及启动再次发育的关键基因和信号通路研究

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摘要: 罗氏沼虾在适宜的温度条件下可常年产卵, 生产上常利用其多次产卵的特性来提高经济效益。为探究罗氏沼虾卵巢再发育的动态变化及关键基因, 研究了其卵巢再次发育过程中卵巢的外部形态、组织学及不同发育时期的转录组学。结果表明, 罗氏沼虾卵巢再发育可分为五期: 卵原细胞积累期、卵母细胞生成期、卵子成熟期、再次排卵期及恢复期。转录组测序获得 99.3 Gb 数据, 注释出 89 614 个 Unigenes, 识别了 32 288 个差异表达基因。加权基因共表达网络分析和蛋白质互作网络分析显示, 核糖体和蛋白酶体通路中的基因在卵巢再次发育中发挥着重要功能, KEGG 分析也发现这两个通路显著富集; RPL24 等核糖体相关基因和蛋白酶体基因家族如 PSMC2 等基因在启动卵巢再次发育中具有重要功能。该研究结果为罗氏沼虾卵巢再发育的分子调控机制提供了理论基础。

关键词: 罗氏沼虾; 卵巢; 再次发育; 转录组学; 组织学

STUDIES ON THE PATTERNS OF OVARY RE-DEVELOPMENT AND SCREENING THE KEY GENES AND SIGNALING PATHWAYS INITIATING RE-DEVELOPMENT OF MACROBRACHIUM ROSENBERGII

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Abstract: Under optimal temperature conditions, *Macrobrachium rosenbergii* can spawn year-round, which is often used to increase economic efficiency. This study examined the dynamics and key genes involved in ovary re-development through external morphology, histology, and transcriptomics. Ovary re-development cycle was classified into five stages: oogonia accumulation, oocyte formation, oocyte maturation, re-spawning and recovery. Transcriptome sequencing generated 99.3 Gb of data, annotating 89614 unigenes and identifying 32288 differentially expressed genes. Both WGCNA and PPI analyses highlighted the importance of ribosome and proteasome pathways, with KEGG analysis furtherly confirming the significant enrichment. Ribosomal gene families like RPL24 and proteasomal gene families such as PSMC2 were identified as key genes in initiating ovary re-development. These findings lay a theoretical foundation for revealing the molecular regulatory mechanisms of ovary re-development.

Key words: *Macrobrachium rosenbergii*; ovary; re-development; transcriptomics; histology

中间球海胆不同遗传距离亲本对后代遗传多样性的影响

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摘要: 为了研究保持中间球海胆群体遗传多样性的方法, 本研究利用 15 个 SSR 位点和 SSR-seq 技术, 选择 3 种遗传距离, 即亲本间遗传距离较远(0.336 40)较近(0.13051)和远近混合(0.299 16)的亲本分组交配, 分别构建远距离群体(F)、近距离群体(N)和混合距离群体(M), 并对 3 个群体内 150 个后代进行了基因分型, 分析了亲本遗传距离对后代遗传多样性的影响。结果表明: 亲本遗传距离最高的 F 组群体, 其遗传多样性为后代最高, F 组群体与 M 组群体遗传多样性相近, N 组群体遗传多样性为最低。研究表明, 3 个群体的遗传多样性相较于亲本群体均有不同程度的降低, 其中 N 群体降低最为严重, F 和 M 群体的遗传多样性程度相近。为保持育种群体的遗传多样性, 在选配时应提高亲本间的遗传距离, 或采用混合交配的方法产生下一代群体。

关键词: 中间球海胆; 遗传距离; 遗传多样性; 遗传结构;

Effects of different genetic distance between parents on genetic diversity of progeny of *Echinothurus intermedius*

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Abstract: In order to study the methods of maintaining the genetic diversity of the stronglylocentrotus intermedius, SSR loci and SSR-SEQ techniques were used in this study to select the parents whose genetic distance was relatively distant (0.336 40), relatively close (0.13051) and distant and mixed (0.299 16). Distant (F), near (N) and mixed distance populations (M) were constructed, and the offspring of the three populations were genotyped, and the influence of parental genetic distance on the genetic diversity of the offspring was analyzed. The results showed that group F with the highest parental genetic distance had the highest genetic diversity, group M was close to group F, and group N had the lowest genetic diversity. The results showed that the genetic diversity of the three populations decreased to different degrees compared with the parental populations, and the N population was the most serious. In order to maintain the genetic diversity of breeding population, the genetic distance between parents should be increased during selection.

Key words:: Strongylocentrotus intermedius; Genetic distance; Genetic diversity; Genetic structure;

马口鱼 YY 超雄鱼制备研究

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摘要：马口鱼生长具有明显的性别二态性，雄性生长速度是雌性的 1.5 倍以上，且雄性具有独特婚姻色条纹，观赏价值更高。本研究旨在培育马口鱼全雄新种质，推动其产业高质量发展。在性别分化关键时期（15-70 日龄），对幼鱼进行雌二醇（17 β -estradiol）投喂处理，设置 E2 组（100 mg/kg E2）和对照组 CR 组（0 E2）。结果显示，E2 组性腺类型为全卵巢性腺（86%）、间性性腺（11.1%）和全精巢性腺（2.9%）。后续采用 XY 雄鱼和 XY 伪雌鱼进行繁殖，成功获得 YY 超雄鱼。XY 雄鱼与 YY 超雄鱼在形态学上无显著差异，需开发性别特异分子标记。利用全基因组关联分析（GWAS），本研究筛选出两段雌性纯合和雄性杂合的 InDel 片段，成功开发性别特异性分子标记，能有效区分 XX、XY 和 YY 三种基因型。后续将通过 YY 超雄鱼与 YY 伪雌鱼进行繁殖，规模化生产 YY 超雄鱼，为马口鱼全雄种质创制和种质控制提供技术保障。

关键词：性别控制；雌二醇；雌性化；马口鱼；超雄鱼；性别特异分子标记

Study on the preparation of *Opsariichthys bidens* YY super-males

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Abstract: *Opsariichthys bidens* shows pronounced sexual dimorphism, with males growing over 1.5 times faster than females and exhibiting distinct color stripes that enhance their ornamental value. This study aims to develop an all-male germplasm of *O. bidens* to enhance industry quality. During the critical sex differentiation period (15 to 70 days post-hatching), juvenile fish were fed with 17 β -estradiol, establishing two groups: the E2 group (100 mg/kg E2) and the control group (0 E2). Results indicated that the E2 group had 86% total ovarian gonads, 11.1% interstitial gonads, and 2.9% total seminal gonads. Breeding XY males with XY pseudo-females successfully produced YY hypermales, which exhibit no significant morphological differences from XY males. To develop sex-specific molecular markers, genome-wide association analysis (GWAS) identified two InDel fragments for female and male heterozygosity, effectively distinguishing XX, XY, and YY genotypes. The large-scale production of YY super-males will establish a technical foundation for the creation and control of all-male *O. bidens* germplasm.

Key words: Sex control; 17 β -estradiol; feminisation; *Opsariichthys bidens*; supermale; sex-specific molecular markers

团头鲂 circR XRBB 通过 miR-155/socs1a 轴 调控嗜水气单胞菌感染后的抗菌免疫反应

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摘要: 环状 RNA (circRNAs) 作为竞争内源性 RNA (ceRNAs) 在多种疾病中发挥重要作用, 可作为生物标志物和治疗靶点。本研究验证了 circR XRBB 的环状结构及剪切位点, 它在嗜水气单胞菌感染后显著下调, 这表明它可能参与了抗微生物免疫。随后, 本研究证明 circR XRBB 过表达抑制促炎因子 (il-6、il-1 β 、tnf- α 和 ifn- γ) 的表达水平。此外, circR XRBB 可以通过海绵作用直接吸附 miR-155, 而 miR-155 模拟物可以恢复 circR XRBB 过表达对炎症因子的抑制作用。进一步研究表明, mir-155 可以靶向 socs1a, mir-155/socs1a 轴是 circR XRBB 调控免疫反应的重要途径之一。总之, 该研究证明了 circR XRBB 在嗜水气单胞菌感染后调节抗菌免疫中的关键作用, 这有助于更好地理解 ceRNA 调控网络, 并为未来鱼病诊断、预防和鱼类抗病育种奠定了基础。

关键词: circR XRBB; miR-155; Socs1a; ceRNA; 免疫反应

Blunt snout bream (*Megalobrama amblycephala*) circR XRBB regulates antimicrobial immune response against *Aeromonas* *hydrophila* infection via miR-155/socs1a axis

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Abstract: Circular RNAs (circRNAs) play an important role in various of human diseases by acting as competing endogenous RNAs (ceRNAs). In this research, we identified a circRNA called circR XRBB that was down regulated following *A. hydrophila* challenge, suggesting its possible involvement in antimicrobial immune. Subsequently, the study demonstrated that circR XRBB overexpression suppressed the expression levels of pro-inflammatory factors. Dual luciferase assay demonstrated that circR XRBB could directly adsorb miR-155 through sponge action. In addition, mir-155 can target socs1a, and the mir-155/socs1a axis is one of the important pathways for circR XRBB to regulate immune response. In conclusion, this research demonstrated that circR XRBB is critical in regulating the antibacterial defense against *A. hydrophila* infection, which contributes to a better understanding of the ceRNA regulatory network and offers a foundation for future strategies in fish disease diagnose, prevention, and breeding for disease resistance in fish.

Key words: circR XRBB; miR-155; Socs1a; ceRNA; Innate immunity

黑鲟 GSDF 基因的克隆与表达特征

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摘要: 性腺体细胞衍生因子(gonadal soma-derived factor, GSDF)与鱼类性别决定及分化密切相关。本文克隆了雌雄同体鱼类黑鲟 AsGsdf 基因 cDNA 序列,分析了黑鲟及其杂交子二代(黑鲟♀×真鲷♂杂交 F2)中该基因在性逆转前期的表达特性。结果显示,AsGsdf 基因开放阅读框为 636bp,编码 212 个氨基酸;序列中包含转化生长因子-β(TGF-β)特有的保守结构域、1 个信号肽、1 个 N-糖基化位点及 9 个磷酸化位点;同源建模获得了 AsGsdf 蛋白的二级与三维结构;同源比较显示,AsGsdf 基因与其它鱼类的核苷酸、氨基酸序列相似性最高均达 99%;进化分析显示 AsGsdf 与鲷科其它鱼类 GSDF 聚为一枝。定量检测得出,基因在性腺中存在极显著高表达;在 11~12 月的性腺表达量呈现为下降再上升的趋势,与对性腺的切片观察一致。该研究结果为 GSDF 基因在黑鲟性转换过程中的作用提供依据。

关键词: 黑鲟;性腺体细胞衍生因子(GSDF);性转换;转化生长因子-β

Cloning and expression analysis of GSDF gene in *Acanthopagrus schlegeli*

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Abstract: Gonadal soma-derived factor (GSDF) plays a crucial role in the sex determination and differentiation of fishes. In the present study, we cloned the cDNA-encoding sequence of GSDF from black porgy *Acanthopagrus schlegeli*, a protandrous hermaphrodite, and examined its tissue expression pattern before the sex-reversal phase. The results shows that the open reading frame (ORF) of AsGsdf gene spaned a region of 636 bp and coded 212 amino acids, with a conserved domain of the TGF-β superfamily and a signal peptide. Secondary and three dimensional structure of AsGsdf were developed by homology modeling. The similarity of the nucleotide and amino acid sequences of the AsGsdf gene with those of other fish was up to 99%. The CDSs of AsGsdf and other Sparidae species were clustered in one branch in the NJ evolutionary tree. AsGsdf transcription was predominantly detected in gonads and its levels were extremely significant higher than those issues. The results provide a basis for studying the GSDF gene in the sex-reversal of *A. schlegeli*.

Key words: *Acanthopagrus schlegeli*, GSDF, Sex-reversal, TGF-β

通过重测序方法以性别分子标记揭示黑斑原 鲃性染色体型

何昊明

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摘要：黑斑原鲃 (*Glyptosternum maculatum*) 是中国西藏自治区的二级保护水生动物，并被 IUCN 红色名录列为极危物种。该物种性别二态性显著，但缺乏明显的外部性别特征，难以通过形态学方法鉴定性别。本研究利用斑点江鲃雄性基因组为参考，通过比较 40 个混合样本（20 个雌性和 20 个雄性）的基因组重测序数据，筛选出与性别显著相关的 SNP 位点。研究确定性别决定区域位于 LG01 的 27Mb-28Mb 区域。所有候选标记均为雄性杂合，表明斑点江鲃的性别决定系统为 XX/XY 型。通过为 XX 位点设计引物，并进行 Sanger 测序验证，成功鉴定出一个与性别完全连锁的位点。这些发现为斑点江鲃性别决定和分化过程中的关键遗传标记提供了重要信息，为开发西藏本土鱼类物种的性别特异性分子标记提供了宝贵的参考。这些分子标记的发现，为斑点江鲃性别控制育种策略的实施奠定了基础，有望提高水产养殖的生产力和效率。

关键词：黑斑原鲃；转录组；性别决定；性别决定基因

***Glyptosternum maculatum*; sex-determining gene ; resequencing**

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Abstract : *Glyptosternum maculatum* is a second-class protected aquatic animal in the Tibet Autonomous Region of China and is listed as Critically Endangered in the IUCN Red List. This species exhibits pronounced sexual dimorphism, but lacks distinct external sexual characteristics, making it difficult to determine sex through morphological methods. This study uses the male genome of *Glyptosternum maculatum* as a reference. It compares the genomic resequencing data of 40 mixed samples (20 females and 20 males) to screen for SNP sites significantly associated with sex. The study identified the sex determination region in the 27Mb-28Mb region of LG01. All candidate markers were heterozygous in males, indicating that the sex determination system of *Glyptosternum maculatum* is of the XX/XY type. By designing primers for the XX sites and performing Sanger sequencing validation, a locus completely linked to sex was successfully identified. These findings provide important information on key genetic markers in the sex determination and differentiation processes of *Glyptosternum maculatum* an

Key words:: *Glyptosternum maculatum*; ; sex determination; generesequencing

扇贝壳闭合力性状的测定与遗传解析

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摘要: 扇贝是双壳贝类中具有较大闭壳肌的种类之一, 其营养丰富、味道鲜美, 是优质“蓝色食物”的重要组成部分, 具有很高的经济价值。但因缺乏无损高效的闭壳肌性状测定技术, 导致闭壳肌性状的测评与遗传育种工作进展缓慢。本研究首先利用拉力计建立了扇贝壳闭合力无损高效测定技术, 获得包括总力、平均力、最大力、闭壳时间四项评价指标; 分析发现栉孔扇贝生长性状与壳闭合力指标呈正相关, 其中闭壳肌重同四项壳闭合力指标均呈显著正相关 ($P < 0.05$), 糖原含量以及精氨酸、亮氨酸及缬氨酸均同壳闭合力指标呈显著正相关 ($P < 0.05$), 栉孔扇贝壳闭合力四项指标均同高温耐受时间呈显著正相关 ($P < 0.05$)。高效的壳闭合力性状的测定将为贝类闭壳肌性状与抗性性状的选育提供技术支持。

关键词: 扇贝, 壳闭合力, 糖原, 热耐受

Rapid and noninvasive assessment of adductor muscle performance through shell-closing strength of Zhikong scallop *Chlamys farreri*

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Abstract: Shell-closing strength (SCS) is a crucial trait of adductor muscle closely associated with the bivalve's swimming ability and health status. However, the investigation and practical application of SCS have been seriously hampered due to the limited availability and complexity of current measurement methodologies. In this study, a rapid and noninvasive method was developed to quantify SCS with four indicators including total force (TF), time of shell closing (TSC), average force (AF), and maximum force (MF) using a simple force gauge device. The optimal measurement time and distance for SCS were three minutes and 0.75 cm, respectively. The analysis revealed that the four SCS indicators of scallops were significantly associated with the adductor muscle weight (AMW) and the adductor muscle glycogen content (AMG). Furthermore, scallops with stronger SCS were proved to have longer survival times under heat stress, with correlation coefficients ranging from 0.25 to 0.47 ($P < 0.05$). The SCS could be useful for selection breeding of scallops to enhance quality and resistance traits.

Key words: scallop, shell closed strength, glycogen, heat tolerance

胰岛素样雄性腺激素诱导日本沼虾性别逆转和分子途径：对繁殖、生长和性别分化的启示

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摘要：本研究探讨了利用双链 RNA 胰岛素样雄性腺激素 (dsIAG) 诱导日本沼虾性别逆转的可能性, 并通过对正常雄虾 (dsM)、正常雌虾 (dsFM)、性逆转后的假雌虾 (dsRM) 和未逆转的雄虾 (dsNRM) 进行性腺转录组分析, 筛选出了与性别相关的通路和基因。经过 6 次注射, 45 天后实验最终产生了 20% 的假雌虾。从组织学观察表明, 假雌虾的卵巢发育慢于正常雌虾。通过对三个比较组的性腺进行转录组测序发现了 1718、1069 和 255 个差异表达基因, 揭示了与生殖和性别分化相关的关键基因, 如 GnRHR、VGR、SG 和 LWS。此外, 该研究还预测, 眼柄和“光传导”、“类固醇合成”通路可能在日本沼虾的性别逆转中发挥重要作用。

关键词：日本沼虾, 性别逆转, 胰岛素样雄性腺激素, 精巢, 卵巢, 繁殖, 生长调节, 转录组, 光周期途径

Insulin-like Androgenic Gland Hormone Induced Sex Reversal and Molecular Pathways in *Macrobrachium nipponense*: Insights into Reproduction, Growth, and Sex Differentiation

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Abstract: This study investigates the potential to use double-stranded RNA insulin-like androgenic gland hormone (dsIAG) to induce sex reversal in *Macrobrachium nipponense*, and screened for sex-related pathways and genes through gonadal transcriptome analyses of normal males (dsM), normal females (dsFM), neo-female sex-reversed individuals (dsRM), and unreversed males (dsNRM). The experiment eventually produced 20% dsRM after six injections and 45 days. Histology, dsRM ovaries developed slower than dsFM. A total of 1,718, 1,069, and 255 differentially expressed genes were identified through transcriptome sequencing of the gonads in three comparison groups, revealing crucial genes related to reproduction and sex differentiation, such as GnRHR, VGR, SG, and LWS. In addition, this study predicted that the eyestalks, ‘phototransduction-fly’ and ‘steroid synthesis’ pathways of *M. nipponense* could play an important role in sex reversal.

Key words: *Macrobrachium nipponense*; sex reversal; IAG; testis; ovary; reproduction; growth regulation; transcriptome; photoperiodic pathways

基于全基因组测序的四指马鲛基因组注释 和系统发育分析

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摘要: 四指马鲛 (*Eleutheronema tetradactylum*) 是一种广盐性鱼类, 主要分布于印度至西太平洋海域, 包括印度至东南亚各沿海, 北至菲律宾, 南至巴布亚新几内亚、澳大利亚北部等沿海。尽管染色体水平的四指马鲛基因组已在 NCBI 发布, 但关于其基因组注释和进化分析还需进一步完善。为了对四指马鲛基因组注释和系统发育进行系统分析, 本研究利用 SMRT 和 Hi-C 技术进行了基因组测序, 组装了高质量的染色体水平的四指马鲛基因组。此基因组大小为 586.1 Mb, 由 106 个重叠群组成, 重叠群 N50 长度为 21.32 Mb。染色体 (26) 锚定率为 98.76%, 共预测了 23,162 个蛋白质编码基因和约 18.24% 的重复序列。高质量参考基因组测序和组装为四指马鲛的进化与遗传相关研究奠定了数据基础。

关键词: 四指马鲛; 全基因组; 组装与注释; 系统进化

无

无
无

Abstract: 无

Key words: 无

基于代谢组解析四指马鲛在低温胁迫下的适应机制

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摘要：为探讨四指马鲛（*Eleutheronema tetradactylum*）对低温胁迫的响应机制，本实验将四指马鲛在低温（18℃）条件下饲养，比较分析肝脏组织在胁迫后第7和14天的氧化应激状态和组织结构情况，并利用LC-MS非靶向代谢组学技术进行组间差异代谢物筛选，确定与差异代谢物的关键代谢通路变化。结果显示，低温胁迫下SOD、CAT和GPx的活性均呈现先上升后下降的趋势，MDA含量在7天和14天均显著升高，且肝细胞出现不同程度的空泡化和核萎缩，表明低温对四指马鲛造成了氧化损伤。在低温胁迫下，7d组鉴定出87种差异代谢物，主要富集于碳水化合物的消化和吸收、谷胱甘肽代谢等6条代谢通路；14d组鉴定出116种差异代谢产物，主要富集于甘油酯代谢和脂肪的消化和吸收等6条代谢通路，表明，脂质、糖类代谢和抗氧化系统在四指马鲛适应低温胁迫中发挥重要作用。本研究结果为该鱼类应对低温胁迫的生理调节机制提供了见解。

关键词：四指马鲛；低温；氧化应激；代谢组学

Metabolomics-based analysis of adaptive mechanism of *Eleutheronema tetradactylum* to low temperature stress

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Abstract： To study low-temperature stress response in *Eleutheronema tetradactylum*, we exposed fish to 18°C and analyzed liver oxidative stress and structure on days 7 and 14. LC-MS metabolomics identified 87 and 116 differential metabolites on days 7 and 14, respectively, enriched in pathways like carbohydrate digestion, glutathione metabolism, glycerolipid metabolism, etc. Results showed initial increase then decrease in SOD, CAT, GPx activities, and elevated MDA, with hepatocyte vacuolation and nuclear atrophy, indicating oxidative damage. Lipid, carbohydrate metabolism, and antioxidant systems play key roles in adaptation. Our findings provide insights into physiological regulation under low-temperature stress.

Key words： *Eleutheronema tetradactylum*; low temperature; Antioxidant enzyme; metabolomics

膳食纤维过量摄入对水产动物的致病作用和机制

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摘要: 由于环境保护和成本控制的需要, 植物性饲料原料在水产配合饲料中的用量越来越高。植物性原料中含有丰富的膳食纤维 (DFs), 但其对水产动物的生理影响仍鲜受关注。研究表明, 黄颡鱼摄食含 20%-30% DFs 的饲料后会出现出血、白便、肠炎、腐皮、烂鳃、肝脂肪变和纤维化、绿肝、白肝、胆囊肿大等症状及暴发性死亡。大口黑鲈和草鱼摄食高 DFs 饲料后也有相似症状。DFs 的致病作用不仅与饲料中 DFs 含量有关, 还与 DFs 种类有关。DFs 的致病机制与其对胆汁酸 (BAs) 稳态和肠道微生物稳态的干扰有关。从 DFs 的致病机制出发, 通过控制 DFs 摄入种类和摄入量、向饲料中添加 BAs 及牛磺酸、防止 DFs 与其他胁迫因子的叠加效应等方式可防控 DFs 诱导的疾病。

关键词: 水产动物, 膳食纤维, 非感染性炎症, 胆汁酸, 肠道微生物

Pathogenic effects and mechanisms of excessive intake of dietary fiber on aquatic animals

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Abstract: Due to the needs of environmental protection and cost control, the amount of plant feedstuffs used in aquatic formula feed is increasing. Plant feedstuffs are rich in dietary fibers (DFs), however, their impacts on aquatic animal physiology are still of little concern. We noticed that the hemorrhage, white feces, enteritis, skin-rotting, gill-rotting, hepatic steatosis and fibrosis, green liver, white liver, gallbladder enlargement and even outbreak death could be induced in yellow catfish *Pelteobagrus fulvidraco* when diet included 20-30% DFs. Similar symptoms had also been observed in largemouth bass *Micropterus salmoides* and grass carp *Ctenopharyngodon Idella* fed high DFs diet. The pathogenic effect of DFs was related not only to the content of DFs in the diet but also to the types of DFs. The pathogenic mechanism of DFs is related to their interference with bile acids (BAs) homeostasis and intestinal microbial homeostasis. Based on the pathogenesis of DFs, the diseases can be prevented and controlled by limiting the intake of DFs, adding BAs and taurine to the diet, and avoiding the superposition effect of DFs with other stress factors.

Key words: Aquatic animal, dietary fiber, non infectious inflammation, bile acid, microflora

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高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

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

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Abstract : This study aimed to investigate the effects of nano-se as a dietary supplement on *Gymnocypris przewalskii*. 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 NSE11 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 cell infiltration in *G. przewalskii*. In addition, the results of intestinal microbiota detection showed that dietary nano-selenium could improve the diversity of the intestinal microbiota and increase the abundance of beneficial bacteria in *G. przewalskii*. 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 przewalskii*, feed additives, antioxidant capacity, immune response, intestinal health

DHA 强化卤虫无节幼体策略及 DHA 对黄姑鱼 (*Nibea albiflora*) 仔鱼生长、代谢和耐低氧能力的影响

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摘要: 卤虫无节幼体缺乏 DHA, 影响其作为仔鱼生物饵料的营养效价。本研究通过测定不同强化条件下的存活率和营养组成和个体大小, 探索有效提高卤虫 DHA 含量的营养强化策略, 即在每升海水中培养 50 个卤虫, 向每吨海水中添加 12 克 50% DHA 油, 并进行 12 小时强化处理, 结果显示该方法显著提高卤虫 DHA 含量而不影响其存活和大小。通过对 12 日龄黄姑鱼仔鱼进行为期 15 天的投喂实验, 发现 DHA 强化的卤虫显著提高仔鱼的生长性能、肝脏脂肪酶活性和耐低氧能力。RNA 测序分析揭示, DHA 促进了脂质吸收和 β -氧化相关基因的表达, 抑制了脂肪酸和胆固醇合成相关基因, 表明 DHA 促进脂肪代谢。此外, DHA 降低了炎症相关基因表达, 提升了补体途径基因表达, 这可能有助于增强仔鱼的低氧耐受性。本研究不仅优化了卤虫的营养强化方法, 还阐释了 DHA 对仔鱼生长的分子机制, 对仔稚鱼培育具有重要指导意义。

关键词: DHA, 卤虫, 黄姑鱼, 生长, 耐低氧, 代谢

Strategies for DHA-Enriched Artemia Nauplii and the Effects of DHA on Growth, Metabolism, and Hypoxia Tolerance in Yellow Drum (*Nibea albiflora*) Larvae

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Abstract: Artemia nauplii generally lack sufficient DHA, reducing their nutritional value as larval feed. This study aimed to enhance the nutritional value of Artemia nauplii through DHA enrichment and investigate DHA's role in marine larvae rearing. By maintaining a density of 50 nauplii per milliliter of seawater and adding 12 grams of 50% DHA oil per ton of seawater for 12 hours, this method significantly increased the DHA content in Artemia nauplii without adversely affecting their survival or size. In a 15-day feeding trial using 12-day-old yellow drum larvae, results showed significant improvements in growth, liver lipase activity, and hypoxia tolerance in larvae fed with DHA-enriched nauplii. RNA-seq analysis of liver and intestinal tissues revealed that DHA upregulated genes related to lipid absorption and β -oxidation while suppressing genes involved in fatty acid and cholesterol synthesis, suggesting enhanced lipid catabolism. Additionally, DHA reduced cytokine gene expression and enhanced complement pathway genes, potentially improving hypoxia tolerance.

Key words: DHA, Artemia tibetiana, yellow drum, growth performance, hypoxia resistance, lipid metabolism

Mfn2 介导的线粒体融合促进黄颡鱼的脂肪酸 β -氧化

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摘要: 【目的】线粒体是脂肪酸 β -氧化的主要场所, 因此, 线粒体的完整性与稳态是脂肪酸 β -氧化的基础。而线粒体作为双层膜结构的细胞器, 需要不断的融合与分裂来维持其稳态。然而, 目前就线粒体如何直接影响脂肪酸 β -氧化尚无证据。此外, 饲料脂肪酸配比优化缓解鱼类肝脂沉积的机制仍有待深入。【方法】因此, 本研究以黄颡鱼为研究对象, 设定不同棕榈油(PA)/鱼油(FO)比例的饲料, 投喂8周后取其肝脏分析。【结果】本研究取得的主要结论如下: 1, 适量棕榈油替代鱼油可通过激活脂肪酸 β -氧化而缓解黄颡鱼肝脂沉积情况; 2, 适量棕榈油替代鱼油可经抑制 Mfn-2 泛素化, 而激活黄颡鱼肝脏内的线粒体融合机制; 3, Mfn-2 可经其自身的 GTPase-domain 与 Cpt-1 α 产生蛋白互作机制, 而互作机制又可以直接促进下游脂肪酸 β -氧化。

关键词: Mfn2; 线粒体融合; 脂肪酸 β -氧化; Cpt1 α ; 脂肪酸配比

Moderate replacement of fish oil with palmitic acid-stimulated mitochondrial fusion promotes β -oxidation by Mfn2 interacting with Cpt1 α via its GTPase-domain

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Abstract: [Objective] Since mitochondrial matrix is the main site where the fatty acids (FAs) β -oxidation takes place. Meanwhile, maintenance of mitochondrial integrity and homeostasis, which is achieved through continual fusion, is extremely critical for FAs β -oxidation. However, despite this well-accepted fact, no study has yet explored whether and how mitochondrial fusion directly promotes FAs β -oxidation. Moreover, the underlying mechanism of a balanced FAs ratio favors hepatic lipid homeostasis are still largely unclear. [Methods] To address these gaps, this study was conducted to investigate the mechanism by which proper dietary FAs ratio promotes hepatic FAs β -oxidation, focusing on the role of Mfn2-mediated mitochondrial fusion regulating Cpt1 α in this process. To this end, a model animal for lipid metabolism, yellow catfish (*Pelteobagrus fulvidraco*), were fed six different diets with a range of FAs ratio in vivo for 8 weeks, and in vitro experiments were conducted to intercept Mfn2-mediated mitochondrial fusion in isolated hepatocytes by transfecting them with si-mfn2, also to demonst

Key words: Mfn2; Mitochondrial Fusion; β -oxidation; Cpt1 α ; Fatty Acids Ratio

维生素 C 通过 TGF- β /Smads 通路介导胶原蛋白合成促进光棘球海胆摄食

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摘要: 为探讨不同剂量维生素 C 通过 TGF- β /Smads 通路介导胶原蛋白合成对光棘球海胆生长和摄食的影响。实验设置不同含量 (0、3000 和 6000mg/kg) VC 的饲料投喂初始体重为 (3.50 \pm 0.20g) 的海胆, 以海带作为对照饮食, 养殖实验 80 天。结果显示: (1) 3000mg/kgVC 显著提升了海胆的摄食量、生长速度、运动和摄食能力 (翻正行为速度、亚里士多德提灯咬合频率和海带块消耗量)。 (2) 3000mg/kgVC 显著增加了海胆围口膜、关节及亚里士多德提灯的胶原蛋白含量。同时围口膜纤维胶原面积最大, 排列最为紧密。 (3) 3000mg/kgVC 显著提高了海胆围口膜中 col1 α , col2 α , col3 α , tgfb β 1, snip1, tgfb β 2 和 p4h β 的表达量。综上, VC 有助于促进海胆的生长和摄食, 这可能是通过 TGF- β /Smads 通路增加海胆围口膜、关节和亚里士多德提灯中的胶原蛋白合成实现的。

关键词: 光棘球海胆; 维生素 C; 生长; 摄食; TGF- β /Smads 通路; 胶原蛋白

Vitamin C promoting the growth and feeding rate of sea urchin (*Mesocentrotus nudus*) by increasing collagen synthesis through the TGF- β /Smads pathway

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Abstract: An 80-day feeding trial was aimed to explore the effects of dietary vitamin C (VC) at different addition levels (0, 3000, and 6000mg/kg) on the growth and feeding rates of sea urchin (*Mesocentrotus nudus*) by increasing collagen synthesis through the TGF- β /Smads pathway. Feeding sea urchins (initial weight:3.50 \pm 0.20g), with kelp used as the control diet. The results indicated that the *M. nudus* in the group with 3000mg/kg VC exhibited significantly higher growth performance, feed intake, kelp consumption, Aristotle's lantern reflex frequency, and righting behavior speed. VC at an addition level of 3000mg/kg increased the collagen content in the peristomial membrane (PM), joint, and Aristotle's lantern of *M. nudus*. VC at an addition level of 3000mg/kg increased the expression levels of col1 α , col2 α , col3 α , tgfb β 1, tgfb β 2, snip1 and p4h β in the PM of *M. nudus*. Research showed that VC helped promote the growth and feeding of sea urchins, which could be achieved by increasing collagen synthesis in the PM, joint, and Aristotle's lantern of sea urchins through the TGF- β /Smads pathway.

Key words: vitamin C, *Mesocentrotus nudus*, growth performance, feeding rate, tgfb β /Smads, collagen

两种体色日本螯类胡萝卜素靶向代谢组学 及低温胁迫后抗氧化特性的比较

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摘要: 为探究大连近海体色灰绿的“花盖”和体色暗红的“赤甲红”两种体色日本螯(*Charybdis japonica*)色素代谢及抗氧化特性差异,本试验通过代谢组学的方法,比较分析了两种体色蟹甲壳和底膜类胡萝卜素种类和含量,并对低温胁迫后抗氧化酶活性进行测定。结果表明:在“花盖”和“赤甲红”头胸甲壳和底膜中存在68种类胡萝卜素,种类无明显差异,后者游离态的 β -胡萝卜素、角黄素和虾青素含量显著高于前者。两种体色蟹的甲壳和底膜共检测出8种呈显著差异的代谢物,其中甲壳中有2种,分别为 β -隐黄质和叶黄素。赤甲红抗氧化酶活性与低温胁迫时间呈负相关,花盖抗氧化酶活性在低温胁迫6h后可恢复至胁迫前水平。研究结果可为蟹类体色形成机理及育种过程中的性状选择提供参考。

关键词: 日本螯; 抗氧化特性; 类胡萝卜素

Targeted metabolomics of carotenoids and comparison of antioxidant characteristics after low-temperature stress in two body color varieties of *Charybdis japonica*.

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Abstract: To explore the differences in physiology, metabolism and antioxidant characteristics of *Charybdis japonica* with gray-green 'Huagai' and dark-red 'Chijiahong' in Dalian coastal waters, this experiment compared and analyzed the types and levels of carotenoids in the carapace and basement membrane of two body color crabs by metabolomics, and measured the activity of antioxidant enzymes after low temperature stress. The results showed that there were 68 carotenoids in the carapace and basement membrane of 'Huagai' and 'Chijiahong', and there was no significant difference in the types. The levels of free β -carotene, canthaxanthin and astaxanthin in the latter was significantly higher than that in the former. A total of 8 metabolites with significant differences were detected in the carapace and basement membrane of the two body color crabs, of which 2 were β -cryptoxanthin and lutein in the carapace.

Key words: *Charybdis japonica*; antioxidant properties; carotenoids

投喂南极磷虾对红螯螯虾幼虾生长、生理生化、免疫及肠道菌群结构的影响

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摘要：文章旨在研究投喂南极磷虾冰鲜肉对红螯螯虾幼虾生长性能、体成分、生理生化指标、免疫机能及肠道菌落的影响。设置了四种投喂组合，分别为：C（只饲喂基础饲料，对照组）、E3（每天投喂 50%南极磷虾）、E2（1d 基础饲料+1d50%南极磷虾循环投喂）、E1（2d 基础饲料+1d50%南极磷虾循环投喂）。饲喂 10 周后，与对照组相比，E2 和 E1 组的增重率和特定生长率显著提高（ $p < 0.05$ ），且 E2 组的成活率最高。肌肉的脂肪酸分析发现 EPA 和 DHA 量与南极磷虾投喂量呈显著正相关，而与氨基酸组成无显著变化。在肌肉与虾壳的虾青素分析中发现 E2 组虾青素含量最高。此外，投喂南极磷虾显著提高了肝胰腺中胰蛋白酶、脂肪酶活（ $p < 0.05$ ），而抗氧化和免疫相关酶活无显著影响。基因检测结果证实，饲喂南极磷虾显著上调了与蜕皮和免疫等相关基因表达水平。肠道菌落分析发现，饲喂南极磷虾改变了肠道菌群丰度，提升了其营养吸收代谢功能。

关键词：南极磷虾；红螯螯虾；生长性能；肠道菌群；脂肪酸营养；

Effects of feeding Antarctic krill on growth, physiology, biochemistry, immunity and Intestinal microbiota of Redclaw Crayfish(*Cherax quadricarinatus*.)

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Abstract: This study comprehensively examined the effects of feeding raw frozen Antarctic krill (*Euphausia superba*) on performance and other aspects of *Cherax quadricarinatus*. Four feeding groups were set: C (fed basal diet, control), E1 (2-day basal diet, 1-day krill), E2 (1-day basal diet, 1-day krill), and E3 (fed krill daily). After feeding for 10 weeks, compared with the C, the weight gain rate and specific growth rate of E2 and E1 groups were significantly increased ($p < 0.05$), and the survival rate of E2 group was the highest. The fatty acid analysis of muscle showed that EPA and DHA were positively correlated with krill feeding, but not with amino acid composition. The E2 had the highest astaxanthin content in muscle and shell. In addition, the activities of trypsin and lipase in hepatopancreas were significantly increased by feeding krill ($p < 0.05$). Meanwhile, feeding krill significantly upregulated the expression levels of genes related to molting and immunity. In addition, feeding krill increased the abundance of gut microbiota and enhancing the nutritional metabolism function.

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

基于多组学技术的香螺对不同饵料响应的分子机制

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摘要: 香螺为我国北方具有较高养殖潜力的经济腹足类。由于香螺对饲料比较挑剔,人工配合饲料尚未研制成功,本文以香螺为研究对象,采用行为学方法比较了香螺对5种饵料(虾夷扇贝、紫贻贝、菲律宾蛤仔、南美白对虾、许氏平鲷)喜好差异,通过分子生物学方法研究了摄食不同饵料后香螺的分子表达机制。结果表明,香螺最喜欢摄食虾夷扇贝。进而通过该饵料的体成分发现L-甘氨酸、L-谷氨酸可能为香螺的诱食物质。为了证实诱食物质对香螺的影响,通过转录组学和代谢组学分析发现,摄食前后香螺水管和嗅检器组织内均有显著差异。其中,水管内共鉴定出3452种DEGs及100种DMs。而嗅检器组织内共4914种DEGs及247种DMs。主要富集在了FoxO信号通路、氨基酰-tRNA生物合成通路等通路,主要包括差异代谢物质有苯丙氨酸、色氨酸、吡啶等。综上,虾夷扇贝饵料在香螺摄食方面表现出较强的摄食、生长和食欲响应等能力。

关键词: 香螺; 偏好性饵料; 诱食物质; 转录; 代谢; 联合分析

Molecular mechanisms of the response of *Neptunea arthritica cumingii* to different baits based on multi-omics techniques

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Abstract: The aim of this experiment was to investigate the effects of preferred baits and predatory substances on the promotion of feeding behavior and appetite response of snails. The possible mechanisms of the feeding enhancement of the snail by the appetizing substances were also explored. The results showed that the scallop was fed with bait for 10 d. The results indicated that the scallop could enhance the expression of energy supply, signaling and feeding-related genes. The obtained DEGs and DMs were enriched in amino acid metabolism, purine metabolism and other nutrient metabolism-related pathways, and the DEGs were enriched in response to appetite regulation, metabolic functions, as well as FoxO signaling pathway and aminoacyl-tRNA biosynthesis pathway. In conclusion, the enrichment of glycine and glutamate in Ezo scallops significantly improved processes such as feeding and appetite response in the scallop. The regulation of nutrient metabolism and other related pathways as well as bioactive metabolites is an important factor in improving the feeding ability of the scallop.

Key words: *Neptunea arthritica cumingii*; Preferred bait; Attractants; Feeding; Transcriptional metabolism

裂壶藻作为一种有前景的西藏卤虫无节幼体强化剂在黄姑鱼苗种培育中的应用研究

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摘要: 卤虫无节幼体内缺乏海水仔鱼生长发育所必需的营养成分, 作为饵料直接影响仔鱼的生长和健康。本研究探讨通过添加裂壶藻来增强西藏卤虫的营养特性以评估该强化策略在黄姑鱼仔鱼中的可行性。结果表明, 在每毫升海水中添加 50 只无节幼体和 40g/t 的裂壶藻进行 12 小时强化, 显著提高了卤虫体内的 DHA 水平, 且未对卤虫存活率和体型产生负面影响。通过对 12 日龄的黄姑鱼仔鱼进行为期 10 天的投喂试验, 发现裂壶藻可以显著改善仔鱼的生长性能, 肝肠组织形态。RNA 测序分析表明, 仔鱼摄食裂壶藻强化的卤虫可降低肝肠组织中脂质合成相关基因的表达, 增加脂肪酸分解代谢相关基因的表达。在后续的转饵实验中, 处理组仔鱼表现出更高的生长性能。此外, 处理组在低氧胁迫下的存活率显著高于对照组, 可能与 RNA 测序显示的非特异性免疫相关基因表达增加有关。本研究强调了裂壶藻强化西藏卤虫无节幼体的潜力, 为改善海水鱼类苗种的培育和整体健康提供新的见解。

关键词: 裂壶藻, 西藏卤虫, 黄姑鱼, 强化剂, 苗种培育

Schizochytrium sp. as a promising *Artemia tibetiana* nauplii fortifier for yellow drum (*Nibea albiflora*) larviculture

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Abstract: Optimal nutrition for *Artemia nauplii* is crucial for marine larvae rearing, as it underpins their growth, development, and overall health. This study aimed to enhance the nutritional profile of *Artemia tibetiana* using *Schizochytrium* sp., assessing its feasibility for yellow drum larvae. Results showed that 50 nauplii/mL seawater and enriching nauplii with 40 g of *Schizochytrium* sp. per ton of seawater for 12 h significantly increased the DHA levels in *A. tibetiana* without affecting survival or size. In a 10-day feeding trial using 12dph yellow drum larvae, results showed significant improvements in growth, liver and intestinal morphology in larvae fed with *Schizochytrium* sp.-enriched *A. tibetiana*. RNA-seq analysis indicated that *Schizochytrium* sp. reduced lipid synthesis gene expression, increasing fatty acid catabolism in intestinal and liver tissues while elevating the expression of immune-related genes. In addition, *Schizochytrium* sp. improved the weaning effect of larvae and showed a higher survival rate under hypoxia stress.

Key words: *Schizochytrium* sp., *Artemia tibetiana*, *Nibea albiflora*, fortifier, larviculture

产虾青素马氏副球菌（*Paracoccus marcusii*）IHA034 的筛选及其对小黄鱼（*Larimichthys polyactis*）生长性能、抗氧化水平及肠道屏障的影响研究

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摘要: 本研究旨在开发基于马氏副球菌 IHA034 的虾青素高产技术并评估 IHA034 缓解小黄鱼 (*Larimichthys polyactis*) 肠道损伤的效果。通过优化培养基成分, 72h 发酵液中虾青素产量可达到 245 mg/L。氧化应激细胞试验表明, IHA034 的代谢产物显著提升小黄鱼的肠道细胞活力。动物试验选取了 450 尾 29.16 ± 0.52 g 的小黄鱼幼鱼, 随机分入基础饲料组 (CON)、虾青素组 (添加 4.0g/kg 虾青素, HP) 和马氏副球菌组 (添加 4.0g/kg IHA034 冻干粉, PM), 每组 3 个重复, 试验期 60 天。结果表明, IHA034 显著提升小黄鱼 ($P < 0.05$) 采食量、增重率和成活率, 提高了血清总 SOD 活性。HP 和 PM 组肠道上皮细胞微绒毛较 CON 组更完整致密。转录组分析表明, PM 组小黄鱼肠道 claudin 等基因表达高于 HP 组。但是, IHA034 区别于虾青素的保护机制有待进一步探索。

关键词: 小黄鱼; 马氏副球菌; 抗氧化; 肠道屏障

Development of astaxanthin-producing *Paracoccus marcusii* IHA034 and its effect on growth performance, antioxidant capacity and intestinal barrier of little yellow croaker (*Larimichthys polyactis*)

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Abstract: This study aimed to develop a *Paracoccus marcusii* IHA034 source high astaxanthin production technology and evaluated the effect of IHA034 on alleviating intestinal damage in little yellow croaker (*Larimichthys polyactis*). By optimizing the medium composition, the yield of astaxanthin could reach 245 mg/L at 72 h. Oxidative stress cell assay showed that the metabolites of IHA034 significantly enhanced the viability of intestinal cells of *L. polyactis*. In 60 d animal experiment, 450 juvenile fish at 29.16 ± 0.52 g were randomly divided into the basal feed group (CON), astaxanthin group (4.0 g/kg astaxanthin, HP), and *Paracoccus marcusii* group (4.0 g/kg IHA034 lyophilized powder, PM) with three replicates in each group. The results showed that IHA034 significantly ($P < 0.05$) enhanced the feed intake, weight gain rate, survival rate, and serum total SOD activity. The microvilli of intestinal epithelial cells were more intact and dense in the HP and PM groups than in the CON group. The expression of claudin in the gut was higher in the PM group than in PM group.

Key words: *Paracoccus marcusii*; *Larimichthys polyactis*; antioxidant capacity; intestinal barrier

膳食益生菌对中间球海胆生长、性腺发育与质量、抗氧化能力、肠道健康及非特异性免疫的影响

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摘要：中间球海胆因大型藻类季节性短缺及单一海带不足以满足其生长与性腺发育，常面临营养问题。益生菌富含营养和生物活性物质，广泛用于水产养殖。本研究开发了一种含沼泽红假单胞菌的益生菌饲料，旨在解决食物和营养短缺问题。实验中， 26.5 ± 0.17 g 的中间球海胆被喂食新鲜海带及不同浓度（0%、0.5%、1%、2%）的沼泽红假单胞菌饲料 60 天。结果表明，益生菌显著提高了海胆的生长、抗氧化酶、免疫酶和消化酶活性，促进了性腺发育和免疫相关基因的表达。1%和 2%组的性腺发育、氨基酸含量等优于海带组，尽管性腺颜色略差。益生菌还显著增加了肠道内红杆菌科的丰度（ $P < 0.05$ ），显示对肠道健康的积极作用。总体而言，1% 沼泽红假单胞菌可以提高海胆的生长、性腺发育、抗氧化能力和免疫功能，为解决大型藻类短缺提供了潜在方案。

关键词：棘皮动物, 中间球海胆, 沼泽红假单胞菌, 肠道微生物群, 性腺品质

Effects of dietary probiotics on growth, gonadal development and quality, antioxidant capacity, intestinal health and non-specific immunity of sea urchin (*Strongylocentrotus intermedius*)

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Abstract: *Strongylocentrotus intermedius* faces nutritional challenges due to seasonal macroalgae shortages and single-species kelp diets, which do not fully support its growth and gonadal development. Probiotics, rich in nutrients and bioactive substances, are widely used in aquaculture to address these issues. This study developed a probiotic feed containing *Rhodopseudomonas palustris* to combat food and nutrient deficiencies. *S. intermedius* (26.5 ± 0.17 g) were fed fresh kelp and probiotic feeds with 0%, 0.5%, 1%, and 2% *R. palustris* for 60 days. Results showed that probiotics significantly improved growth, antioxidant, immune, and digestive enzyme activity, while promoting gonadal development and immune gene expression. The 1% and 2% groups showed better gonadal development and amino acid content than the kelp group, despite slightly poorer gonad color. Probiotics also increased *Rhodobacteraceae* abundance in the intestines ($P < 0.05$), positively impacting gut health. Overall, 1% *R. palustris* improves growth, gonadal development, and immunity, offering a solution to macroalgae shortages.

Key words: Echinoid, *Strongylocentrotus intermedius*, *Rhodopseudomonas palustris*, Gut microbiota, Gonadal traits

吊笼养殖附着物替代海泥可以促进刺参的生长和肠道健康

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摘要: 在吊笼养殖过程中, 大量来自吊笼的附着物会在滩涂聚集, 造成环境污染和资源浪费。本研究旨在探讨吊笼养殖附着物作为刺参饲料原料的可行性。在投喂 60d 的刺参中使用不同浓度的吊笼养殖附着物(0、25、50、75、100%)。50% 的吊笼养殖附着物替代海泥显著提高了刺参生长, 降低了饲料系数, 显著提高了肠道消化酶活性, 改善了肠道结构, 丰富了肠道微生物多样性。用 75% 和 100% 的吊笼养殖附着物替代海泥显著提高了海参的总抗氧化能力和总超氧化物歧化酶。通过对增重率的二次回归分析, 估算出适宜的吊笼养殖附着物替代水平为 44.28%。结果表明, 吊笼养殖附着物具有作为刺参饲料新原料的潜力。

关键词: 刺参, 吊笼养殖附着物, 消化酶活力, 肠道菌群, 肠道结构

Replacing sea mud with attachment of suspension cage can improve growth and gut health for sea cucumber *Apostichopus japonicus*

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Abstract: During the suspension cage culture procedure, a substantial quantity of attachments from the suspension cage will amass in the tidal flats, resulting in environmental pollution and resource wastage. The aim of the present study was to explore the feasibility of using attachments of suspension cage (ASC) as a raw feed material for sea cucumbers. Different ASC concentrations (0, 25, 50, 75, and 100%) were used in sea cucumber (*Apostichopus japonicus*) fed for 60d. Replacing Sea mud with 50% ASC significantly improved sea cucumber growth, reduced the feed coefficient, significantly increased the activity of intestinal digestive enzymes, improved the intestinal structure, and enriched intestinal microbiome diversity. Replacing sea mud with 75% and 100% ASC significantly improved sea cucumber total antioxidant capacity and total superoxide dismutase. Based on the quadratic regression analysis for the weight gain rate, the appropriate levels of ASC substitution were estimated as to be 44.28%. The results suggested the potential of ASC as a new raw feed material for sea cucumbers.

Key words: *Apostichopus japonicus*, attachments suspension cage, digestive enzyme, intestinal flora, intestinal structure

饲料中添加复合乳酸菌对刺参生长、 肠道生理及免疫指标的影响

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摘要：为探究复合乳酸菌（LAB）对海参生长性能、肠道生理和非特异性免疫的影响，实验采用平均体重为 2.43 ± 0.02 克的海参进行。设计了五个实验组，每组有 3 次重复，每次重复 20 只海参。海参接受含有不同浓度复合 LAB 的饲料，饲喂时间为 56 天。研究发现，各试验组海参的体重增长和特定生长率显著提高。各实验组消化、免疫及抗氧化酶活性均显著高于对照组。丙二醛（MDA）的含量持续下降。各实验组海参肠道绒毛高度和宽度显著提高。实验组的免疫和生长相关基因的表达水平高于对照组。

关键词：海参，乳酸菌，生长性能，免疫

Effects of Composite Lactic Acid Bacteria on the Growth, intestinal physiology and Nonspecific immunity of Sea cucumber(*Apostichopus japonicus*)

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Abstract: To explore the effects of composite lactic acid bacteria (LAB) on the growth performance, intestinal physiology, and non-specific immunity of sea cucumbers, the experiment was conducted using sea cucumbers with an average weight of 2.43 ± 0.02 grams. Five experimental groups were designed, with each group having 3 replicates and each replicate consisting of 20 sea cucumbers. The sea cucumbers were fed with feed containing different concentrations of composite LAB for a period of 56 days. The study found that the body weight gain and specific growth rate of sea cucumbers in each experimental group were significantly improved. The activity of digestive, immune, and antioxidant enzymes in each experimental group was significantly higher than that in the control group. The content of malondialdehyde (MDA) continued to decrease. The height and width of the intestinal villi in sea cucumbers of each experimental group were significantly increased. The expression levels of immune and growth-related genes in the experimental groups were higher than those in the control group.

Key words: Sea cucumber, composite lactic acid bacteria, growth performance, immunity

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

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

关键词: 脂肪源; 脂肪沉积; 抗氧化能力; 炎症反应; 大口黑鲈

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

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Abstract: In this study, different fat sources (fish oil FO, soybean oil SO, linseed oil LO and coconut oil CO) were supplemented to the diets to investigate their effects on growth performance, lipid deposition, antioxidant capacity and inflammatory response of largemouth bass. The results showed that the weight gain rate and specific growth rate in FO group were significantly higher than those in LO group and CO group. The content of liver triglyceride in SO group was significantly higher than that in other groups. At the transcriptional level, the expression of genes related to lipid synthesis and lipolysis in SO group was significantly higher than that in FO group. LO and SO substitution of fish oil significantly decreased MDA content and increased CAT and T-SOD activity in the liver of largemouth bass. However, replacing fish oil with vegetable oil significantly increased the expression of liver inflammatory response and ER stress-related genes. In conclusion, soybean oil might be used as an alternative lipid source for largemouth bass.

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

亚麻籽油替代鱼油后添加阿卡地新对大黄鱼生长性能和肝脏脂肪沉积的影响

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摘要: 本研究以鱼油组 (6%鱼油, FO)、亚麻籽油组 (亚麻籽油完全替代鱼油, LO) 和亚麻籽油 + 阿卡地新 (150 mg/kg) 组 (LA) 3 种饲料投喂大黄鱼 (92.24 ± 0.30 g) 8 周。结果显示, 与 FO 组相比, LO 和 LA 组大黄鱼增重率显著降低, 饲料系数显著升高。SGR 以 FO 组最高, LA 组最低。LO 组肌肉 p-AMPK 表达和 p-AMPK/AMPK 显著低于 FO 和 LA 组。与 FO 和 LO 组相比, LA 组肌肉 p-TOR 表达和 p-TOR/TOR 显著下降。且 FO 组 p-S6 表达和 p-S6/S6 显著高于 LO 和 LA 组。同时, 与 FO 组相比, LO 组肝脏粗脂肪和甘油三酯含量显著增加, 肝细胞空泡化严重, 细胞核偏移, 脂滴积累, 而添加阿卡地新可明显改善以上情况。总之, 亚麻籽油替代鱼油后添加 AMPK 激动剂 (阿卡地新) 可恢复大黄鱼肌肉中 AMPK 磷酸化水平, 缓解肝脏脂肪沉积, 但未能改善生长, 反而抑制肌肉 TOR 通路, 进一步降低 SGR。

关键词: 大黄鱼; 亚麻籽油; AMPK; 生长性能; 脂肪沉积

Effects of Acadesine (AICAR) Supplementation in a Linseed Oil-based Diet on Growth Performance and Lipid Deposition in Liver of Large Yellow Croaker (*Larimichthys Crocea*)

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Abstract: Large yellow croaker (92.24 ± 0.30 g) were fed fish oil-based diet (FO), linseed oil-based diet (LO) and LA (LO diet added with 150 mg kg⁻¹ acadesine) for 8 weeks in this study. The results showed that weight gain rate was markedly decreased in the LO and LA groups than in the FO group, while the opposite was true for the feed conversion ratio. The FO and LA groups exhibited the highest and lowest specific growth rate (SGR) respectively. The LO group had markedly lower p-AMPK expression and p-AMPK/AMPK in muscle than the other groups. p-TOR expression and p-TOR/TOR were markedly decreased in the LA group than in other groups. p-S6 expression and p-S6/S6 were markedly higher in the FO group than in other groups. Crude lipid and triglyceride contents in liver were markedly higher in the LO group than in the FO group. Dietary linseed oil induced serious vacuolization, nuclear translocation and lipid droplet deposit in liver. Acadesine inclusion obviously improved above phenomena. In conclusion, acadesine inclusion in a linseed oil-based diet restored AMPK phosphorylation and alleviated

Key words: Large yellow croaker; Linseed oil; AMPK; Growth performance; Lipid deposition

双酚 S 诱导淡水小龙虾氧化应激、脂质代谢紊乱和自噬功能障碍的机制研究

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

关键词: 内分泌干扰物, 环境污染物, 甘油磷脂代谢, 肝胰腺毒性, 克氏原螯虾

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

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Abstract: Bisphenol S (BPS) is widely used in plastic products, food packaging, electronic products, and other applications. This study aimed to explore the mechanisms of lipid metabolism disorders induced in freshwater crayfish by exposure to different concentrations of BPS (0, 1, 10, and 100 $\mu\text{g/L}$) over 14 d. The results indicated that BPS exposure led to oxidative stress by inducing elevated levels of ROS and inhibiting the activity of antioxidant-related enzymes. BPS exposure led to increased lipid content in the serum and hepatopancreas, which was associated with elevated lipid-related enzyme activity and increased expression of related genes. BPS exposure decreased levels of PC and PI, disrupted GPI metabolism, and caused lipid deposition in the hepatopancreatic. These phenomena may have occurred because BPS exposure reduced the transport of fatty acids and led to hepatopancreatic lipid deposition by inhibiting the transport and synthesis of PC and PI in the hepatopancreas, thereby inhibiting the PI3K-AMPK pathway.

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

不同海带制品对不同规格中间球海胆的投喂效果研究

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摘要: 为评估不同海带制品对中间球海胆的投喂效果, 对大小两种规格(壳径分别为 3cm 和 1cm)的海胆分别投喂海水泡发盐渍海带、海水泡发干海带、淡水泡发盐渍海带、淡水泡发干海带及鲜海带(对照组)共 5 种海带制品, 测量并比较了各组海胆的体重、特定生长率(SGR)及饵料系数(FCR)。结果表明, 不同海带制品对大、小规格海胆的 FCR 和 SGR 均有显著影响($p < 0.05$)。对大规格海胆投喂海水泡发干海带组、淡水泡发干海带组和鲜海带组的 SGR 显著高于其他处理组; 对小规格海胆投喂海水泡发干海带组和鲜海带组的 SGR 显著高于其他处理组。对大规格海胆投喂海水泡发干海带组、淡水泡发干海带组和鲜海带组的 FCR 显著低于其他处理组, 对小规格海胆投喂海水泡发干海带组和鲜海带组的 FCR 显著低于其他处理组。本研究表明, 海水泡发干海带在提升中间球海胆的生长及饵料利用效率方面具有显著优势, 适合作为鲜海带的替代饵料。

关键词: 中间球海胆, 海带制品, 特定生长率, 饵料系数

Study on the Feeding Effects of Different Kelp Products on *Hemicentrotus pulcherrimus* of Various Sizes

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Abstract: Here's your compressed abstract, keeping the key points within 1100 characters:

This study evaluated the effects of five kelp products on *Hemicentrotus pulcherrimus* in two size groups (3 cm and 1 cm shell diameter). Urchins were fed seawater-rehydrated salted kelp, seawater-rehydrated dried kelp, freshwater-rehydrated salted kelp, freshwater-rehydrated dried kelp, and fresh kelp (control). Body weight, specific growth rate (SGR), and feed conversion ratio (FCR) were measured. Results showed seawater-rehydrated dried kelp significantly improved SGR and FCR in both groups ($p < 0.05$), with performance comparable to or surpassing fresh kelp. Freshwater-rehydrated dried kelp had stronger effects on larger urchins but weaker on smaller ones. Seawater-rehydrated dried kelp also exhibited the lowest FCR, indicating superior feed conversion efficiency. Freshwater-rehydrated dried kelp remained effective despite slightly increasing FCR later in the experiment. Overall, seawater-rehydrated dried kelp is a promising alternative to fresh kelp, with freshwater-rehydrated dried kelp showing potent

Key words:: *Hemicentrotus pulcherrimus*, kelp products, specific growth rate (SGR), feed conversion ratio (FCR)

凝结芽孢杆菌对四指马鲛幼鱼生长性能、 肠道消化酶活性及 肠道菌群的影响

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摘要: 本研究探讨了凝结芽孢杆菌对四指马鲛幼鱼的生长性能、肠道消化酶活性、肠道形态和肠道菌群的影响。在基础饲料上喷洒 1×10^8 cfu/g 的凝结芽孢杆菌，投喂初始体重为 (4.2 ± 0.5) g 的健康四指马鲛幼鱼 8 周。结果显示，实验组与对照组之间的饲料转化率差异极显著 ($P < 0.01$)，而体重增长率、特定生长率、存活率和肥满度差异显著 ($P < 0.05$)。实验组的胰蛋白酶和淀粉酶活性显著降低 ($P < 0.05$)，而两组间的脂肪酶活性差异不显著。与对照组相比，实验组肠绒毛显著增高。两组间的厚壁菌门相对丰度存在显著差异 ($P < 0.05$)，其余菌门差异并不显著 ($P > 0.05$)。根据功能预测分析，实验组中聚糖生物合成和代谢、消化系统计数值显著增加 ($P < 0.05$)，其他功能途径的计数值无显著差异 ($P > 0.05$)。结果表明，饲料中添加凝结芽孢杆菌对幼鱼的生长性能及肠道健康具有积极影响。

关键词: 四指马鲛；凝结芽孢杆菌；生长性能；消化力；肠道菌群

Effects of *Bacillus coagulans* on growth performance, digestive enzyme activity and intestinal flora of the juvenile fourfinger threadfin (*Eleutheronema tetradactylum*)

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Abstract: The effects of *Bacillus coagulans* (BC) on growth performance, intestinal digestive enzyme activity, intestinal morphology, and intestinal flora of juvenile fourfinger threadfin (*Eleutheronema tetradactylum*) were investigated in the present study. Healthy juvenile *E. tetradactylum* with an initial body weight of 4.2 ± 0.5 g were fed a basal diet sprayed with 1×10^8 cfu/g *B. coagulans* for 8 weeks. The differences in the feed conversion ratio, weight gain rate, specific growth rate, survival rate, and condition factor were significant ($P < 0.05$). In the experimental group, trypsin and amylase activities decreased significantly. Compared to the control group, the height of the intestinal villi was greater. Based on the function prediction analysis, the count values for the glycan biosynthesis, metabolism, and digestive system pathways were significantly increased in the experimental group ($P < 0.05$). These results indicate that dietary *B. coagulans* supplementation is effective in promoting the growth performance and intestinal health of juvenile *E. tetradactylum*.

Key words: *Eleutheronema tetradactylum*; *Bacillus coagulans*; Growth performance; Intestinal flora; Probiotics

两种菜粕营养改进策略对大口黑鲈生长、代谢、抗氧化与免疫的影响

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摘要: 充分利用菜粕可作为我国非粮蛋白饲料资源开发的高效途径, 饲料添加谷氨酰胺和叶酸可作为两种提高菜粕限用量的有效策略。为了探讨菜粕利用的提升途径, 设计了两部分实验进行研究。第一部分实验设置 7 组等氮等能饲料, 基础饲料(45%鱼粉, 对照组), 25%菜粕(31%鱼粉, RM 组), 在菜粕组基础上添加 1%, 2%, 3%, 4%, 5%谷氨酰胺二肽复合物。第二部分实验设置 6 组等氮等能饲料, 包括基础饲料(41%鱼粉, F 组)、12%菜粕饲料(34%鱼粉, R 组), 以及在 R 组基础上添加 2-8 mg/kg 叶酸。结果显示: 菜粕会导致大口黑鲈机体生长和消化受阻, 营养代谢紊乱, 抗氧化能力下降, 肝脏受到损伤, 肠道菌群多样性下降, 条件致病菌丰度升高。谷氨酰胺和叶酸可通过促进蛋白质合成, 脂质代谢, 提高抗氧化和免疫能力来改善菜粕的负面效应, 可作为两种极具潜力的新型添加剂。

关键词: 大口黑鲈; 菜粕; 谷氨酰胺; 叶酸; 生长; 代谢

Effects of two rapeseed meal nutrient enhancement strategies on growth, metabolism, antioxidant and immunity of largemouth bass(*Micropterus salmoides*)

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Abstract: The utilisation of rapeseed meal can be used as an efficient way to develop non-food protein feed resources in China, and the addition of glutamine and folic acid to feed can be used as two effective strategies to improve the limited utilisation of rapeseed meal. To explore the way to improve the use of rapeseed meal, a two-part experiment was designed for the study. The results showed that rapeseed meal resulted in impaired growth and digestion, disturbed nutrient metabolism, decreased antioxidant capacity, liver damage, decreased diversity of gut microbiota, and increased abundance of conditionally pathogenic bacteria in largemouth bass. Glutamine and folic acid can ameliorate the negative effects of meal by promoting protein synthesis, lipid metabolism, and antioxidant and immune capacity, and can be used as two new additives with great potential.

Key words: Largemouth bass; Rapeseed meal; Glutamine; Folic acid; Growth; Metabolism

循环水与流水养殖对光唇鱼肌肉营养成分的影响

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摘要：本试验旨在研究循环水养殖和流水养殖模式下光唇鱼的肌肉营养品质差异。实验分析了流水和循环水养殖光唇鱼的肌肉营养成分、脂肪酸含量、氨基酸含量、矿物质元素的含量。结果显示：流水养殖组肌肉水分、粗脂肪、十一种脂肪酸、六种氨基酸、锌及砷含量均显著高于循环水养殖组（ $P < 0.05$ ）。循环水养殖组肌肉粗蛋白、五种脂肪酸、铁及铜显著高于流水养殖组（ $P < 0.05$ ）。研究表明，流水养殖提高了光唇鱼肌肉粗脂肪、多种氨基酸、脂肪酸、锌及砷含量，循环水养殖则提高光唇鱼肌肉粗蛋白、多种脂肪酸、铁及铜含量，因此这两种模式都适宜养殖光唇鱼。

关键词：循环水；流水；光唇鱼；肌肉；营养成分

Effects of circulating water and running water culture on muscle nutrients of *Acrossocheilus*

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Abstract： The aim of this experiment was to study the difference of muscle nutritional quality of *acrossocheilus chinensis* in circulating water culture and running water culture. The muscle nutrients, fatty acids, amino acids and mineral elements of *Acrossocheilus* cultured in running water and circulating water were analyzed. The results showed as follows: The contents of muscle moisture, crude fat, 11 fatty acids, 6 amino acids, zinc and arsenic in running water culture group were significantly higher than those in circulating water culture group ($P < 0.05$). The crude protein, five fatty acids, iron and copper of muscle in recirculating water culture group were significantly higher than those in running water culture group ($P < 0.05$). The results showed that running water culture increased the contents of crude fat, various amino acids, fatty acids, zinc and arsenic, while circulating water culture increased the contents of crude protein, various fatty acids, iron and copper, so both models were suitable for farming.

Key words:： Circulating water; Running water; *Acrossocheilus*; Muscle; Nutrient composition

饲料中添加植物甾醇可促进高淀粉饲喂下大口黑鲈幼鱼的生长性能、饲料利用率、抗氧化能力和葡萄糖代谢功能

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摘要: 为探究饲料中添加植物甾醇对高淀粉饲喂下大口黑鲈 (*Micropterus salmoides*) 幼鱼的影响, 设置了四个饲喂组: 分别配制含有质量比为 10% 和 15% α -淀粉的膨化浮质等氮等能饲料; 在 15% α -淀粉配方基础上, 分别在其中添加 0.1% 和 0.5% 的植物甾醇。实验结果表明, 高淀粉的饲喂显著降低了大口黑鲈幼鱼的成活率、体增重和特定生长率, 而在添加植物甾醇后三项指标获得显著提高。随着植物甾醇添加量的升高, 饲料系数、腹腔脂肪比、血浆中胆固醇、甘油三酯、葡萄糖、丙二醛、天冬氨酸转氨酶和丙氨酸转氨酶水平及肝糖原含量显著降低; 幽门胃蛋白酶和脂肪酶水平、肝脏葡萄糖激酶和丙酮酸激酶水平显著升高。综上所述, 饲料中添加植物甾醇可提高大口黑鲈幼鱼的生长性能、葡萄糖利用代谢和抗氧化能力, 并缓解高淀粉饲喂造成鱼体的血糖应激。

关键词: 植物甾醇; 大口黑鲈; 高淀粉; 生长性能; 饲料利用率; 抗氧化水平; 葡萄糖代谢

Phytosterol Supplementation Enhances the Growth Performance, Feed Utilization, Antioxidant Status and Glucose Metabolism of Juvenile Largemouth Bass (*Micropterus salmoides*) Fed a High-Starch Diet

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Abstract: A 56-day feeding trial was conducted with four dietary feeds: extruded floating isonitrogenous and isoenergetic diets were formulated to contain 10% and 15% α -starch; on basis of a 15% α -starch diet, two diets were supplemented with 0.1% and 0.5% phytosterol, respectively. The results showed that high-starch dietary significantly lowered the survival rates, weight gain and specific growth rates, when supplemented with phytosterols, three indexes significantly increased. As phytosterol concentration increased, the feed conversion ratio, intraperitoneal fat ratio, plasma cholesterol, triglyceride, glucose, malondialdehyde, aspartate transaminase and alanine transaminase levels and hepatic glycogen content significantly decreased; protease and lipase levels in the pyloric zone, glucokinase and pyruvate kinase levels markedly increased. In summary, dietary phytosterol supplementation promoted the growth performance, glucose utilization and metabolism, antioxidant status as well as alleviated the negative stimulation of glycemia stress in largemouth bass fed a high-starch diet.

Key words: phytosterol; *Micropterus salmoides*; high-starch diet; growth performance; feed utilization; antioxidant status; glucose metabolism

蚕豆饲料中乳酸菌添加水平对草鱼生长性能和消化机能影响

董鹏林

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摘要：本研究的目的是评估不同浓度的乳酸菌对草鱼（*Ctenopharyngodon idella*）生长性能和消化功能的影响。在实验设计中，以蚕豆饲料为基础，分别添加了0%、1%、2%、3%和4%的乳酸菌进行喂养，并监测了草鱼的生长速度、饲料转化效率以及消化酶活性等关键指标。研究结果显示，随着乳酸菌添加量的增加，草鱼的生长速度和饲料转化效率均显著提高，尤其是在添加2%和3%乳酸菌的组别中，效果更为显著。同时，消化酶活性也得到了明显提升，这说明乳酸菌能够增强草鱼的消化吸收能力。然而，研究还发现，当乳酸菌的添加量过高（例如4%）时，会对草鱼的生长产生抑制作用，这提示在实际饲料配制时，应谨慎选择乳酸菌的添加比例。综合分析表明，适量的乳酸菌添加能够显著提升草鱼的生长性能和消化功能，为水产养殖业中饲料的优化提供了理论依据和实践指导。

关键词：草鱼, 乳酸菌, 蚕豆饲料, 生长性能, 消化机能

Effect of lactic acid bacteria supplementation in broad bean feed on carp growth performance and digestive function

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Abstract: The purpose of this study is to evaluate the effect of different concentrations of *Lactobacillus* on the growth performance and digestive function of grass carp (*Ctenopharyngodon idella*). In the experimental design, 0%, 1%, 2%, 3% and 4% lactic acid bacteria were added based on the broad bean feed, and key indicators such as growth rate, feed conversion efficiency and digestive enzyme activity were monitored. The results showed that the growth rate and feed conversion efficiency of grass carp increased significantly with the addition of lactic acid bacteria, especially in the groups of 2% and 3% lactic acid bacteria. At the same time, the activity of digestive enzymes was also significantly improved, which indicates that lactic acid bacteria can enhance the digestion and absorption capacity of grass carp. However, the study also found that when the addition of lactic acid bacteria was too high (such as 4%), it suggests that the added proportion of lactic acid bacteria should be carefully selected in actual feed preparation. Comprehensive analysis shows that the appropriate amount of lactic acid bacteria can significantly improve the growth performance and digestive function of grass carp, and provides theoretical basis and practical guidance for the optimization of feed in aquaculture industry.

Key words: grass carp, lactic acid bacteria, broad bean feed, growth performance, digestive function

白斑综合征病毒和对虾内参基因双重荧光定量 PCR 检测方法的建立

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摘要: 本研究旨在建立一种白斑综合征病毒 (WSSV) 和对虾内参基因双重荧光定量 PCR 检测方法, 提高 WSSV 检测的灵敏度和特异性。首先, 基于 WSSV 基因组保守序列设计合成特异性引物和 TaqMan 探针, 建立 WSSV 单重荧光定量 PCR 检测体系, 经特异性和重复性试验证实, 该方法对 WSSV 具有良好的特异性和重复性。在此基础上, 设计合成了凡纳滨对虾内参基因引物和探针, 并对引物碱基进行优化替换, 建立了 WSSV-对虾内参基因双重荧光定量 PCR 检测体系。敏感性试验结果显示, 该双重检测体系对 WSSV 的检测下限可达 15 拷贝/ μL , 在 $6.6 \times 10^5 \sim 6.6$ 拷贝/ μL 范围内, WSSV 质粒标准品的起始模板量对数值与 Ct 值呈良好的线性关系 ($R^2=0.998$)。同时, 内参基因的引入可有效区分样本中由核酸提取或操作问题引起的假阴性结果。

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

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

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

endogenous control gene of *Litopenaeus vannamei* were designed and synthesized, and the primer bases were optimized to establish a duplex qPCR detection system. [Results] The sensitivity test results showed that the detection limit of the duplex system for WSSV was 15 copies/ μ L, and there was a good linear relationship between the logarithmic value of the initial template amount and the Ct value of WSSV plasmid standards within the range of $6.6 \times 10^5 \sim 6.6$ copies/ μ L ($R^2=0.998$). Moreover, the introduction of the endogenous control gene effectively distinguished false-negative results caused by nucleic acid extraction or operational issues in the samples.

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

杂交鳢脾脏细胞系的建立及其对杂交鳢弹状病毒敏感性的探究

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

关键词：杂交鳢 脾脏 细胞系 杂交鳢弹状病毒

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

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

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

乌梅和黄芩水提物对致病性嗜水气单胞菌的体外抑菌效果及抑菌机理初探

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摘要: 【目的】探讨乌梅和黄芩水提物对水产养殖业中主要病原菌嗜水气单胞菌的抑菌作用和机制。【方法】通过实验探明乌梅和黄芩水提物对嗜水气单胞菌的最低抑菌浓度 (MIC)，对该菌集群运动、脂肪酶活性、蛋白酶活性及溶血活性及毒力基因表达的影响。【结果】乌梅和黄芩水提物对嗜水气单胞菌的 MIC 均为 6.25 mg/mL；乌梅和黄芩水提物对集群能力和蛋白酶的抑制效果呈剂量依赖性，均在 3.12 mg/ml 时抑制效果最强，其中乌梅抑制效果更佳；乌梅和黄芩水提物对脂肪酶的抑制效果均在 1.56 mg/ml 达最佳，此浓度下黄芩抑制效果更佳；乌梅和黄芩水提物对溶血活性的抑制效果均在 3.12 mg/ml 达最佳，此浓度下黄芩效果更佳；毒力基因 Act、AerA、Aha、Hly 和 OMP 在乌梅、黄芩添加影响下表达均下调，其中 Aha 基因下调最显著。【结论】乌梅和黄芩水提物是潜在的嗜水气单胞菌替抗物。

关键词: 乌梅；黄芩；嗜水气单胞菌；

Preliminary study on the in vitro antibacterial effects and mechanisms of water extracts of *Fructus Mume* and *Scutellaria baicalensis* Georgi against pathogenic *Aeromonas aeruginosa*

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Abstract: 【Objective】The objective of this study is to investigate the antibacterial effect and mechanism of aqueous extracts from *Mume Fructus* and *Scutellaria baicalensis* Georgi on *Aeromonas hydrophila*, the main pathogen in aquaculture. 【Method】The effects of the aqueous extracts of *Mume Fructus* and *Scutellaria baicalensis* Georgi on *Aeromonas hydrophila* were investigated by experiments on the swarm motility, lipase activity, protease activity, hemolytic activity and virulence gene expression of the bacterium. 【Result】The MIC of aqueous extracts of *Mume Fructus* and *Scutellaria baicalensis* Georgi against *Aeromonas hydrophila* was 6.25 mg/mL. The inhibition effect of aqueous extracts of *Mume Fructus* and *Scutellaria baicalensis* Georgi on clustering capacity and protease was dose-dependent, and the inhibition effect was the strongest at 3.12 mg/ml, and the inhibition effect of *Mume Fructus* was better. The inhibition effect of aqueous extracts of *Mume Fructus* and *Scutellaria baicalensis* Georgi on lipase was the best at 1.56 mg/ml, and the inhibition effect of *Skullcap* was better at this concentration. The inhibition effect of aqueous extracts of *Mume Fructus* and *Scutellaria baicalensis* Georgi on hemolytic activity were the best at 3.12 mg/ml, and the effect of *Scutellaria baicalensis* Georgi was better at this concentration. The expressions of virulence genes Act, AerA, Aha, Hly and OMP were all down-regulated under the influence of the addition of *Wumei* and *Scutellaria baicalensis*, and the Aha gene was the most down-regulated. 【Conclusion】The aqueous extracts of *Ume* and *Scutellaria baicalensis* are potential hydrophilic aeromonas substitute resistants.

Key words: *Mume Fructus*; *Scutellaria baicalensis* Georgi; *Aeromonas hydrophila*.

虎斑乌贼皮肤溃疡综合征的蛋白质组学分析

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摘要：皮肤溃疡综合征(SUS)是虎斑乌贼养殖过程中的一个严重问题。然而，我们对这种疾病认知有限。本文旨在通过蛋白组学方法分析探究患病乌贼体内差异表达蛋白和生物学通路。实验分为健康组和患病组，各组3个生物学重复，每个重复4只虎斑乌贼。与健康组相比，患病组筛选到85个差异表达蛋白(DEPs)、其中36个上调蛋白和49个下调蛋白。GO富集结果表明，DEPs主要富集于细胞内组分组织或生物发生，原子核和离子结合过程。对KEGG富集通路进行分析，上调的DEPs主要富集在细胞外基质(ECM)-受体相互作用途径。实时定量PCR结果显示，患病乌贼体内MMP14和MMP19 mRNA表达显著上升。此外，患病乌贼的蛋白酶活性高于健康组。

关键词：虎斑乌贼、蛋白质组学、皮肤溃疡综合征、基质金属蛋白酶

Comparative proteomic analysis of the protein profile in the cuttlefish *Sepia pharaonis* associated with skin ulceration syndrome

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Abstract : Skin ulceration syndrome (SUS) is becoming a severe problem in the breeding and culturing process of the cuttlefish *Sepia pharaonis*. However, limited knowledge is available about the occurrence of this devastating disease. In this study, proteomic analysis was used to identify the differentially expressed proteins (DEPs) and the biological pathways enriched in SUS-diseased *S. pharaonis*. Both the healthy group and diseased group were analyzed in triplicate, with 4 cuttlefish in each replicate. The results showed that 85 DEPs were identified between the two groups, including 36 upregulated proteins and 49 downregulated proteins in the diseased group compared to the healthy group. GO enrichment analysis revealed that the DEPs were mainly enriched in cellular component organization or biogenesis, nucleus and ion binding processes. The results of the KEGG pathway analysis indicated that extracellular matrix (ECM)-receptor interaction was the most enriched upregulated pathway.

Key words:: *Sepia pharaonis* 、 Proteomic analyses 、 Skin ulceration syndrome、 Matrix metalloproteinases

眼点淀粉卵涡鞭虫感染黄鳍棘鲷致病寄生靶器官确定

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摘要: 眼点淀粉卵涡鞭虫是一种海水鱼类体表寄生鞭毛虫, 严重感染时可导致感染鱼迅速死亡。为确定导致感染鱼死亡的关键致病寄生靶器官, 本研究分别比较了鳃局部感染、皮肤局部感染和整体感染时感染鱼体表寄生虫丰度和存活情况之间的关系。结果表明, 眼点淀粉卵涡鞭虫严重感染鳃组织会导致感染鱼死亡且滋养体在鳃上的发育速度显著高于皮肤和鳍条 ($P < 0.05$)。感染鱼鳃丝结构混乱, 上皮细胞变性并出现大量淋巴细胞浸润。感染鱼皮肤未见明显的组织病理学变化。TUNEL 实验结果表明, 滋养体寄生位点附近存在大量细胞凋亡。微生物组分析结果显示, 眼点淀粉卵涡鞭虫感染显著降低了感染鱼鳃组织微生物群落的丰富度和多样性 ($P < 0.05$), 且黄杆菌属、诺卡氏菌属等常见水生生物致病菌丰度显著增加。综上, 鳃组织被寄生虫严重感染和病变是导致感染鱼死亡的关键。

关键词: 眼点淀粉卵涡鞭虫; 致病机理; 局部感染; 微生物群落

Gill lesions are the main cause of death in yellowfin seabream (*Acanthopagrus latus*) following infection with *Amyloodinium ocellatum*

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Abstract: This study used a local infection method to identify the pathogenic target organ responsible for the death of infected fish. Comparing the relationship between the abundance of trophonts in gills and skin with the mortality of infected fish using local infection showed that severe gill infections cause the mortality of infected fish. The gill filaments of the infected fish were structurally disordered, with pronounced lesions associated with the presence of trophonts, such as epithelial cell degeneration and massive lymphocytic infiltration. However, the skin showed no obvious pathological changes. The TUNEL assay showed a significant presence of apoptotic cells concentrated in the area of *A. ocellatum* infection. *A. ocellatum* infection significantly reduced ($p < 0.05$) the richness and diversity of the gill microbial community of *A. latus*. Infection by *A. ocellatum* increased the relative abundance of several putative pathogenic bacteria (*Flavobacterium* and *Nocardia*) in the gill and skin of *A. latus*.

Key words: *Amyloodinium ocellatum*; Pathogenesis; Local infection; Microbiome

镀锌材料是一种有效防控鱼类眼点淀粉卵涡鞭虫感染的方法

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摘要: 眼点淀粉卵涡鞭虫是一种海水鱼类寄生鞭毛虫, 可造成鱼类大量死亡和经济损失。本研究评估了浸泡镀锌材料海水对防控眼点淀粉卵涡鞭虫重复感染的效果及其对涡孢子、滋养体和包囊阶段的毒性效果。结果发现浸泡镀锌材料海水显著降低载虫量, 有效保护了患病鱼。涡孢子感染能力被显著抑制, 载虫量减少 89.5%, 滋养体驱离率达 46.24%。浸泡镀锌材料海水中锌离子浓度持续升高, 而黄鳍棘鲷肝脏中锌转运体表达显著下调, 提示黄鳍棘鲷通过减少锌离子内流以维持细胞内锌稳态来适应高锌环境。这些结果表明, 使用镀锌材料是一种有效的防控鱼类眼点淀粉卵涡鞭虫感染的方法。

关键词: 眼点淀粉卵涡鞭虫; 镀锌材料; 防控; 锌离子; 锌转运体

Galvanized material is a promising approach to control *Amyloodinium ocellatum* infection in fishes

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Abstract: *Amyloodinium ocellatum* is a dinoflagellate that infects marine fish, causing mass mortality and economic loss. This study evaluated the efficacy of the seawater immersed with galvanized materials (IGM seawater) in controlling *A. ocellatum* reinfection. Furthermore, the toxicity of IGM seawater to the dinospores infectivity, tomites development, and trophonts parasitism was determined. The results revealed that the IGM seawater significantly decreased parasite abundances and protected the infected fishes. The infectivity of dinospores was significantly inhibited in the [0.4–2 d] group by 89.50% and the reduction of trophonts was 46.24%. The zinc ion concentrations in the IGM seawater were continuously increased. While the expression of zinc transporters in the liver of *A. latus* was significantly down-regulated. Therefore, *A. latus* acclimatizes to a high-zinc environment by reducing zinc ions influx to maintain intracellular zinc homeostasis. These results imply that using galvanized material is a promising approach to controlling *A. ocellatum* infection in fish.

Key words: *Amyloodinium ocellatum*; galvanized materials; control; zinc ion; zinc transporters

抗簇生蟹奴病的药物筛选和治疗效果研究

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摘要: 簇生蟹奴专营寄生在中华绒螯蟹体内, 导致蟹蜕壳困难、性腺萎缩, 对种质资源保护和养殖产业造成经济损失, 目前缺乏有效治疗手段。本研究旨在探索六种药物(甘草、生姜、丁香、苦参、绿茶和硫酸奎宁)对簇生蟹奴病的治疗效果。这些药物能显著提高患病蟹的存活率, 促进蟹奴外体脱落, 并损伤其细胞结构。免疫学检测显示, 治疗组蟹的血蓝蛋白(Hc)水平及胰腺中多种酶活性增强。qPCR 分析揭示了药物对蟹免疫通路的不同激活效果: 甘草、丁香和苦参能上调治疗组蟹酚氧化酶原(proPO)表达, 生姜则降低了其表达; 甘草、绿茶和硫酸奎宁显著上调丝氨酸蛋白酶抑制剂(Serpin3)和脂多糖和 β -1,3-葡聚糖结合蛋白(LGBP)的表达, 生姜和丁香则下调; 丝氨酸蛋白酶(SP)在甘草、丁香、苦参和硫酸奎宁组中表达上调, 生姜组则降低。综合分析表明, 这些药物能激活蟹的免疫通路, 有效抑制簇生蟹奴的繁殖, 其中丁香和甘草效果最佳。

关键词: 簇生蟹奴; 中华绒螯蟹; 免疫通路; 治疗效果

Drug screening and treatment efficacy research for *Polyascus gregaria* in *Eriocheir sinensis*

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Abstract: *Polyascus gregaria* specifically infects the *Eriocheir sinensis*, resulting in molting difficulties, and gonad atrophy leading to reproductive failure. This poses a substantial threat to genetic resource preservation and aquaculture industry development, as there is currently no effective treatment available. This study aims to explore the treatment effects of six types of drugs (Licorice, Ginger, Clove, *Sophora flavescens*, Green tea, and Quinine sulfate) on the treatment of *P. gregaria*. The study found that these drugs can significantly improve survival rates in treated crabs, increase the shedding rate, and damage the cell structure of externa. Immunological assays revealed that the levels of hemocyanin (Hc) in the treated crabs and the activities of immune-related enzymes in the hepatopancreas were enhanced. qPCR analysis revealed the different activation effects of the drugs on the immune pathway: licorice, clove, and *sophora flavescens* could upregulate the expression of prophenoloxidase (proPO) in the treatment group, while ginger reduced its expression; Licorice, green tea, and quinine sulfate significantly upregulated the expression of serine protease inhibitor (Serpin 3) and lipopolysaccharide and β -1,3-glucan binding protein (LGBP) in the treatment group, while their expression decreased in the ginger and clove groups. Serine protease (SP) expression is upregulated in the licorice, clove, *Sophora flavescens*, and quinine sulfate groups but decreased in the ginger group. Overall, the analysis indicates that these drugs activate immune pathways in crabs and effectively inhibit *P. gregaria* reproduction. Notably, clove and licorice exhibit significant therapeutic effects.

Key words: *Polyascus gregaria*; *Eriocheir sinensis*; immune pathways; therapeutic effects

一种作用于东星斑体表鱼蛭的消除装置

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摘要: 水产养殖产业链中以东星斑为代表的各类石斑鱼受到鱼蛭寄生现象较难解决, 长期以来的药物治疗或人工处理方式费时费力, 且复发率较高。本实验设计一种养殖治疗装置以解决鱼蛭大量寄生问题, 通过紫外线照射装置、水过滤装置、沉淀装置、观察装置, 利用管道、单向阀、抽鱼泵连接病鱼池, 以水质处理器、电机、充气泵等为辅助设备对鱼蛭进行消除处理。各装置均安装不同孔径滤网, 设置单向阀以解决病鱼不定向游动、鱼蛭脱落难、未及时处理造成的反复寄生问题。处理装置设额定功率全光谱灯对鱼体进行短时照射后进入观察装置静养防止应激导致病鱼死亡。实验处理 30min 后, 鱼蛭开始脱落; 处理 1h, 鱼蛭继续脱落, 体表寄生出现聚缩, 鱼正常活动; 3h, 鱼蛭明显大批量脱落, 鱼体粘液增多; 7h, 大多数鱼蛭脱落死亡, 体表出现白色丝状物。本装置可使鱼蛭大批量脱落, 极大提高病鱼康复概率, 不会造成交叉感染或寄生等一系列问题, 且投入成本可控, 具有一定推广价值。

关键词: 东星斑, 鱼蛭, 病害, 消除装置

A device for eliminating leeches on the surface of the *Plectropomus leopardus* body

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Abstract : In the aquaculture industry, grouper species like *Plectropomus leopardus* are often parasitized by leeches, a persistent issue hard to address with long-term drug/manual treatments due to high recurrence. This experiment designed a breeding treatment device integrating UV irradiation, water filtration, sedimentation, observation tools, pipelines, check valves, fish pumps, etc., to eliminate leeches. It features filters with various apertures and a one-way valve to tackle issues from fish's nondirectional swimming, leech detachment difficulty, and timely handling. The device also uses a full-spectrum lamp to briefly irradiate fish before observation, with resting periods to prevent stress-related deaths. Results showed leeches began falling off after 30 minutes, significantly after 1 hour, and mostly dead after 7 hours, with fish showing increased mucus and unidentified white filaments. This device efficiently removes leeches, enhances fish recovery, avoids cross-infection/re-parasitism, and is cost-effective, holding promotion potential.

Key words:: *Plectropomus leopardus*, leech, disease, elimination device

草金鱼白点病的诊断和防治方法

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摘要: 草金鱼具有观赏价值高、易饲养等诸多优点,但冬季水温较低时易感染小瓜虫,小瓜虫病是一种草金鱼常见的寄生虫病。小瓜虫作为单细胞原生体外寄生虫,其成虫呈球形且全身披纤毛,直径约 0.8mm。在感染鱼体后,肉眼可见鱼体表面有白点附着,因此该病也被称为白点病。本文以草金鱼来源的小瓜虫为研究对象,新购入的草金鱼在水族观赏鱼缸养殖环境下发病,病鱼出现食欲减退、消瘦、体表白点、皮肤溃烂、鳍条腐烂、呼吸困难等症状。通过显微镜观测鱼体的体表粘液、鳃、鳍等部位,确定为小瓜虫病。治疗采用了升温治疗法,将水温提升至 31℃ 以上和药浴治疗法,亚甲基蓝浸泡结合高锰酸钾处理养殖缸,成功控制病情。分析病因可知,新购入的草金鱼缸苗未隔离观察,鱼缸清洁和消毒不到位,以及冬季气温骤变导致的低温环境利于小瓜虫繁殖等因素促使发病。

关键词: 小瓜虫病; 草金鱼; 疾病防治; 生活史

Diagnosis and control of white spot disease in grass carp

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Abstract: Grass carp have many advantages such as high ornamental value and easy to feed, but they are easy to be infected with *Cucurbita pepo* in winter when the water temperature is low, and *Cucurbita pepo* is a kind of common parasitic disease of grass carp. As a unicellular protozoan ectoparasite, *Cucumis sativus* is spherical and ciliated, with a diameter of about 0.8 mm, and when infected, white dots can be seen on the surface of the fish, which is why the disease is also called white spot disease. In this paper, *Cucumis sativus*, which is a source of grass carp, was used as the object of study. Newly purchased grass carp developed the disease under the breeding environment of aquariums and ornamental fish tanks, and the diseased fish showed the symptoms of loss of appetite, emaciation, white dots on the surface of the body, ulceration of the skin, decay of fins, and respiratory difficulties.

Key words: melioidosis; grass carp; disease control; life history

罗非鱼养殖系统中抗生素的溯源、传播、 生物累积和关键影响因子研究

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摘要：抗生素是新污染物。本研究对罗非鱼养殖中抗生素的来源和传播等开展研究。在养殖水源水中抗生素总浓度是池塘水的 3.58~5.49 倍 ($p<0.05$)。在养成罗非鱼鱼体的抗生素总浓度为 $17.20\pm 1.51\text{ng/g}$ ，远低于国家规定的 100ng/g 限值，鱼肉中仅 $2.89\pm 0.10\text{ng/g}$ 。生物累积因子为 $21.56\sim 7827.48\text{L/kg}$ 。从饲料中投入的抗生素为 0.18g ，而从养殖水源水输入可达 0.75g ，其抗生素来源贡献度为 80.65% 。罗非鱼养殖系统中抗生素的环境归趋主要为池塘水 (51.61%)，自然降解 (25.81%)，罗非鱼 (17.20%)，沉积物 (5.38%)。研究表明，引流自周边水域环境的养殖水源水是池塘养殖生态系统抗生素的主要来源，水源水中含有磺胺喹噁啉等 10 多种农业农村部禁用和限用而在饲料中无检出的抗生素。SS 和 COD 是影响抗生素分布和传播的关键影响因子。

关键词：健康养殖，水产品质量安全，抗生素，溯源，环境归趋

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Abstract: /

Key words: /

溶解氧对刺激隐核虫发育规律研究

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摘要: 刺激隐核虫是一种专性寄生于海水鱼类的纤毛虫, 离开宿主后黏附在海水网箱深处缺氧网衣上, 是海水鱼刺激隐核虫病重要感染源。为探究缺氧环境中刺激隐核虫的发育特征, 本研究设定 6、4、3、2 和 1mg/L 的溶解氧含量, 分析刺激隐核虫包囊前体, 包囊和幼虫在不同溶解氧水平下发育规律。结果显示, 缺氧抑制包囊孵化率, 各组包囊孵化率分别为 96.93, 91.38, 89.69, 70.69 和 57.82%, 缺氧组的孵化率显著性降低 ($P<0.05$)。包囊孵化幼虫数目分别为 185.91、178.72、82.33、78.09 和 64.47, 缺氧组包囊孵化幼虫数目显著性减少 ($P<0.05$)。缺氧下包囊孵化幼虫感染力显著性降低 ($P<0.05$), 6, 2 和 1 mg/L 海水包囊孵化幼虫感染后载虫量分别为 104.67, 35.33 和 18.33。本研究分析刺激隐核虫在缺氧中的发育规律, 为刺激隐核虫病的监测和预警工作提供参考。

关键词: 刺激隐核虫, 海水溶解氧, 网箱养殖

The effect of varying dissolved oxygen levels on the developmental patterns of *Cryptocaryon irritans*

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Abstract: *Cryptocaryon irritans* is an obligate ciliated protozoan of marine fish. *C. irritans* can adhere to the hypoxic net clothing at the depths of marine cages after leaving the host, which is a primary infection source of *C. irritans* in cage culture farms. To examine the changes of *C. irritans* in hypoxia, this study set dissolved oxygen levels at 6, 4, 3, 2, and 1 mg/L, analyzing the developmental patterns of the protomonts, tomonts, and theronts under different DO conditions. The results showed that hypoxia inhibited the hatching of tomonts. The excystment rate of tomonts seawater was 96.93, 91.38, 89.69, 70.69, and 57.82 % ($P<0.05$), respectively. The number of theronts released from tomonts were 185.91, 178.72, 82.33, 78.09, and 64.47, respectively ($P<0.05$). The parasite abundance per fish in 6, 2, and 1 mg/L DO seawater were 104.67, 35.33, and 18.33 ($P<0.05$). This study analyzes the developmental patterns of *C. irritans* under hypoxia, providing a reference for the monitoring and early warning of Cryptocaryoniasis.

Key words: *Cryptocaryon irritans*, Seawater dissolved oxygen, Net cage culture

海水中眼点淀粉卵涡鞭虫涡孢子荧光定量 PCR 检测方法的建立

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摘要: 眼点淀粉卵涡鞭虫(*Amyloodinium ocellatum*)是海洋鱼类最重要的体外寄生虫之一, 能引起眼点淀粉卵涡鞭虫病并导致养殖鱼大规模死亡。在本研究中, 基于 *A. ocellatum* 的核糖体 DNA 的内部转录间隔区 (ITS rDNA), 成功建立了使用 ITS-F3 和 ITS-R3 引物对的实时荧光定量 PCR (qPCR) 检测方法, 用于定量检测海水中的眼点淀粉卵涡鞭虫。通过使用真空泵抽滤海水的方式收集涡孢子, 并通过光学显微镜和扫描电子显微镜 (SEM) 检查, 显示涡孢子被吸附在醋酸纤维素膜的表面。海水寄生虫数量与 Ct 值之间的线性关系遵循模型 $y = -3.0607x + 29.919$, 决定系数 (R^2) 为 0.985。检测结果显示出高度的可重复性, 并且与其他海水寄生虫没有交叉反应。该检测方法在每 300 mL 海水中有 8 和 10 个涡孢子的浓度下 100% 检测到涡孢子。

关键词: 眼点淀粉卵涡鞭虫、黄鳍棘鲷、实时定量 PCR、定量检测

Development of a quantitative real-time PCR assay for the detection of dinospores of *Amyloodinium ocellatum* in seawater samples

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Abstract: *Amyloodinium ocellatum* is one of the most important ectoparasites of marine fish, causing amyloodiniosis and mass mortality in aquaculture. In this study, a quantitative real-time PCR (qPCR) assay using the ITS-F3 and ITS-R3 primer pair based on the internal transcribed spacers of nuclear ribosomal DNA (ITS rDNA) of *A. ocellatum* was successfully established for the detection and quantification of dinospores in seawater. The dinospores were collected by suction filtration of seawater using a vacuum pump, and examination by light microscopy and scanning electron microscopy (SEM) showed that the dinospores were adsorbed on the surface of the cellulose acetate membrane. The linear relationship between seawater parasite abundance and Ct values followed the model $y = -3.0607x + 29.919$ with a coefficient of determination (R^2) of 0.985. The results of the assay showed high reproducibility and no cross-reactivity with other aquatic pathogens. The detection method successfully identified 100% of dinospores at concentrations of 8 and 10 spores per 300 mL of seawater.

Key words: *Amyloodinium ocellatum*; *Acanthopagrus latus*; quantitative real-time PCR; quantitative detection

密斑刺鲀（*Diodon hystrix*）假交替单胞菌的分离鉴定

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摘要: 养殖室中暂养的密斑刺鲀（*Diodon hystrix*）体表溃烂、眼睛白浊，从眼部分离得到菌株 Z，革兰氏阴性、短杆状；菌落呈圆形、有光泽的表面和规整的边缘，并且在中心区域微微凸起，菌落在初期培养时清晰透明，随着培养时间的延长，颜色变为微黄色，生理生化实验发现对葡萄糖、麦芽糖、果糖、N-乙酰葡萄糖胺、侧金盏花醇呈阳性，对蔗糖、半乳糖、卫茅醇、尿素、甘露醇、 β -半乳糖苷酶等呈阴性，结合以上菌体形态特征、革兰氏染色实验、生理生化性状以及 16S rDNA 序列分析，同时结合系统进化树的构建，最终鉴定菌株 Z 是假交替单胞菌（*Pseudomonas aeruginosa*）。对该菌株进行药敏试验，结果表明对头孢唑啉、头孢拉定、四环素、诺氟沙星等 12 种抗生素敏感，对头孢呋辛、红霉素 2 种抗生素中度敏感，对头孢他啶、头孢曲松、青霉素对 5 种抗生对密斑刺鲀（*D. hystrix*）的病害防治起到参考作用。

关键词: 密斑刺鲀；假交替单胞菌；分离鉴定

Isolation and Identification of *Pseudomonas aeruginosa* from *Diodon hystrix*

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Abstract: *Diodon hystrix* temporarily kept in a breeding room exhibited symptoms of lethargy, skin ulceration, and turbid eyes. A bacterial strain, designated as Z, was isolated from the eyes. The strain was Gram-negative, short rod-shaped; colonies were circular with a glossy surface and regular edges, slightly raised in the central area. Initially, the colonies were clear and transparent during early cultivation, but turned light yellow as the culture time increased. Physiological and biochemical tests revealed positive reactions to glucose, maltose, fructose, N-acetylglucosamine, and adonitol, and negative reactions to sucrose, galactose, dulcitol, urea, mannitol, β -galactosidase. Based on the morphological characteristics, Gram staining, physiological and biochemical properties, and 16S rDNA sequence analysis, along with the construction of a phylogenetic tree, strain Z was ultimately identified as *Pseudomonas aeruginosa*. Antibiotic sensitivity tests showed that the strain was sensitive to 12 antibiotics, moderately sensitive to 2 antibiotics, resistant to 5 antibiotics.

Key words: *Diodon hystrix*; *Pseudomonas aeruginosa*; Isolation and identification

大口黑鲈源杀鱼爱德华氏菌的生物学特性及其浸泡感染致病性分析

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摘要: 杀鱼爱德华氏菌是一种对多种鱼类具有感染性的病原菌, 给我国水产养殖业造成巨大的经济损失。研究采用浸泡法对健康大口黑鲈进行感染, 感染的大口黑鲈临床症状主要为皮肤破溃出血、肝弥漫性出血、脾肿大; 最显著的组织病理学变化是出血坏死性炎症。环境胁迫实验结果表明, 鱼的累积死亡率随着细菌浓度的增加而增加, 较低的养殖温度 (18℃)、较短的浸泡时间 (15min) 及较低的溶解氧 (1.5mg/L) 可导致大口黑鲈较高的死亡率。菌载量分析表明, 杀鱼爱德华氏菌主要通过鳃黏膜入侵鱼体, 聚集在脾脏后随着循环系统快速扩散并定殖到各个组织。透射电镜结果显示, 杀鱼爱德华氏菌可内化于吞噬细胞并定殖。实时荧光定量 PCR 分析表明, 感染后杀鱼爱德华氏菌逃避大口黑鲈免疫系统的监测、引起全身性炎症, 抑制宿主细胞凋亡, 非特异性免疫在感染中发挥主要作用。

关键词: 大口黑鲈; 杀鱼爱德华氏菌; 浸泡感染; 致病性

Biological characteristics of *Edwardsiella piscicida* from Largemouth bass and pathogenicity analysis of immersion infection

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Abstract: *Edwardsiella piscicida* causes huge economic losses to China's aquaculture industry. In this study, healthy largemouth bass was infected by soaking method. The clinical symptoms of infected largemouth bass were mainly skin ulcer bleeding, liver diffuse bleeding and splenomegaly. The most significant histopathological change is hemorrhagic necrotizing inflammation. The results of environmental stress experiments showed that lower culture temperature (18 °C), shorter soaking time (15min) and lower dissolved oxygen (1.5mg / L) could lead to higher mortality of largemouth bass. The bacteria mainly invade the fish through the gill mucosa, accumulate in the spleen, spread and colonize to various tissues. The internalization and colonization of bacteria in phagocytes were observed by transmission electron microscopy. qPCR analysis showed that the bacteria evaded the monitoring of the immune system of largemouth bass after infection, caused systemic inflammation, and inhibited host cell apoptosis. Non-specific immunity played a major role in infection.

Key words: Keywords: Largemouth bass ; *Edwardsiella piscicida* ; immersion infection ; pathogenicity

斜带石斑鱼白细胞介素 22 基因克隆鉴定 及功能研究

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摘要: 在哺乳动物中, IL-22 被认为是调节屏障表面免疫和稳态的关键细胞因子。虽然 IL-22 在不同种类的鱼类中已经有了功能表征, 但关于 IL-22 在不同器官/组织/细胞类型中的不同反应的研究较少。本文从石斑鱼中鉴定并克隆了 IL-22 基因 (命名为 Ec-IL-22)。在所有检测的组织中均检测到该基因, 并在 LPS 和 poly (I: C) 的刺激下, 在肠、鳃、脾、头肾、头肾/肠原代白细胞中被诱导, 以及哈维弧菌和 SGIV 感染后同样, IL22 表达量上调。此外, DSS 刺激后, 可诱导肠和肠原代白细胞中 Ec-IL-22 的表达。在重组 Ec-IL-22 蛋白刺激后, 原代肠/头肾白细胞促炎细胞因子的 mRNA 水平显著上调。本研究结果提高了对鱼类 IL-22 在不同器官/组织/细胞类型中的表达模式和功能特征的认识。

关键词: 斜带石斑鱼, IL-22, 表达模式, 肠/头肾白细胞, 促炎细胞因子

Identification and functional characterization of interleukin-22 (IL-22) in orange-spotted grouper (*Epinephelus coioides*)

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Abstract : In mammals, IL-22 is considered as a critical cytokine regulating of immunity and homeostasis at barrier surfaces. Although IL-22 have been functional characterization in different species of fish, the studies about distinct responses of IL-22 in different organs/tissues/cell types is rather limited. Here, we identified and cloned IL-22 gene (named as Ec-IL-22) from grouper (*Epinephelus coioides*). Ec-IL-22 gene was detected in all oranges/tissues examined, and was induced in intestine, gill, spleen, head kidney, and primary head kidney/intestine leukocytes following the stimulation of LPS and poly (I:C), as well as *Vibrio harveyi* and Singapore grouper iridovirus infection (SGIV). In addition, the stimulation of DSS could induce the expression of Ec-IL-22 in intestine and primary leukocytes from intestine. Importantly, the treatment of recombinant Ec-IL-22 induced the mRNA level of proinflammatory cytokines in primary intestine/head kidney leukocytes. The present results improve the understanding of expression patterns and functional characteristics of fish IL-22 in different organs/ti

Key words:: *Epinephelus coioides*, IL-22 , Expression patterns , Intestine/head kidney leukocytes , Proinflammatory cytokines

大口黑鲈病毒病疫苗研制

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摘要: 大口黑鲈是我国主要的特色鱼类养殖品种之一, 养殖产量逐年增加, 2023 年达 80.25 万吨, 被称为第五大家鱼。但是大口黑鲈养殖业快速发展的同时, 病害问题已成为产业发展的瓶颈问题, 尤其是整个养殖期均暴发的蛙虹彩病毒病以及苗种期暴发的弹状病毒病、双节段 RNA 病毒病等, 对养殖产业构成了严重威胁, 导致大口黑鲈苗种成活率极低。针对上述病毒病, 我们研发了鲈蛙虹彩病毒病弱毒疫苗及灭活疫苗, 鲈弹状病毒病弱毒疫苗, 鲈双节段 RNA 病毒病弱毒疫苗及 DNA 疫苗; 确定了病毒最适增殖细胞系; 构建了细胞库、种毒库; 对疫苗浸泡、注射的有效性、安全性等进行了系统评价; 并对免疫机制进行了初探; 同时对弱毒株保护剂进行了大规模筛选, 获得一种长效保存病毒的复方保护剂。上述疫苗的研制, 满足了苗种需要浸泡免疫、成鱼需要注射免疫的需求, 将为大口黑鲈病毒病的防治提供技术和产品支持, 为保障大口黑鲈养殖产业的绿色、健康、可持续发展奠定基础。

关键词: 大口黑鲈, 蛙虹彩病毒, 弹状病毒, 双节段 RNA 病毒, 疫苗

Vaccine development for viral diseases of largemouth bass

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Abstract: Largemouth bass is one of the main characteristic fish species in China. However, with the rapid development of the largemouth bass aquaculture industry, disease issues have become a bottleneck problem for the industry's development. In particular, viral diseases pose a serious threat to the aquaculture industry, such as ranavirus disease, which occurs throughout the entire cultivation period, as well as rhabdovirus and birnavirus diseases that occur during the fingerling stage. In response to the aforementioned viral diseases, we have developed attenuated vaccines and inactivated vaccines for largemouth bass ranavirus disease, attenuated vaccine for largemouth bass iridovirus disease, and attenuated vaccine and DNA vaccine for largemouth bass birnavirus disease. The effectiveness and safety of vaccine by immersion and injection have been systematically evaluated, and a compound protectant for long-term preservation of the virus has been obtained. These vaccines will provide technical and product support for the prevention and control of largemouth bass viral diseases.

Key words: Largemouth bass, Ranavirus, Rhabdovirus, Birnavirus, vaccine

利用合成生物学在水产中应用乳酸菌

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摘要：乳酸菌是一种益生菌，能够水解蛋白质，产有机酸和细菌素等。随着人们对乳酸菌特殊功能需求的提升，传统筛菌方法由于其技术繁复、周期长、成功率低等缺点，逐渐成为制约乳酸菌行业发展的瓶颈。合成生物学技术的出现，将具有特定功能的基因电路网络导入细胞基因组中，让细胞来完成设计者设想的各种任务，可为解决水产养殖中绿色养殖难题提供新的机遇。

关键词：乳酸菌；合成生物学

Application of lactic acid bacteria in aquaculture by synthetic biology

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Abstract : Lactic acid bacteria are a kind of probiotics that can hydrolyze proteins and produce organic acids and bacteriocins. As people's demand for the special functions of lactic acid bacteria increases, traditional screening methods have gradually become a bottleneck restricting the development of the lactic acid bacteria industry due to their disadvantages such as complicated techniques, long cycles, and low success rates. The emergence of synthetic biology technology, which imports gene circuit networks with specific functions into the cell genome and lets cells complete various tasks envisioned by designers, can provide new opportunities for solving the problem of green aquaculture in aquaculture.

Key words: : Lactic acid bacteria; Synthetic biology

抗菌肽 Spamosin26-54 通过结合脂质介导病毒裂解对三种水生包膜病毒表现出抗病毒活性

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摘要: 水产养殖业面临着各种包膜病毒感染造成的巨大经济损失, 如白斑综合征病毒 (WSSV), 蛙虹彩病毒 (RGV), 鳃鲰疱疹病毒 (AngHV)。对广谱抗病毒药物的迫切需求促使人们对抗病毒肽进行探索, 其中具有抗病毒活性的抗菌肽 (AMPs) 越来越受到人们的关注。Spamosin26-54 (源自拟穴青蟹) 是一种很有应用前途的抗菌肽。在本研究中, 我们发现 Spamosin26-54 对三种包膜病毒 (WSSV、RGV 和 AngHV) 具有显著的抑制作用。透射电镜观察表明, Spamosin26-54 对病毒粒子具有直接的破坏作用。脂质结合结果显示, Spamosin26-54 对磷脂酸 (PA) 和磷脂酰丝氨酸 (PS) 具有较强的亲和力, 其可能通过结合脂质诱导病毒裂解。在三种病毒感染的动物模型中, Spamosin26-54 可以降低组织中的病毒载量, 提高存活率或降低感染率。

关键词: 抗菌肽, Spamosin26-54, 水生包膜病毒, 抗病毒活性, 脂质结合

The antimicrobial peptide Spamosin26-54 exhibits antiviral activity against three aquatic enveloped viruses through lipid-binding-mediated virus lysis

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Abstract: The aquaculture industry is faced with huge economic losses caused by various enveloped virus infections, such as white spot syndrome virus (WSSV), Rana grylio virus (RGV), and Anguillid Herpesvirus 1 (AngHV). The urgent need for readily available broad-spectrum antiviral agents has led to the exploration of antiviral peptides (AVPs), among which antimicrobial peptides (AMPs) with antiviral activity have attracted increasing attention. Spamosin26-54 (derived from *Scylla paramamosain*) is a promising antimicrobial agent. In this study, we found that Spamosin26-54 significantly against the three enveloped viruses (WSSV, RGV, and AngHV). Transmission electron microscopy observations showed that Spamosin26-54 had a direct destructive effect on virions. ELISA assay highlighted that Spamosin26-54 had a potent affinity for phosphatidic acid (PA) and phosphatidylserine (PS). Notably, in three animal models of viral infection, Spamosin26-54 reduced viral loads in tissues, increased survival, or decreased infection rates.

Key words: Antimicrobial peptide, Spamosin26-54, Aquatic enveloped viruses, Antiviral activity, Lipid binding

联合 miRNA 与病理学的研究为菲律宾蛤仔抗 鳃弧菌的免疫应答提供了新的视角

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

关键词: 菲律宾蛤仔、鳃弧菌、高通量测序、免疫应答

Integrated microRNA study and pathological analysis provides new insights into the immune response of *Ruditapes philippinarum* under *Vibrio anguillarum* challenge

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Abstract: Manila clam(*Ruditapes philippinarum*) is an important shellfish product. The breeding of clams is often affected by *V. anguillarum* and causes large-scale death. In this study, we found that the bacterial load in the hepatopancreas of clam peaked at 2d after *V. anguillarum* infection, while the activity of lysozyme reached the peak at 12 h. Tissue observation reveals that the infected hepatopancreas cells lost normal structure or necrosis. Additionally, six small RNA libraries were constructed using hepatopancreas of clams. A total of 15 differentially expressed microRNA were identified at 48 h after *V. anguillarum* infection, including 8 upregulated and 7 downregulated miRNAs. GO and KEGG enrichment results indicated the prediction of 48 known miRNAs and 127 new miRNAs, corresponding to 2,171 target genes. Functional annotations indicate significant changes in several signaling pathways, including endocytosis, bacterial recognition proteins, the FoxO pathway, and the mTOR. This study provides a new idea to explore the immune regulation mechanism of shellfish after *V. anguillarum* infection.

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

整合转录组学和代谢组学揭示恩诺沙星诱导舒伯特气单胞菌的耐药机制

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摘要: 舒伯特气单胞菌感染对水产养殖业造成了严重经济损失。本研究通过逐步提高抗菌药物浓度, 成功诱导出该菌对恩诺沙星的耐药菌株, 并利用转录组学和代谢组学分析其耐药机制。结果显示, 恩诺沙星对敏感菌株 (WL23S) 的最小抑菌浓度为 0.03125 $\mu\text{g}/\text{mL}$, 而对耐药菌株 (WL23R) 则高达 32 $\mu\text{g}/\text{mL}$, 提高了 1024 倍。WL23R 在移除抗性压力后仍保持耐药性, 且对多种非诱导抗菌药物也产生了交叉耐药性。两菌株的生长速率没有显著差异, 突显了 WL23R 的强适应性。转录组学分析显示 WL23R 中与外排泵相关的基因的表达显著上调, 且差异基因主要富集于氨基酸代谢和 ABC 转运蛋白通路。代谢组学揭示了耐药菌株与氨基酸水平、氨基酸生物合成/代谢通路活性及 ABC 转运蛋白通路的影响。综合组学分析表明, ABC 转运蛋白是耐药性机制中的核心通路。本研究强调了外排系统和 ABC 转运蛋白在舒伯特气单胞菌多重耐药性中的关键作用。

关键词: 舒伯特气单胞菌, 恩诺沙星, 耐药机制, 多重外排泵, ABC 转运蛋白

Integration of transcriptomics and metabolomics reveals the mechanism of enrofloxacin resistance in *Aeromonas schubertii*

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Abstract: *Aeromonas schubertii* infections have led to significant economic losses in aquaculture. This study developed enrofloxacin-resistant *A. schubertii* strains by gradually increasing antibiotic concentrations and examined the resistance mechanisms using transcriptomics and metabolomics. The results showed that the minimum inhibitory concentration (MIC) of enrofloxacin for the sensitive strain (WL23S) was 0.03125 $\mu\text{g}/\text{mL}$, while for the resistant strain (WL23R), it increased 1024-fold to 32 $\mu\text{g}/\text{mL}$. WL23R maintained its resistance even without antibiotic exposure and exhibited cross-resistance to other antimicrobials. Transcriptomic analysis revealed upregulation of efflux pump-related genes in WL23R, with differential genes linked to amino acid metabolism and the ABC transporter pathway. Metabolomics indicated that resistance impacted amino acid levels and related metabolic activities. The combined analysis identified the ABC transporter as a key resistance mechanism. This study emphasizes the critical role of efflux systems and ABC transporters in *A. schubertii* multidrug resistance.

Key words: *Aeromonas schubertii*, enrofloxacin, artificially induced, transcriptomics and metabolomics, resistance mechanism, multiple efflux pump, ABC transporters

肿瘤坏死因子受体相关因子 6 (TRAF6) 通过 NF- κ B 通路参与调节中华绒螯蟹在蜕皮前期的免疫反应

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摘要: 蜕皮是甲壳动物重要的生物学现象, 蜕皮过程主要分为前期、后期和间期三个时期。目前, 甲壳动物蜕皮过程中的免疫调节机制仍不清楚。本研究从中华绒螯蟹中鉴定出一个具有两个 TRAF 型锌指结构域的 TRAF6 基因 (EsTRAF6), 探讨了其在蜕皮过程中的免疫调控作用。研究发现, EsTRAF6 在蜕皮前期显著高表达, 且在不同蜕皮阶段嗜水气单胞菌刺激后, EsTRAF6 和免疫因子如 Relish 和抗脂多糖因子 (ALFs) 的表达水平均显著显著。进一步研究发现, 蜕皮激素能够显著上调 EsTRAF6 和 EsRelish 的表达量。抑制 EsTRAF6 后, 抗脂多糖因子 (ALFs) 在蜕壳前期的表达水平显著下降, 并且 NF- κ B 的磷酸化水平也显著降低。综上所述, 本研究表明蜕皮激素 20E 能够诱导 EsTRAF6 的表达, 且 EsTRAF6 在蜕壳前期可以通过激活 NF- κ B 促进脂多糖因子 (ALFs) 的表达。

关键词: 肿瘤坏死因子受体相关因子 6、蜕壳、免疫反应、中华绒螯蟹

The involvement of tumor necrosis factor receptor-associated factor 6 in regulating immune response by NF- κ B at pre-molt stage of Chinese mitten crab (*Eriocheir sinensis*)

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Abstract: Molting is a crucial biological process of crustaceans, which can be divided into three main stages: pre-molt, post-molt and inter-molt. However, the exact mechanism of immunological modulation during molting remains unclear. In this study, a Tumor necrosis factor receptor-associated factor 6 (TRAF6) gene with two TRAF-type zinc finger domains was identified from *Eriocheir sinensis*, and investigated its role in regulating immune response during molting process. The mRNA expression level of EsTRAF6 at pre-molt stage was highest. After *Aeromonas hydrophila* stimulation, EsTRAF6, EsRelish and EsALFs transcripts considerably increased at three molting stages. The mRNA and protein expression levels of EsTRAF6 and EsRelish were significantly increased at 12 h after 20-hydroxyecdysone (20E) injection. Inhibition of the EsTRAF6 transcript, there was a notable decrease of the EsALFs transcripts and the phosphorylation level of NF- κ B at pre-molt stage. Collectively, our results suggest that EsTRAF6 could be induced by 20E and promoted the EsALFs expression by activating NF- κ B at pre-molt stage.

Key words: Tumor necrosis factor receptor-associated factor 6 (TRAF6), molting, immune response, *Eriocheir sinensis*

黄颡鱼源海豚链球菌的生物学特性、致病性及其全基因组分析

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摘要: 为阐明黄颡鱼源海豚链球菌的生物学特性、致病性及其全基因组特征, 为该病诊断和防治提供理论支撑。本研究选取了黄颡鱼源海豚链球菌 ZQ2205 为研究对象, 对其生长特性、致病力及全基因组序列特征进行分析。研究表明, 菌株 ZQ2205 为 β 溶血, 胞外产物具有脂肪、淀粉和蛋白酶活性, 无纤维素酶活性, 并对酸碱和盐度适应范围较广, 最适生长 pH 为 9, 盐度小于 20‰。攻毒结果显示, 该菌株具有较高毒力, 剂量低至 0.5 CFU/g 即可致黄颡鱼幼鱼死亡, 对鱼体多个器官造成显著损伤, 检测发现脾脏和肾脏菌载量最高。全基因组测序显示其总长度为 2, 128, 105 bp, 编码 2, 035 个基因, 共发现 18 种毒力因子和预测到 21 个抗生素耐药基因和 18 个抗生素靶基因。综上所述, 黄颡鱼源海豚链球菌 ZQ2205 具有强致病性、多重耐药性, 且对环境适应性强, 其全基因组信息揭示了毒力和耐药性特征, 对该病防控具有重要意义。

关键词: 黄颡鱼; 海豚链球菌; 生物学特性; 致病性; 全基因组

Biological characteristics, pathogenicity, and whole genome bioinformatics analysis of *Streptococcus iniae* from *Tachysurus fulvidraco*

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Abstract: To elucidate the biological characteristics, pathogenicity, and whole-genome features of *Streptococcus iniae* derived from *Tachysurus fulvidraco*, the *S. iniae* (ZQ2205) was selected to study. Results showed that ZQ2205 exhibits β -hemolytic activity, with extracellular lipase, amylase, and protease activities, but no cellulase activity. It adapts broadly to pH and salinity, growing optimally at pH 9 and salinity below 20‰. Challenge tests demonstrated that the ZQ2205 has high virulence, with a dose as low as 0.5 CFU/g causing death in *T. fulvidraco* juveniles and significant damage to multiple organs, especially the spleen and kidneys, where the highest bacterial loads were detected. Whole-genome sequencing revealed a total length of 2, 128, 105 bp, encoding 2, 035 genes. A total of 18 virulence factors and 21 antibiotic resistance genes, along with 18 antibiotic target genes, were identified. Collectively, strain ZQ2205 possesses high pathogenicity and multidrug resistance with robust environmental adaptability.

Key words: *Tachysurus fulvidraco*; *Streptococcus iniae*; Biological Characteristics; Pathogenicity; Whole-genome

一种防控多子小瓜虫病杀虫涂料研发

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摘要: 铜离子具有天然抗菌杀虫功能, 其铜制剂常用于水产养殖中病害防治。前期研究发现接触铜合金片表面的多子小瓜虫 (*Ichthyophthirius multifiliis*) 也会发生死亡。本研究根据多子小瓜虫滋养体脱离宿主之后沉降到水体底部形成包囊过程中, 包囊会粘附于池子底部的特性, 将铜合金颗粒掺入涂层中, 并将涂于实验桶或器皿中, 观其防控效果。结果显示, 添加了 5% 的铜合金颗粒涂料, 病鱼的保护率可达 100%, 而对照组的病鱼因严重的二次感染全部死亡。体外实验中, 包囊在接触铜涂层表面 6 小时后包囊的死亡率达到了 86.67%, 第 24 h 包囊体内的铜离子浓度从 8.67 mg/kg 增加至 801 mg/kg。安全性评估结果显示鱼暴露于铜合金涂层养殖 30 天, 其血清、肝脏或肌肉组织中铜浓度与对照组无显著差异。本研究为工厂化循环水养殖中控制多子小瓜虫病提供了一种安全绿色有效的策略。

关键词: 多子小瓜虫; 铜合金颗粒; 涂层; 预防控制;

Development of an antiparasitic paint for prevention and control of *Ichthyophthirius multifiliis*

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Abstract: Copper ions have natural antibacterial and insecticidal properties, and the copper preparations are commonly used in aquaculture for disease control. Previous studies have found that *Ichthyophthirius multifiliis* perish upon contact with copper alloy surfaces. We coated experimental buckets with a copper alloy-infused coating to assess its effect on *I. multifiliis*, which detaches from hosts to form tomonts. The results showed that the protective rate for diseased fish soared to 100% with the application of a 5% copper alloy particle coating, while all diseased fish in the control group perished due to reinfections. In vitro experiments revealed that the mortality rate of tomonts reached 86.67% after merely 6 hours of contact with the copper-coated surface. Moreover, the copper ion concentration within the tomonts saw a dramatic increase, jumping from 8.67 mg/kg to 801 mg/kg after 24 hours. Safety assessment showed that after a 30-day exposure to the copper alloy-coated environment, there was no significant difference in copper concentration within the fish between two groups.

Key words: *Ichthyophthirius multifiliis*, Copper alloy particle, Paint, Control

饲料中添加复方中草药对大菱鲆抗杀鲑气单胞菌感染的影响

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摘要: 为研究复方中草药对大菱鲆抗氧化能力、非特异性免疫功能以及抗杀鲑气单胞菌感染能力的影响。本研究在基础饲料中添加 1%、2% 2 种剂量的复方中草药, 各自投喂大菱鲆 7 天和 14 天, 分别取血清检测免疫球蛋白 M、溶菌酶及超氧化物歧化酶的活性; 取头肾、鳃及脾脏 RT-qPCR 检测免疫相关基因表达差异; 并对不同组别进行杀鲑气单胞菌感染, 进行存活率统计及病理切片分析。结果表明, 1% 组投喂 7 天后, 免疫球蛋白 M、溶菌酶、超氧化物歧化酶活性显著高于对照组, 14 天后有所降低; 2% 组投喂 7 天后免疫球蛋白 M、超氧化物歧化酶活性无显著变化, 溶菌酶活性上升。此外, 1% 组投喂 7 天, RT-qPCR 检测发现头肾、鳃和脾组织中 TNF、TGF 的 mRNA 表达量上调; 之后用杀鲑气单胞菌感染, 大菱鲆的存活率及病理切片结果均表明其效果显著高于基础饲料组。以上研究表明基础饲料中添加 1% 此复方中草药投喂 7 天可显著提升大菱鲆抗杀鲑气单胞菌感染能力。

关键词: 大菱鲆; 复方中草药; 杀鲑气单胞菌; 抗氧化能力; 非特异性免疫功能

Effects of compound Chinese herbs added to feed on the resistance of *Scophthalmus maximus* to *Aeromonas salmonicida* infection

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Abstract : To explore effects of compound Chinese herbs on antioxidant capacity, nonspecific immune function and resistance to *A. salmonicida* infection in turbot, the study added 2 doses of the medicine to a basic diet, then fed turbot for 7 and 14 days respectively. Serum samples were used to assess activities of IgM, LZM, and SOD. Immune-related gene expression was analyzed through RT-qPCR in head kidney, gill and spleen. Groups were infected with *A. salmonicida*; survival rate and pathological analysis were conducted. Results showed higher activities of IgM, LZM and SOD of 1% group than the control group in 7 days, and they decreased after 14 days. Meanwhile IgM or SOD were stable in 2% group, but LZM rose. RT-qPCR showed increase of mRNA expression of TNF and TGF in aforesaid tissues in 1% group. Infected with *A. salmonicida*, survival rates and pathological results signally improved compared with the control group. Findings suggest that adding 1% compound Chinese herbs in 7 days can enhance turbot's ability to resist *A. salmonicida*.

Key words: : *Scophthalmus maximus*; Compound Chinese herbal medicine; *Aeromonas salmonicida*; Antioxidant capacity; Non-specific immune function

引起日本对虾红体病病原菌分离鉴定及致病性研究

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摘要: 为分析连云港市赣榆区佳信养殖基地中一例日本对虾发生红体病的病因, 本研究对可能引起该病的病原菌进行了筛选鉴定。获得红体日本对虾后, 分别取其鳃、肝胰腺、肠道、肌肉四个组织进行病原菌的分离和纯化。对纯化后的优势菌进行革兰氏染色、生化实验、16S rRNA 测序鉴定、人工回染实验和药敏试验。测序结果显示, 该菌与模式菌株 *Bacillus cereus* 同源性为 99%, 结合菌株的形态特征, 鉴定该菌为蜡样芽孢杆菌。回染实验结果显示, 从注射病菌组的凡纳滨对虾的肝胰腺和肠道中均能提取出单一的优势菌群, 且对照组样品的组织中未见该菌, 对这一优势菌纯化培养后进行革兰氏染色检验, 发现该菌为革兰氏阳性菌, 呈单个或者长链状排列, 具有明显的蜡样芽孢杆菌特征。表明蜡样芽孢杆菌也能感染凡纳滨对虾。

关键词: 日本对虾; 蜡样芽孢杆菌; 病原菌鉴定; 回染实验; 药敏试验

Isolation, Identification, and Pathogenicity Study of Pathogens Causing Red Body Disease in *Penaeus japonicus*

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Abstract: To analyze the cause of red body disease in a case of *Penaeus japonicus* from the Jiaxin Aquaculture Base in Ganyu District, Lianyungang City, this study screened and identified the pathogenic bacteria that might cause the disease. After obtaining the red-body *Penaeus japonicus*, four tissues (gills, hepatopancreas, intestine, and muscle) were taken for pathogen isolation and purification. The purified dominant bacteria were subjected to Gram staining, biochemical experiments, 16S rRNA sequencing identification, artificial re-infection experiments, and drug sensitivity tests. Sequencing results showed that the bacteria had 99% homology with the type strain *Bacillus cereus*, and combined with the morphological characteristics of the strain, it was identified as *Bacillus cereus*. Re-infection experiment results showed that a single dominant bacterial group could be extracted from the hepatopancreas and intestine of *Penaeus vannamei* injected with the bacteria, and no such bacteria were found in the tissues of the control group samples.

Key words: *Penaeus japonicus*; *Bacillus cereus*; pathogen identification; re-infection experiment; drug sensitivity test

生物絮团中微塑料对罗非鱼的影响

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摘要: 微塑料 (MPs) 在水产养殖中广泛存在, 包括在生物絮团技术 (BFT) 养殖系统中。与其他水产养殖系统相比, BFT 系统拥有最丰富的微生物群落, 且多数为益生菌。因此, 本研究评估了 BFT 系统中不同浓度的 MPs 对罗非鱼 (*Oreochromis niloticus*) 的影响。结果表明, MPs 对水质、罗非鱼生长和消化酶活性没有明显影响。然而, MPs 在肝脏中积累最多 (5.65 ± 0.74 ug/mg), 造成肝体指数显著增加, 并降低了肌肉粗蛋白和脂肪 ($p < 0.05$)。此外, MPs 暴露后, 抗氧化酶、丙二醛和 Na⁺/K⁺-ATPase 的酶活性没有明显变化。生物絮团和罗非鱼肠道微生物群落也没有明显变化。这些结果表明, MPs 在 BFT 系统中对罗非鱼几乎没有影响。本研究有助于评估 MPs 在水产养殖系统中的生态风险, 并更好地理解 BFT 系统中养殖动物对 MPs 的综合响应。

关键词: 微颗粒, 生物絮团, 综合生物标志物, 微生物群里

Impacts of Nile Tilapia (*Oreochromis niloticus*) exposed to microplastics in bioflocs system

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Abstract: Microplastics (MPs) are abundant in aquaculture water, including in bioflocs aquaculture systems. Compared with other aquaculture systems, biofloc technology systems have the richest microbes and are beneficial to cultivated organisms. Therefore, this study provides a comprehensive assessment of the potential effects of MPs on aquaculture organisms in bioflocs systems. Here, Nile Tilapia (*Oreochromis niloticus*) were exposed to MPs (polystyrene; 32–40 μm diameter) with 0, 80 items/L (30 ug/L), and 800 items/L (300 ug/L) for 28 days in a bioflocs aquaculture system. The results showed that the MPs generally had no apparent effect on water quality, tilapia growth, or digestive enzyme activity. MPs did not affect the content of glutathione, glutathione peroxidase, oxidized glutathione, and malondialdehyde, or the enzyme activity of Na⁺/K⁺-ATPase. Exposure to MPs did not significantly influence the microbial communities of the bioflocs and tilapia guts ($p < 0.05$). These results suggest that MPs barely affected tilapia in the bioflocs system.

Key words: Microparticle, Biofloc technology, Integrated biomarkers response, Microbial community

中华鲟胸鳍细胞系的建立及其生物学特性

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摘要: 为保障中华鲟 (*Acipenser sinensis*) 种群健康与疾病防控, 本研究通过组织块培养技术, 从中华鲟胸鳍组织中成功建立了一株成纤维样细胞系, 命名为 ASXFine。该细胞系增殖速度快, 24 小时可传代一次, 且已稳定传代 40 代以上。ASXFine 细胞可在 M199 和 DMEM 培养基中生长, 最适培养温度为 28°C, 经液氮冷冻保存 6 个月后复苏, 仍保持旺盛生长能力。细胞转染实验表明该细胞系能够有效转染外源基因表达质粒。此外, ASXFine 细胞对大口黑鲈鱼虹彩病毒 (LMBV) 具有较高的敏感性。综上, ASXFine 细胞系为中华鲟健康养殖和疾病防控提供了重要的细胞模型, 同时也为水生动物病毒学、基因组学研究及疫苗开发提供了新的实验材料, 具有广泛的应用前景。

关键词: 中华鲟, 胸鳍, 组织块培养, 成纤维样, LMBV

The establishment and biological characteristics of pectoral fin cell line of Chinese Sturgeon *Acipenser sinensis*

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Abstract: To ensure the population health and disease prevention of Chinese sturgeon (*Acipenser sinensis*), this study successfully established a fibroblast-like cell line from the pectoral fin tissue of Chinese sturgeon based on in vitro tissue block culture technology and named it ASXFine. This cell line proliferates rapidly, can be passaged once every 24 hours, and has been stably passaged for more than 40 generations. ASXFine cells can grow in M199 and DMEM culture media, with the optimal culture temperature being 28°C. After being frozen in liquid nitrogen for 6 months, they can still maintain vigorous growth ability. Cell transfection experiments have shown that this cell line can effectively transfect exogenous gene expression plasmids. In addition, ASXFine cells are highly sensitive to largemouth black bass iridovirus (LMBV). In summary, the ASXFine cell line provides an important cell model for the healthy breeding and disease prevention and control of Chinese sturgeon, and also provides new experimental materials for aquatic animal virology, genomics research and vaccine development.

Key words: *Acipenser sinensis*, pectoral fin, in vitro tissue culture technique, fibroblast-like cells, LMBV

大黄鱼中新型抗菌肽 LCAMP 的体外抗菌活性和体内抗河流弧菌感染的作用

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摘要: 在本研究中, 来自大黄鱼的 LCAMP 具有广谱抗菌活性; 而且 LCAMP 对河流弧菌、荧光假单胞菌和恶臭假单胞菌的生物膜均具有抑制作用。外源性 LPS 的添加降低 LCAMP 对细菌的活性; 此外, LCAMP 破坏细胞膜的完整性, 导致 ATP 的泄漏和细胞内 ROS 的积累。值得注意的是, LCAMP 显著提高河流弧菌感染后大黄鱼的存活率; 而且 LCAMP 降低促炎细胞因子 (TNF α 和 IL-1 β) 的表达量, 提高免疫相关基因 (IL4、piscidin、hepcidin 和溶菌酶) 的表达水平, 以及增强溶菌酶的酶活。综上所述, 本研究发现的新型抗菌肽 LCAMP 具有体外抗菌活性和体内抗感染和抗炎的作用, 表明其作为抗河流弧菌感染的治疗药物潜力。

关键词: 大黄鱼; 抗菌肽; LCAMP; 抗菌活性; 河流弧菌感染

A novel antimicrobial peptide LCAMP from large yellow croaker (*Larimichthys crocea*) shows potent antimicrobial activity in vitro and enhances resistance to *Vibrio fluvialis* infection in vivo

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Abstract : In this study, LCAMP derived from *Larimichthys crocea* exerted broad-spectrum antimicrobial activity. LCAMP exhibited biofilm inhibition against *Vibrio fluvialis*, *Pseudomonas fluorescens* and *Pseudomonas putida*. The addition of exogenous LPS decreased bacterial sensitivity to LCAMP. Moreover, LCAMP disrupted the integrity of the membrane, leading to leakage of ATP and accumulation of intracellular ROS. Notably, LCAMP could significantly improve the survival rate of *L. crocea* under *V. fluvialis* infection. In addition, LCAMP reduced the expression of two pro-inflammatory cytokines (TNF α and IL-1 β), increased the expression levels of immune-associated genes (IL4, piscidin, hepcidin and lysozyme), and enhanced the enzymatic activity of lysozyme. Taken together, the novel antimicrobial peptide LCAMP identified in this study possesses in vitro antimicrobial activity and in vivo anti-infective and anti-inflammatory effects, suggesting its potential as a therapeutic agent against *V. fluvialis* infection.

Key words:: *Larimichthys crocea*; Antimicrobial peptide; LCAMP; Antimicrobial activity; *Vibrio fluvialis* infection

姜黄提取物对加州鲈生长、抗氧化能力及抗病力的影响

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摘要：为了探究姜黄提取物对加州鲈生长、抗氧化能力及抗病力的影响，在饲料中分别添加1%的姜黄醇提物和水提物，进行4周的投喂试验。结果显示，投喂姜黄提取物对加州鲈幼鱼生长无显著影响。醇提物组 SOD、CAT、T-AOC、ACP 显著高于对照组及水提物组 ($P < 0.05$)，MDA 显著低于对照组及水提物组 ($P < 0.05$)。姜黄水提物组 SOD、T-AOC、AKP、ACP 显著高于对照组 ($P < 0.05$)，MDA 及 CAT 显著小于对照组 ($P < 0.05$)。用药组脾脏 IL-8、IL-10、TNF- α 、IFN- γ 、Mx-1 和 PKR 基因表达量均显著高于对照组 ($P < 0.05$)，其中醇提物组 IL-10、Mx-1 和 PKR 基因表达量较水提物组高 ($P < 0.05$)，水提物组 IFN- γ 基因表达量较醇提物组高 ($P < 0.05$)。研究表明，饲料中添加适量的姜黄醇提物和水提物投喂4周能显著提高加州鲈抗氧化能力及抗病力，以姜黄醇提物效果更优。

关键词：姜黄醇提物；姜黄水提物；生长；抗氧化；抗病力

Effect of *Curcuma longa* Extracts on Growth, Antioxidant Activity and Disease Resistance of *Micropterus salmoides*

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Abstract: In order to study the effects of *Curcuma longa* extracts on the growth, antioxidant capacity and disease resistance of *Micropterus salmoides*, the experimental groups were fed with diets containing ethanol or water extracts of *C. longa* at the level of 1% for 4 weeks. The results showed that *C. longa* extracts had no significant influence on body weight. The SOD, CAT, T-AOC, AKP and ACP activities in the ethanol extract group were significantly higher than those in other groups, while MDA content was significantly lower. The SOD, T-AOC and ACP activities in the water extract group were significantly higher than those in the control group, while the MDA content and CAT activity were significantly lower. The gene expression levels of IL-8, IL-10, TNF- α , IFN- γ , Mx-1 and PKR in the treatment groups were dramatically higher than those in the control group. These findings indicated that a diet supplemented with *C. longa* extracts for 4 weeks can markedly enhance the antioxidant capacity and disease resistance of *M. salmoides*, with the ethanol extract of *C. longa* showing better effects.

Key words: ethanol extract of *Curcuma longa*; water extract of *Curcuma longa*; growth; antioxidant capacity; disease resistance

日粮中添加枯草芽孢杆菌对大口黑鲈生长、免疫以及肠道菌群的影响

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摘要: 益生菌在水产养殖中广泛应用于提高生长性能和抗病能力。本研究筛选了健康大口黑鲈肠道中的枯草芽孢杆菌 YB-4, 并通过饲喂试验评估其益生特性。将试验鱼随机分为对照组 (普通饲料) 和 YB-4 组 (添加 1×10^8 CFU 枯草芽孢杆菌), 持续 8 周。结果显示, YB-4 组鱼的增重率和特定生长率显著高于对照组, 肠道绒毛长度和数量有所增加, 但差异不显著。YB-4 组血清中的乳酸脱氢酶 (LDH) 和谷胱甘肽还原酶 (GR) 显著高于对照组。免疫指标测定显示, YB-4 组在肝脏和脾脏的碱性磷酸酶 (AKP) 高于空白组。毒性实验表明, YB-4 组的鱼存活率显著高于对照组。肠道微生物分析显示, YB-4 组索氏鲸杆菌丰度显著增加, 且微生物群落组成有显著差异。综上, 添加枯草芽孢杆菌 YB-4 可改善大口黑鲈的肠道菌群、促进生长、增强免疫力及抗病能力。

关键词: 大口黑鲈; 枯草芽孢杆菌; 生长指标; 抗病力; 肠道菌群

The effects of adding *Bacillus subtilis* to the diet on the growth, immunity, and intestinal microbiota of *Micropterus salmoides*

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Abstract: Probiotics are commonly used in aquaculture to boost growth and disease resistance. This study isolated *Bacillus subtilis* YB-4 from the intestines of healthy *Micropterus salmoides* and assessed its probiotic effects through an 8-week feeding trial. Fish were divided into a control group (regular feed) and a YB-4 group (1×10^8 CFU of *B. subtilis*). Results showed that the YB-4 group had significantly greater weight gain and specific growth rates, along with higher serum levels of lactate dehydrogenase (LDH) and glutathione reductase (GR). Immunological assessments indicated increased alkaline phosphatase (AKP) in the liver and spleen. The YB-4 group also exhibited a significantly higher survival rate and increased abundance of *Cetobacterium somerae* in the intestines, indicating notable changes in microbial community composition. In summary, adding *B. subtilis* YB-4 enhances intestinal microbiota, promotes growth, and boosts immunity and disease resistance in *M. salmoides*.

Key words: *Micropterus salmoides*, *Bacillus subtilis*, Growth parameters, Disease resistance, Intestinal microbiota

高温胁迫下 CgmiR307 靶向 CgNrf2 调控长牡蛎氧化应激过程

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摘要: miRNA 是一类内源性非编码小 RNA, 通过转录后调控参与机体对各种环境胁迫的响应过程。本研究探讨了长牡蛎 CgmiR307 调节高温胁迫下氧化应激过程的作用机制。结果发现, 通过软件预测和双荧光素酶报告实验证实 CgmiR307 靶向结合 CgNrf2 的 3'-UTR 区域结合位点。在鳃组织中, CgmiR307 和 CgNrf2 的表达水平显著高于其他组织。在注射 CgmiR307 模拟物并进行高温胁迫后, 鳃组织中 CgNrf2、CgSOD 和 CgCAT 的 mRNA 表达水平, SOD 和 CAT 的活性以及 T-AOC 显著下降, 而 MDA 含量显著增加。注射 CgmiR307 抑制剂并进行高温胁迫后, 鳃组织中 CgNrf2、CgSOD 和 CgCAT 的 mRNA 表达水平、SOD 和 CAT 活性及 T-AOC 明显升高, 而 MDA 含量显著降低。以上结果表明, CgmiR307 通过抑制高温胁迫下 CgNrf2 的表达参与调节长牡蛎氧化应激过程。

关键词: 长牡蛎、CgmiR307、CgNrf2、氧化应激、抗氧化

CgmiR307 involved in the regulation of Nrf2-dependent oxidative response in the Pacific oyster *Crassostrea gigas* under high-temperature stress

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Abstract: miRNA, a type of endogenous small non-coding RNA, is involved in the response to various environmental stresses, through post-transcriptional regulation. In the study, the role of CgmiR307 in the regulation of oxidative response under high-temperature stress by targeting CgNrf2 was investigated in the Pacific oyster *Crassostrea gigas*. CgmiR307's binding sites in CgNrf2's 3'-UTR were confirmed using dual-luciferase assay. The expression levels of CgmiR307 and CgNrf2 in gill were higher than other tissues. After CgmiR307 agomir injection, the expression levels of CgNrf2, CgSOD and CgCAT in gill, the activities of SOD and CAT and T-AOC decreased that in the control group, while MDA content increased. After CgmiR307 antagomir injection, these factors increased, while MDA content decreased. These results demonstrated that CgmiR307 was involved in the regulation of oxidative response by inhibiting the expression of CgNrf2 under high-temperature stress. These findings contributed to the understanding of miRNA regulation of Nrf2 in the response to high-temperature stress in molluscs.

Key words: Pacific oyster *Crassostrea gigas*; CgmiR307; CgNrf2; oxidative response; antioxidant

刺激隐核虫 *Cathepsin L* 基因的克隆及 功能初探

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摘要: 刺激隐核虫是一种海水寄生虫, 常寄生在硬骨鱼类体表及鳃丝部位, 导致海水白点病, 严重时可致鱼类死亡。有研究发现蛋白酶在 *C. irritans* 的感染和发育中起关键作用, 可以作为基于免疫治疗的潜在分子靶点。为探究刺激隐核虫 (*C. irritans*) 的生长发育机制, 并开发新的防治策略。本研究首先通过生物信息学方法鉴定了刺激隐核虫中的 *CathL* 基因, 并利用 CRISPR/Cas9 技术进行基因编辑。通过 qPCR 和序列分析, 验证了敲除组虫体 *CathL* 基因表达水平显著降低, 基因序列缺失, 表明敲除位点成功作用。实验结果显示, *CathL* 基因敲除组的孵化幼虫数量减少, 但形态未受影响, 说明 *CathL* 在刺激隐核虫的生长发育阶段发挥重要作用。本研究为硬骨鱼类养殖业提供了一种潜在的防治刺激隐核虫病的新方法, 有助于减轻其对我国沿海经济鱼类养殖的负面影响。然而, *CathL* 基因的具体功能和作用机制仍需进一步研究。

关键词: CRISPR/Cas9; *Cathepsin L*; 刺激隐核虫; 功能分析; 基因编辑

Cloning and Functional Analysis of *Cathepsin L* in *Cryptocaryon irritans*

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Abstract: *Cryptocaryon irritans* parasitizes marine fish and causes fatal marine fish “white spot disease”. The protease was found to play a key role in the infection and development of *C. irritans* and could serve as a potential molecular target for immune-based therapies. To explore the growth and development mechanism of *C. irritans* and to develop new prevention and control strategies, this study first identified the *CathL* gene in *C. irritans* through bioinformatics methods and used CRISPR/Cas9 technology for gene editing. Through RT-qPCR and sequence analysis, it was verified that the expression level of the *CathL* gene in the knockout group of expression was significantly reduced, and the gene sequences with partial sequence deletions, indicating that the knockout site was successfully effective. The experimental results showed that the hatching of *C. irritans* tomonts in the *CathL* gene knockout group was reduced, but the morphology was not affected, indicating that *CathL* plays an important role in the growth and development stage of *C. irritans*.

Key words: CRISPR/Cas9; *Cathepsin L*; *Cryptocaryon irritans*; function analysis; Gene Editing

西藏特有鱼类黑斑原鲢不同组织微生物群落特征及致病性研究

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摘要: 为了解健康与病死黑斑原鲢不同组织微生物群落特征及致病性, 对健康和病死黑斑原鲢的不同组织进行了微生物的培养同时进行了 16S rRNA 测序, 分析了健康和病死黑斑原鲢不同组织的组织学差异、微生物群落特征及致病性。结果显示, 健康和病死黑斑原鲢皮肤和鳃在病理分析上存在一定差异; 健康和病死黑斑原鲢皮肤菌群之间 α 多样性指数存在显著差异; 健康和病死黑斑原鲢鳃菌群在主坐标分析上存在显著差异; 健康和病死黑斑原鲢肠道、皮肤和鳃优势菌门均主要为厚壁菌门、拟杆菌门、变形菌门。OTUs 聚类分析结果表明, 病死鱼不同组织中绿弯菌门、脱硫弧菌门、放线菌门、粘球菌门丰度较高, 而嗜盐古菌门在健康鱼不同组织丰度较高。差异分析发现, 希瓦氏菌属仅在肠道中分布, 在健康鱼丰度相对较高; 病死鱼不同组织的气单胞菌属丰度均高于健康鱼。

关键词: 黑斑原鲢; 微生物; 鳃; 皮肤; 肠道; 高通量测序

Molecular Characterization and Pathogenic Potential of Microbiota Associated with Tissue-Specific Niches in the Tibetan Endemic Fish Species *Glyptosternum maculatum*

WU mengyu

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Abstract: This study aimed to explore the microbial community characteristics and pathogenicity in various tissues of healthy and diseased *Glyptosternum maculatum*. Microorganisms were isolated and 16S rRNA sequencing was performed. Analysis revealed histological and microbial community differences between healthy and diseased fish, particularly in the skin and gills ($P < 0.05$). The α diversity and PCoA of gill microbiomes also showed significant variance. Firmicutes, Bacteroidetes, and Proteobacteria were dominant in all tissues. OTUs analysis showed higher abundances of Chloroflexi, Desulfovibrionaceae, Actinobacteria, and Myxococcota in deceased fish, versus Halobacterot in healthy ones. LEfSe analysis indicated *Shewanella* was more abundant in the intestines of healthy fish, while *Aeromonas* was more prevalent in deceased fish, suggesting it is a potential pathogen. These findings provide insights into the microbial structure of *G. maculatum* tissues and inform targeted disease management in aquaculture.

Key words: *Glyptosternum maculatum*; microorganisms; gills; skin; intestines; High-throughput sequencing

副溶血性弧菌 LF1113 的全基因组测序和比较基因组学解析

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摘要: 石斑鱼是南方沿海最重要的养殖鱼类之一，目前有工厂化养殖，室外水泥养殖，土池养殖、海上网箱养殖等多种养殖方式，养殖密度高，易感弧菌病，因此是石斑鱼养殖过程中需要重点防治的疾病之一。副溶血性弧菌由于传播速度快，致死率高，危害性大，已经在世界范围内对石斑鱼养殖产业造成了巨大的经济损失。2022年12月初，从文昌某珍珠龙胆石斑鱼养殖场分离到一株致病性的副溶血性弧菌，利用 Pacbio 测序平台和 Illumina Hiseq 测序平台进行全基因组测序、组装和功能注释。并进一步做了比较基因组分析、进化树分析和致病性评价。为有效的防控石斑鱼养殖细菌病害提供了基础。

关键词: 副溶血性弧菌；珍珠龙胆；全基因组测序；基因组比较；毒力；

The analysis of complete genome sequence and comparative genomics of *Vibrio parahaemolyticus* LF1113 in Hainan

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Abstract: *Vibrio parahaemolyticus* is a Gram-negative, halophilic and polymorphic coccobacillus. It is world-widely distributed and has resulted in great economic losses since its first appearance. In this study, a pathogenic strain was isolated from diseased pearl gentian grouper and identified as *V. parahaemolyticus* based on the sequencing results of 16S rDNA gene. In order to gain a comprehensive understanding of this isolation, the whole genome sequencing was conducted. Phylogenetic analysis of the complete genomes of 16 *Vibrio* species showed that LF1113, ATCC17802, ATCC33787, 2210633, FORC 004, and 160807 were the most closely related. Animal experiments demonstrated that the isolated LF1113 strain was pathogenic in a fish model. This study is the first study to describe the complete genome sequence of a *V. parahaemolyticus* isolate, which infected pearl gentian grouper from an outbreak in a fish factory farm in Hainan. The results will expand our understanding of genetic characteristics, pathogenesis, diagnostics and disease prevention of *V. parahaemolyticus*, and lay the foundati

Key words: *Vibrio parahaemolyticus* Pearl gentian grouper Whole genome sequencing Genomic comparison Virulence

达氏鲟幼鲟急性肠炎的病原鉴定及药敏分析

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摘要: 为探究达氏鲟 (*Acipenser dabryanus*) 育苗阶段的急性肠炎而引起死亡的原因及致病菌, 本研究从饵料丰年虾、水蚯蚓、养殖水体和患病鱼肠道分离纯化得到四种优势菌 DSX-0420、DSX-0421、DSX-0422 和 DSX-0423。对这四种菌株进行生理生化和 16S rDNA 分析, 结果表明饵料丰年虾 DSX-0420 菌株为弧菌; 水蚯蚓 DSX-0421、养殖水体 DSX-0422 和患病鱼肠道 DSX-0423 菌株均为嗜水气单胞菌, 且三种菌同源性达 99%。对 DSX-0420、DSX-0423 进行人工回归感染试验, 其中患病鱼肠道 DSX-0423 菌株感染的试验鱼与自然发病的肠炎症状相同, 结果表明致病菌株为 DSX-0423。并对 DSX-0423 菌株进行药物敏感性分析, 结果表明该菌株对四环素和菌必治高度敏感; 对庆大霉素、头孢哌酮和链霉素中度敏感。

关键词: 达氏鲟; 急性肠炎; 嗜水气单胞菌; 病原鉴定

Isolation and identification acute bacterial enteritis from larvae *Acipenser dabryanus* and its antibiotic sensitivity

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Abstract: In order to identify the pathogen which caused bacterial enteritis and killed a number of larvae *Acipenser dabryanus* during seedling stage, the bacterial strain of DSX-0420, DSX-0421, DSX-0422 and DSX-0423 were isolated from intestinal tract of diseased fish, *Artemia salina*, *Limnodrilus hoffmeisteri*, and aquaculture water, by mean of physiological characteristics and 16S rDNA sequence analysis, the result show that strain DSX-0420 was identified as *Vibrio*; DXS-0421, DSX-0422 and strain DXS-0423 were identified as *Aeromonas hydrophila*, and the strain of three with 99% homology. And the strain of DSX-0420 and DSX-0423 were used in the artificial infection experiment, the strain of DSX-0423 displaying similar to nature infection cases, and caused death, so the strain DXS-0423 was the etiological agent of this disease. Meanwhile, the strain DXS-0423 was highly sensitive to tetracycline, ceftriaxone sodium and medium sensitivity to gentamicin, cefoperazone, streptomycin. In conclusion, The pathogen of acute enteritis was *Aeromonas hydrophila* in this seedling stage, which can be treated wi

Key words: *Acipenser dabryanus*; Acute bacterial enteritis; *Aeromonas hydrophila*; Identification

大黄鱼感染盾纤毛虫死亡高峰期的 差异可变剪切和差异表达分析

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摘要: 大黄鱼正面临着细菌、病毒和寄生虫病的各种威胁, 尤其是盾状纤毛虫。本研究对大黄鱼进行人工攻毒, 并对实验组死亡高峰期的鱼和对照组的鱼的鳃组织进行了转录组和可变剪切分析。在 7d/0h、8d/0h 和 9d/0h 分别发现了 400、427 和 311 个差异可变剪切事件。同时, 发现 761 个差异表达基因, 其中 154 个在三个时间点同时存在。GO 和 KEGG 富集分析表明, DAS 基因和 DEGs 主要集中在自我修复、免疫和代谢相关途径上。与凝血相关的 DEGs 包括 FGA、FGB、FGG 和凝集素结构域基因。细胞因子、Caspase-1、TRIM13、TRIM16 和 TRIM39 共同参与免疫反应。C3 既是 DEG, 又是 DAS。此外, STRING 软件用于可视化相互作用调控网络并预测中枢基因。总共有 22 个 DEG 同时存在于至少两组中。这一信息为进一步寻找盾状纤毛虫抗性基因和阐明鱼类与寄生虫的相互作用提供了参考依据。

关键词: 大黄鱼, 盾纤毛虫, 转录组分析, 可变剪切

Alternative splicing events and differently expressed genes during peak mortality in large yellow croaker (*Larimichthys crocea*) infected with scuticociliate

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Abstract: The large yellow croaker faces threats from bacterial, viral, and parasitic diseases, especially scuticociliate. This study conducted artificial infections and analyzed gill tissues from the experimental group at peak mortality and the control group using transcriptome and alternative splicing analyses. A total of 400, 427, and 311 differential alternative splicing events were identified at 7d/0h, 8d/0h, and 9d/0h, respectively. Additionally, 761 differentially expressed genes (DEGs) were detected, with 154 present at all three time points. GO and KEGG enrichment analyses showed that DAS genes and DEGs primarily involved self-repair, immune, and metabolic pathways. Coagulation-related DEGs included FGA, FGB, FGG, and lectin domain genes. Cytokines, Caspase-1, TRIM13, TRIM16, and TRIM39 were involved in immune responses. C3 was identified as both a DEG and DAS. STRING software visualized the interaction network, revealing 22 DEGs present in at least two groups. This information aids in identifying resistance genes against *Didinium* and understanding fish-parasite interactions.

Key words: *Larimichthys crocea*, scuticociliate, transcriptome, alternative splicing

靶向宿主的抗病毒物质在水产养殖中应用的理论和实践

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摘要： 主流的抗病毒策略包括疫苗防控和药物防控，药物防控的技术路线分为靶向病毒的抗病毒药物开发和靶向宿主的抗病毒药物开发两大方向。我国水产养殖病害有种类多、发病广、危害大、缺疫苗、无药物的特点，从中草药中筛选靶向宿主的抗病毒物质具有绿色、广谱和应用方便的显著优点。过去 10 年，我们课题组以草鱼出血病的药物开发为目标，基于病毒和宿主的相互作用开发了基于病毒吸附受体、应激反应等新靶点筛选了系列绿色小分子，在药代动力学数据的支撑下确定了使用剂量，以饲添的形式应用于我国各大草鱼主养区，均取得了良好的草鱼出血病防控效果。

关键词： 靶向宿主的抗病毒药物，草鱼出血病，草鱼呼肠孤病毒，靶点，药代动力学

Theory and practice of developing host-targeting antivirals in aquaculture

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Abstract : The mainstream anti-viral strategies include vaccine control and drug control. The technical route for drug control is divided into two directions: the development of anti-viral drugs targeting viruses and the development of anti-viral drugs targeting hosts. The fish diseases in aquaculture in China are characterized by two many disease types, widespread outbreaks, great harm, lack of vaccines, and no drugs. Selecting anti-viral substances targeting hosts from traditional Chinese medicine has the significant advantages of being green, broad-spectrum, and easy to apply. Over the past 10 years, our research group has aimed to the development of drugs for grass carp hemorrhagic septicemia , and developed a series of green and small molecules based on the interaction between viruses and hosts, such as virus adhesion receptors and stress response proteins. With the support of pharmacokinetic data, we determined the dosage and applied it in the form of feed additives in major grass carp production areas in China, achieving good control of grass carp hemorrhagic septicemia.

Key words:: Host-targeting antivirals, grass carp hemorrhagic disease, grass carp reovirus, target, pharmacokinetics

溶藻弧菌富含 sRNA 的外膜囊泡:生物膜被 组装的决定性建造者

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摘要: 生物被膜能够增强细菌在宿主体内的生存能力, 已成为一个重要的临床问题。近期研究揭示了外膜囊泡 (OMVs) 在生物被膜形成中的关键作用。本研究成功提取、纯化并表征了来自溶藻弧菌 (*Vibrio alginolyticus*) 的 OMVs, 发现这些 OMVs 不仅促进生物被膜的形成, 还富含小 RNA (sRNA)。生物信息学分析表明, 这些 sRNA 靶向多种调控基因, 可能在生物膜形成过程中发挥重要作用。为了验证这一点, 我们构建了缺失高丰度 sRNA 的突变体, 并评估了它们对细菌生理的影响, 包括生长、运动、细胞外基质的产生和生物被膜的发育。研究结果表明, sRNA 在这些过程中发挥着关键作用, 并调节与生物膜形成相关的基因表达。本研究强调了 OMVs 在调节细菌生物膜形成中传递 sRNA 的重要性, 为理解细菌的致病机制提供了新的见解。

关键词: 外膜囊泡, 生物被膜形成, sRNA, 溶藻弧菌

sRNA-Enriched Outer Membrane Vesicles of *Vibrio alginolyticus*: Decisive Architects of Biofilm Assembly

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Abstract : Biofilms enhance bacterial survival within the host, presenting a significant clinical challenge. Recent studies have highlighted the critical role of outer membrane vesicles (OMVs) in biofilm formation. In this study, we successfully isolated, purified, and characterized OMVs derived from *Vibrio alginolyticus*. Our findings reveal that these OMVs not only promote biofilm formation but are also enriched in small RNAs (sRNAs). Bioinformatic analyses indicate that these sRNAs target various regulatory genes, suggesting a potential role in biofilm development. To validate this, we constructed mutants and OMVs lacking high-abundance sRNAs and assessed their impact on bacterial physiology, including growth, motility, extracellular matrix production, and biofilm development. The results demonstrate that sRNAs play a crucial role in these processes and regulate the expression of genes associated with biofilm formation. This study underscores the importance of OMVs in transferring sRNAs to regulate bacterial biofilm formation, providing new insights into the pathogenic mechanisms of bacteria.

Key words:: Outer Membrane Vesicles; Biofilm Formation; small RNAs; *Vibrio alginolyticus*

大口黑鲈微生物群落变化分析

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摘要: 为探讨不同养殖阶段大口黑鲈肠道和水质微生物的组成及其影响因素, 本研究采用 16S rRNA 高通量测序技术, 对鱼的肠道和水质微生物组成进行了检测, 并与环境因子相关性进行了分析。结果显示 8 月份与其他月份的肠道微生物组成区系存在显著差异, 变形菌门 (31.22%) 和厚壁菌门 (26.49%) 为优势类群, 其数量过度增长会抑制有益菌生长, 减少微生物多样性。结果也显示, 8 月份肠道的 OTU 数量明显低于其他月份, 这会影响鱼类肠道生态平衡, 增加感染疾病风险。水体中的优势类群则为变形菌门和放线菌门, 放线菌门过度生长会使水体微生物多样性下降, 水质恶化, 影响鱼类的营养代谢。结果显示, 总磷、总氮与肠道微生物区系, 水温、化学需氧量与水体微生物区系均存在显著相关性, 这几类水质因子升高会导致水质恶化, 增加水中病原菌, 提高鱼类疾病风险。

关键词: 大口黑鲈; 水质因子; 菌群结构; 养殖池塘

Analysis of microbial community changes in largemouth bass

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Abstract: To investigate the composition and influencing factors of microorganisms in the intestinal tract and water environment of *Micropterus salmoides* during aquaculture, 16S rRNA high-throughput sequencing technology was used to analyze the microbial composition of intestinal tract and pond water in different periods of *Micropterus salmoides*, and its correlation with environmental factors was analyzed. The results showed that there were significant differences in the composition of intestinal microflora between August and other months. Proteobacteria (31.22 %) and Firmicutes (26.49 %) were the dominant groups. Excessive growth of their number would inhibit the growth of beneficial bacteria and reduce microbial diversity. The results also showed that the number of OTUs in the intestine in August was significantly lower than that in other months, which would affect the intestinal ecological balance of fish and increase the risk of infectious diseases. The dominant groups in the water body are Proteobacteria and Actinobacteria. The excessive growth of Actinobacteria will reduce the microbial di

Key words: *micropterus salmoides*, water quality factors, microbial community structure, aquaculture ponds

高温胁迫下虾夷扇贝糖代谢重编程增强供能并修复 DNA 损伤

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摘要: 全球气候变暖导致海水温度升高, 严重影响冷水性贝类虾夷扇贝 (*Patinopecten yessoensis*) 的生长生存。本研从糖原代谢角度揭示虾夷扇贝响应高温胁迫的分子机制。结果发现, 高温 (25°C) 胁迫 3h 后, 闭壳肌中的乳酸和 ROS 含量显著升高, 同时 Glycolysis/Gluconeogenesis 通路被显著富集到; 对糖酵解指标进行检测发现丙酮酸激酶 (PK), 乳酸脱氢酶 (LDH) 活性, 丙酮酸和 NAD⁺ 含量均显著升高, 提示糖酵解增强, 同时 NAD⁺-NADH 循环回补糖酵解。高温胁迫 6h 后, 磷酸戊糖途径 (PPP) 通路均被显著富集, 同时 PK 活性和 NADP⁺ 含量也显著升高。与高温胁迫 3h 后相比, 高温胁迫 6h 后, LDH 活性和丙酮酸含量无显著性变化, 而 PK 活性显著降低, 提示糖酵解途径被减弱, 机体可能通过激活 PPP 途径清除 ROS、修复受损的 DNA。以上研究为深入揭示贝类响应高温胁迫的分子机制奠定基础。

关键词: 虾夷扇贝, 高温胁迫, 糖酵解途径, 磷酸戊糖途径, DNA 损伤

Glycometabolism reprogramming in scallop *Patinopecten yessoensis* to enhance energy supply and repair DNA damage under high temperature

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Abstract: Global climate warming has led to a continuous rise in seawater temperature, severely affecting the growth of the cold-water shellfish *Patinopecten yessoensis*. This study aimed to reveal the response mechanism of *P. yessoensis* to high temperature from the perspective of glycogen metabolism. At 3h after high temperature (25°C) treatment, the content of lactate, ROS significantly increased. The Glycolysis/Gluconeogenesis pathway was notably enriched, we further found that the activities of PK and LDH as well as the content of pyruvate and NAD⁺ significantly increased, suggesting that glycolysis enhanced and NAD⁺-NADH cycling. At 6 h after high temperature treatment, The PPP were enriched considerably. Concurrently, G6PD activity also increased significantly. Compared to the results at 3 h, PK activity, ROS, and PARP1 protein significantly decreased, and the PPP pathway was activated to scavenge ROS and repair damaged DNA. These results would help us understand the mechanism of scallops to respond to high temperature stress.

Key words: *Patinopecten yessoensis*, High temperature stress, Glycolysis, Pentose phosphate pathway, DNA damage

副溶血弧菌感染下缢蛏免疫与糖代谢的 权衡策略对其抗病能力影响

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摘要: 缢蛏 (*Sinovacula constricta*) 是我国四大海水养殖贝类之一, 高温病害引起的大规模死亡事件是其产业发展的重要限制因素。我们对缢蛏攻毒过程的存活曲线和每日将死个体转录组变化进行分析, 可将缢蛏响应副溶血弧菌感染分为四个时期: 死亡早期、死亡中期、死亡晚期和最终存活。期间, 缢蛏依次经历了细胞凋亡、能量供需和病原体清除。基于 STEM 和 WGCNA 分析发现糖代谢相关基因表达随着缢蛏的存活时间而增加。我们进一步通过注射葡萄糖抑制剂 (2-DG) 抑制其糖代谢确认糖代谢对缢蛏抗病力的影响, 结果显示, 在副溶血弧菌感染 12 小时和 48 小时后, 缢蛏的葡萄糖和乳酸含量增加, 糖酵解关键基因上调表达, 促炎相关通路显著富集; 而 2-DG 处理后, 缢蛏糖酵解关键基因下调, IL-17、NF- κ B 和 TNF 通路受到抑制, 死亡率增加。研究结果表明糖代谢重编程可以通过缢蛏促炎应答调控缢蛏抗病力。

关键词: 缢蛏; 副溶血弧菌; 糖代谢; 抗病力; 免疫应答

The impact of the trade-off strategy between immunity and glycometabolism on the disease resistance of razor clams infected with *Vibrio parahaemolyticus*

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Abstract: The response of razor clams to *Vibrio parahaemolyticus* infection was divided into four stages: early death, mid death, late death, and final survival, based on the survival curve of razor clams during the process of infection and transcriptome analysis of deceased individuals on a daily basis. During this period, razor clams underwent cell apoptosis, energy supply and demand, and pathogen clearance, and the surviving individuals eventually developed strong resistance to *Vibrio parahaemolyticus*. Based on STEM and WGCNA analysis, it was found that the expression of sugar metabolism related genes increases with the survival time of razor clams. We further confirmed the effect of glucose metabolism on the disease resistance of razor clams by injecting glucose inhibitor (2-DG) to inhibit their glucose metabolism. The results showed that after 12 and 48 hours of *Vibrio parahaemolyticus* infection, the glucose and lactate content of razor clams increased, key genes for glycolysis were upregulated, and pro-inflammatory pathways IL-17, MAPK, and NF- κ B were upregulated.

Key words: *Sinonovacula constricta*; *Vibrio parahaemolyticus*; Glycometabolism; Disease resistance; Immune response

黄颡鱼细菌病流行病学调查与 药敏快速检测技术研究

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摘要: 针对黄颡鱼细菌性病害频发而流行病学数据不足的问题, 本团队于 2022 年 3 月至 2023 年 9 月在珠三角地区进行了细菌病流行病学调查。共采集 375 份病鱼样品, 获得 210 株病原菌。结果显示, 细菌病的发生率在不同季节间差异较大, 尤其以春季最为集中, 占比高达 79.05%, 而在病原菌的构成中, 以海豚链球菌为主, 占比达 32.38%。采用微量肉汤药敏检测结果显示, 病原菌普遍具有较高耐药率, 且超过半数的菌株呈现多种耐药。此外, 为克服传统药敏时效差的缺点, 本研究以海豚链球菌为例, 对多种实验条件进行了系统的对比和优化, 包括不同培养基、培养温度、时间、菌液浓度以及混入组织液匀浆液等因素对纸片琼脂扩散法抑菌结果的影响, 在参考 CLSI 标准对测数据差异进行修正的基础上, 建立了一种快速药敏检测方法: 取濒死病鱼肝、脾、肾组织, 加入 10 倍体积 PBS 匀浆, 涂布 CBA 平板, 30℃ 培养 16~24 h 后判定结果。

关键词: 黄颡鱼; 流行性病学调查; 多重耐药性; 药敏检测

Epidemiological investigation of bacterial diseases in *Tachysurus fulvidraco* and research on rapid antimicrobial susceptibility testing technology

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Abstract: In view of the frequent occurrence of bacterial diseases of *Tachysurus fulvidraco* and insufficient epidemiological data, our team conducted an epidemiological investigation of bacterial diseases in the Pearl River Delta region from March 2022 to September 2023. A total of 375 diseased fish samples were collected and 210 pathogenic strains were obtained. The incidence of bacterial diseases was highest in spring, reaching 79.05%, with *Streptococcus iniae* being the predominant pathogen (32.38%). Drug sensitivity tests revealed high resistance rates, with over half of the strains showing multidrug resistance. In addition, in order to overcome the disadvantages of traditional drug sensitivity difference, a variety of experimental conditions, including different media, culture temperature, time, bacterial fluid concentration, and the antibacterial results of the paper agar diffusion method, on the basis of the CLSI standard, established a rapid drug sensitivity detection method. This method can produce drug sensitivity results within 24 h.

Key words: *Tachysurus fulvidraco*; Epidemiological investigation; Multi-drug resistance; Antibiotic susceptibility testing

基于补体 C3 的激活与调节机制探讨大黄鱼和黄姑鱼对刺激隐核虫抗感染差异的分子机理研究

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摘要: 刺激隐核虫病是由一种专性寄生纤毛虫—刺激隐核虫(*Cryptocaryon irritans*)寄生硬骨鱼类引起的疾病。鱼体感染刺激隐核虫后, 体表和鳃丝上呈现肉眼可见的小白点, 也被称为“白点病”。其爆发速度快, 传播范围广, 若未及时采取有效措施, 鱼群将大规模死亡。前期研究发现, 黄姑鱼不易感染刺激隐核虫病且补体旁途径发挥重要作用。本研究中, 我们以大黄鱼和黄姑鱼的补体 C3 为研究对象, 首先分析补体 C3 蛋白的结构特点, 其次通过 ELISA、Western blot 及免疫荧光等实验技术检测刺激隐核虫对血清中 C3 的消耗和分解以及虫体表面 C3 的沉积。结果表明, 大黄鱼和黄姑鱼 C3 蛋白的糖基化和信号肽有所不同, 与大黄鱼血清共同孵育后, 血清中 C3b 含量降低; 经过血清孵育后的幼虫沉淀进行 Western blot 分析显示, 刺激隐核虫幼虫表面不仅沉积了 C3b 的 α 链和 β 链, 还出现了更为显著的 iC3b 条带。

关键词: 刺激隐核虫、免疫、补体 C3

Based on the activation and regulation mechanism of complement C3, the molecular mechanism of the difference between large yellow croaker and *Nibea albiflora* against stimulated *Cryptocaryon irritans* infection was studied

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Abstract: cryptocaryoniasis is a disease caused by an obligate parasitic ciliate, *Cryptocaryon irritans*, which parasitizes bony fish. After the fish is infected with *Cryptocaryon irritans*, small white spots visible to the naked eye appear on the body surface and gill filaments, which is also known as "white spot disease". The outbreak is fast and spreading, and if effective measures are not taken in time, fish will die on a large scale. Previous studies have found that *Nibea albiflora* is not susceptible to stimulus *Cryptocaryon irritans* and the complement bypass pathway plays an important role. In this study, we took the complement C3 of large yellow croaker and *Nibea albiflora* as the research object, and detected the depletion and decomposition of C3 protein and the deposition of C3 on the surface of the insect by ELISA, Western blot and immunofluorescence, to explore the differences in the anti-infectivity of different species in the totoaba family to *Cryptocaryon irritans*, and to reveal how complement C3 plays a key role in the role of its regulatory factors.

Key words: *Cryptocaryon irritans*, immunity, complement C3

鱼类 NLRX1 变体靶向 STING 负调控干扰素 抗病毒免疫反应的机制研究

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摘要: 哺乳类 NLRX1 是 NLR 受体家族中的一个独特成员, 具有负调控干扰素 (IFN) 抗病毒免疫反应的能力。NLRX1 等包含内含子的基因有多个转录本存在, 然而对其剪接变体的功能知之甚少。我们在斑马鱼中发现了 NLRX1 的一个变体 NLRX1-tv4, 研究发现它是鱼类 IFN 反应的负调节因子。斑马鱼 NLRX1-tv4 表达模式与全长 NLRX1 相似, 尽管相比全长 NLRX1 缺少一个 N 端结构域, 但它过表达仍会抑制 IFN 抗病毒反应, 促进病毒在鱼类细胞中的复制。从机制上讲, NLRX1-tv4 通过募集 E3 泛素连接酶 RNF5 来驱动 K48 链接的泛素化, 靶向 STING 蛋白进而通过蛋白酶体途径使其降解。通过构建 NLRX1-tv4 的突变体表明, 其 N 端和 C 端区域都具有抑制 STING 介导的 IFN 抗病毒反应的相似潜力。我们的研究表明, 与全长 NLRX1 一样, 斑马鱼的 NLRX-tv4 也作为一个负调控因子进而抑制鱼类 IFN 抗病毒反应。

关键词: NLRX1, 干扰素反应, E3 连接酶, 泛素化修饰, 调控机制

A zebrafish NLRX1 isoform downregulates fish IFN responses by targeting the adaptor STING

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Abstract: NLRX1 is a unique member of the nucleotide-binding domain and leucine-rich repeat (NLR) family showing an ability to negatively regulate IFN antiviral immunity. NLRX1 has more than one transcript due to alternative splicing; however, little is known about the function of its splicing variants. Here, we identified a transcript variant of NLRX1, NLRX1-tv4, as a negative regulator of fish IFN response. NLRX1-tv4 was slightly induced by viral infection. Despite the lack of an N-terminal domain that exists in the full-length NLRX1, overexpression of NLRX1-tv4 still impaired fish IFN antiviral response and promoted viral replication in fish cells. Mechanistically, NLRX1-tv4 targeted STING for proteasome-dependent protein degradation by recruiting an E3 ubiquitin ligase RNF5 to drive the K48-linked ubiquitination, eventually downregulating the IFN response. The N-terminal and C-terminal regions of NLRX1-tv4 both exhibited a similar potential to inhibit STING-mediated IFN antiviral response. Our findings reveal that NLRX-tv4 functions as an inhibitor to shape fish IFN antiviral response.

Key words: NLRX1, interferon response, E3 ubiquitin ligase, ubiquitination modification, regulatory mechanism

许氏平鲉 (*Sebastes schlegelii*) TRAF 基因的鉴定及其响应杀鱼爱德华氏菌感染的表达模式研究

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摘要: 肿瘤细胞坏死因子受体相关因子(TRAF)是机体内一种具有信息传导作用的胞内因子, 承担多个受体家族的信号转导工作, 在固有免疫以及获得性免疫方面都发挥出重要作用。TRAF 作为一类胞内接头蛋白, 对多条信号途径的活化具有一定的影响, 包括细胞的增殖、生存、凋亡、炎症反应、免疫反应等。目前, 已有研究表明鱼类中的 TRAF 基因也发挥重要的免疫防御作用。因此, 以许氏平鲉为研究对象, 基于基因组和转录组的数据库, 进行了许氏平鲉 TRAF 基因的全基因组鉴定。在许氏平鲉中共鉴定到 9 个 TRAF 基因, 并对这些 TRAF 基因的长度和氨基酸个数进行了统计分析。同时, 分析了这 9 个 TRAF 基因的结构特征。选取了包括许氏平鲉在内的 6 种鱼类进行 TRAF 基因的共线性分析。结果显示, TRAF 基因在硬骨鱼类中较为保守。通过系统发育分析, 更好的解析了 TRAF 家族基因的进化关系, 同时也证明了我们对其鉴定及命名的准确性。

关键词: TRAF; 信号传导; 表达模式; 许氏平鲉; 免疫应答

IDENTIFICATION AND ANALYSIS OF TUMOR NECROSIS FACTOR RECEPTOR-ASSOCIATED FACTORS (TRAF) AND THEIR EXPRESSION PATTERN IN SEBASTES SCHLEGELII AFTER EDWARDSIELLA PISCICIDA INFECTION

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Abstract : Tumor cell necrosis factor receptor-related factor (tumor necrosis factor receptor-associated factors, TRAF) is an intracellular factor with information conduction effect in the body, which is responsible for the signal transduction efforts in many receptor families and plays an important role in both innate immunity and acquired immunity. As an intracellular adaptor protein, TRAF has a certain influence on the activation of multiple signaling pathways, including cell proliferation, survival and apoptosis participate in inflammatory and immune responses. At present, studies have shown that TRAF genes in fish also play an important role. Therefore, the whole genome of TRAF gene of *Sebastes schlegelii* was identified based on the database of genome and transcriptome. A total of nine TRAF genes were identified in *S. schlegelii*, and the length and number of amino acids of these TRAF genes were analyzed. Meanwhile, the structural characteristics of these nine TRAF genes were analyzed. Six species of fish including *S. schlegelii* were selected for the collinearity analysis of TRAF gene. Resu

Key words:: TRAF ; signaling transduction ; expression patterns ; *Sebastes schlegelii* ; immune response

基于鮰鱼诺卡氏菌感染大黄鱼的头肾转录组学研究

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摘要：大黄鱼是我国重要的经济海洋鱼类，由鮰鱼诺卡氏菌引发的传染病严重暴发，造成巨大的经济损失。然而，大黄鱼对此类细菌感染的免疫反应及鮰鱼诺卡氏菌的致病机制尚不完全清楚。我们使用高通量测序技术来研究未感染和鮰鱼诺卡氏菌感染 1、3、7、14 天的大黄鱼头肾的转录组。KEGG 富集分析结果表明差异表达基因主要在免疫和代谢相关通路中富集，免疫途径中 Toll 样受体信号通路、ECM 受体相互作用、细胞因子-细胞因子受体相互作用等途径的富集，表明感染后大黄鱼的免疫系统被激活，代谢途径中柠檬酸循环和氧化磷酸化途径的显著富集，表明 ATP 合成可能加快，以确保免疫反应时的能量供应。这些发现都增加了我们对鮰鱼诺卡氏菌感染下大黄鱼的防御机制的和鮰鱼诺卡氏菌致病机制的认识。

关键词：大黄鱼，鮰鱼诺卡氏菌，转录组，免疫，代谢

Transcriptomic analysis of the head kidney in large yellow croaker (*Larimichthys crocea*) infected with *Nocardia seriolae*

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Abstract: *Larimichthys crocea* is a significant marine fish species in China, it suffers substantial economic losses due to outbreaks of infectious diseases caused by *Nocardia seriolae*. Presently, the immune response of the *L. crocea* to such bacterial infections and the pathogenic mechanisms of *N. seriolae* remain inadequately understood. We employed high-throughput sequencing to investigate the transcriptome of the head kidney in uninfected fish and those infected with *N. seriolae* at 1, 3, 7, and 14 days post-infection. KEGG enrichment analysis revealed that DEGs were predominantly enriched in immune and metabolic pathways. The enrichment of Toll-like receptor signaling, ECM-receptor interaction, and cytokine-cytokine receptor interaction indicates an activation of the immune system. The enrichment of Oxidative phosphorylation and Citrate cycle suggests accelerated ATP synthesis to ensure energy supply during the immune response. These findings enhance our understanding of the defense mechanisms of *L. crocea* under *N. seriolae* infection and the pathogenic mechanisms of *N. seriolae*.

Key words: *Larimichthys crocea*, *Nocardia seriolae*, Transcriptome, Immunity, Metabolism

加州鲈 pIgR 抗体制备及免疫应答特征研究

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摘要: 多聚免疫球蛋白受体 (pIgR) 对于保护生物体免受病原体入侵至关重要。本研究在制备了抗加州鲈重组 pIgR 抗体后, 分析了浸泡和腹腔注射嗜水气单胞菌后 pIgR 和 IgM 的免疫应答特征。研究表明, pIgR 的转录水平与皮肤、胃、肠、脾和头肾中 IgM 的转录水平相似, 但 pIgR 上升速度比 IgM 更快。在浸泡组中 pIgR 表达在皮肤中较高, 在腹腔免疫组中则在脾脏中较高。IgM 表达在皮肤和鳃中较高, 在腹腔免疫组中则在脾脏和肝中较高。ELISA 结果显示 IgM 和 pIgR 蛋白水平在皮肤黏液、鳃黏液、肠道黏液和胆汁中上调, 在浸泡组中皮肤黏液和鳃黏液更早达到较高的峰值水平, 而在注射组中胆汁达到较高的峰值水平。这些结果表明, 浸泡和腹腔免疫上调了分泌液中 pIgR 和分泌型 Ig 的表达, 为深入研究硬骨鱼类 pIgR 在黏膜免疫中的作用提供了数据支撑。

关键词: 加州鲈; 多聚免疫球蛋白受体; 嗜水气单胞菌; 黏膜免疫

Antibody preparation and immune response of pIgR in largemouth bass (*Micropterus salmoides*) following immunization with inactivated *Aeromonas hydrophila*

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Abstract: The polymeric immunoglobulin receptor (pIgR) is crucial in protecting organisms against pathogen invasion. However, further clarification regarding its mucosal immune responses is required, particularly when considering various vaccine administration routes. Herein, polyclonal antibodies against largemouth bass (*Micropterus salmoides*) recombinant pIgR was prepared. Moreover, pIgR and IgM response features were investigated after immunization via bath and intraperitoneal injection with *Aeromonas hydrophila*. The findings indicated that the pIgR transcription level was comparable to that of IgM in the skin, gills, intestine, liver, spleen, and head kidney. Nonetheless, pIgR increased at a quicker rate and peaked earlier than IgM. The pIgR was overexpressed in the skin in the bath immersion group and the spleen in the intraperitoneal immunization group. Meanwhile, IgM expression levels exhibited higher results in the skin and gills in the bath immersion group as well as the liver and spleen in the intraperitoneal immunization group. The ELISA results demonstrated an elevation of IgM and

Key words: Largemouth bass (*Micropterus salmoides*); Polymeric immunoglobulin receptor (pIgR); *Aeromonas hydrophila*; Mucosal immunity

通过 sRNA15 和 sRNA80 揭示溶藻弧菌生物被膜形成的转录后调控机制

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摘要：生物被膜是细菌对抗逆境的有力屏障，可以有效保护细菌免受药物、环境压力以及宿主免疫系统的胁迫和攻击。在前期研究中，我们在溶藻弧菌中发现了两种新型 sRNA——sRNA15 和 sRNA80。生物信息学分析显示，sRNA15 和 sRNA80 靶向多种调节基因，可能在溶藻弧菌的生物被膜形成中发挥着关键作用。为了验证它们在生物被膜形成中的作用及其机制，我们构建了 sRNA15 和 sRNA80 的缺失突变株，发现其对溶藻弧菌的生长、运动、细胞外基质的产生以及生物被膜的发育具有显著影响。此外，通过 GFP 报告基因分析、EMSA、Northern Blot、mRNA 半衰期分析和蛋白质体外翻译等技术，我们证实了 sRNA15 和 sRNA80 在转录后调节 rpoS 方面的重要作用，揭示了它们在溶藻弧菌生物被膜形成中的关键功能。

关键词：生物被膜、小 RNA、转录后调控、溶藻弧菌

Deciphering the Post-Transcriptional Regulation of Biofilm Formation in *Vibrio alginolyticus* by Small RNAs sRNA15 and sRNA80

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Abstract : Biofilms are powerful barriers that bacteria employ to combat adversity, effectively shielding them from the stress and attacks posed by antibiotics, environmental pressures, and host immune systems. In our previous research, we identified two novel small RNAs in *Vibrio alginolyticus*: sRNA15 and sRNA80. Bioinformatic analyses revealed that sRNA15 and sRNA80 target multiple regulatory genes, suggesting their crucial roles in biofilm formation in *V. alginolyticus*. To validate their contributions and elucidate the underlying mechanisms in biofilm formation, we constructed deletion mutants of sRNA15 and sRNA80. Our findings indicated significant effects on the growth, motility, extracellular matrix production, and biofilm development of *V. alginolyticus*. Furthermore, employing various techniques such as GFP reporter gene analysis, EMSA, Northern blotting, mRNA half-life assessment, and in vitro protein translation, we confirmed the pivotal role of sRNA15 and sRNA80 in the post-transcriptional regulation of rpoS, unveiling their key functions in the biofilm formation of *V. alginolyticus*.

Key words:: Biofilm Formation、Small RNAs、Post-Transcriptional Regulation、*Vibrio alginolyticus*

虾青素对微囊藻毒素-LR 胁迫下凡纳滨对虾生长性能、肠道结构及肠道微生物的影响

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摘要: 微囊藻毒素-LR (MC-LR) 是一种由蓝藻在水华期间释放的多肽化合物。凡纳滨对虾是全球重要的养殖种类。对虾养殖中常发生蓝藻水华爆发, 对其可持续养殖构成严重威胁。本研究旨在探讨虾青素对凡纳滨对虾暴露于微囊藻毒素诱导的胁迫下的保护作用。实验设置三组: 一组投喂含 MC 的饲料, 一组投喂含 MC+AX 的饲料, 第三组为对照组, 投喂基础饲料。饲喂 15 天后, 与 MC 组相比, MCAX 组的特定生长率 (SGR) 显著升高, 而与对照组之间无显著差异。同样, 与 MC 组和对照组相比, MCAX 组的体重增长率 (PWG) 也显著更高。与对照组相比, MC 组的上皮细胞遭受了严重的损伤并与基底膜发生脱离。肠道微生物群分析显示, MC 组与 MCAX 组在群落组成上存在显著差异。菌属比较中, MC 组弧菌丰度增加。研究结果表明, AX 通过调节肠道微生物群组成, 对凡纳滨对虾的生长性能和抵抗力产生积极影响, 有助于减轻 MC 在水产养殖中的有害影响。

关键词: 凡纳滨对虾; 微囊藻毒素-LR; 虾青素; 生长性能; 肠道微生物

Effects of Astaxanthin on Growth Performance, Gut Structure, and Intestinal Microorganisms of *Penaeus vannamei* under Microcystin-LR Stress

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Abstract: Microcystin-LR (MC-LR) are biologically active cycloheptapeptide compounds that are released by cyanobacteria during water blooms and are extensively found in aquatic ecosystems. The *Penaeus vannamei* is a significant species in global aquaculture. However, the high level of eutrophication in aquaculture water frequently leads to outbreaks of cyanobacterial blooms, posing a significant threat to its sustainable cultivation. Astaxanthin (AX) is commonly utilized in aquaculture for its physiological benefits, including promoting growth and enhancing immune function in cultured organisms. This study aimed to examine the protective effect of astaxanthin on *P. vannamei* exposed to microcystin-induced stress. The experiment consisted of three groups: one group was fed formulated feed containing MC (100 µg/kg), another group was fed formulated feed containing MC (100 µg/kg) + AX (100 mg/kg), and the third group was fed basic feed (control group). After 15 days of feeding, the specific growth rate (SGR) was significantly higher in the MCAX group (2.21% day⁻¹) compared to the MC group (0.77% da

Key words: *P. vannamei*; MC-LR; astaxanthin; growth performance; intestinal microbiota

曼氏无针乌贼 (*Sepiella japonica*) IL-17 的分子特征、表达模式及抑菌功能分析

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摘要: 白细胞介素 17 (IL-17) 在脊椎动物的炎症反应中发挥着关键作用, 但在头足类动物中的功能却知之甚少。本研究从曼氏无针乌贼 (*Sepiella japonica*) 中获得了 20 个 IL-17 转录本, 并将其分为 8 类 (Sj_IL-17-1 至 Sj_IL-17-8)。系统发育分析显示 Sj_IL-17-5、Sj_IL-17-6 和 Sj_IL-17-8 与其他转录本的同源性较低。这些基因在 10 种乌贼组织中广泛表达, 且在血淋巴中表达最高。Sj_IL-17-2、Sj_IL-17-3、Sj_IL-17-6、Sj_IL-17-7 和 Sj_IL-17-8 在患病或哈维氏弧菌浸泡感染后显著上调。此外, 我们纯化了 Sj_IL-17-4 和 Sj_IL-17-7 蛋白, 后续的抑菌实验显示随着蛋白浓度的升高, 细菌生长率逐渐下降, 表明它们均具有抑制细菌生长的功能。本研究旨在深入了解 Sj_IL-17 基因在曼氏无针乌贼对细菌感染免疫反应中的作用。

关键词: 曼氏无针乌贼; 白细胞介素 17; 分子特征; 表达模式; 抑菌功能

Molecular characterization, expression and antibacterial function of interleukin-17 in the common Chinese cuttlefish (*Sepiella japonica*)

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Abstract: Interleukin-17 (IL-17) cytokine family is crucial in vertebrate inflammatory responses, but little is known about its role in cephalopods. In this study, twenty IL-17 transcripts obtained from *Sepiella japonica* were categorized into eight groups (Sj_IL-17-1 to Sj_IL-17-8). Multiple alignments and phylogenetic analysis showed that Sj_IL-17-5, Sj_IL-17-6 and Sj_IL-17-8 had low homology with the other Sj_IL-17s. Eight Sj_IL-17 mRNAs were expressed in ten examined tissues, with the highest expression in hemolymph. Five genes (Sj_IL-17-2, Sj_IL-17-3, Sj_IL-17-6, Sj_IL-17-7 and Sj_IL-17-8) were notably up-regulated either in sick *S. japonica* or after *V. harveyi* immersion infection, indicating their role in immune response against bacterial infection. Additionally, we expressed and purified Sj_IL-17-4 and Sj_IL-17-7 proteins, and subsequent antibacterial assays revealed a dose-dependent decrease in bacterial growth, showing their significant function of killing bacteria. This study provides insight into the role of Sj_IL-17 genes in cuttlefish immune defense against bacterial infections.

Key words: *Sepiella japonica*; IL-17 genes; Molecular characterization; Expression profile; Antibacterial function

抗生素在刺激隐核虫感染大黄鱼过程中的作用研究

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摘要：随着集约化水产养殖的发展，水产养殖场的水质也在不断下降，导致细菌性疾病显著增加，为了预防或治疗水产养殖中的细菌感染使用了大量的抗生素。在当前抗生素使用无法避免且刺激隐核虫病频发的情况下，研究抗生素的使用是否会影响刺激隐核虫对鱼类的感染就显得尤为重要。因此，我们选择了水产上常用的恩诺沙星和硫酸新霉素探究了抗生素的使用是否会影影响刺激隐核虫感染大黄鱼。首先，我们使用抗生素处理刺激隐核虫，发现经过抗生素处理的刺激隐核虫幼虫死亡时间延后，感染率提升了 12.2%。之后我们用抗生素短期浸浴大黄鱼，发现，抗生素处理增强了大黄鱼对刺激隐核虫的抵抗力，且抗生素组脱落的包囊有更低的孵化率。鉴于此，我们采集了大黄鱼的鳃组织，进行了转录组测序，尝试从 RNA 层面研究了出现此现象的原因。发现抗生素处理提前激活了大黄鱼的免疫反应、影响了大黄鱼趋化因子对刺激隐核虫的响应、影响了大黄鱼的糖代谢。

关键词：刺激隐核虫；大黄鱼；抗生素

Study on the role of antibiotics in the infection process of *Cryptocaryon irritans* in large yellow croaker

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Abstract: Intensive aquaculture has degraded water quality, leading to increased bacterial diseases, prompting heavy antibiotic use. Given the prevalence of *Cryptocaryon irritans* disease, studying antibiotic impact on fish infection is vital. We assessed enrofloxacin and neomycin sulfate's influence on *Cryptocaryon irritans* infection in large yellow croaker. Tests showed delayed larval death and a 12.2% infection rate increase with antibiotic treatment. Short-term immersion enhanced fish resistance and reduced cyst hatching. Gill tissue transcriptome sequencing revealed antibiotic-induced early immune activation, modulated chemokine response, and altered glucose metabolism.

Key words: large yellow croaker; *Cryptocaryon irritans*; antibiotic

罗氏沼虾新疾病（白化病）的转录组学分析：对其发病原因和防治方法的初步探究

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摘要：罗氏沼虾（*Macrobrachium rosenbergii*）是世界上最大的淡水虾类，目前已发展成为多个国家和地区水产养殖的重要经济物种。在中国，一种新的疾病（白化病）的出现严重影响了雌性罗氏沼虾的肉质和繁殖性能。该病主要在雌虾中出现，主要临床症状为全身白化、肝胰腺萎缩和甲壳下出现水泡。本研究对白化虾的肝胰腺和肌肉组织进行了组织病理学和转录组学分析。组织切片结果显示白化虾肝胰腺中肝小管受损，管间间隙变大，肌肉中肌纤维发生萎缩。KEGG 富集分析结果显示，肝胰腺中与白化病有关的主要通路为 Lysosome、Glycosaminoglycan degradation、Pentose and glucuronate interconversions、Starch and sucrose metabolism、Biosynthesis of unsaturated fatty acids、Sphing

关键词：罗氏沼虾；白化病；转录组；营养；繁殖

Transcriptomic Analysis of a Novel Disease (White Syndrome) in *Macrobrachium rosenbergii*: Preliminary Investigation into Its Pathogenesis and Control Measures

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Abstract : *Macrobrachium rosenbergii*, the world's largest freshwater prawn, has emerged as a significant economic species in aquaculture in numerous countries and regions. In China, the emergence of a novel disease, White Syndrome (WS), has profoundly affected the meat quality and reproductive performance of *M. rosenbergii*. This disease predominantly affects female prawns, characterized by systemic whitening, hepatopancreatic atrophy, and the presence of blisters beneath the carapace. In this study, we conducted histopathological and transcriptomic analyses on the hepatopancreas and muscle tissues of afflicted prawns. Histological sections revealed damaged hepatopancreas tubules with enlarged intercellular spaces and muscle fibers exhibiting atrophy in white prawns. KEGG enrichment analysis indicated significant enrichment of pathways associated with WS in the hepatopancreas, including Lysosome, Glycosaminoglycan degradation, Pentose and glucuronate interconversions, Starch and sucrose metabolism, Biosynthesis of unsaturated fatty acids, Sphingolipid metabolism, Steroid biosynthesis, and Fatty

Key words:: *Macrobrachium rosenbergii*; White Syndrome; Transcriptome; Nutrition; Reproduction

细胞自噬在罗氏沼虾抵御细菌感染中的作用机制研究

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摘要: 细胞自噬受到自噬相关基因 (ATGs) 的调控, 在机体抵御微生物入侵的过程中起着关键作用。然而, 罗氏沼虾的细胞自噬调控及其抗感染机制仍然未知。我们通过 Western blot、qRT-PCR、扫描电镜观察等发现嗜水气单胞菌可以诱导罗氏沼虾的自噬激活。接着, RNA-seq 分析雷帕霉素刺激的罗氏沼虾鳃组织, 鉴定出 1684 个上调和 1500 个下调的 DEGs。此外, 综合分析了雷帕霉素刺激和嗜水气单胞菌感染罗氏沼虾的两个 RNA-seq 数据, 鉴定出 15 个同时上调和 25 个同时下调的 DEGs, 他们主要参与调控代谢和免疫途径。进一步, 我们克隆、分析了罗氏沼虾 ATG5 与 Beclin1 的功能。结果显示 ATG5 和 Beclin1 在各组织中广泛表达; 主要定位在细胞质中; 细菌和 LPS 刺激后, 都主要上调表达; 他们的重组活性蛋白对部分病原细菌的生长具有一定的抑制效果。以上结果, 初步揭示了罗氏沼虾细胞自噬的调控与抗菌感染机制。

关键词: 罗氏沼虾, 细胞自噬, 自噬相关基因, 细菌感染, 免疫防御

Mechanism research of autophagy on antibacterial response in *Macrobrachium rosenbergii*

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Abstract: Autophagy is regulated by autophagy related proteins (ATGs), which plays a crucial role against invading microorganisms. However, the mechanism underlying autophagy in *Macrobrachium rosenbergii* remains largely unknown. Here, we demonstrate that *Aeromonas hydrophila* activates autophagy, according to western blot, qRT-PCR, and transmission electron microscopy observations. RNA-seq analysis of *M. rosenbergii* gills treated with rapamycin revealed 1684 upregulated and 1500 downregulated DEGs. A comprehensive joint analysis of the two transcriptomic databases for *A. hydrophila* infection and rapamycin treatment, identified 15 upregulated and 25 downregulated DEGs. Furthermore, ATG5 and Beclin1 in *M. rosenbergii* were identified and characterized, they were widely expressed in all tissues and distributed in the cytoplasm, and were induced after *A. hydrophila* and LPS stimulation. The recombinant proteins could inhibit the growth of several pathogenic bacteria. These results preliminarily revealed the regulation of autophagy and antibacterial infection mechanism in *M. rosenbergii*.

Key words: *Macrobrachium rosenbergii*, Autophagy, ATG, Bacterial infection, Immune defense

基于羟肟酸/紫尿酸铁显色反应和智能手机的牡蛎中弯曲菌现场灵敏比色检测便携生物传感平台

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摘要: 贝类中的弯曲菌污染会一种人类健康高风险, 其可导致弯曲菌病的发生。因此, 需要一种有效的贝类养殖弯曲菌的检测方法。本研究介绍了一种便携式贝类弯曲菌比色生物传感检测平台, 由三个模块组成: 富集模块 1、结合和传导模块 2 以及智能手机模块 3。模块 1 是特异性核酸适配体修饰的 96 孔板, 用于以简便、高通量和特异性地捕获弯曲菌。模块 2 可与被捕获的弯曲菌结合, 并在与 Fe^{3+} -紫尿酸复合物反应后将其转化为放大的颜色信号。模块 1 的捕获效率为 97.24%。加入模块 2 可对弯曲菌进行比色指示, 检测范围为 101 到 106 CFU/mL。利用分选的弯曲菌单细胞, 验证其实际检测限为 8 CFU/mL。模块 3 可以超灵敏识别所产生的颜色并将其转换为细胞密度。利用这种生物传感器-智能手机平台能对实际样品中的弯曲菌进行高通量比色检测, 检测准确率达 80%。本研究示例了一种贝类养殖弯曲菌高效现场检测的生物比色传感平台。

关键词: 弯曲菌; 牡蛎; 比色生物传感; 便携平台; 现场检测

Ultrasensitive on-site colorimetric detection of *Campylobacter* in oyster with a portable biosensing platform based on hydroxamate/ Fe^{3+} -violurate chromogenic reaction and smartphone

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Abstract: The contamination of *Campylobacter* in shellfish poses a health risk for its pathogenicity associated with campylobacteriosis. An efficient method to detect this risk is required. We introduce a portable colorimetric biosensing platform that comprises three modules: an enrichment module 1, a binding and transduction module 2, and a smartphone-based module 3. Module 1 is an aptamer-modified 96-well plate for the specific capture of *Campylobacter* in a simple and high-throughput manner. Module 2 can bind the captured *Campylobacter* cells and transduce them into amplified color signals upon reaction with Fe^{3+} -violurate complexes. The colorimetric biosensing features a detection range of 101 to 106 CFU/mL, and an actual limit of detection of 8 CFU/mL validated by *Campylobacter* single-cells. The generated colors can be recognized and converted into cell densities by module 3 with ultrasensitivity. This biosensor-smartphone platform accomplishes an accuracy of 80%, showcasing a proof of principle for efficient on-site detection of *Campylobacter* contamination regarding shellfish farming.

Key words: *Campylobacter*; Oysters; Colorimetric biosensing; Portable platform; On-site detection

尼罗罗非鱼 LCP1 基因的克隆及其在灭活无乳链球菌免疫刺激后的应答

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摘要: 【目的】LCP1 基因对 T 细胞和 B 细胞的迁移以及 T 细胞的激活发挥核心作用, 在哺乳动物的先天免疫系统中扮演着关键角色, 但在鱼类中的功能尚未被充分阐明。【方法】从尼罗罗非鱼中克隆出了 LCP1 基因, 命名为 OnLcp1, 并对该基因进行生物信息学分析和亚细胞定位分析。采用双荧光素酶报告系统检测了 NF- κ B、STAT1、ISRE、IFN-1 和 IFN-3 等转录因子对 LCP1 基因启动子活性的影响。运用荧光定量 PCR 技术分析了经无乳链球菌刺激后 OnLcp1 在各组织中 mRNA 的表达情况。【结果】结果显示, OnLcp1 包含 1857 个碱基对, 编码一个 618 氨基酸的蛋白质, OnLcp1 蛋白被鉴定含有 EF 臂结构域 (钙结合结构域) 和两个串联的肌动蛋白结合结构域 (ABD), 每个肌动蛋白结合结构域均包含两个钙调蛋白同源 (CH) 结构域。OnLcp1 是一个无跨膜的细胞外蛋白, 与人类 LCP1 蛋白的三维结构高度相似。

关键词: 尼罗罗非鱼; LCP1; 无乳链球菌; mRNA 表达分析

Molecular Cloning of LCP1 in Nile Tilapia (*Oreochromis niloticus*) and immune response against *Streptococcus agalactiae* stimulus

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Abstract: 【Objective】The LCP1 gene plays a crucial role in the migration and activation of T and B cells, as well as in the activation of T cells, and it is a key player in the innate immune system of mammals. However, its function in fish has not been fully elucidated. 【Method】The gene encoding LCP1 from Nile tilapia was successfully cloned and named OnLcp1. Bioinformatics analysis was conducted on this gene, and its subcellular localization was determined. Dual luciferase reporter gene experiment was used to detect the impact of transcription factors such as NF- κ B, STAT1, irse, IL-1 and IL-3 on promoter activity of LCP1 gene. The expression pattern of OnLcp1 mRNA in various tissues after the stimulation of *Streptococcus agalactiae* was studied using fluorescence quantitative PCR method. 【Result】The results showed that OnLcp1 comprised 1857 base pairs and encoded a 618-amino acid protein. The OnLcp1 protein contained EF-hand domains (calcium-binding domains) and two tandem actin-binding domains (actin-binding domains), with each actin domain containing two calmodulin homology (CH) domains. OnLc

Key words: Nile tilapia; LCP1; *Streptococcus agalactiae*; mRNA expression analysis

斜带石斑鱼对哈维氏弧菌攻毒反应中白细胞介素-15受体(IL-15R α) α 链的分子和功能研究

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摘要: 白细胞介素-15 (IL15) 是一种促炎细胞因子, 可以诱导炎症细胞因子的产生。本研究鉴定了斜带石斑鱼的 IL - 15 受体 α 链 (Ec-IL15R α) 作为 IL - 15 的天然调节因子, 并对鱼的免疫应答功能进行了测定和表征。Ec-IL15R α 包含一个 720 bp 的开放阅读框, 编码 239 个氨基酸, 包括 4 个典型的保守半胱氨酸残基和一个高度保守的 sushi 结构域。亚细胞定位研究表明, Ec-IL15R α 位于细胞质和细胞膜中。在 11 个组织中检测到 Ec-IL15R α , 其中肝脏和血液中表达量最高。同时, 在感染哈维氏弧菌后的 9 个组织中, Ec-IL15R α 转录水平显著升高。在 ConA、PHA、LPS 和 poly I:C 刺激下, Ec-IL15R α 在头肾淋巴细胞中显著上调。在体外分析中, rEc-IL15R α 重组蛋白刺激 HKL 增殖和 IL1R、IL6R、IL10 和 IL16 的表达。

关键词: IL15R α ; 哈维氏弧菌; 斜带石斑鱼; 头肾淋巴细胞; 蛋白质功能

Molecular and Functional Characterization of α Chain of Interleukin-15 Receptor (IL-15R α) in Orange-Spotted Grouper (*Epinephelus coioides*) in Response to *Vibrio harveyi* Challenge

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Abstract: Interleukin-15 (IL15) is a proinflammatory cytokine that could induce the production of inflammatory cytokines. In this study, the α chain of the IL15 receptor of *Epinephelus coioides* (Ec-IL15R α), a natural regulator of IL15, was identified, and immune response functions of fish were determined and characterized. Ec-IL15R α contains a 720 bp open reading frame that encodes 239 amino acids, including four typical conserved cysteine residues with a highly conserved sushi domain. Ec-IL15R α is closely related to *Epinephelus lanceolatus* and is the most clustered with teleost. Subcellular localization studies showed that Ec-IL15R α was situated in the cytoplasm and cell membrane. Ec-IL15R α was detected in 11 tissues, with the highest expression in the liver and blood. Meanwhile, the Ec-IL15R α transcriptional levels substantially increased in nine tissues after *Vibrio harveyi* infection. Ec-IL15R α was significantly up-regulated in HKLs by ConA, PHA, LPS and poly I:C stimulation. In vitro analysis, the recombinant protein of rEc-IL15R α stimulates HKL proliferation and IL1R, IL6R, IL10, and IL16 expression.

Key words: IL15R α ; *Vibrio harveyi*; orange-spotted grouper; HKLs; protein function

银鲳对美人鱼发光杆菌的免疫响应及其免疫逃逸机理的初步探究

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摘要：银鲳在高温季节易感染美人鱼发光杆菌（PDD），致高死亡率。本研究从染病银鲳分离出高致病性菌株 YC211109，回归感染实验发现鱼体广泛出血及坏死。转录组测序显示，抗原呈递相关基因下调，吞噬体信号通路显著富集。分离的银鲳单核-巨噬细胞具马蹄形细胞核及呼吸爆发特征，高吞噬能力。透射电镜显示 PDD 在细胞膜形成孔道并破坏溶酶体膜，推测其通过分泌毒力因子破坏膜结构。基因组测序显示其含四种溶血素，HlyA 为成孔毒素。构建的 HlyA-PDD 和 EGFP+PDD 突变株感染巨噬细胞后共定位显示溶酶体数量减少且菌与溶酶体信号分离，而 HlyA-延缓该现象，故 HlyA 可能帮助细菌逃逸至胞质。MHC 与 GILT 负责抗原呈递，且感染后两类基因表达模式具相反趋势。利用 shRNA-GILT-对鱼体干扰,表明其协助 PDD 逃逸溶酶体。综合来看，本研究揭示了银鲳对 PDD 的免疫响应及其免疫逃逸机制。

关键词：银鲳 美人鱼发光杆菌 免疫逃逸

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

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Abstract : During the high-temperature season, silver pomfret (*Pampus argenteus*) is highly susceptible to infection by *Photobacterium damsela* subsp. *Damsela* (PDD), resulting in elevated mortality rates. In this study, a highly pathogenic strain, YC211109, was isolated from diseased silver pomfret. Regression infection experiments revealed widespread hemorrhage and necrosis in the fish. Transcriptome sequencing indicated downregulation of antigen presentation-related genes and significant enrichment of the phagosome signaling pathway. Isolated monocyte-macrophages from silver pomfret exhibited horseshoe-shaped nuclei, respiratory burst activity, and high phagocytic capacity. Transmission electron microscopy showed that PDD forms pores in the cell membrane and disrupts the lysosomal membrane, suggesting that the bacterium secretes virulence factors to damage membrane structures. Genome sequencing revealed the presence of four hemolysins, with HlyA identified as a pore-forming toxin. Co-localization studies using HlyA-PDD and EGFP+PDD mutant strains in macrophage infection showed a reduction in

Key words:: *Pampus argenteus* *Photobacterium damsela* subsp. *Damsela* Immune Evasion

纳米材料介导的海洋弧菌的可视化核酸 检测和毒力基因沉默

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摘要：海洋弧菌导致的水产生物病害造成重大经济损失，引起了相关领域研究者的广泛关注。目前水产病害也缺乏绿色、高效的防控方法。以鳎弧菌引起的大菱鲆白鳍病为对象，本研究合成和利用核酸胶体金材料对鳎弧菌的 LAMP 扩增产物实现了快速、特异的可视化检测。进一步地，利用纳米材料递送反义寡核苷酸进入鳎弧菌，实现了对鳎弧菌金属蛋白酶毒力基因的高效沉默，并应用于大菱鲆的白鳍病有效防控。本研究借助交叉学科研究方法，为水产病害的检测和防控提供了新思路。

关键词：纳米材料 核酸 鳎弧菌 基因沉默

Nanomaterials-mediated naked-eye detection and target gene silencing of *Vibrio marinopraesens*

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Abstract: The aquatic biological diseases caused by *Vibrio marinopraesens* have caused significant economic losses, which have attracted extensive attention from researchers in related fields. At present, there is also a lack of green and efficient prevention and control methods for aquatic diseases. In this study, the LAMP amplification products of *Vibrio eel* caused by *Vibrio eel* were synthesized and detected by nucleic acid colloidal gold materials to achieve rapid and specific visual detection. Furthermore, nanomaterials were used to deliver antisense oligonucleotides into *Vibrio eel*, which achieved efficient silencing of the *vil* gene of *Vibrio eel* metalloproteinase, and was applied to the effective prevention and control of white fin disease in turbot. With the help of interdisciplinary research methods, this study provides new ideas for the detection, prevention and control of aquatic diseases.

Key words: Nanomaterials, nucleic acid, *Vibrio marinopraesens*, gene silencing

银鲳感染鮳鱼诺卡氏菌不同感染阶段的免疫策略

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摘要：银鲳是东海重要的经济鱼类，细菌病严重限制了银鲳人工养殖的规模化。其中，常见的细菌为诺卡氏菌，是一种广泛分布的机会性病原体，能够导致病程延长及高死亡率。在本研究中，我们分析了银鲳在不同感染阶段（对照、感染 5 天和 15 天）的肝、脾和肾脏组织。通过 HE 染色观察到肉芽肿结节的形成，并发现肾结节中有大量凋亡细胞。感染后，肝脏和肾脏的 AKP、ACP 和 LZM 水平明显升高，而 LPS 则下降。通过转录组富集到 PI3K-Akt 和 p53 等通路。关键差异表达基因的研究表明，与生物合成和代谢相关的基因上调，而与免疫反应和凋亡相关的基因下调。我们还建立了银鲳脾细胞系，确认了诺卡氏菌的最佳侵入阈值。JC-1 实验显示膜电位在感染后逐渐下降。同时选取了重要的差异表达基因补体 C1，通过干扰及过表达初步验证了其在诺卡氏菌感染中的功能。总的来看，本研究揭示了银鲳感染诺卡氏菌后复杂的免疫反应机制，为控制该病原体提供了潜在的研究方向。

关键词：银鲳、诺卡氏菌、免疫策略、补体

Immune strategies of silver pomfret (*Pampus argenteus*) infected with *Nocardia seriolae* at different infection stages

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Abstract: Silver pomfret (*Pampus argenteus*) is an important economic fish species in the East China Sea, but bacterial diseases severely limit its aquaculture. A common pathogen is *Nocardia seriolae*, an opportunistic bacterium that can prolong illness and increase mortality rates. In this study, we analyzed the liver, spleen, and kidney tissues of silver pomfret at different infection stages. Histological examination revealed granulomatous nodules and numerous apoptotic cells. After infection, levels of alkaline phosphatase (AKP), acid phosphatase (ACP), and lysozyme (LZM) significantly increased in the liver and kidney, while lipopolysaccharide (LPS) levels decreased. Transcriptomic analysis highlighted enriched pathways such as PI3K-Akt and p53. Research on key differentially expressed genes (DEGs) showed upregulation of biosynthesis and metabolism-related genes, while immune response and apoptosis-related genes were downregulated. We also established a silver pomfret spleen cell line to confirm the optimal invasion threshold for *Nocardia*. JC-1 assays demonstrated a gradual decline in membra

Key words:: Silver pomfret ; *Nocardia seriolae*; Immune strategies ; Complement

白细胞介素-34 作为肠道屏障功能的正调节因子减轻团头鲂的细菌性肠炎

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摘要: 白细胞介素-34 是调节哺乳动物肠道功能的重要细胞因子, 其在鱼类肠道疾病中的潜在作用正在探索中。本研究通过观察团头鲂 IL-34 (MaIL-34) 对肠道屏障功能的影响, 探讨其在细菌性肠炎中的作用。MaIL-34 与其他硬骨鱼 IL-34 具有相似的结构和进化特征, 并参与了对团头鲂嗜水气单胞菌感染的肠道免疫应答。体内实验表明, 重组 MaIL-34 (rMaIL-34) 蛋白可显著减轻嗜水气单胞菌引起的肠道损伤。其机制可能是通过抑制 Notch 信号通路, 促进杯状细胞增殖和黏蛋白表达, 从而维持黏膜层的完整性。同时, rMaIL-34 降低了嗜水气单胞菌诱导的肠道通透性, 维持了肠道紧密连接的完整性。此外, rMaIL-34 通过抑制肠道氧化应激-凋亡-炎症级联反应增强了团头鲂对细菌感染的抵抗力。在微生物学水平上, rMaIL-34 改善了肠道菌群分布, 并增强了肠道微生物群在能量代谢、抗生素生物合成和氧化磷酸化方面的功能。

关键词: 黏膜屏障; 杯状细胞; 紧密连接; 肠道菌群; 氧化应激; 细胞凋亡; 炎症

Interleukin-34 as a positive regulator of intestinal barrier function for alleviating bacterial enteritis in *Megalobrama amblycephala*

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Abstract : *Megalobrama amblycephala* IL-34 (MaIL-34) exhibited conserved structural and evolutionary features with teleosts IL-34 and was involved in the intestinal immune response to *Aeromonas hydrophila* infection. In vivo experiments revealed that recombinant MaIL-34 (rMaIL-34) protein significantly mitigated intestinal damage caused by *A. hydrophila*. This mitigating effect may be due to that rMaIL-34 maintains the integrity of mucosal layer by inhibiting the Notch signaling, promoting goblet cell proliferation and mucins expression. Meanwhile, rMaIL-34 reduced *A. hydrophila* induced intestinal permeability and maintained the integrity of intestinal tight junctions. Furthermore, rMaIL-34 enhanced the resistance of *M. amblycephala* to bacterial infection by inhibiting the intestinal oxidative stress-apoptosis-inflammation cascade. On the microbiological level, rMaIL-34 improved the distribution of intestinal microbiota, and enhanced intestinal microbiota functionality in energy metabolism, antibiotic biosynthesis, and oxidative phosphorylation.

Key words:: Mucosal barrier; Goblet cell; Tight junction; Intestinal microbiota; Oxidative stress; Apoptosis; Inflammation

刺激隐核虫表面抗原对大黄鱼免疫保护效果探究

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摘要：刺激隐核虫大规模爆发导致的大黄鱼“海水白点病”给养殖户们造成了巨大的经济损失，目前尚无安全有效的治疗方法。寄生虫表面抗原是虫体主要的免疫显性抗原，在入侵宿主过程中发挥了重要作用，可能是免疫预防的主要靶点之一。本研究初步评价了刺激隐核虫两个表面抗原（CI-521 和 CI-522）的原核重组蛋白对大黄鱼在刺激隐核虫攻毒后的免疫保护效果。免疫荧光实验结果表明，两种抗原主要分布在刺激隐核虫幼虫表面。经密码子优化后表达获得的原核重组蛋白经验证具有良好的免疫原性。腹腔注射免疫大黄鱼，使用 42000 虫/鱼剂量攻毒后，96 h 内的相对保护率分别为 88.90%（CI-521）和 47.6%（CI-522）。荧光定量 PCR 测定免疫后不同时间点大黄鱼肝脏、脾脏、体肾和头肾组织内免疫相关基因表达量发现，免疫注射重组表面抗原后可显著增加鱼体内免疫相关基因的表达量。

关键词：刺激隐核虫，免疫预防，表面抗原

Surface antigens of *Cryptocaryon irritans* is a promising vaccine of "white spot" disease

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Abstract : This study preliminarily evaluated the immunoprophylaxis effect of prokaryotic recombinant proteins stimulating two surface antigens of *Cryptocaryon irritans* (CI-521 and CI-522) on the large yellow fish following parasite attack. The results of immunofluorescence demonstrated that the two antigens were predominantly distributed and localized on the surface of *Cryptocaryon irritans*. The prokaryotic recombinant proteins obtained through codon optimization and expression were verified to possess good immunogenicity. The relative protection rates within 96 h after intraperitoneal injection immunization of recombinant proteins, using a dose of 42,000 theronts/fish for tapping, were 88.90% (CI-521) and 47.6% (CI-522), respectively. The qPCR to determine the changes in the expression of immune-related genes in liver, spleen, somatic kidney, and head kidney tissues of fish at different time points after immunization revealed that recombinant surface antigen post-immunization significantly increased the expression of immune-related genes in the fish.

Key words:: *Cryptocaryon irritans*, immunoprophylaxis, surface antigen

西北印度洋中尺度涡对鸢乌贼时空分布的影响

付迎悦

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摘要: 鸢乌贼(*Sthenoteuthis oualaniensis*)是具有重要经济价值的头足类之一,在西北印度洋海域蕴藏有丰富的资源量,该海域受季风的影响中尺度涡分布广泛,但对栖息于该海域鸢乌贼的影响尚不清晰。本研究基于角动量涡旋检测与追踪算法获得的涡旋追踪数据集匹配渔业数据,统计了西北印度洋中尺度涡的时空分布,分析了不同类型涡旋和鸢乌贼资源丰度和分布的关系,并结合广义加性模型解析了中尺度涡基本特征量与鸢乌贼资源分布之间的关联。结果表明,西北印度洋中尺度涡发生的高频海域在北部区域,且存在明显的月间和年际变化。振幅、相对涡度大的中尺度涡内更容易聚集高的鸢乌贼资源丰度。

且这种差异于涡旋内部区域更加明显。研究表明,西北印度洋中尺度涡会影响鸢乌贼的资源分布,需要进一步结合

环境因子探究其影响机制。

关键词: 中尺度涡; 鸢乌贼; 资源丰度和分布; 西北印度洋

Impacts of mesoscale eddies on the spatial and temporal distribution of *Sthenoteuthis oualaniensis* in the Northwest Indian Ocean

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Abstract: *Sthenoteuthis oualaniensis*, a cephalopod species with significant economic value, is widely distributed and abundant in the Northwestern Indian Ocean. This region is characterized by rich and active mesoscale eddies influenced by various factors such as monsoons. Currently, the impacts of mesoscale eddies on *S. oualaniensis* in the Northwestern Indian Ocean are still unknown. Therefore, this study utilized data derived from the angular momentum eddy detection and tracking algorithm (AMEDA) for eddy detection and tracking and matched the eddies with fisheries data. The spatiotemporal distribution of mesoscale eddies in the Northwestern Indian Ocean was examined, and the relationships between different types of eddies and the abundance and distribution of *S. oualaniensis* were evaluated. Moreover, this study applied the generalized additive model (GAM) to assess the association between the fundamental characteristics of mesoscale eddies and the abundance and distribution of *S. oualaniensis*. The results revealed that high-frequency occurrences of mesoscale eddies were observed in

Key words: mesoscale eddy; *Sthenoteuthis oualaniensis*; abundance and distribution; Northwest Indian Ocean

基于 NODE-GAM 模型和 XGBoost 模型的太平洋大眼金枪鱼渔场预报

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摘要： 本文根据 8 艘中国超低温延绳钓渔船 2018-2021 年在太平洋的作业数据，结合海水温度、海表面盐度、叶绿素 a 浓度等同期海洋环境数据，构建广义可加性神经遗忘决策集成模型（NODE-GAM）和 XGBoost 模型，以对比分析两模型对太平洋大眼金枪鱼渔场的预测效果。结果表明：NODE-GAM 模型的 MSE 为 0.0850，RMSE 为 0.292。XGBoost 模型的 MSE 为 0.221，RMSE 为 0.470。相比之下，NODE-GAM 模型在预测精度和稳定性方面表现更优。NODE-GAM 模型和 XGBoost 模型预测的渔场位置与捕捞位置都基本重合，主要集中在赤道两侧，10°N-10°S 之间的海域。此外，XGBoost 模型在预测渔场丰度时表现较差。

关键词： 太平洋；大眼金枪鱼；NODE-GAM；XGBoost 模型；环境因子；时空分布

Pacific bigeye tuna fishery forecasting based on NODE-GAM and XGBoost models

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Abstract: This paper, based on the operational data of eight Chinese ultra-low-temperature longline fishing vessels in the Pacific Ocean from 2018-2021, combined with the seawater temperature, sea-surface salinity, chlorophyll a concentration, and other marine environmental data for the same period, we constructed the generalized additivity neural oblivious decision-integration model (NODE-GAM) and the XGBoost model, to comparatively analyze the prediction effect of the two models on the Pacific bigeye tuna fishing ground. The results show that the NODE-GAM model has an MSE of 0.0850, an RMSE of 0.292, while the XGBoost model has an MSE of 0.221, an RMSE of 0.470. Compared with the XGBoost model, the NODE-GAM model performs better in prediction accuracy and stability. The NODE-GAM and the XGBoost models predicted fishery locations that largely overlapped with fishing locations, mainly concentrated on both sides of the equator, between 10°N and 10°S. In addition, the XGBoost model performed poorly in predicting fishery abundance.

Key words: Pacific Ocean; bigeye tuna; NODE-GAM; XGBoost model; environmental factors; spatial and temporal distribution

中西太平洋围网渔业兼捕渔获物组成 分布研究

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摘要：金枪鱼围网渔业在带来大量金枪鱼渔获物的同时，也因其较低的选择性直接导致了大量的兼捕发生。本研究根据中西太平洋围网渔业的渔业数据和兼捕数据，对兼捕渔获物的时空分布、物种间兼捕率差异、与金枪鱼的联系等进行分析，为评估与保护兼捕鱼种资源提供一定的参考和理论依据。

关键词：金枪鱼围网渔业；渔获物组成；兼捕；资源养护；

Research on the Composition and Distribution of Bycatch in Purse Seine Fishery in the Central and Western Pacific Ocean

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Abstract: While the tuna Seine fishery brings in a large number of tuna catches, it also directly leads to a large number of bycatch because of its low selectivity. Based on the fishery data and bycatch data of Seine fisheries in the Central and Western Pacific Ocean, this study analyzed the temporal and spatial distribution of bycatch, the difference of bycatch rate among species, and the relationship with tuna, etc., in order to provide a certain reference and theoretical basis for the evaluation and protection of bycatch resources.

Key words: Tuna Seine fishery; Composition of the catch; Bycatch; Resource conservation;

基于 Iot 的秋刀鱼渔捞数据收集研究

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摘要：渔捞日志等相关记录是渔业生产过程中重要的数据记录，可用于鱼类生境研究、种群评估和渔业管理。为了更准确地收集捕捞日志等数据，本研究以太平洋秋刀鱼渔业为例，开发了基于物联网技术的相关捕捞可追溯系统，并使用二维码测试和收集了渔获包装信息。结果表明：物联网系统可以提高渔业数据采集的可靠性和准确性；IoT 系统数据可改进 CPUE 估算，在当前无法获取每一网次产量的情况下，使用每天产量估算 CPUE 优于使用每天平均网次产量估算。

关键词：物联网；渔捞日志；CPUE；

Data collection for fishing logbook by using Traceability System

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Abstract： Fishing logbook and other related records are important data records in the process of fishery production, which can be used in the study of fish habitat, stock assessment and fishery management. To collect fishing logbooks and other data more accurately, this study takes the Pacific saury fishery as a case study, develops a relevant catch traceability system based on IoT technology, and uses QR code to test and collect some IoT packed catch information. A Better data collection for fishing logbook was analyzed by combining VMS data and SST data. The results indicate that: IoT systems can improve the reliability and accuracy of fishing data collection.

Key words:： Iot System; Fishing logbook;CPUE

基于耳石微化学技术的秋刀鱼生活史特征的初步研究

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摘要: 秋刀鱼(*Coloabis saira*)是一种冷水性洄游鱼类,广泛分布于北太平洋海域,是我国重要的远洋作业鱼种,目前对于秋刀鱼生活史过程中的洄游模式的探究尚不明确。本文基于在西北太平洋公海采集的秋刀鱼样本,分析了秋刀鱼样本生活史过程中耳石 Sr/Ca 值、Ba/Ca 值的变化特征。研究表明:(1)性别对耳石核心区 Sr/Ca 值差异无显著影响($P>0.05$),耳石核心区对应的 Ba/Ca 值与其他所有点位对应的 Ba/Ca 值也均没有显著性差异($P>0.05$)。(2)通过建立线性回归方程,耳石 Sr/Ca 值与海表面温度梯度呈负相关关系。由此推断,海表面温度梯度的升高,引起饵料丰富聚集,Ca 含量的升高,进而导致秋刀鱼样本耳石中 Sr/Ca 值的降低。以期为今后北太平洋秋刀鱼栖息地变动规律、洄游模式等方面的研究提供参考。

关键词: 秋刀鱼、耳石、Sr/Ca、Ba/Ca、生活史

A preliminary study on life history characteristics of Pacific saury based on otolith microchemistry

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Abstract: Pacific saury is a cold water migration fish, widely distributed in the north Pacific Ocean, which is an important ocean-going fish in China. At present, the migration pattern of saury during its life history is not clear. In this paper, we analyzed the variation characteristics of otolith Sr/Ca and Ba/Ca during the life history of saury samples collected in the open sea of Northwest Pacific Ocean. The results showed as follows: (1) Gender had no significant effect on Sr/Ca in the otolith core region ($P>0.05$), and Ba/Ca corresponding to the otolith core region were not significantly different from those corresponding to other sites ($P>0.05$). (2) By establishment the linear regression equation, the Sr/Ca of otolith is negatively correlated with sea surface temperature gradient. It is inferred that the increase of sea surface temperature gradient leads to the accumulation of bait and the increase of Ca content, which leads to the decrease of Sr/Ca in the otolith of saury samples. In order to provide a reference for the study of habitat change and migration pattern of saury.

Key words: Pacific saury, otolith, Sr/Ca, Ba/Ca, life history

基于几何形态测量的西北太平洋日本鲭的 个体生长规律

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摘要: 为探究西北太平洋海域日本鲭的个体生长规律, 利用基于地标点的几何形态测量方法对2021—2022年“淞航”号调查船在西北太平洋海域采集的210尾日本鲭样本进行形态学分析。与其他方法相比, 利用地标点方法能够有效揭示鱼体表型多样性, 反映不同阶段鱼体的变化情况, 揭示其个体生长规律。结果发现不同叉长组的日本鲭的外部形态存在显著差异。主成分分析和多元回归分析均显示, 叉长组越小的个体, 其分区越明显, 3个叉长组间的分区位置存在重叠, 不同叉长组具有相同的生长模式, 日本鲭形态生长速率随叉长的增加而逐渐减小。薄板样条变形网格结果表明, 叉长越小的日本鲭个体, 其腹部, 尾部越小, 日本鲭的外部形态随着叉长的改变而发生变化。结论认为, 西北太平洋日本鲭生长形态随着叉长的增加而逐渐发生改变。

关键词: 几何形态测量;西北太平洋;日本鲭;生长规律;

Growth regularity of *Scomber japonicus* based on geometric morphometrics in Northwest Pacific Ocean

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Abstract: In order to explore the growth regularity of *Scomber japonicus* in Northwest Pacific Ocean, 210 samples collected by the "Songhang" from 2021 to 2022 used landmarks based on geometric morphometrics. Compared with other methods, the use of landmark methods can effectively reveal the phenotypic diversity of fish, reflect the changes in fish at different stages, and explore their individual growth regularity. The results showed that there were significant differences in the external morphology of *S. japonicus* across different fork length groups. Both principal component analysis and multivariate analysis of covariance showed that *S. japonicus* with smaller fork length had more distinct zones, with overlapping zones among the three different fork length groups. Different fork length groups had the same growth regularities. The growth rate of *S. japonicus* gradually decreased with increasing fork length. The thin-plate spline indicates that the smaller the fork length of *S. japonicus*, the smaller their abdomen and tail. The morphology of *S. japonicus* changes with the change of fork length.

Key words: geometric morphometrics; Northwest Pacific Ocean; *Scomber japonicus*; growth regularity

未来气候情境下中国东海鲈鱼栖息地的时空分布

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摘要: 为探究未来气候变化下东海鲈鱼 (*Scomber japonicus*) 适宜栖息地的分布规律, 本文基于 CMIP6 气候模式输出的 2.5 m (Temp_2.5 m)、25 m (Temp_25 m) 和 50 m (Temp_50 m) 水温数据来探究 3 种未来气候情境下 (SSP126、SSP370 和 SSP585) 东海鲈鱼栖息地的时空变化。结果表明: 2015-2100 年东海鲈鱼渔场 HSI 和适宜栖息地面积比例在 SSP126、SSP370 和 SSP585 情境下整体呈显著下降趋势, 而不适宜栖息地面积呈显著上升趋势。不同气候变化情境下, 东海鲈鱼适宜栖息地在 2015-2020、2055-2060 和 2095-2100 三个时间段内主要分布在 122o~126oE, 28o~30oN 范围内, 不适宜栖息地主要分布在渔场中部; 此外, 鲈鱼适宜栖息地重心有向北移动趋势。研究表明, 未来全球变暖的气候背景不利于形成有利的鲈鱼栖息地。

关键词: 东海鲈鱼; 栖息地; 空间分布; 气候变化; 不同水层温度; 中国东海

Spatio-temporal distribution of habitat patterns of *Scomber japonicus* in East China Sea under future climatic conditions

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Abstract: To investigate the effects of future climate change on habitat pattern of *Scomber japonicus* in the East China Sea, water temperature at depths of 2.5 m (Temp_2.5 m), 25 m (Temp_25 m) and 50 m (Temp_50 m) under SSP126, SSP370 and SSP585 scenarios sourced from the CMIP6 climate model were selected. This study analyzed temporal and spatial habitat changes of *Scomber japonicus* under different climate conditions in the future. The HSI on the fishing ground and proportion of suitable habitat of *Scomber japonicus* in the East China Sea from 2015 to 2100 show a similar downward trend under SSP126, SSP370 and SSP585 scenarios. However, the proportion of unsuitable habitat area of *Scomber japonicus* in the East China Sea from 2015 to 2100 increased under SSP126, SSP370 and SSP585 scenarios. The suitable habitats of *Scomber japonicus* are mainly distributed in the waters of 122o~126oE and 28o~30oN during 2015-2020, 2055-2060 and 2095-2100, while the unsuitable habitat was mainly distributed in the middle of fishing ground.

Key words: *Scomber japonicus*; Habitat pattern; Spatial distribution; Climate change; Water temperature at different layers; East China Sea

不同空间尺度下秋刀鱼 CPUE 标准化研究

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摘要：单位捕捞努力量渔获量(Catch Per Unit Effort, CPUE) 作为相对资源量指标或资源分布密度指数，通常被假设成与资源量成正比关系，CPUE 标准化在渔业资源评估研究中广泛应用。选取不同的时空分辨率会对 CPUE 标准化产生影响，从而影响资源评估。本研究利用太平洋秋刀鱼渔业数据，结合海洋环境数据，基于广义加性模型（GAM）按照不同的空间尺度划分为 9 组数据，分析计算得到最适模型，进行名义 CPUE 的标准化。结果显示：（1）最适 GAM 模型中除了月、经纬度、海表面温度、海表面温度差和叶绿素浓度等 6 个变量外，交互项年和经度、年和纬度、月和经度、经度和纬度对 CPUE 的影响较大。（2）不同的空间尺度最适 GAM 模型对标准化的结果不同，根据五折交叉验证分析，选取均方误差最小的 2° （奇数） $\times 2^{\circ}$ （奇数）为最适空间尺度。

关键词：CPUE 标准化，GAM 模型，空间分辨率

Research on CPUE standardization of saury at different spatial scales

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Abstract： Catch Per Unit Effort (CPUE) is used as a relative indicator of resource abundance or distribution density, typically assumed to be proportional to resource quantity. CPUE standardization is widely applied in fishery resource assessment. This study analyzes Pacific saury fishing data combined with ocean environmental data using Generalized Additive Models (GAM) across nine spatial scales. Results indicate that, in the optimal GAM model, six variables significantly impact CPUE, with notable interactions between year and longitude, year and latitude, month and longitude, and longitude and latitude. Different spatial scales yield varying standardization results, the scale of 2° (odd) $\times 2^{\circ}$ (odd) was identified as the most suitable due to its minimal mean squared error. Consequently, when assessing Pacific mackerel resources, it is crucial to consider the impacts of temporal and spatial factors, such as year, month, and geographical coordinates, on CPUE standardization.

Key words:： CPUE standardization, GAM model, spatial resolution

南海渔业生态系统结构分析

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摘要：南海是中国近海重要的海洋生态系统之一，气候变化和渔业捕捞等因素会影响其结构和功能。此前，有关南海生态系统结构长期动态的研究多聚焦于物种层面，对渔业生态系统整体结构的研究相对较少。因此，本研究根据 Sea Around US 提供的 1950-2019 年南海渔业生态系统渔业产量数据，结合 FishBase 和 SeaLifeBase 提供相关物种的最适温度以及 Sea Around Us Biodiversity 提供的对应物种的营养级进行研究分析，旨在全面了解 70 年间南海渔业生态系统结构的长期变化特征。结果显示，南海渔业产量稳步上升，其中中国的产量占比最高。自 1981 年以来，南海机动渔船数量和功率稳步上升，到 1990 年后逐步稳定；而非机动渔船数量和吨位则急剧下降。跃变分析发现南海渔业生态系统跃变集中发生在 20 世纪 80 年代中期、90 年代中期及 21 世纪 10 年代早期，较好地反映了不同年代的渔业捕捞现状。

关键词：南海；渔业产量；海洋生态系统；长期变化

Analysis of fishery ecosystem structure in the South China Sea

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Abstract : In recent years, there has been increasing evidence that climate change can affect the biodiversity, structure, and function of marine ecosystems, a phenomenon known as marine ecosystem transition. Studies have shown that climate change is likely to increase the frequency of regime shift phenomena, and climate change often interacts with fishing, contributing to these shifts in marine ecosystems. The ecosystem of the South China Sea lies at the intersection of the north-south air flow, with the Pacific Ocean to the east and the Indian Ocean to the west. It is located at the confluence of Walker Circulation patterns influenced by the Indian Ocean and the Pacific Ocean. It is the most complex region in the global climate system and the most sensitive region for large-scale air-sea interaction. At present, most studies on the response of the fishery ecosystem to climate change in the South China Sea focus on the species level, and few studies on the fishery ecosystem.

Key words: : The South China Sea; fishery catch; marine ecosystem; long-term change

西北太平洋秋刀鱼资源丰度变化与 气候—海洋变化的关系

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摘要: 秋刀鱼(*Coloabis saira*)是西北太平洋海域重要经济鱼类, 具有生命周期短、生长速度快、高集群性等特点; 其资源年间波动显著, 且受气候—海洋变化的影响。本研究利用 2000-2023 年的太平洋秋刀鱼渔业数据, 评估了厄尔尼诺-南方涛动 (ENSO)、太平洋年代际振荡 (PDO)、太平洋环流振荡 (NPGO) 等关键气候-海洋指数之间及对资源变动的影响; 采用向量自回归 (VAR) 模型预测秋刀鱼捕捞渔获量。结果表明: (1) PDO 与 El Niño3.4 指数呈现显著相关, 北太平洋环流振荡指数与南方涛动指数 (SOI) 的变化趋势基本相似。(2) VAR 模型显示, 除自身资源量波动外, 太平洋年代际振荡、厄尔尼诺-南方涛动和北太平洋环流振荡对秋刀鱼的资源丰度变化有显著影响。因此, 在预测秋刀鱼资源量时, 应将气候-海洋变化纳入考量。

关键词: 资源丰度, 气候-海洋指数, VAR 模型

The Relationship between the Abundance Changes of Autumn Swordfish Resources in the Northwest Pacific and Climate Ocean Changes

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Abstract: *Coloabis saira* is an important economic fish species in the Pacific Ocean, characterized by a short life cycle and fast growth rate; Its resources fluctuate significantly between years and are influenced by climate ocean changes. This study used Pacific saury fishery data from 2000 to 2023 to evaluate the impact of key climate ocean indices such as El Niño-Southern Oscillation and Pacific decadal oscillation on resource changes; Using vector autoregression (VAR) model to predict the catch of autumn swordfish. The results show that: (1) PDO is significantly correlated with the El Niño index, and the trend of the North Pacific circulation oscillation index is basically similar to that of the Southern Oscillation index. (2) The VAR model shows that, in addition to fluctuations in its own resources, inter decadal oscillations in the Pacific, El Niño-Southern Oscillation, and North Pacific circulation oscillations have a significant impact on changes in the abundance of saury resources. Therefore, when predicting the abundance of saury, climate ocean changes should be taken into account.

Key words: Resource abundance, climate ocean index, VAR model

东海带鱼延绳钓渔场分布特征

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摘要：带鱼延绳钓是获取带鱼资源的重要作业方式之一，其具有生态友好性，捕捞的带鱼深受市场欢迎。本文利用 2023 年浙江玉环延绳钓渔船的生产数据和同期卫星遥感的海洋环境数据，通过 GAM 模型分析了环境因子与单位捕捞努力量渔获量（CPUE）的关系。结果表明：东海带鱼延绳钓作业渔场分布在 26.75°~30.25°N，122.25°~127.25°E；带鱼渔获量与单位捕捞努力量渔获量（CPUE）随着月份的变化都呈现出逐渐降低的趋势；5-6 月渔场重心从温台渔场向北偏东转移，6-7 月渔场重心向东小范围移动，7-8 月渔场重心向西南转移到舟山渔场；月份（Month）、纬度（Latitude）、经度（Longitude）、海表面温度（SST）对 CPUE 存在显著影响（ $P < 0.05$ ）；作业渔场最适 SST 范围为 24°~26°C，最适 Chl-a 范围为 0.1-1 mg/m³。研究结果可为带鱼资源的科学管理和可持续利用提供依据。

关键词：带鱼延绳钓；渔场重心；海洋环境因子；广义可加模型（GAM）；时空分布；

Distribution Characteristics of Longline Fishing Grounds for *Trichiurus japonicus* in the East China Sea

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Abstract: Longline fishing constitutes one of the crucial methods for acquiring *Trichiurus japonicus* resources. It is environmentally friendly, and the *Trichiurus japonicus* caught are highly favored in the market. Based on the production data of longline fishing vessels in Yuhuan, Zhejiang Province in 2023 and the marine environment data of satellite remote sensing during the same period, the relationship between environmental factors and catch per unit fishing effort (CPUE) was analyzed through the GAM model. The findings indicated that longline fishing for *Trichiurus japonicus* in the East China Sea was distributed within 26.75°–30.25°N and 122.25°–127.25°E. The catch of *Trichiurus japonicus* and the catch per unit fishing effort (CPUE) demonstrated a decreasing tendency along with the variation of month. From May to June, the center of gravity shifted from the Wentai fishing ground to the north and east. From June to July, it moved eastward, and from July to August, it shifted to the southwest towards the Zhoushan fishing ground.

Key words: longline fishing for *Trichiurus japonicus*; Center of gravity of fishing ground; Marine environmental factors; Generalized additive model (GAM); Spatiotemporal distribution;

西北太平洋远东拟沙丁鱼的摄食策略和 营养生态位差异：稳定同位素和 脂肪酸分析的见解

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摘要：远东拟沙丁鱼广泛分布于西北太平洋海域，是重要的捕捞对象。为研究在个体发育过程中的食性转变以及生态位的差异，本研究根据 2021 年 6—7 月在西北太平洋公海采集的远东拟沙丁鱼肌肉样本，通过稳定同位素和脂肪酸分析法去研究在不同体长和性别之间稳定同位素值和脂肪酸种类及其含量。结果显示，雌、雄个体的稳定同位素值和脂肪酸组成不存在显著差异 ($P < 0.05$)。不同体长组之间的 $\delta^{15}\text{N}$ 和 $\delta^{13}\text{C}$ 值差异显著 ($P < 0.05$)， $\delta^{13}\text{C}$ 和 $\delta^{15}\text{N}$ 值在不同体长组间表现出先减小后增大的趋势。远东拟沙丁鱼不同体长组的生态位宽度呈先增加后减少的趋势，且不同体长组的生态位重叠都低于 55%。主成分分析 (PCA) 结果显示，远东拟沙丁鱼有 10 种主要脂肪酸，其中除 C18:0、C24:1n-9 和 C18:3n-3 之外其他脂肪酸含量在不同体长组间都存在显著差异 ($P < 0.05$)。

关键词：远东拟沙丁鱼；稳定同位素分析；脂肪酸分析；生态位；食性分化

Feeding Strategies and Trophic Niche Divergence of *Sardinops melanostictus* in the Northwest Pacific: Insights from Stable Isotope and Fatty Acid Analyses

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Abstract: *Sardinops melanostictus* (*S. melanostictus*) is widely distributed in the Northwest Pacific and is an important target for fisheries. To investigate dietary shifts and ecological niche differentiation during individual development, we analyzed muscle samples of *S. melanostictus* collected from the Northwest Pacific open sea between June and July 2021. Stable isotope and fatty acid analyses were employed to examine the differences in stable isotope values, fatty acid composition, and content across various body lengths and sexes. The results showed no significant differences ($P < 0.05$) in stable isotope values and fatty acid composition between male and female individuals. Significant differences in $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values were found among the different body length groups ($P < 0.05$). Both $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values exhibited a trend of initially decreasing and then increasing with body length. The niche width of *S. melanostictus* increased initially and then decreased with body length, with niche overlap among different body length groups remaining below 55%. Principal component analysis (PCA) rev

Key words: *S. melanostictus*; stable isotope analysis; fatty acid analysis; niche; dietary differentiation

打开黑盒模型：热带大西洋海域金枪鱼丰度预测的案例研究

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摘要: 准确预测鱼类丰度对于渔业可持续管理至关重要。本研究聚焦于热带大西洋海域的四种高度洄游鱼类：大眼金枪鱼、长鳍金枪鱼、黄鳍金枪鱼和剑鱼。利用 2016 年至 2019 年的金枪鱼延绳钓渔捞日志数据及各种环境数据集，建立了一个可解释的 LightGBM-SHAP 模型来预测各鱼种 CPUE，并分析关键环境特征对它的影响。通过比较 CPUE 和 SHAP 值的核密度分布，验证了 LightGBM-SHAP 模型的预测准确度较高 ($R^2 > 0.84$)。研究发现：(1) 对大眼金枪鱼影响最大的因素是月份、经度和纬度；(2) 长鳍金枪鱼的主要驱动因素是 ST100、SSH 和 D350；(3) 黄鳍金枪鱼的主导因素是纬度、月份和 D250；(4) 箭鱼的关键因素是纬度、月份和 D450。研究强调了根据环境条件选择适当渔场和调整策略的重要性。

关键词: LightGBM, SHAP, 鱼类丰度, 预测, 热带大西洋海域

Opening the black box model: a case study of tuna fish abundance prediction in the tropical Atlantic Ocean

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Abstract: Accurately predicting fish abundance is crucial for sustainable fisheries management. This study focuses on four highly migratory fish species: bigeye tuna, albacore tuna, yellowfin tuna, and swordfish in the tropical Atlantic Ocean. Utilizing tuna longline logbook data from 2016 to 2019 and various environmental datasets, we established an interpretable LightGBM-SHAP model to predict CPUEs and analyze the impact of key environmental characteristics. The predictive accuracy of LightGBM-SHAP model was high ($R^2 > 0.84$), as validated by comparing kernel density distributions of CPUE and SHAP values. This study found that: (1) the most influential factors were month, longitude, and latitude for bigeye tuna; (2) for albacore tuna, ST100, SSH, and D350 were the primary drivers; (3) latitude, month, and D250 were the dominant factors for yellowfin tuna; (4) latitude, month, and D450 were key factors for swordfish. This study highlights the importance of selecting appropriate fishing grounds and adjusting strategies based on environmental conditions.

Key words: LightGBM, SHAP, Fish Abundance, Prediction, Tropical Atlantic Ocean

热带中西太平洋围网 FSC 和 DFADs 渔获群落多样性分析

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摘要: 中上层鱼类群落在鱼类组合中占主导地位, 并且由于其高丰度、垂直洄游行为和全球分布而构成海洋生态系统的重要组成部分。围网渔业是热带中西太平洋(Western and Central Pacific Ocean, WCPO)海洋渔业的一个关键组成部分, 主要目标品种是鲣鱼(*Katsuwonus pelamis*)、黄鳍金枪鱼(*Thunnus albacares*)和大眼金枪鱼(*Thunnus obesus*)。本研究利用 2014—2022 年 WCPO 围网渔业数据并结合环境因子数据, 采用 Mantel 检验和相关性分析等分析方法分析了围网自由游泳集群(Free-swimming school, FSC)和漂流人工集鱼装置(Drifting fish aggregating devices, DFADs)两种不同捕捞策略下的渔获群落的多样性、鱼类共存机制及环境响应。

关键词: 围网; 渔获群落; FSC; DFADs; Mantel 检验; 共存机制

Catch community diversity analysis of purse seine in the tropical Western and Central Pacific Ocean

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Abstract: Epipelagic fish communities dominate fish assemblages and are an important part of marine ecosystems due to their high abundance, vertical migration behavior, and global distribution. Purse seine fisheries are key components of marine fisheries in the tropical Western and Central Pacific Ocean (WCPO), primarily targeting skipjack tuna (*Katsuwonus pelamis*, SKJ), yellowfin tuna (*Thunnus albacares*, YFT), and bigeye tuna (*Thunnus obesus*, BET). In this study, WCPO purse seine fishery data from 2014 to 2022, combined with environmental factor data, were used, and Mantel tests and correlation analysis were employed to analyze the diversity, fish coexistence mechanisms, and environmental responses of catch communities under the following two different fishing strategies: free-swimming school (FSC) and drifting fish aggregating device (DFAD). Mantel tests indicated that nitrate (NO_3^-), the Oceanic Niño Index (ONI), and pH significantly impact the diversity of the FSC community, whereas NO_3^- significantly affects the diversity of the DFAD community.

Key words: purse seine; catch communities; FSC; DFAD; Mantel test; coexistence mechanisms

淀粉基可降解渔具材料的制备与应用研究

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摘要：以可降解捕捞渔具来应对我国渔业面临的白色污染及幽灵捕捞问题长期以来备受关注，然而，可降解材料的高成本及力学性能不足成为制约其应用的关键因素。针对以上问题，本文通过接枝共聚、微交联以及界面相容性改性等制备了改性淀粉基可降解渔网材料，显著提升了淀粉基渔网材料的力学性能；系统研究材料在不同时间和温度条件下的降解行为，建立了可降解渔网材料降解行为的时间-温度等效原理，并基于层状填料聚集态结构调控优化了降解过程的可控性。与传统的不可降解渔网相比，淀粉基可降解渔网装配的蟹笼在促进蟹类逃逸方面具有显著优势，可有效降低幽灵捕捞发生率。

关键词：淀粉，可降解渔网，降解行为，逃逸行为

Preparation and application of starch-based degradable fishing gear

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Abstract: The development and use of degradable fishing gear have long been prioritized as a means to address the persistent issues of white pollution and ghost fishing. Despite this focus, the high costs and limited mechanical strength of degradable materials have posed significant barriers to their widespread adoption. In response to these challenges, a modified starch-based egradable fishing net material was prepared through techniques such as grafting copolymerization, micro-crosslinking, and interface compatibility modification, which collectively result in significant improvements in its mechanical properties. Furthermore, the time-temperature equivalence principle for the degradation behavior of these materials was also established, providing a theoretical framework for understanding their long-term performance. By adjusting the aggregation structure of layered fillers, the controllability of the degradation process was optimized. A comparative analysis with traditional non-degradable fishing nets revealed that starch-based degradable nets facilitated crab escape.

Key words:: Starch, degradable fishing net, degradation behavior, escape behavior

时空尺度对不同联合物种分布模型的影响： 以西北太平洋中上层渔业种类为例

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摘要：为了综合评估时空尺度对联合分布模型的影响，对比了 32 种时空组合形式下 4 个联合物种分布模型的性能。结果表明，时空尺度对联合物种分布模型性能具有明显的影响，且模型之间具有一定的差异。研究显示，时间尺度越长，空间尺度越精细，模型的模拟和预测性能更好，稳定性越强；空间尺度对种间关系的评估影响较大，空间尺度越精细，正种间关系强度减弱，负种间关系增强；模型中 HMSC 表现出较好的中和性能，而 Boral 模型的稳定性最差。整体而言，最优的联合物种分布模型为 HMSC，对应的最优时空尺度为年和 0.25° 。

关键词：时空尺度；联合物种分布模型；种间关系；中上层渔业种类

The Impact of Spatio-Temporal Scales on Different Joint Species Distribution Models: A Case Study of mesopelagic Fish in Northwest Pacific

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Abstract : To comprehensively assess the impact of spatio-temporal scales on joint distribution models, this study compared the performance of four joint species distribution models across 32 different spatio-temporal combinations. The results indicated that spatio-temporal scales significantly influence the performance of joint species distribution models, with notable differences observed between the models. The study revealed that longer temporal scales and finer spatial scales enhance the simulation and prediction performance of the models, as well as their stability. Furthermore, spatial scale has a substantial impact on the assessment of interspecies relationships; as the spatial scale becomes finer, the strength of positive interspecies relationships decreases while negative interspecies relationships strengthen. Among the models, HMSC demonstrated better equilibrating performance, while the Boral model exhibited the poorest stability. Overall, the optimal joint species distribution model was identified as HMSC, with the optimal spatio-temporal scales being annually and 0.25° .

Key words:: Spatio-temporal scale, Joint species distribution model, Interspecies relationship, Mesopelagic fish

西南大西洋阿根廷滑柔鱼栖息地与 中尺度涡的关系分析

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摘要：本研究探讨了阿根廷滑柔鱼 (*Illex argentinus*) 在气旋和反气旋涡旋中的分布模式，分析了海表面温度 (SST)、200 米深度的温度 (T200m) 和叶绿素 a (Chl-a) 等环境因素对其资源量的影响，并评估了涡旋内阿根廷滑柔鱼的栖息地适宜性指数 (HSI) 的分析结果显示，气旋涡旋中的资源丰度明显高于反气旋涡旋，且 HSI 的高值区域与滑柔鱼资源的高值区域相重叠，表明涡旋的类型及其内部环境条件对滑柔鱼的资源分布和栖息地选择具有显著影响，气旋涡内低温、高营养盐的环境条件更有利于该物种资源的生长和维持。

关键词：中尺度涡；阿根廷滑柔鱼；栖息地模型；

Analysis of the Relationship between the Habitat of *Illex argentinus* with Mesoscale eddies in the Southwest Atlantic

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Abstract: This study explored the distribution patterns of *Illex argentinus* in eddies, analyzed the impact of environmental factors such as sea surface temperature (SST), 200m water temperature (T200m), and chlorophyll a (Chl-a) on its abundance, and evaluated the habitat suitability index (HSI) of *Illex argentinus* in eddies. The results indicated that the abundance in cyclonic eddies was higher than that in anticyclonic eddies, and the areas of high HSI overlapped with the areas of high resources, suggesting that the type of eddies and their internal environmental conditions had significant impact on the resource distribution and habitat selection of *Illex argentinus*.

Key words: Ocean mesoscale eddies; *Illex argentinus*; Habitat suitability index model

两种鱿鱼的跨太平洋栖息地模式的年代际变化

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摘要: 利用栖息地适宜性指数 (HSI) 模型研究了 1950-2015 年间西北太平洋柔鱼和东南太平洋茎柔鱼栖息地的变化。模型基于两个影响鱿鱼出现的环境因子: 海面温度 (SST) 和海面高度异常 (SSHA)。观察到这两种鱿鱼的栖息地变化具有明显的跷跷板模式, 与太平洋十年涛动 (PDO) 的正负相位变化一致。两种鱿鱼在 PDO 负相位阶段, 柔鱼渔场的 SST 异常和 SSHA 增加。由于适宜的 SST 和 SSHA 的减少, 柔鱼的适宜栖息地面积明显缩小。与此相反, 在 PDO 负相位阶段, 茎柔鱼渔场的 SST 下降和 SSHA 减少导致更多的适宜生境形成。形成了更多适宜的 SST 和 SSHA, 从而使茎柔鱼的适宜栖息地扩大。此外, 在 PDO 负相位阶段, 对柔鱼和茎柔鱼最有利的 SST 向北移动, 这两种鱿鱼的适宜栖息地也向北移动。当 PDO 为暖相位时, 两种鱿鱼的变化与负相位相反。

关键词: 西北太平洋柔鱼; 茎柔鱼; 太平洋年代际涛动; 年代际变化; 栖息地适宜性指数; 太平洋

Trans-Pacific multidecadal changes of habitat patterns of two squid species

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Abstract: The HSI model involved two environmental variables: sea surface temperature (SST) and sea surface height anomaly (SSHA). Significant seesaw-like patterns of environmental variability and habitat changes, consistent with the regime shift of positive and negative Pacific Decadal Oscillation (PDO), were observed for the two squid species. In a negative PDO phase, SST anomaly and SSHA increased on the fishing grounds of *O. bartramii*. The areas of suitable habitat of *O. bartramii* contracted markedly due to the decrease in suitable SST and SSHA. In contrast, cooling SST and decreasing SSHA on the fishing grounds of *D. gigas* during a negative PDO phase led to the formation of more suitable SST and SSHA, yielding expansive suitable habitats for *D. gigas*. Moreover, the most favorable SST for *O. bartramii* and *D. gigas* moved northward in the negative PDO regime, and the suitable habitat for both squids shifted into the northern regions as well. When the climate regime shifted into a positive PDO phase, the responses of the two squids were opposite to those in the negative PDO phase.

Key words: Neon flying squid; Jumbo flying squid; Pacific decadal oscillation; Multidecadal change; Habitat suitability index; Pacific Ocean

南极磷虾桁杆拖网作业参数调节对网具性能的影响

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摘要：南极磷虾具有集群分布不规则和昼夜垂直移动等特点，数天至数周的连续泵吸捕捞需要根据探鱼仪映像调节网位至南极磷虾群密度中心分布水层，以实现瞄准捕捞。本研究基于水槽模型试验，开展不同拖速、曳纲长度和下纲单边重锤重量等作业参数对渔具性能的影响规律研究。GAM 结果表明，拖速、曳纲长度和下纲单边重锤重量 3 个作业参数均对拖网网位变化具有显著影响($P < 0.05$)；网位与拖速呈现负相关，与曳纲长度和重锤重量呈正相关。曳纲长度对网具阻力、网口高度和能耗系数的影响不显著($P > 0.05$)；拖速和下纲单边重锤重量 2 个作业参数对网具阻力、网口高度和能耗系数均具有显著影响($P < 0.05$)，网具阻力与拖速和下纲单边重锤重量呈正相关；网口高度与拖速呈负相关，与下纲单边重锤重量呈正相关；能耗系数与拖速呈正相关，与下纲单边重锤重量呈负相关。研究结果揭示了作业参数对网具性能的影响规律，为南极磷虾渔业生产实践提供科学指导。

关键词：模型试验，桁杆拖网，连续捕捞，网位

Fishing parameters impact on the performance of Antarctic krill beam trawl

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Abstract: Antarctic krill (*Euphausia superba*) has irregular swarm distribution and diurnal vertical movement characteristics. The beam trawl must regulate the net position to the high-density layer of the krill swarms during continuous fishing. This study explored the impact of towing speed, warp length, and groundline weights on the performance of a beam trawl used in Antarctic krill fisheries. The results showed that these three factors significantly impact net position, negatively correlated with towing speed, and positively correlated with the warp length and weights. Two factors, towing speed and groundline weights, significantly impact resistance, net opening, and energy consumption coefficient. The research results reveal the influence of operational parameters on the performance of beam trawl, which can provide valuable guidance for improving the efficiency of krill fishing operations.

Key words: Model test; Beam trawl; Continuous fishing; Net position.

Nordmøre 装置的栅条间距和姿态对拖网网囊稳定性的影响

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摘要： Nordmøre 栅栏是一种广泛用于虾拖网渔业中减少副渔获物的栅型兼捕减少装置。其栅条间距和姿态的改变不仅影响网囊结构水动力，对网囊系统的稳定性也会产生一定影响。本研究通过动水槽模型试验，探究了栅条间距（15mm、25mm、35mm、45mm）和倾角（30°、45°、60°）对网囊系统阻力和形态的影响变化，结果表明：（1）网囊阻力随着栅栏倾角和流速的增大而增大，但随栅条间距的增大而减小。当栅栏倾角为 60°时，网囊的平均阻力较倾角为 30°和 45°时分别增大了 60%和 20%。（2）随着栅栏倾角的增大，网囊轮廓形态扩张效果显著，网囊垂直方向的中心点位置偏低；随着流速增大，网囊整体形态呈收缩趋势。（3）测试中发现，网囊阻力呈一定程度波动规律，随流速增大，网囊阻力振荡效果越显著；当栅栏倾角为 30°时，网囊阻力振荡效果最为显著，栅栏倾角为 45°时，网囊阻力振荡效果较弱。

关键词： 栅型兼捕减少装置；栅条间距；倾角；阻力；稳定性

The impact of bar spacing and orientation of Nordmøre devices on the stability of the trawl cod-end

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Abstract： The results showed that: (1) The drag of the cod-end increases with the increase of the grid's inclination angle and flow velocity, but decreases with the increase of bar spacing. When the grid inclination angle is 60°, the average drag of the cod-end is increased by 60% compared to when the angle is 30° and by 20% compared to when the angle is 45°. (2) As the inclination angle of the grid increases, the expansion effect on the contour morphology of the cod-end becomes significant, with the vertical center point of the cod-end positioned lower; as the flow velocity increases, the overall shape of the cod-end tends to contract. (3) Experimental observations reveals that the drag of the cod-end exhibits a certain degree of fluctuation, becoming more pronounced with increasing flow velocity; when the grid inclination angle is 30°, the drag oscillation effect is the most significant, When the inclination is 45°, the drag oscillation effect of the cod-end is weaker; the average amplitude of the drag oscillation at 30° inclination angle is increased by 30% compared to that at 45° angle.

Key words:： sorting grid; bar spacing; inclination angle; drag; stability

基于结构方程模型的淡水补充对马达加斯加西海岸印度白虾 CPUE 的影响

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摘要: 探索渔业资源与环境因子的关系, 掌握种群分布对环境变化的响应机制, 是实现渔业可持续发展的基础。然渔业资源的变化受多个环境因素的综合影响, 这些因素之间存在复杂且相关的关系。目前的研究主要集中于环境因子对种群分布和资源丰度等直接影响, 而忽视了环境因素之间的相互作用。本研究选取 2014—2019 年马达加斯加西海岸印度白虾(*Fenneropenaeus indicus*)为研究对象, 采用结构方程模型对印度白虾 CPUE 与降水、径流、SST、SSHA 和 Chl-a 之间的关系进行了分析。结果表明: 径流、SST、SSHA 和 Chl-a 对 CPUE 有直接影响, 其中径流、SST 和 Chl-a 与 CPUE 呈显著正相关, SSHA 与 CPUE 呈显著负相关; 降水通过影响 SST 和 SSHA, 间接影响 CPUE; 径流通过影响 SSHA 进而影响 CPUE。研究结果揭示了马达加斯加西海岸环境因子通过直接或间接影响印度白虾种群资源变动的潜在机制。

关键词: 印度白虾; CPUE; SEM; 淡水补充; 环境因子

Effects of freshwater replenishment on the *Fenneropenaeus indicus* CPUE the west coast of Madagascar based on structural equation modeling

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Abstract: Understanding the relationship between fisheries resources and environmental factors is essential for sustainable fisheries development. Variations in resources are influenced by complex, interrelated factors, yet current research often overlooks their interactions. This study explores how environmental factors and their interrelationships affect *Fenneropenaeus indicus* stocks off Madagascar's west coast. Using a structural equation model (SEM), data from 2014-2019 were analyzed to assess relationships between *F. indicus* CPUE (Catch Per Unit Effort) and variables like precipitation, runoff, SST, SSHA, and Chl-a. The model showed that runoff, SST, SSHA, and Chl-a directly impacted CPUE, with runoff, SST, and Chl-a correlating positively, and SSHA negatively. Precipitation indirectly influenced CPUE via SST and SSHA, while runoff impacted CPUE through SSHA. These findings highlight mechanisms by which freshwater inputs and marine factors affect *F. indicus* variability on Madagascar's west coast.

Key words: *Fenneropenaeus indicus*; Catch Per Unit Effort (CPUE); structural equation model (SEM); freshwater replenishment; environmental factors

西北太平洋渔业物种的生活史策略研究

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摘要：生活史特征及其变化是海洋渔业和海洋生态系统研究的重要内容，对基本生活史信息的了解被认为是渔业管理和保护的基本标准。本文从已发表的文献中收集了西北太平洋海域渔业生物的生活史特征(即繁殖和生长动态)。根据生活史策略的理论分类，对一百多种生物的生活史特征进行了分类。PC1即体型和生长因子，受最大长度、最大年龄、性成熟长度和生长系数的影响最大，得分为正的物种代表体型大、生长慢、寿命长、体型成熟大的物种。生殖因子PC2受繁殖力和成熟卵径的影响最大，表现为繁殖力低、卵大。研究结果提供了管理选择的概念框架，可用于对典型种群反应进行分类，为渔业的可持续发展提供科学依据。

关键词：渔业管理；生活史特征；西北太平洋

Study on life history strategies of fishery species in the northwest Pacific

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Abstract: The characteristics and changes of life history are important content in the study of marine fisheries and marine ecosystems, and the understanding of basic life history information is considered a basic standard for fisheries management and protection. A suite of life history traits (i.e. reproduction and growth vital statistics) of fishery species in the Northwest Pacific Ocean were collected from reliable published literatures. The life history traits of more than 100 species were grouped according to the theoretical classifications of life history strategies. The PC1, namely size and growth factor, was most influenced by the maximum length, maximum age, length at sexual maturity and growth coefficient, with positive scores representing species that are large, slow growing, long-lived and mature at large size. The PC2, namely reproductive factor, was most influenced by the fecundity and matured egg diameter, representing low fecundity and large eggs. The research results provide a conceptual framework of management options, they can be used to classify typical population responses

Key words:: fisheries management; life history trait; the northwest Pacific

拖网网囊结构振荡特性对网囊长度的响应变化

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摘要: 网囊位于拖网渔具系统的末端, 网囊长度决定着拖网结构的稳定特性, 进而影响网囊的选择性。为了分析网囊长度对中层拖网网囊结构水动力特性的影响, 本研究制作了长度为 1.0m、1.5m 和 2.0m 网囊模型 (网囊 C1、C2 和 C3), 测试其在不同流速和渔获物条件下的阻力和形态。结果显示: (1) 无渔获物时, 随着流速的增大, 网囊 C1、C2 和 C3 长度分别增加了 8.10%、7.07% 和 4.88%; 存在渔获物时, 网囊通道狭窄, 末端膨大, 网囊长度增加。(2) 网囊结构水阻力随网囊长度的增加而增加, 空网囊时 C3 为 C1 的 1.09 倍; 存在渔获物时 C3 为 C1 的 1.04 倍。(3) 空网囊的阻力振幅在低流速时随网囊长度的增加而减少, 但在高流速时情况相反; 网囊中有渔获物时, 网囊的阻力振幅随网囊长度的增加而增加。(4) 网囊纵向位置振荡周期受网囊长度变化的影响较小, 但其振幅受影响较大; 随着网囊长度的增加, 网囊横向位置振荡周期缩短, 振幅增大。

关键词: 拖网; 网囊长度; 阻力; 形态; 振荡特性

Variation of the oscillatory characteristics of the trawl codend structure in response to the length of the codend

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Abstract: To investigate the impact of codend length on the hydrodynamic characteristics of codend structures in mid-water trawling, this study evaluates the resistance and morphology of codend models under varying flow velocities and fish catch conditions. The findings reveal that: (1) In absence of fish catch, The length of the codend increases with the increase of the flow rate; when fish are present, a constricted codend channel leads to an enlarged end section; (2) Hydrodynamic resistance escalates with increasing codend length; (3) For empty codends at low flow speeds, resistance amplitude diminishes as codend length increases but conversely rises at high flow speeds; when containing fish catches within them this amplitude consistently increases alongside longer codend; (4) The longitudinal position oscillation period of the codend is less influenced by the variation of the codend length, but its amplitude is significantly affected by the codend. With the increase in the length of the codend, the oscillation period of the lateral position of the codend shortens and the amplitude increases.

Key words: Trawl; Length of codend; Drag; shape; Oscillation characteristics

基于 RF-SHAP 方法的中西太平洋围网鲣资源变动与环境因子关系研究

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摘要：本文建立了一个可解释的基于机器学习的分析框架，整合随机森林和 SHapley 加法规划来解释三种气候模式下鲣 CPUE 与环境因子的全局效应和交互效应，得出：（1）厄尔尼诺、拉尼娜、正常年份的预测结果 R2 分别为 0.67、0.52、0.51，拟合优度结果较好；（2）在全局效应结果下，对厄尔尼诺年份影响较大前五的环境因子为 Lon、chl、sla、s105、u105，拉尼娜年为 sst、chl、Lon、sla、u105，正常年为 Lon、s105、sst、sla、Lat；（3）在交互效应下，厄尔尼诺年 Lon 与 chl 和 sla 交互效应较强，拉尼娜年 sst 与 chl 和 Lon 交互效应较强。

关键词：鲣鱼；环境因子；机器学习；随机森林；SHAP

Study on the relationship between resource changes and environmental factors in the western and central Pacific purse seine bonito based on RF-SHAP methodology

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Abstract： In this paper, an interpretable machine learning-based analytical framework integrating random forests and SHapley additive planning is developed to explain the global and interactive effects of bonito CPUE with environmental factors under three climate models, which yields (1) the prediction results of El Niño, La Niña, and normal years have R2 of 0.67, 0.52, and 0.51, respectively, with better goodness-of-fit results, and (2) under the global effect results, the top five environmental factors with large effects on El Niño years are Lon, chl, sla, s105, u105, La Niña years are sst, chl, Lon, sla, u105, and normal years are Lon, s105, sst, sla, and Lat; (3) under the interaction effect, El Niño year Lon interacts with chl and sla were stronger, and La Niña years sst had stronger interaction effects with chl and Lon.

Key words:: Skipjack tuna; Environmental factors; Machine learning; Random forest; SHAP

漂流人工集鱼装置影响下的随附金枪鱼类分布建模

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摘要：漂流人工集鱼装置（Drifting Fish Aggregating Devices, DFADs）能够吸引金枪鱼类聚集为随附群，在金枪鱼围网渔业中广泛应用。大规模使用 DFADs 导致金枪鱼的行为习性发生变化，对环境的变化更加敏感。本研究将中西太平洋海域 DFADs 回声探测数据与海洋环境因子结合，采用机器学习模型对 DFADs 随附金枪鱼类的时空分布进行建模，并研究了 DFADs 轨迹特征与海洋环境特征等对鱼群随附行为的影响。结果表明，（1）采用机器学习模型对回声探测数据建模基本可以准确揭示 DFADs 影响下的金枪鱼类集群分布；（2）DFADs 轨迹的弯曲度、漂流距离和漂流速度等对鱼群随附行为的影响显著；（3）海洋环境因子如初级生产力、叶绿素 a 浓度和溶解氧浓度对随附鱼群生物量的影响较大。

关键词：漂流人工集鱼装置；机器学习模型；轨迹特征；海洋环境因子

Modeling the Distribution of Associated Tuna Species Under the Influence of Artificial Drift Fish Aggregating Devices

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Abstract: Drifting Fish Aggregating Devices (DFADs) are capable of attracting tuna species to form associated schools, and are widely used in tuna purse seine fisheries. The large-scale use of DFADs has led to changes in the behavioral habits of tuna, making them more sensitive to environmental changes. This study combines echo detection data from DFADs in the Western and Central Pacific Ocean with oceanic environmental factors, and employs machine learning models to model the spatio-temporal distribution of tuna species associated with DFADs. Additionally, the study investigates the impact of DFADs' trajectory characteristics and oceanic environmental characteristics on the fish aggregation behavior. The results indicate that: (1) Modeling echo detection data using machine learning models can generally accurately reveal the distribution of tuna aggregations influenced by DFADs; (2) The curvature, drift distance, and drift speed of DFADs' trajectories have significant effects on the aggregation behavior of fish; (3) Oceanic environmental factors such as primary productivity, chlorophyll-a conc

Key words: Drifting Fish Aggregating Devices (DFADs); Machine Learning Model; Trajectory Characteristics; Oceanic Environmental Factors

海豚声波驱赶对罩网捕捞的影响研究

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摘要: 灯光罩网是南海外海的一种主要捕捞方式, 夜晚作业时点斑原海豚(*Stenella attenuata*)常常聚集在渔船周围进行捕食活动, 导致被网具兼捕死亡。基于前期研发的宽带声波驱豚系统 (acoustic deterrent system, ADS), 本研究在渔船上开展了多年度的海上应用测试, 以确定了驱豚系统的有效性以及对捕捞的影响。3 个年度共驱赶了 90 晚次海豚, 成功驱赶 72 次, 成功率为 80%。对于海豚被驱赶的夜晚, 渔船平均 CPUE 为 4.96 ± 3.06 kg/min; 与海豚未出现的夜晚 CPUE 之间无显著性差异 (5.04 ± 4.44 kg/min)。海豚出现但未被驱赶的夜晚, 平均 CPUE 为 3.78 ± 3.10 kg/min, 显著低于海豚未出现的夜晚。GAM 模型表明, 月份、经度、流向、纬度、风向, 海豚数量及风速是影响渔船产量的几个关键因素。

关键词: 热带点斑原海豚; 海豚声波驱赶; CPUE; GAM

Field tests of an acoustic deterrent to reduce pantropical spotted dolphin bycatch in a light-falling net fishery

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Abstract: A field test was conducted to determine the effect of an acoustic deterrent system (ADS) on dolphins and fish catch aboard a commercial fishing vessel in the South China Sea. For successful deterrence (when dolphins were repelled by the acoustic signal), mean nightly CPUE (4.96 ± 3.06 kg/min) did not differ significantly from the mean CPUE on nights during which no dolphins appeared (5.04 ± 4.44 kg/min). For nights when dolphins were not successfully deterred (when the acoustic signal failed to repel them), mean CPUE (3.78 ± 3.10 kg/min) differed significantly from nights on which no dolphins were observed. General additive model results indicate that month, longitude, flow direction, latitude, wind direction, dolphin number, and wind speed affect fish catch. Overall, our ADS did not affect fish catch. The ADS may be improved by manually controlling pulse frequency, transmission interval, and type to deter different dolphin species and improve efficiency.

Key words: Pantropical spotted dolphin; *Stenella attenuata*; acoustic deterrent; catch per unit effort (CPUE); generalized additive model (GAM)

渤海湾海域中国毛虾资源开发状态

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摘要: 本研究基于 2021-2023 年渤海湾张网调查所获得的中国毛虾 (*Acetes Chinensis*) 体长、体质量数据, 研究了毛虾生长参数、死亡系数和单位补充渔获量(yield per recruitment, YPR), 为中国毛虾的管理提供科学指导和理论依据。中国毛虾体长体质量关系和生长方程的拟合结果表明: 其条件因子 a 估计值为 4.5×10^{-3} , 其异速生长系数 b 的估计值为 1.25。其渐近体长 L_{∞} 的估计均值为 57.63 cm, 生长速率 K 的均值为 0.25/年。通过 Pauly 经验公式求得中国毛虾的自然死亡系数(M)为 0.50。体长转换的渔获曲线求得总死亡系数为 1.01, 进而求得现阶段的捕捞死亡系数(F)为 0.50, 开发率为 0.49。

关键词: 中国毛虾; 单位补充量模型; 体长频率分析; 个体生物学特征; 渤海湾

Development status of *Acetes* Chinese resources in Bohai Bay

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Abstract: Based on the data of body length and body weight of *Acetes Chinensis* obtained from the survey of stow net in Bohai Bay from 2021 to 2023, this study studied the growth parameters, mortality coefficient and yield per recruitment (YPR) of *Acetes Chinensis*, and provided scientific guidance and theoretical basis for the management of *Acetes Chinensis*. The fitting results of body length-weight relationship and growth equation of *A.chinensis* showed that the estimated value of condition factor a was 4.5×10^{-3} , and the estimated value of allometric growth coefficient b was 1.25. The estimated mean value of the asymptotic body length L_{∞} is 57.63 cm, and the mean value of the growth rate K is 0.25 / year. The natural mortality coefficient (M) of *A.chinensis* was calculated to be 0.50 by Pauly 's empirical formula. The total mortality coefficient was 1.01, and the current fishing mortality coefficient (F) was 0.50, and the development rate was 0.49. The fishing mortality (F) was 0.26, 0.75 and 0.42 month⁻¹, respectively, and the optimum initial length (L_c) was 28.06, 30.25 and 25.9,

Key words: *Acetes* Chinese ;yield per-recruit model,; body length frequency analysis ; individual biological characteristics ; Bohai Bay

不同规格罩网沉降性能的影响因素分析

李杰

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摘要: 灯光罩网是南海外海鸢乌贼 (*Symplectoteuthis oualaniensis*) 等资源开发的主要渔具, 为促进外海罩网渔业的健康发展, 有必要研究不同规格罩网网具的沉降性能。该研究通过广义可加模型 (Generalized additive model, GAM) 对不同规格 (3 种主尺度、7 组网口纲每米配重) 罩网沉降深度的影响因素进行分析, 结果发现: (1) 沉降深度的最优 GAM 模型包括网衣纵向拉直高度、网口纲每米配重、放网时间、表层流速、风速, 且均对沉降深度影响显著; (2) 网衣纵向拉直高度的增大对沉降深度产生正面影响; (3) 随网口纲每米配重的增大, 沉降深度呈递增趋势; (4) 随放网时间的增大, 沉降深度先显著增大, 再略有变小, 后显著增大; (5) 随表层流速的增大, 沉降深度呈递减趋势; (6) 随风速增大, 沉降深度先略微降低, 后维持不变, 再显著升高。研究将为罩网生产作业与网具优化改进提供技术支持。

关键词: 罩网; 沉降深度; 不同网具规格; 影响因素; GAM

Analysis of influencing factors on settlement performance of different specifications falling-nets

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Abstract: This study collected data of the settlement depth and operating parameters, environmental parameters of different specifications falling-net through measurement at sea. Based on the Generalized Additive Model, the influencing factors of settlement depth of different specifications falling-net were analyzed. The results showed that: (1) The optimal GAM model for settlement depth (D) included the longitudinal straight height of the netting (H), the weight per meter of the opening rope (W), the shooting time (T), the surface flow speed (VF), and the wind speed (VW), all these factors had a significant impact on D ; (2) The increase in H had a positive impact on D ; (3) With the increase of W , D showed an increasing trend; (4) As T increased, D first significantly increased, then slightly decreased, and then significantly increased; (5) As VF increased, D showed a decreasing trend; (6) As VW increased, D first slightly decreased, then remained unchanged, and then significantly increased. The research will provide technical support for the production operation and the optimization of falling-net gear.

Key words: falling-net; settlement depth; different gear specifications; influencing factors; GAM

南海北部张网方形和菱形混合网目网囊的选择性研究

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摘要: 为探索南海北部张网方形和菱形混合网目网囊的不同网目尺寸对主要渔获的网目选择性, 使用套网法开展了 4 种不同网目尺寸 (25mm、30mm、35mm 和 40mm) 的方形和菱形混合网目网囊的选择性对比试验, 根据相对重要性指数 (IRI), 确定风鲚作为选择性研究的指标种。使用 Logistic 模型拟合不同网目尺寸下风鲚的选择性曲线, 采用极大似然法估算模型参数。结果显示, 网囊网目尺寸为 25mm、30mm、35mm 和 40mm 时, 风鲚的 50% 选择体长 $L_{0.5}$ 分别为 108.48mm、109.02mm、114.36mm 和 115.94mm, 选择范围 SR 分别为 39.37mm、84.99mm、75.26mm 和 38.73mm; 风鲚的 $L_{0.5}$ 随着网目尺寸的增大而增大, 而 SR 逐渐减小; 根据该 $L_{0.5}$ 和网目大小得出最小网目尺寸为 47.03mm; 方形和菱形混合网目网囊没有显著提高风鲚的释放率, 表明该网囊并不适用于南海北部张网渔业。

关键词: 南海; 张网; 最小网目尺寸; 选择性; 套网法

Selective Study of combined square and diamond mesh codend of stow net in the Northern part of South China Sea

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Abstract: In order to evaluate the mesh selectivity of combined square and diamond mesh codend for the main catches of stow net, comparative experiments were conducted using the covered net method with four different mesh sizes. The selectivity of combined square and diamond mesh was evaluated, and the target species, *Coilia mystus*, was determined as the indicator species for the selectivity study based on the Importance Index (IRI). Logistic models were employed to fit the selectivity curves of *C. mystus* under different mesh sizes, and model parameters were estimated using maximum likelihood estimation. The results showed that the 50% selection length $L_{0.5}$ of *C. mystus* increased with increasing mesh size, while SR gradually decreased. Based on this $L_{0.5}$ and mesh size relationship, the minimum mesh size for *C. mystus* was determined to be 47.03mm. The combined square and diamond mesh did not significantly improve the release rate for *C. mystus*, and it indicated that the combined square and diamond mesh is not suitable for the stow net in the northern South China Sea.

Key words: stow net; combined square and diamond mesh codend; codend; selectivity performance

黄鳍鲷趋光行为对光照特征的响应

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摘要：为探究光照特征（光谱频率、光照强度和光照时间）对黄鳍鲷（*Sparus latus*）趋光行为的影响，本研究以黄鳍鲷幼苗为实验对象，共设置全光谱白光（400-800nm）、蓝光（450-470nm）、红光（645-665nm）和绿光（530-550nm）4种颜色的LED光，实验分析了黄鳍鲷在各种光照特征下的趋光分布情况。结果表明：（1）黄鳍鲷幼苗对4种光谱频率表现出不同程度的趋光性，趋光反应由强到弱依次为：蓝光、白光、红光、绿光。（2）鱼群趋光率在白光下与光照强度呈正相关，在红光与绿光下呈负相关，蓝光下无明显反应。光照强度对黄鳍鲷幼鱼的诱集效果有显著的影响（ $P < 0.05$ ）。（3）在任一光谱频率下，当黑暗环境转变为光照环境时，鱼群会出现远离光源的应激反应，随着光照时间的延长，其趋光率无明显变化，即光照时间对黄鳍鲷幼鱼的趋光率影响不显著（ $P > 0.05$ ）。

关键词：黄鳍鲷，趋光行为，光照频率，光照强度

Phototropic behaviour of Yellowfin Seabream in response to light characteristics

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Abstract： To investigate the effects of light characteristics (specifically spectral frequency, light intensity, and light duration) on the phototropic behavior of yellowfin seabream (*Sparus latus*), this study was conducted with yellowfin hatchlings. Four types of full-spectrum light were used: white light (400-800 nm), blue light (450-470 nm), red light (645-665 nm), and green light (530-550 nm). Using LED lighting, the experiment analyzed the phototropic distribution of yellowfin seabream under these varying light conditions. The results indicated that: (1) Yellowfin seabream fry exhibited varying degrees of phototropism in response to the four spectral frequencies, with the phototropic responses ranked from strongest to weakest as follows: blue light, white light, red light, and green light; (2) Light intensity significantly affected the phototropic behavior of yellowfin seabream fry ($P < 0.05$); (3) When transitioning from a dark to a light environment, fish exhibited a stress response by moving away from the light source.

Key words:： *Sparus latus*, phototropic behaviour, light frequency, light intensity

基于贝叶斯最大熵的中西太平洋鲣资源预测

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摘要： 鲣是中西太平洋围网渔业主要目标鱼种。由于大洋环境的复杂性，其资源丰度在时空上呈现多样化的变化形式。深入了解鲣资源时空演变格局及其环境因子对于科学研究和生产需求具有重要意义。为此，本文开展鲣的时空变化预测，并探讨环境因子对其影响的机制。贝叶斯最大熵是地统计学的一种，该方法有坚实灵活的理论基础，无需数据满足空间平稳及正态分布的假设，可充分利用不确定信息，且预测结果包括无偏、最优、非线性的预测值和时空随机变量完整、非高斯形态的概率密度函数。贝叶斯与鲣的融合，可以在数据不完整的情况下提升数据预测精度，充分发挥数据的最大价值。

关键词： 鲣；贝叶斯最大熵；环境因子；时空

Prediction of skipjack resources in the Western and Central Pacific based on Bayesian maximum entropy

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Abstract: Skipjack tuna is the main target species of purse seine fishery in the central and western Pacific Ocean. Due to the complexity of the ocean environment, its resource abundance shows a variety of changes in time and space. In-depth understanding of the spatial and temporal evolution pattern of skipjack resources and its environmental factors is of great significance for scientific research and production needs. Therefore, this paper carried out the prediction of spatio-temporal changes of skipjack tuna and discussed the mechanism of the influence of environmental factors on it. Bayesian maximum entropy is a kind of geostatistics. This method has a solid and flexible theoretical basis. It does not need the assumption that the data satisfies the spatial stationary and normal distribution. It can make full use of uncertain information, and the prediction results include unbiased, optimal, and non-linear prediction values and spatial-temporal random variables. Complete, non-Gaussian probability density function. The fusion of Bayesian and skipjack can improve the accuracy of data predict

Key words:: Skjpack; Bayesain Maximum Entropy; Environment factors; Space-time

内衬网比例和重锤重量对南极磷虾桁杆拖网水动力性能的影响

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摘要: 合理的内衬网比例对于实现南极磷虾的可持续捕捞具有重要意义。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 1/15 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(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) 当流速增加,桁杆拖网模型网网口高度降低,网具整体收缩,阻力增大且振荡越剧烈。
(2) 当内衬网比例减少,模型网阻力和能耗系数呈下降趋势,阻力振幅减小,而网口高度无明显变化;相同条件下,当内衬网比例减少 20%,拖网阻力降低 21%,能耗系数减少 11.5%。
(3) 重锤重量的增加与拖网阻力和能耗系数呈正相关,但与网口高度和阻力振幅呈负相关。
(4) 当内衬网比例为 80%,重锤重量为 2 kg,流速为 0.3m/s 时,网口垂直扩张最佳,拖网阻力小且稳定性高。

关键词: 南极磷虾; 桁杆拖网; 内衬网; 重锤; 水动力

The effects of liner ratio and sinker weight on the hydrodynamic performance of Antarctic krill beam trawl

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Abstract: A 1/15 scale model of the net was constructed based on a modified Tanoue criterion, and experiments were conducted in a circulating flume to investigate the effects of liner net proportion and sinker weights on the overall shape, drag, energy consumption coefficient, and stability of the beam trawl model. The results indicate that: (1) As the flow velocity increased, the height of the trawl net opening decreased, the overall net structure contracted, drag increased, and oscillation became more severe. (2) A reduction in liner net proportion resulted in a downward trend in both the model's drag and energy consumption coefficient, with a reduction in drag amplitude, while the net opening height remained largely unchanged. (3) The increase in sinker weight was positively correlated with trawl drag and energy consumption coefficient, but negatively correlated with the net opening height and drag amplitude. (4) When the liner net proportion was 80%, sinker weight was 2 kg, the vertical expansion of the net opening was optimal, drag was minimized, and stability was high.

Key words: Antarctic krill; beam trawl; liner net; sinker weight; hydrodynamic

Super shoot TED 对模拟渔获物入网轨迹的 导向试验研究

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摘要： Super shoot TED 是一种用于拖网渔业中的海龟释放装置（Turtle Excluder Device, TED），其在减少海龟误捕方面效果显著，但对渔获物入网运动轨迹的影响尚不明确。本研究通过动水槽试验，分析了不同释放姿态和栅栏间距条件下，Super shoot TED 对模拟渔获物入网轨迹的影响。实验将网囊区域划分为缓冲区、装置区和收集区，测量各区域内渔获物运动速度的变化。结果显示：（1）上部、中部、下部释放的渔获物轨迹均呈现先加速后减速的趋势，尤其是上部释放的轨迹波动较大，进入收集区后趋于一致。（2）未安装 TED 时，渔获物速度相对稳定；安装 TED 后，各区域速度出现显著差异。（3）来流速度为 0.8m/s 时，缓冲区速度约为 0.7m/s，装置区为 0.6m/s，收集区速度上升至 0.7m/s。本研究为 Super shoot TED 的优化设计及渔具选择性改进提供了科学依据。

关键词： Super shoot TED；动水槽试验；渔获物；轨迹；安装倾角

Experimental Study on the Guiding Effect of the Super shoot TED on the Trajectory of Simulated Catch Entering the Net

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Abstract: The Super shoot TED is a Turtle Excluder Device (TED) used in trawl fisheries, effective in reducing sea turtle bycatch, but its influence on fish entry trajectories remains unclear. This study analyzed how different release positions and bar spacings of the Super shoot TED affect simulated fish movement using flume tank experiments. The net was divided into three zones: buffer, device, and collection, with fish movement speeds measured in each. Results indicated: (1) Fish released from upper, middle, and lower positions initially accelerated, then decelerated, with upper releases showing more trajectory fluctuations before stabilizing in the collection zone. (2) Without TED installation, fish speeds remained stable, but with TED installed, speed differences across zones were significant. (3) At a flow rate of 0.8 m/s, the average speed in the buffer zone was 0.7 m/s, device zone 0.6 m/s, and collection zone 0.7 m/s. These findings provide a scientific basis for optimizing the Super shoot TED's design and improving gear selectivity.

Key words:: Super shoot TED; Flume tank experiment; Catch; Trajectory; Installation tilt angle

舟山普陀区蚂蚁岛多锚张纲张网渔具渔法 调查分析

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摘要：本文对舟山市普陀区蚂蚁岛多锚张纲张网的渔具结构、装配技术、经济效益、存在问题等进行调查，得出以下结论：（1）多锚张纲张网是近两年新兴的捕捞作业方式，该渔具在传统多锚单片张网基础上进行结构改良，采用浮沉子替代桁杆实现网口垂直扩张，通过多个铁锚固定网衣的水平方向，每片网衣安装4个网囊，依靠潮流冲击迫使捕捞对象进网，达到捕捞目的，故属于多锚张纲张网。（2）该网具作业方式具有操作简便、渔获鲜度高、离岸近等特点，一般3~5天返回一次，使渔民兼顾经济效益和家庭生活，属于家庭和睦型作业方式。（3）该网具主要利用水流迫使捕捞对象进入网内，对海底环境不会造成影响，属于环境友好型渔具。（4）该网具作业过程中存在对大型经济鱼类幼鱼兼捕问题，可能对渔业资源可持续利用造成一定影响，因此建议将网囊网目尺寸增大至35mm，以减少大型经济鱼类的幼鱼兼捕，促进渔业可持续发展。

关键词：渔具渔法；多锚张纲张网；普陀区蚂蚁岛；家庭友好型；最适网目尺寸

Investigation and analysis of fishing gear and method of multi-anchor canvas stow net on Ant Island, Putuo District, Zhoushan

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Abstract : This study investigates the structure of fishing gear, assembly technology, economic benefits, problems of the multi-anchor canvas stow net on Ant Island, Putuo District, Zhoushan .The following conclusions were drawn; (1) multi-anchor canvas stow net which was structurally improved on the basis of the traditional multi-anchor single piece stow net .This fishing gear adopts the floating sinker instead of the beam to realize vertical expansion of the net opening. Multiple iron anchors are used to secure the horizontal position of the fishing gear, with each panel containing four cod-ends. (2) This method is characterized by its simplicity, high freshness of the catch, and proximity to shore. (3) A problem identified with this fishing method is the incidental capture of juvenile large economic fish species, which may affect the sustainable utilization of fishery resources. It is recommended to increase the mesh size of the cod-end to 35mm to reduce bycatch of juvenile large fish and promot the sustainable development of fisheries.

Key words:: Fishing gear and methods;Multi-anchor canvas stow net;Ant island, Putuo district; Family friendly;Optimum mesh size

水文环境塑造了南极布兰斯菲尔德海峡冰鱼 (*Chionodraco rastrospinosus*) 的遗传种群 结构：线粒体 CO I 和 ND2 基因提供的证据

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摘要：眼斑雪冰鱼 (*Chionodraco rastrospinosus*) 是南极地区数量最为丰富的鱼类之一，在南大洋的生态系统中扮演着连接初级生产者与高级捕食者的关键角色，对维持南极地区生态平衡起着重要的作用。了解眼斑雪冰鱼种群的遗传结构和分化情况有助于对其资源进行合理的管理。本研究利用线粒体 CO I 和 ND2 基因序列，对布兰斯菲尔德海峡的三个眼斑雪冰鱼群体 (BS1/BS2/BS3) 共 133 个样本进行遗传多样性和种群遗传结构分析。综上所述，布兰斯菲尔德海峡内眼斑雪冰鱼遗传多样性丰富，已经分化成两个明显的地理种群，建议看作两个独立的渔业管理单元分别进行管理，并优先保护 BS3 群体，加强对其种群资源和遗传多样性的监测，长期追踪变化，适时制定科学合理的保护和管理措施以保证其资源的可持续性发展。

关键词：布兰斯菲尔德海峡；眼斑雪冰鱼；种群遗传结构；遗传多样性；CO I；ND2

Hydrography shapes the genetic population structure of ocellated icefish (*Chionodraco rastrospinosus*) in the Bransfield Strait, Antarctic: Evidence from mitochondrial CO I and ND2 genes

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Abstract: The ocellated icefish, *Chionodraco rastrospinosus*, is among the most abundant fishes in the Antarctic region. This species contributes significantly to the Southern Ocean ecosystem by linking primary producers with higher-level predators, but is vulnerable to the climate change due to the limited geographic distribution. The population structure of this species remains unknown due to the limited data collection and the indistinguishable morphology of species from genus *Chionodraco*, which hampers the conservation of this vulnerable species. We analyzed the mitochondrial CO I and ND2 sequences of 133 *C. rastrospinosus* specimens from three areas (BS1, BS2, and BS3) in the Bransfield Strait (BS), which influenced by different water masses, to assess genetic diversity and population structure. Our study found that *C. rastrospinosus* in the BS exhibited high genetic diversity and diverged into two distinct geographic populations, and the hydrography is the key driver that shapes this population structure of *C. rastrospinosus* in the BS.

Key words: Bransfield Strait, *Chionodraco rastrospinosus*, genetic diversity, population structure, CO I, ND2

旅顺塔河湾海域浮游动物群落结构及 优势种生态位分化研究

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摘要: 浮游动物是海洋生态系统中重要的饵料生物, 其群落结构和分布反映了水域的生产力。为研究旅顺塔河湾海域浮游动物群落结构及影响生态位分化的环境因子, 于 2021 年 9 月、2022 年 3 月、4 月和 11 月对塔河湾海域进行了调查。结果表明, 浮游动物共 4 门 31 种, 年平均密度为 $12.42 \times 10^3 \text{ ind/m}^3$, 以桡足类为主 (13 种, 占 41.94%), 浮游动物丰富度指数为 0.83~2.44, 多样性指数为 0.84~2.42, 均匀度指数为 0.14~0.84。浮游动物丰度和物种多样性与水温、盐度、溶解氧、 $\text{NH}_3\text{-N}$ 和 $\text{NO}_3\text{-N}$ 等环境因子的皮尔逊相关性显著。优势种有 13 种, 主要由广生态位物种组成, 其中 *Oithona similis* 四季均为优势种; 优势种的生态位重叠程度与季节有关, 生态位严重重叠比例夏季最高, 冬季最低; 冗余分析表明, 水温、盐度、溶解氧和 DIP 是影响浮游动物优势种生态位分化的主要环境因子。

关键词: 浮游动物; 生态位; 环境因子; 冗余分析; 旅顺塔河湾

Zooplankton structure and ecological niche differentiation of dominant species in Tahe Bay, Lushun, China

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Abstract: To investigate the zooplankton structure and the environmental factors affecting ecological niche differentiation in the waters of Tahe Bay, Lushun, a survey was conducted in September 2021, March, April and November 2022 in the waters of Tahe Bay. The results showed that there were 31 species in representation of four phyla, with an annual mean density of $12.4 \times 10^3 \text{ ind/m}^3$, dominated by Copepoda (41.94%). The Pearson's correlation of zooplankton abundance and community diversity with environmental factors such as water temperature, salinity, DO, $\text{NH}_3\text{-N}$, and $\text{NO}_3\text{-N}$ was significant in the waters of Tahe Bay. There were 13 dominant species, mainly consisting of broad niche species, among which *Oithona similis* was the dominant species in all four seasons; the degree of niche overlap of the dominant species was related to the seasons, with the highest in the summer and the lowest in the winter; the redundancy analysis showed that the water temperature, salinity, DO and DIP were the main environmental factors affecting ecological niche differentiation of the dominant species of zooplankton.

Key words: zooplankton; ecological niche; environmental factors; redundancy analysis; Tahe Bay of Lushun

万宁洲仔岛附近海域游泳生物群落结构及其与环境因子的关系

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摘要：为了解万宁洲仔岛附近海域游泳生物群落结构特征，分析了该海域游泳生物种类组成、优势种、渔获率和群落结构特征，并构建游泳生物群落结构数据矩阵。研究共采集到游泳生物62种，隶属于11目28科45属，其中鱼类最多，共有42种，虾类8种，蟹类6种，头足类3种，虾蛄类3种。相对重要性指数（IRI）分析显示，渔获物中IRI>1000的优势种有3种。单因素方差分析（ANOVA）显示多样性指数（H'）和均匀度指数（J'）在不同区域存在显著性差异。相似性百分比分析（SIMPER）表明贡献率最高的物种为长蛇鲻。冗余分析（RDA）显示叶绿素a和溶解氧是影响万宁洲仔岛附近海域游泳生物群落结构的主要环境因子。研究表明万宁洲仔岛附近海域游泳生物渔获量高密度区主要出现在岛礁近岸海域，可能与生活史规律及海域重点环境因子影响有关。

关键词：万宁洲仔岛；群落结构；环境因子；RDA分析

The relationship between community structure of nekton and environmental factors in Zhou Zai Island Wanning

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Abstract : The species composition, dominant species, fishing rate and community structure characteristics of swimming organisms in the waters near Zhou Zai Island, Wanning were analyzed, and the data matrix of swimming organisms community structure was constructed. A total of 62 species of swimming creatures were collected, belonging to 11 orders, 28 families and 45 genera, among which 42 species of fish, 8 species of shrimp, 6 species of crab, 3 species of cephalopod and 3 species of squilla. The relative importance index (IRI) analysis showed that there were 3 dominant species with IRI > 1000 in the catches. Univariate analysis of variance (ANOVA) showed that the diversity index (H') and evenness index (J') were significantly different in different regions. The similarity percentage analysis (SIMPER) showed that the species with the highest contribution rate was *Saurida elongata*. Redundancy analysis (RDA) showed that chlorophyll a and dissolved oxygen were the main environmental factors affecting the community structure of swimming organisms in the waters near Zhou Zai Island, Wanning

Key words:: Zhou Zai Island, Wanning; community structure; environmental factors; RDA analysis

人工繁育中华鲟成体在长江口放流后可以 进行溯河洄游

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摘要: 中华鲟自葛洲坝截流以来种群锐减, 自然繁殖已中断多年, 开展人工增殖放流是目前维持中华鲟种群和后续实现种群重建的关键措施。在当前的放流实践中, 放流规格和地点选择都具有一定的随意性, 其中一个关键争议点——未在仔稚鱼时期经历从产卵场到海洋的降河洄游过程的中华鲟性成熟后是否能够进行繁殖洄游找到产卵场? 本研究分析了在长江口开展的人工繁育中华鲟成体亚成体放流实验, 及用卫星标记 (PAT) 监测的其迁移状况。结果显示, 2004-2021 年长江口共放流人工繁育中华鲟成体亚成体 (3 龄及以上) 874 尾, 其中做了 PAT 标志的有 71 尾, 监测回收 PAT 标志信息 31 份, 分析发现获得有效监测信息的 20 尾 11~12 龄个体中, 有 3 尾出现了逆流沿长江溯河洄游的行为。该结果或可说明仔稚鱼时期经历从产卵场到海洋的降河洄游过程并非中华鲟性成熟后进行溯河洄游的必要条件。为了进一步论证该结论、弄清放流后的繁殖洄游过程, 还需更精细的实验研究。

关键词: 中华鲟, 种群重建, 放流, 洄游, 长江口, 成体

Adult artificially bred Chinese sturgeon (*Acipenser sinensis*) can migrate upstream following the Yangtze River after being released into the Yangtze River Estuary

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Abstract: Chinese sturgeon (*Acipenser sinensis*) is critically endangered. Releasing artificially bred individuals is currently the crucial measure to sustain and recover the natural population. About the releasing practice, there is a hypothesis: Chinese sturgeon that has not experienced the downstream migration process from the spawning ground to the ocean during the larval and juvenile stages cannot start reproductive migration and locate the spawning ground after reaching sexual maturity. The current study analyzed the release experiments of artificially bred adult and sub-adult Chinese sturgeon conducted in the Yangtze River Estuary, as well as their migration data monitored using satellite tagging (Pop-up Archival Tags, PAT). The results showed that a total of 874 artificially bred adult and sub-adult Chinese sturgeons were released into the Yangtze River Estuary from 2004 to 2021. 3 of the 20 individuals aged 11-12 years with valid PAT monitoring data exhibited upstream migration behavior along the Yangtze River. The result suggests that the hypothesis maybe wrong.

Key words: *Acipenser sinensis*, adult, release, migration, Yangtze River Estuary

气候变化对浙江近海三种头足类生物潜在生境分布的影响

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摘要：头足类多为短生命周期海洋生物，其生境容易受环境和气候变化影响。本研究使用2017-2023年浙江沿岸拖网调查资料，运用物种分布模型预测了本世纪末4种RCP气候情境下3种头足类生物（杜氏枪乌贼、多钩钩腕乌贼和曼氏无针乌贼）的潜在生境分布。结果显示：随机森林具有较好且稳定的预测效果，各组AUC均高于0.8且标准差小于0.05。影响头足类生境分布的主要环境因子为SST和SSS，不同种对SST和SSS变化的响应程度具有差异。高排放情境下头足类的潜在生境适生区主要向浙江南部沿岸和北部外海扩散，不同种之间具有一定差异，不同气候情境下的高适生区几何质心变化不明显。本研究可为应对气候变化背景下的头足类栖息地养护提供重要科学依据。

关键词：头足类；气候变化；随机森林；浙江近海；空间格局

The impact of climate change on the potential habitat distribution of three cephalopod species in the coastal waters of Zhejiang

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Abstract: Cephalopods are mostly short-lived marine organisms with habitats susceptible to climate change. Trawl survey data from 2017 to 2023 of Zhejiang offshore was employed to forecast the potential habitat distribution of three cephalopod organisms in 4 RCP climate scenarios at the end of the century by utilizing species distribution model. The results showed random forest exhibited robust and consistent predictive performance, with AUC exceeding 0.8 and standard deviation below 0.05 for each group. The primary environmental factors affecting the distribution of cephalopod habitats were SST and SSS. The response of different species to changes in SST and SSS differed. The potential habitats under high emission scenarios are predicted to expand to the southern coast of Zhejiang and the northern offshore, with some species-specific variations. The geometric centre of gravity of the high suitable habitat remained relatively stable under different climatic scenarios. The findings provide a crucial scientific foundation for the conservation of cephalopod habitats in response to climate change.

Key words: cephalopods; climate change; random forest; Zhejiang offshore; spatial pattern

东海不同群体大黄鱼的耳石稳定同位素分析及溯源

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摘要：大黄鱼作为我国重要的渔业资源，其先后经历了敲鼓作业、过度捕捞等带来的资源破坏，又受到了禁渔休渔、增殖放流的保护措施。目前我们最关心的问题就是增殖放流的成效以及大黄鱼群体间是否混合。为了查明这一情况，我们选择对大黄鱼耳石稳定同位素取样分析，结合方差分析，聚类分析等方法找到不同群体类别的差异特征，并进一步推测大黄鱼的产卵场、越冬场、洄游路径等。结果表明，在耳石核心处的 C 同位素可以很好的区分出养殖群体与野生群体。耳石核心处的 O 同位素可以区分野生群体中的外海群体与近海群体。此外通过对核心处到之后冬龄处的 C、O 稳定同位素的变化差异，可以将始终在养殖场的样本与增殖放流样本进行区分。其中我们发现，1) 舟山海域的野生大黄鱼有明显的混合情况；2) 养殖样本因逃逸或放流等原因也会出现在近海海域。这些可能出现的洄游情况反映了舟山近海的大黄鱼群体已经发生了明显的混合，并且增殖放流种可能已经融入野生群体当中。

关键词：大黄鱼、耳石稳定同位素、增殖放流

无

无
无

Abstract:

Key words:: 无

流速对草鱼卵巢发育的影响

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摘要: 水利工程的生态运行对渔业资源的保护至关重要。流速会影响产漂流性卵鱼类的繁殖生态。探索流速对草鱼卵巢发育的影响, 对于了解自然繁殖对生态水流的响应至关重要。本研究中, 我们对草鱼进行了组织学分析、生化分析, 并检测了草鱼下丘脑-垂体-性腺轴中关键基因的转录情况。虽然流速刺激对草鱼卵巢发育特征无明显影响, 但雌二醇和孕酮水平明显升高。cyp17a1、cyp19a1a、hsd17b1 的基因表达水平受到显著调控。此外, 适当的流速刺激可以通过提高抗氧化酶的活性来改善机体健康状况。研究结果为水电工程生态运行和河流生态恢复提供了基础知识和数据支持。

关键词: 草鱼, 流速, 卵巢, 性激素, 氧化应激

Influences of Water Velocity on Ovarian Development in Adult Grass Carp (*Ctenopharyngodon idellus*)

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Abstract: Ecological operation of hydraulic engineering is essential for the conservation of fishery resources. Water velocity is known to affect the spawning of fishes delivering drifting eggs. In particular, exploring the effects of water velocity stimulation on ovarian development in grass carp is essential to understand the response of natural reproduction to ecological flows. We performed histology analysis, biochemical assays, and examined the transcripts of key genes in the hypothalamus-pituitary-gonad axis in grass carp. Although there was no discernible difference on the ovarian development characteristics of grass carp under water velocity stimulation, estradiol and progesterone were elevated. The gene expression levels of cyp17a1, cyp19a1a, hsd17b1 were significantly regulated. In addition, appropriate water velocity stimulation could enhance body health status by increasing the activities of antioxidant enzymes. The results of this study provide the fundamental knowledge and data support for ecological operation of hydropower projects and river ecological restoration.

Key words: grass carp, water velocity, ovary, sex hormones, oxidative stress

秘鲁外海群茎柔鱼体内汞的生物积累首次 评估：群体、性别、摄食生态的影响

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摘要：本研究探讨了东太平洋茎柔鱼体内总汞浓度的生物积累特征，并分析胴长、性别和摄食生态等因素对其体内汞含量的影响。通过对 2020 年 6 月至 12 月期间捕获的 108 个茎柔鱼样本的肌肉组织进行分析，我们发现 THg 浓度随胴长的增加而上升，但均未超过中国国家食用标准。性别差异分析显示，雌性个体的 THg 浓度在中型和大型群体中显著高于雄性。稳定同位素（ $\delta^{13}\text{C}$ 和 $\delta^{15}\text{N}$ ）和脂肪酸分析揭示了不同群体的摄食习性和营养级，以及与 THg 浓度的相关性。主成分分析（PCA）表明，体重、 $\delta^{13}\text{C}$ 、EPA 和 THg 在第一主成分中有较大贡献，而经度和 ARA 在第二主成分中有较大贡献。此外，THg 与 $\delta^{13}\text{C}$ 、 $\delta^{15}\text{N}$ 和 DHA/EPA 比值在不同群体中呈现不同的相关性模式。研究结果强调了对头足类动物体内污染物积累进行研究的重要性，并为海洋生态系统中污染物的生物地球化学循环提供了新的见解。

关键词：茎柔鱼；汞；稳定同位素；脂肪酸

First assessment of mercury bioaccumulation in jumbo squid (*Dosidicus gigas*) off Peru: the impact of sized group, sex, and feeding ecology.

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Abstract: This study investigated the bioaccumulation characteristics of total mercury in jumbo squid from the eastern Pacific Ocean, analyzing the influence of factors such as mantle length, sex, and feeding ecology. We analyzed the muscle tissue of 108 squid samples. THg concentrations increased with mantle length, but all values remained within Chinese national edible standards. Females in medium and large-sized groups had significantly higher THg concentrations than males. Stable isotope and fatty acid analyses revealed the feeding habits and trophic levels of different groups and their correlation with THg levels. Principal component analysis identified body weight, $\delta^{13}\text{C}$, EPA, and THg as significant contributors to the first principal component, while longitude and ARA contributed to the second. Correlations between THg, $\delta^{13}\text{C}$, $\delta^{15}\text{N}$, and the DHA/EPA ratio varied among groups. These findings highlight the importance of pollutant bioaccumulation research in cephalopods, providing insights into the biogeochemical cycling of pollutants in marine ecosystems.

Key words: *Dosidicus gigas*; mercury; stable isotope; fatty acid

大连不同群体长牡蛎生殖季节性腺发育对比

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摘要: 本研究对中国北方大连合计 6 个地点的长牡蛎进行取样调查, 对不同地点的长牡蛎的性腺进行组织学观察, 其中包括 3 个养殖群体 (旅顺, 杏树屯, 广鹿岛) 和 6 个野生群体 (旅顺, 杏树屯, 广鹿岛, 三山岛, 付家庄, 老虎滩)。通过对性腺的组织学观察、卵母细胞直径的测量、精母细胞的生长来描述长牡蛎的性腺发育变化。本研究首次通过观察比较了同地区不同养殖方式的长牡蛎性腺发育, 结果为了解和研究双壳类动物中影响繁殖的主要环境因素提供了参考依据, 为长牡蛎后续的种质保护、管理和开发提供了新的见解。

关键词: 长牡蛎; 性腺发育 ; 不同群体

Comparison of gonadal development during the reproductive season in different populations of the *Magallana gigas* from Dalian

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Abstract: In this study, the gonads of *Magallana gigas* from six sites in Dalian, northern China, including three cultured populations (Lvshun, Xingshutun, Guanglu Island) and six wild populations (Lvshun, Xingshutun, Guanglu Island, Sanshan Island, Fujiazhuang, and Laohutan), were sampled for histological observation. Changes in gonadal development were assessed through histological observations, measurements of oocyte diameters, and the growth of spermatocytes. This study represents the first comparative analysis of gonadal development in *Magallana gigas* under different culturing methods within the same region. The findings provide valuable insights into the primary environmental factors influencing bivalve reproduction and offer a foundation for future germplasm conservation, management, and development strategies for *Magallana gigas*.

Key words: *Magallana gigas*; gonadal development ; different populations

全球灯笼鱼渔业资源研究热点与发展趋势——基于 Citespace 的图谱量化研究

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摘要: 摘要: 在多年海洋过度捕捞的压力下, 海洋生态系统失衡破坏, 全球渔业资源衰退严重, 灯笼鱼逐渐成为新的渔业资源目标物种, 引起了各界学者的广泛关注和高度重视。本文基于 1977-2023 年的 CNKI 和 WOS 数据库中灯笼鱼领域研究的文献样本数据, 通过可视化文献分析软件 CiteSpace, 从文献计量角度对全球灯笼鱼渔业资源相关研究论文的年出版量、关键词、作者、机构、地区和国家等进行合作网络分析、关键词共现分析、聚类分析和突现词探测等, 进而直观了解灯笼鱼领域研究的前沿热点和变化趋势, 梳理不同学科发展脉络并对其结果给予客观建议, 以期为国内外研究学者整体掌握全球灯笼鱼渔业资源研究状况提供科学借鉴和理论依据。

关键词: 灯笼鱼科; 渔业资源; Citespace; 知识图谱

Research hotspots and development trends of global lanternfish fishery resources-A quantitative study based on Citespace map

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Abstract: Abstract: Under the pressure of years of ocean overfishing, the imbalance and destruction of marine ecosystems, and the serious decline of global fishery resources, lanternfish has gradually become a new target species of fishery resources, which has aroused extensive concern and great attention of scholars from all walks of life. In this paper, based on the literature sample data of the research in the field of lanternfish in the CNKI and WOS databases from 1977-2023, we conducted collaborative network analysis, keyword co-occurrence analysis, clustering analysis, and cluster analysis on the annual publication volume, keywords, authors, institutions, regions, and countries of the research papers related to the global fishery resources of lanternfish from the perspective of bibliometrics by means of CiteSpace, the software for visual literature analysis. From the perspective of bibliometric analysis, CiteSpace analyzed the annual publications of lanternfish-related research papers, keywords, authors, regions and countries, etc., and conducted cooperative network analysis, keyword co-o

Key words: Keywords: Myctophidae; fishery resources; Citespace; knowledge map

基于提升回归树的西白令海狭鳕资源分布环境影响因子分析

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摘要：本文以 2013—2019 年我国西白令海狭鳕（*Gadus chalcogrammus*）渔业生产数据为基础，采用提升回归树模型，构建西白令海狭鳕渔场预报模型，并以 2020 年实际作业数据对预报模型验证。研究显示，预报模型的 AUC 值为 0.96，kappa 系数为 0.79，准确率为 89%；叶绿素 a 浓度、pH 和海表温度三者相对重要性之和超过 75%；模型预测概率大于 0.6 的海域包含了 2020 年实际作业数据中 85.8% 的作业网次和 87.8% 的 CPUE，且模型预报与实际作业的渔场位置以及 CPUE 分布高度吻合。

关键词：狭鳕；渔场预报；提升回归树；西白令海

A Boosted Regression Tree Based Forecast Model for walleye pollock Fishing Grounds in the Western Bering Sea

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Abstract: This article is based on the fishery production data of *Gadus chalcogrammus* in the West Bering Sea of China from 2013 to 2019. Using an improved regression tree model, a forecast model for the *Gadus chalcogrammus* fishery in the West Bering Sea is constructed, and the forecast model is validated with actual operational data in 2020. The research results indicate that the AUC (area under the curve) value of the prediction model is 0.96, the kappa coefficient is 0.79, and the accuracy is 89%. The comprehensive relative importance of chlorophyll-a concentration, pH value, and sea surface temperature (SST) exceeds 75%. In the validation using 2020 data, areas with model-predicted probabilities greater than 0.6 included 85.8% of the operational net deployments and 87.8% of the Catch Per Unit Effort (CPUE) recorded in 2020. This indicates a strong alignment between the predicted fishing ground locations and the actual operational fishing areas, with the predicted fishing ground center closely matching the CPUE distribution.

Key words: walleye pollock; fishing ground forecasting; boosting regression trees; Western Bering Sea.

长江口邻近海域渔业群落结构特征与 环境因子的关系

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摘要: 随着长江十年禁渔和长江口邻近海域的生态修复和增殖放流活动逐步增强, 渔业生物群落结构特征受到的显著影响, 研究渔业生物的群落特征及与环境因子关系对于指导渔业生态修复活动具有一定的现实意义。本文根据在长江口邻近海域开展的连续两年(2022-2023年)春季底拖网调查, 研究渔业生物的群落结构特征(种类组成、优势种、区系格局), 探究群落结构特征的年际变化的驱动因素。结果表明, 两年的渔业生物区系分布主要为长江口近岸、长江口南部和长江口北部三个群聚, 三个群聚中近岸群聚主要为河口型种类(优势种为绿鳍鱼、龙头鱼、鮫鯪和舌鳎), 南部群聚主要为暖温型种类(优势种为舌鳎、细条天竺鲷和小黄鱼), 北部为冷水团控制种类(优势种为细点圆趾蟹、葛式长臂虾和脊腹褐虾)。根据两年群聚和生态类群的差异性检验分析, 2023年的各类群丰度显著减少, 平均个体大小下降($p < 0.05$)。

关键词: 渔业生物; 群落结构; 季节变化; 环境因子

Relationship between fishery community structure characteristics and environmental factors in the adjacent waters of the Yangtze River Estuary

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Abstract: With the gradual implementation of the ten-year fishing ban on the Yangtze River and the enhancement of ecological restoration and stock enhancement activities in the adjacent waters of the Yangtze River Estuary, the structure of fishery biological communities has been significantly impacted. Studying the characteristics of these communities and their relationships with environmental factors holds practical significance for guiding fishery ecological restoration activities. This study based on two consecutive years (2022-2023) of spring bottom trawl surveys conducted in the waters near the Yangtze River Estuary, examines the community structure characteristics of fishery organisms (species composition, dominant species, and community patterns) and explores the driving factors of interannual variations in these characteristics. The results show that the distribution of fishery biological communities over the two years mainly consisted of three groups: nearshore, southern, and northern communities near the Yangtze River Estuary. The nearshore group was primarily composed of estuarine sp

Key words: Fishery organisms; community structure; seasonal variation; environmental factors

饲用虾青素对青海湖裸鲤生长性能、抗氧化能力、免疫功能及转录水平的影响

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摘要: 为了阐明由虾青素诱导的青海湖裸鲤的碱性应激反应机制, 并为虾青素在青海湖裸鲤饲料中的应用提供理论基础。总共有 900 条初始平均体重为 21.02 ± 1.15 克的 *G.przewalskii* 幼鱼被分为 5 组, 每组有 3 个重复, 每个重复 60 条鱼。对照组 (AS0) 被喂食基础饲料, 而实验饲料则分别添加了 25 毫克/千克 (AS25)、50 毫克/千克 (AS50)、100 毫克/千克 (AS100) 或 200 毫克/千克虾青素 (AS200)。经过 8 周的养殖后, 分析了饲料中虾青素对 *G.przewalskii* 生长性能、抗氧化能力和免疫功能的影响。随后, 我们对补充了虾青素的 *G.przewalskii* 进行了碱性应激实验, 以分析虾青素对 *G.przewalskii* 在转录组水平上的碱性应激抵抗力的影响。

关键词: 虾青素; 青海湖裸鲤; 抗氧化剂; 免疫反应; 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. Subsequently, we conducted an alkaline stress experiment on *G.przewalskii* supplemented with astaxanthin to analyze the impact of astaxanthin on the alkaline stress resistance of *G.przewalskii* at the transcriptome level.

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

新疆特克斯河新疆高原鳅生物学研究

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摘要: 【目的】研究特克斯河新疆高原鳅系统生物学特性, 为其种质资源开发利用奠定基础, 夯实新疆特有鱼类基础生物学数据。【方法】2022~2023年在特克斯河采集新疆高原鳅488尾样本, 运用经典生物学方法鉴定其形态特征, 分析其年龄、生长等生物学特性。【结果】新疆高原鳅体延长, 头略扁平, 头后稍隆起, 吻钝、口下位较宽, 背廓呈弧状, 前躯粗圆, 呈纺锤形, 尾柄起点处的宽度明显大于尾柄高, 皮肤光滑, 无鳞, 侧线完全。体长和体重均不符合正态分布, 年龄均值为 (1.74 ± 0.77) +, 最大年龄为4+, 最小年龄为0+, 其中优势年龄个体为2+, 占46.80%。体长和体重相关方程为: $W = 1.15 \times 10^{-5}L^{2.968}$ ($R^2 = 0.92$); 生长方程为: $L_t = 161.13(1 - e^{-0.32(t + 0.20)})$ 和 $W_t = 40.82(1 - e^{-0.32(t + 0.20)})^{2.968}$, 渐近体长L。

关键词: 特克斯河; 新疆高原鳅; 形态特征; 年龄与生长

Biological characteristics of *Triplophysa Strauchii* in Turks River

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Abstract: 【Objective】To study the systematic biology characteristics of *Triplophysa Strauchii* in Turks River, Lay a foundation for the development and utilization of its germplasm resources, and consolidate the basic biological data of fish endemic to Xinjiang. 【Method】From 2022 to 2023, 488 samples of *T. Strauchii* were collected in the Turks River, and their morphological characteristics were identified by classical biological methods, and their biological characteristics such as age and growth were analyzed. 【Result】*T. Strauchii* has elongated body, slightly flattened head, slightly raised head, blunt snout, wider lower mouth, curved back outline, thick round forebody, fusiform, width of caudal stalk starting point is obviously larger than caudal stalk height, smooth skin, no scale, and complete lateral line.. The mean age of *T. Strauchii* was (1.74 ± 0.77) +, the maximum age is 4+, the minimum age is 0+. Among them, the dominant age was 2+, accounting for 46.80%. The correlation equation between standard length and body weight is as follows: $W = 1.15 \times 10^{-5}L^{2.968}$ ($R^2 = 0.92$); The growth equation

Key words:: Turks River; *Triplophysa Strauchii*; Morphology characteristic; Age and growth

禁渔期内湘江银鮡个体繁殖力与卵径研究

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摘要: 银鮡是湘江的优势种类, 但对繁殖特征的了解较少。本研究于 2023 年 5-6 月在湘江共采集 65 尾性成熟雌性个体, 分析个体繁殖力与卵径。结果表明: 体长范围为 60.52~142.23mm, 体重范围为 5.30~62.10g。个体绝对繁殖力、体长相对繁殖力、体重相对繁殖力以及成熟卵径的平均值分别为 11160 ± 7910 粒、 100.29 ± 62.37 粒/mm、 421.86 ± 240.20 粒/g、 0.91 ± 0.07 mm。性成熟个体年龄范围为 1 至 3 龄, 个体绝对繁殖力随着年龄的增大而增大, 体重相对繁殖力随着年龄的增大而减小, 体长相对繁殖力随年龄的增大趋于稳定。个体繁殖力与生物学特征关系显示个体绝对繁殖力和体长相对繁殖力均随着体长、体重、卵巢重的增大而增大, 体长小于 93.74mm 时体重相对繁殖力随体长的增大而增大, 大于 93.74mm 时随体长的增大而减小。

关键词: 银鮡; 繁殖力; 卵径; 湘江; 禁渔

Individual fecundity and egg size of Xiangjiang *Squalidus argentatus* during the closed season

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Abstract: *Squalidus argentatus* is a dominant species in the Xiangjiang River, but less is known about reproductive characteristics. In this study, a total of 65 sexually mature females were collected from May-June 2023 in Xiangjiang River to analyse individual fecundity and egg diameter. The mean values of absolute fecundity, relative fecundity for body length, relative fecundity for body weight and mature egg diameter were 11160 ± 7910 , 100.29 ± 62.37 grains/mm, 421.86 ± 240.20 grains/g, 0.91 ± 0.07 mm, respectively. The age range of sexually mature individuals was from 1 to 3 years old, and the absolute fecundity of individuals increased with age, the relative fecundity of body weight decreased with age, and the relative fecundity of body length tended to stabilise with age. The relationship between individual fecundity and biological characteristics showed that both absolute fecundity and body length relative fecundity increased with body length, body weight and ovary weight, and body weight relative fecundity increased with body length when body length was less than 93.74 mm, and decreased with bod

Key words: *Squalidus argentatus*; fecundity; egg diameter; Xiangjiang River; ban on fishing

以脂肪酸为营养标志物分析阿根廷滑柔鱼卵子发生的营养分配特点

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摘要: 脂肪酸在头足类胚胎发育过程中具有关键作用。为阐明阿根廷滑柔鱼卵子发生过程中的营养分配特点, 本研究根据 2019 年在西南大西洋索饵场采集的阿根廷滑柔鱼样本, 以脂肪酸生物化学标志物为营养参考指标, 利用非度量多维尺度和相似性分析了不同发育时期卵巢和输卵管卵子的脂肪酸组成差异。结果显示, 卵巢和输卵管卵子含有脂肪酸 30 种, 其中 19 种占总脂肪酸含量的 0.2% 以上。在不同成熟阶段, 卵巢总脂肪酸含量差异显著, 输卵管卵子总脂肪酸含量和单个脂肪酸相对含量均无显著差异。此外, 二者脂肪酸组成存在组织差异性, 输卵管卵子含有更丰富的饱和脂肪酸, 但不饱和脂肪酸含量显著低于卵巢。研究表明, 阿根廷滑柔鱼卵子的脂肪酸组成独立于卵巢组织的脂肪酸组成变化, 成熟卵子营养积累模式为最优化分配积累而非质量的最大化。

关键词: 阿根廷滑柔鱼; 脂肪酸; 营养分配; 卵子发生; 繁殖

Nutrient allocation to eggs in female Argentine shortfin squid, *Illex argentinus* using fatty acids as nutrient indicator

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Abstract: Fatty acids play a critical role in embryonic development of cephalopods. However, little information is available on the allocation of fatty acids to eggs during oogenesis, limiting our understanding regarding how these animals maximize reproductive performance in terms of energy and nutrient use. We explored the nutrients for egg production during maturation for Argentine shortfin squid by comparing the fatty acid profiles between the ovary and eggs in the oviducts. The overall fatty acids in the ovary varied significantly among maturity stages, while the eggs had a consistent amount of total fatty acids and relative amount of individual fatty acids. There were consequently significant differences in the fatty acid profiles between the ovary and eggs by maturity stage and in total. Cumulatively, our results reveal that this squid produces eggs with consistent levels of nutrients virtually regardless of how the nutrient profile of the ovary varies during maturation, providing insight into the egg production process relation to nutrient allocation.

Key words: Argentine shortfin squid; *Illex argentinus*; fatty acid; nutrient allocation; egg production; reproduction

湘江流域丰水期浮游动物群落结构及其水质评价

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摘要: 浮游动物是河流生态系统中重要的初级消费者, 对水环境敏感, 可作为水质评价的重要指标。为了解湘江流域丰水期浮游动物群落结构及水质状况, 于 2024 年 7 月对湘江流域浮游动物群落特征进行调查, 基于现存量、生物多样性指数及综合水质标识指数进行水质评价, 并探讨影响浮游动物群落结构的环境因子。结果表明: 共鉴定出浮游动物 22 种, 以轮虫为主 (11 种), 浮游动物平均丰度和生物量分别为 246.6 ind./L 和 0.3 mg/L, 优势种为晶囊轮属、无节幼体、哲水蚤桡足幼体。浮游动物共划分 7 个功能群, 以 RF 和 RC 功能群为主。铅、铜、锌和氨氮是影响浮游动物群落结构的主要环境因子。浮游动物现存量、生物多样性指数和综合水质标识指数评价湘江流域水质为轻度污染。本研究为湘江流域的水质评价及生态保护提供了科学依据, 丰富了河流水质生物学评价体系中的浮游动物应用。

关键词: 湘江流域; 浮游动物; 群落结构; 环境因子; 水质生物学评价

Zooplankton community structure and water quality assessment in the Xiangjiang River Basin during the wet season

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Abstract: Zooplankton are key consumers in river ecosystems and sensitive indicators of water quality. In July 2024, a survey was conducted in the Xiangjiang River Basin to assess zooplankton community structure and water quality. Zooplankton abundance, biodiversity indices, and water quality index were used for the assessment, while environmental factors influencing community structure were also examined. A total of 22 zooplankton species were identified, with rotifers (11 species) being dominant. The average zooplankton abundance and biomass were 246.6 ind./L and 0.3 mg/L, respectively. Dominant species included *Asplanchna* sp., Nauplius and Calanidae Copepodite. The community was divided into seven functional groups, with RF and RC being predominant. Pb, Cu, Zn and NH₃⁺-N were key factors affecting the community structure. Overall, the basin was classified as mildly polluted. This study provides a scientific foundation for water quality assessment and ecological protection in the Xiangjiang River Basin.

Key words: Xiangjiang River Basin; Zooplankton; Community structure; Environmental factor; Water quality assessment

长江口鱼类群落分布对潮沟水文连通性动态变化的响应

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摘要：水文连通性的动态变化影响河口湿地与其邻近水域之间的物理、化学及生物的交流，特别与鱼类等水生生物群落息息相关，深刻影响着河口湿地整个生态系统的健康及稳定性。本研究以位于长江口崇明东滩的高、中、低程潮沟为对象，通过原位监测和遥感技术相结合，选取3类（结构连通性、水文连通性、景观网络）共9个指标（潮沟横截宽度、DEM、潮沟级别、潮汐大小潮、水文连接时间、淹水滞留时长、节点数、河链数、节点连接率 β ）比较分析在大小潮期间，不同潮沟水文连通程度对鱼类群落分布的影响。结果表明：选取的9个指标均与鱼类丰度和生物量有显著性差异（ $P < 0.05$ ），表明河口湿地对鱼类群落的重要性。为了进一步得知潮汐作用对鱼类群落分布的影响，我们以横截面积为协变量进行聚类和相关性分析，结果表明：不同水文连通性下的物种差异性明显。

关键词：河口湿地、鱼类群落、水文连通性、潮汐作用

The response of fish community distribution at the Yangtze River Estuary to the dynamic changes of tidal creek hydrological connectivity

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Abstract : The dynamic changes in hydrological connectivity affect the physical, chemical, and biological exchanges between estuarine wetlands and their adjacent waters, which are particularly closely related to the communities of aquatic organisms such as fish and profoundly impact the health and stability of the entire ecosystem of the estuarine wetlands. This study focuses on high, medium, and low tidal creeks in the Dongtan area of Chongming at the Yangtze River Estuary. By combining in situ monitoring with remote sensing technology, a total of 9 indicators from 3 categories (structural connectivity, hydrological connectivity, and landscape network) were selected. These include the cross-sectional width of the tidal creek, DEM, level of the tidal creek, spring and neap tides, hydrological connection time, floodwater retention time, number of nodes, number of stream chains, and node connection rate β . The study compares and analyzes the impact of different degrees of hydrological connectivity on the distribution of fish communities during spring and neap tides.

Key words:: Estuarine Wetlands、Fish Communities、Hydrological Connectivity、Tidal Action

通过生理学、转录组和代谢组的综合分析，揭示了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, $0.61 \pm 0.19\text{kg}$; MRT, $1.39 \pm 0.27\text{kg}$; LRT, $2.58 \pm 0.38\text{kg}$ ）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：综合生理学、转录组学和代谢组学分析显示，SRT 具有更大的抗氧化和免疫能力，而 LRT 具有更大的代谢和脂肪沉积能力。三倍体虹鳟的生长伴随着氨基酸和脂肪酸的活性生物合成、代谢和免疫力的改变，这确保了快速生长、脂肪沉积和对环境胁迫的反应。

关键词：三倍体虹鳟；体重；抗氧化能力；免疫反应；新陈代谢

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, $0.61 \pm 0.19\text{ kg}$; MRT, $1.39 \pm 0.27\text{ kg}$; LRT, $2.58 \pm 0.38\text{ kg}$) were examined. In summary, integrated physiological, transcriptomic and metabolomic analyses revealed that SRT had greater antioxidant and immune capacity, whereas LRT had greater metabolic and fat deposition capacity. The growth of triploid rainbow trout is accompanied by alterations in the active biosynthesis, metabolism of amino acids and fatty acids and immunity, which ensures rapid growth, fat deposition, and response to environmental stress.

Key words: Triploid rainbow trout; Body weights; Antioxidant capacity; Immune response; Metabolism

头足类角质颚形态的生态驱动与 功能性演化机制研究

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摘要: 头足类动物是广泛分布于各种海洋生态系统中的海洋软体动物。作为头足类的“齿舌”，角质颚具有广泛的功能，其形态特征在系统发育和生态学上已经得到了确认。然而，大多数头足类物种的角质颚形态特征所受到的生态压力仍不清楚，并且角质颚形态与其功能之间的关系尚未得到探讨。在本研究中，研究人员收集了 45 种头足类动物的 1344 个上颚和 1395 个下颚的侧面轮廓图像，以基于基因的系统发育框架为基础，评估了角质颚形态的系统发育、生态及功能信号，并揭示了角质颚形态可能的生态和功能意义。结果表明，上颚和下颚的形态表现出中等但略低的系统发育信号，并且通过相关性分析发现，角质颚形态与营养生态位、栖息地及分布范围相关。生活在不同栖息地、具有不同角质颚功能的头足类物种，其角质颚形态存在显著差异。研究表明，角质颚在生态和功能类型上的演化可以归因于其形态对捕食、栖息地、分布范围及功能类别的适应性进化。

关键词: 头足类角质颚；几何形态测量学；生态形态学；功能形态学；多样性

Ecological Drivers and Functional Evolutionary Mechanisms of Cephalopod Beak Morphology

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Abstract: Cephalopods are marine molluscs widely distributed in various marine ecosystems. As the “radula” of cephalopods, the beak has broad functions and the phylogenetic and ecological features of beak shapes have been confirmed. However, the ecological pressures on the morphological features of the beak of most cephalopods remain unknown and the relationship between beak morphology and its function has not been explored. In the study, lateral profile images of 1344 upper beaks and 1395 lower beaks of 45 cephalopods were obtained to evaluate the phylogenetic, ecological, and functional signals of beak morphology with the established phylogenetic framework based on genes and reveal the possible ecological and functional significance of beak shapes. The shapes of the upper and lower beaks showed a moderate but slightly low phylogenetic signal, with correlation analysis indicating that beak morphology is linked to trophic niche, habitat, and distribution. Cephalopods with different beak functions across various habitats exhibited significant differences in beak shape. The study demonstrated th

Key words:: Cephalopod Beak; Geometric morphometrics; Ecomorphology; Functional morphology; Diversification

从系统碳代谢角度探讨缢蛭混养对水产养殖池塘水-气界面 CO₂ 通量的影响机制

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摘要: 在全球变暖的背景下, 水产养殖池塘在全球碳循环中的作用日益受到关注。作为海水养殖池塘重要的混养物种, 贝类会对水-气界面二氧化碳 (CO₂) 通量产生显著影响, 但其影响机制尚不清晰。本研究对混养了 3 个不同密度缢蛭的蟹-虾-贝养殖池塘和蟹-虾养殖池塘的 CO₂ 通量和系统碳代谢特征进行了测定。结果显示, 养殖期间所有二元和三元混养系统均为大气 CO₂ 的汇, 净系统生产力是 CO₂ 通量的主要调控因子。缢蛭高低混养密度会产生相反的生态学效应, 即低密度混养会引发“上行效应”最终提高总初级生产力和系统呼吸, 而高密度混养可能通过“下行效应”产生相反的生态效应。缢蛭高低混养密度下, 其对初级生产力的影响始终大于系统呼吸作用, 导致混养系统水-气界面 CO₂ 汇的功能在混养低密度缢蛭时增强, 而在高混养密度时减弱。由于水体 pH 对 CO₂ 通量具有较好的预测能力, 因此对水体 pH 进行监测和管理可能是调节海水养殖池塘 CO₂ 源汇功能的有效途径。

关键词: 滤食性贝类; 混养池塘; 二氧化碳通量; 系统碳代谢; 影响机制

Influencing mechanism of farming clams on the CO₂ flux from aquaculture ponds: Insights from ecosystem carbon metabolism

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Abstract: Aquaculture ponds have gained increasing attention for their potential roles in the global carbon cycle. Clams exert a notable impact on CO₂ flux at the water-air interface, however, the mechanism is still unclear. This study measured the CO₂ flux and the ecosystem carbon metabolism from four polyculture ponds with different clam densities. The results showed that all the ponds acted as atmospheric CO₂ sinks during the farming season and net ecosystem production was a dominant regulator of CO₂ uptake. Farming clams at low density may exert a “bottom-up” effect, promoting gross primary production (GPP) and ecosystem respiration (ER), while a high density can have a “top-down” effect that would have the opposite ecological effects. The effect of farming clam on GPP was always greater than that on ER, leading to the CO₂ sink function being enhanced at low clam densities and weakened at high densities. Given the good predictive ability of water pH on CO₂ flux, monitoring and management of water pH could be an effective way to regulate the CO₂ sink function of mariculture ponds.

Key words: Clam farming; Polyculture ponds; CO₂ flux; Ecosystem carbon metabolism; Influencing mechanism

大豆低聚糖和蛋白核小球藻对生物絮凝系统水质和微生物群落结构的协同效应

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摘要: 研究旨在探讨大豆低聚糖 (SBOS) 和小球藻在生物絮团系统对水产养殖尾水的水质和微生物群落结构的协同作用。SBOS 和小球藻对水质产生了显著的协同效应 ($P<0.05$)。硝酸盐浓度在第 1 天、亚硝酸盐氮浓度在第 5 天、亚硝酸盐和总氮浓度在第 7 天显著降低 ($P<0.05$)。同时使用的处理组 (CS 组) 生物絮团体积显著增加 ($P<0.05$)。SBOS 组中黄杆菌和芽孢杆菌的数量显著增加 ($P<0.05$)，而 CP 组中固氮菌和硝化细菌的比例显著增加 ($P<0.05$)。CS 组芽孢杆菌和分枝杆菌显著增加，而气单胞菌等有害细菌减少 ($P<0.05$)。细菌群落的功能预测分析表明，CS 组的氮循环和有机物降解途径显著上调 ($P<0.05$)。总之，SBOS 与小球藻在 BFT 系统中的联合应用对优化微生物结构、改善水质具有积极的协同效应。

关键词: 大豆低聚糖; 小球藻; 菌群结构; 协同效果; 生物絮团

Synergistic effects of soybean oligosaccharides and chlorella pyrenoidosa on water quality and microbial community structure in biofloc system

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Abstract: This study investigated the synergistic effect of soybean oligosaccharides (SBOS) and chlorella pyrenoidosa (CP) on water quality and microbial community structure of aquaculture effluent in BFT system. SBOS and CP showed a significant synergistic effect on water quality ($P<0.05$). Nitrate content on day 1, nitrite content on day 5, and nitrite and TN content on day 7 were significantly decreased, biofloc volume of the co-used treatments (CS) was increased significantly ($P<0.05$). Flavobacterium and Bacillus was significantly increased in SBOS group, nitrogen-fixing and nitrifying bacteria was significantly increased in CP group. Bacillus and Mycobacterium increased significantly in CS group, while Aeromonas decreased ($P<0.05$). Functional prediction analysis showed that nitrogen cycle and organic matter degradation pathways were significantly upregulated in CS group ($P<0.05$). In conclusion, combined application of SBOS and CP in BFT system has a positive synergistic effect on optimizing microbial structure and improving water quality.

Key words: soybean oligosaccharides; Chlorella pyrenoidosa; microflora; synergistic effects; biofloc

沅江下游大眼鳊仔鱼密度和生长的 时空差异性研究

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摘要: 本研究于 2021 年和 2022 年 5 月至 9 月在沅江梯级大坝下常德江段、河湖交汇处牛鼻滩和西洞庭湖采集样品。2021 年和 2022 年分别采集到大眼鳊仔鱼 575 尾和 2679 尾。2021 年最高密度出现西洞庭湖的 6 月份, 最高径流量出现在 7 月, 2022 年最高密度发生在高径流期 6 月份, 河湖过渡区的密度最高; 2022 年的最高密度远大于 2021 年。仔鱼的体长范围是 4.93-18.07mm, 日龄范围是 3-16 天, 三个采样点耳石的核心直径没有显著性差异 ($P=0.741$), 三个采样点的生长率没有显著性差异 ($p=0.17$), 西洞庭湖的生长率(0.79mm/d)高于常德(0.60mm/d)和牛鼻滩江段(0.65mm/d)。2021 年和 2022 年仔鱼的孵化日期分别从 5 月至 7 月和 6 月至 7 月, 2021 年西洞庭湖孵化高峰期在 6 月中旬, 2022 年牛鼻滩的孵化高峰期在 6 月中旬。研究结果表明河湖过渡区是最重要的育幼场。

关键词: 大眼鳊, 生长, 仔鱼, 耳石

Spatial and temporal variations on density and growth of *Siniperca kneri* larvae in the lower Yuanjiang River

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Abstract: Samples were collected at Changde, river-lake transition zone, and the West Dongting Lake below decadal dams in the Yuanjiang River from May to September 2021 and 2022. A total 507 and 2679 were collected in 2021 and 2022, respectively. Larval density was the highest at the West Dongting Lake in June 2021 and at the transitional zone in June 2022. The highest density was higher in 2022 than in 2021. Water discharge was high in early July 2021 and middle June 2022. Body length ranged from 4.93 mm to 18.07 mm and aged from 3 d to 16 d. Diameter of otolith core was not significantly different among sampling sites ($p=0.741$). Larval growth rate was not significantly different among sampling sites ($p=0.17$). Growth rate was higher at the West Dongting Lake (0.79 mm/d) than at the transitional zone (0.65 mm/d) and Changde (0.60mm/d). Hatch date spanned from May to July 2021 and June to July 2022, with the peak in middle June 2021 at the West Dongting Lake and in middle June 2022 at the transitional zone. The results implied that the transitional zone was the most important nursery ground.

Key words: *Siniperca kneri*, growth, larvae, otolith

非经典生物操纵后淡水水库鱼类密度、大小和生物量的水声学评估

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摘要: 监测水库大规模放养鱼类后的鱼类密度和生长等渔业资源的变化非常重要。本研究利用 BioSonics DT-X (201 kHz) 于 2020 年对浙江省对河口水库鱼类密度、大小分布和生物量的季节变化进行了研究。春季 (3.1 ind/1000 m³) 鱼密度显著低于夏季 (7.0 ind/1000 m³)、秋季 (9.95 ind/1000 m³) 和冬季 (6.7 ind/1000 m³) ($P < 0.01$)。夏季、秋季和冬季鱼类密度无显著差异。春季 (-40.55 dB) 显著高于夏季 (-41.44 dB) 和秋季 (-42.11 dB) ($P < 0.01$), 其他季节 (-39.06 dB) 显著低于冬季 ($P < 0.01$); 夏秋两季无显著差异 ($P > 0.01$)。捕捞结果显示, 鲢和鳙是水库的主要优势种, 数量少, 且大多是年轻个体。

关键词: 水声学; 鱼类资源; 非经典生物操纵; 水库

Hydroacoustic assessment of fish density, size, and biomass in a freshwater reservoir after non-classical biomanipulation

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Abstract: Monitoring changes in fishery resources such as fish density and growth following large-scale fish-stocking in reservoir is important. In this study BioSonics DT-X (201 kHz) was used in 2020 to assess the seasonal changes of fish density, size distribution and biomass in Duihekou Reservoir, which is located in Zhejiang province, China. Fish density in spring (3.1 ind./1000 m³) was significantly lower than that in summer (7.0 ind./1000 m³), autumn (9.95 ind./1000 m³) and winter (6.7 ind./1000 m³) ($P < 0.01$). No significant difference in fish density is apparent between summer, autumn, and winter. Additionally, the average target strength (TS) values in spring (-40.55 dB) are significantly higher than in summer (-41.44 dB) and autumn (-42.11 dB) ($P < 0.01$), while TS values in other seasons are significantly lower than in winter (-39.06 dB) ($P < 0.01$); no significant difference is observed between summer and autumn values ($P > 0.01$). Catch reveals silver and bighead carp to be dominant species, for the population to be small, and to mostly comprise young individuals. These findings enhance

Key words: Hydroacoustics; Fish resources; Non-classical biomanipulation; Reservoir

牡蛎养殖对大鹏澳海域氮源影响的研究

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摘要: 溶解无机营养物质在维持海洋生态系统的物质和能量平衡方面起着关键作用, 影响着海洋生物的生存和动态演替。本研究对深圳大鹏湾牡蛎增殖海域溶解无机营养物的源汇动态进行了调查。在过去的十年中, 调查区内的 N/P 比发生了显著的变化, 表明营养限制从氮的限制转向了磷或磷-硅的限制。这种引起的 N/P 比以及 Si/N 和 Si/P 比的变化可能促进蓝藻的生长, 并随后改变硅藻、甲藻和蓝藻的比例。人类干扰强度和降水的季节波动决定了海湾营养物质的季节和空间分布, 从而影响了海湾生态系统的新陈代谢。本研究有利于理解人类活动影响的海湾溶解无机营养物的源汇特征, 为滤食性贝类与这些营养物质的关系提供了科学数据。

关键词: 牡蛎; 养殖; 氮源; 大鹏澳

Study on the effect of oyster culture on nitrogen source in Dapeng cove

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Abstract: Dissolved inorganic nutrients play a key role in maintaining the material and energy balance of marine ecosystems, affecting the survival and dynamic succession of marine organisms. In this study, the source and sink dynamics of dissolved inorganic nutrients in the Dapengcove of Shenzhen were investigated. Over the past decade, the N / P ratio in the survey area has changed significantly, indicating that nutrient limitation has shifted from nitrogen limitation to phosphorus or phosphorus-silicon limitation. This induced change in N / P ratio and Si / N and Si / P ratios may promote the growth of cyanobacteria and subsequently change the ratio of diatoms, dinoflagellates and cyanobacteria. The seasonal fluctuation of human disturbance intensity and precipitation determines the seasonal and spatial distribution of nutrients in the bay, thus affecting the metabolism of the bay ecosystem. This study is helpful to understand the source and sink characteristics of dissolved inorganic nutrients in the bay affected by human activities, and provides scientific data for the relationship between

Key words: Oyster ; Breeding ; Nitrogen Source ; Dapeng Cove

采桑湖浮游动物群落结构及驱动因素

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摘要: 为探讨采桑湖浮游动物群落结构及其主要驱动因素, 本研究于 2023 年 7 月、11 月和 2024 年 1 月、4 月在采桑湖设置 8 个采样点, 调查浮游动物群落结构及其相关环境因子。共鉴定出浮游动物 43 种, 其中轮虫 22 种, 桡足类 12 种, 枝角类 9 种。采桑湖浮游动物各季节平均丰度为 1067.13 ind./L, 平均生物量为 18.32 mg/L; 丰度以轮虫为主, 生物量以桡足类占优, 二者在各季节间均存在显著差异。优势种的季节更替率分别为夏秋季 50%、秋冬季 72%、冬春季 70%。冬季浮游动物群落结构较为复杂且稳定, 春季结构相对简单且不稳定。基于浮游动物生物多样性指标评估水体营养状态, 结果表明采桑湖处于中营养化水平。典范对应分析 (CCA) 显示, 浮游动物群落的季节变化主要受电导率 (Cond)、总磷 (TP)、溶解氧 (DO)、水温 (WT) 等环境因子的影响。研究结果为采桑湖生态环境保护及水生生物资源的可持续开发提供了科学依据。

关键词: 采桑湖; 浮游动物; 群落结构; 环境因子; 水质评价

The community structure of zooplankton in Caisang Lake and its driving factors

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Abstract: To investigate the community structure of zooplankton in Caisang Lake and its main driving factors, this study conducted surveys at 8 sampling sites in July and November 2023, and in January and April 2024. The zooplankton community structure and related environmental factors were examined. A total of 43 zooplankton species were identified, including 22 species of Rotifera, 12 species of Copepoda and 9 species of Cladocera. The average zooplankton abundance across seasons in Caisang Lake was 1067.13 ind./L, with an average biomass of 18.32 mg/L. Rotifera species dominated in abundance, while Copepoda species dominated in biomass. Seasonal turnover rates of dominant species were 50% between summer and autumn, 72% between autumn and winter, and 70% between winter and spring. The zooplankton community structure was more complex and stable in winter but relatively simple and unstable in spring. Zooplankton biodiversity indices indicated that Caisang Lake is at a mesotrophic level. Canonical Correspondence Analysis (CCA) showed that seasonal changes in the zooplankton community were

Key words: Caisang Lake; Zooplankton; Community structure; Environmental factors; Water quality assessment

温度对中华鲟孵化时间和胚胎发育指标的影响

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摘要: 胚胎发育阶段对中华鲟物种保护和繁殖至关重要, 但水温对这一过程的具体影响研究较少。本研究首先使用三个水温组 (16、19 和 22℃) 进行梯度孵育试验, 探讨水温对中华鲟胚胎发育的影响, 随后利用五个统计模型通过回归分析拟合发育数据, 以确定胚胎孵化时间和温度之间的相关性, 最终通过养殖中华鲟实际胚胎发育数据来验证水温发育指标。结果表明, 在 16-22℃ 的温度范围内, 水温与中华鲟胚胎发育率呈正相关。S 模型是基于水温预测中华鲟胚胎孵化期的最佳模型, 从开始孵化到出苗的过程中, 我们估计了 14 至 25.9℃ 之间的每日发育指数, 范围在 10.66 至 32.22% 之间。本研究基于水温建立的中华鲟胚胎发育指数可以预测中华鲟孵化时间, 有助于及时转移出膜鱼苗, 降低因转移不及时造成的鱼苗窒息死亡率, 为中华鲟人工群体养殖提供科学指导。

关键词: 孵化时间, 发育指标, 水温, 中华鲟

Temperature effects on incubation time and embryo developmental indices in Chinese sturgeon

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Abstract: The embryonic development phase is crucial for the preservation and propagation of the Chinese sturgeon, yet the specific influence of water temperature on this process remains inadequately documented. This study conducted experiments using three temperature groups (16, 19, and 22 °C) to investigate the impact of temperature on the embryonic development of Chinese sturgeon. Subsequently, five statistical models were utilized to fit the developmental data through regression analysis, in order to determine the correlation between incubation time and temperature of the embryos. Data from cultured Chinese sturgeon embryos were finally utilized to validate water-temperature development indices. Over the temperature range of 16 - 22 °C, water temperature was positively related to the rate of embryonic development in Chinese sturgeon. The S model was the best for predicting the incubation period of Chinese sturgeon embryos from temperature. Based on the progression from incubation to initial hatching, we estimated daily development indices, ranging from 10.66 to 32.22 % between 14 and 25.9 °C.

Key words: Incubation time, developmental indices, water temperature, Chinese sturgeon

缢蛏对海水养殖池塘水质改善的潜在作用： 综合单因子和水质指数(WQI)评价方法

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摘要: 滤食性贝类是海水池塘养殖重要的经济品种, 能通过其生理活动产生显著的生态效应。为探究滤食性贝类对养殖水质改善的潜在作用, 本研究构建了5组养殖系统, 即三疣梭子蟹-日本囊对虾养殖系统(PM)及在此基础上混养了4个不同密度缢蛏的混养系统(由低到高分别为PMS1, PMS2, PMS3, PMS4), 综合采用单因子分析和水质指数(WQI)评价了不同系统水质变化。结果显示, 水体pH、叶绿素a、悬浮颗粒物和总氮随缢蛏混养密度增加显著降低, 而化学需氧量、透明度、无机氮、无机磷和总磷显著升高, Cu^{2+} 和 Zn^{2+} 含量则无显著差异。除磷酸盐外, 其他指标均符合国家海水养殖尾水II类排放标准以上, 且氨氮和亚硝氮含量在生物耐受范围内。WQI值随缢蛏密度增加先升后降, PMS2最高, PMS4最低。本研究结果表明, 在蟹-虾综合养殖系统中混养适当密度(本实验条件下为 50g m^{-2})的缢蛏, 可有效改善水质, 提升养殖环境可持续性。

关键词: 水质指标; 缢蛏混养; 单因子评价; WQI

The potential impact of clams on water quality improvement in mariculture ponds: a combined analysis of single factor evaluation and water quality index (WQI) methods

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Abstract: Filter-feeding bivalves are an important economic species in mariculture ponds and can exert significant ecological effects through physiological activities. To explore their potential impact on the improvement of water quality, razor clams were stocked in a crab-shrimp system at four densities (PMS1, PMS2, PMS3, PMS4), the water quality was assessed and contrasted using a single-factor approach and a Water Quality Index (WQI) method. The results showed that water pH, Chl-a, suspended particulate matter and TN decreased significantly with increasing clam density, while COD, transparency, DIN, PO_4^{3-} and TP increased significantly, and there was no difference in Cu^{2+} and Zn^{2+} . Except for PO_4^{3-} , the other parameters met the Class II standard for the discharge of marine aquaculture tailwater. As the clam density increased, WQI initially rose, peaking in PMS2, but subsequently declined, attaining its lowest point in PMS4. The results suggest that co-culturing razor clams at 50g m^{-2} in the crab-shrimp can effectively enhance water quality and promote environmental sustainability.

Key words: Razor clam; Mariculture ponds; Water quality index; Single factor evaluation

长江濒危水生动物亟需重建家园：基于长江 鲟自然繁殖行为重塑的实践启示

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摘要：摘要：长江生物多样性危机备受全球关注，长江濒危水生动物种群恢复状况是检验长江大保护成效的重要参考。在当前长江保护法颁布、长江十年禁渔实施的背景下，长江水生态环境得到改善，水生生物资源恢复总体向好。然而，一些生活史独特、生境需求高、资源严重衰退的珍稀物种仍然难以扭转的濒危态势。本报告以“野外灭绝”长江鲟为例，分析了栖息地破坏是制约其种群恢复重建的关键因素。基于多年的研究攻关，在构建和厘清长江鲟自然繁殖需求模型基础上，2023年通过创制新型产卵巢实现天然水域调控繁殖的成功，2024年再次突破长江鲟天然水域产卵场改造技术并实现改造产卵场中的自然繁殖成功，为长江鲟野外种群重建奠定了坚实理论和实践基础同时结合当前长江十年禁捕后的资源监测结果，指在强干扰的背景下紧靠增殖放流、保护区建设与管理等保护对策是严重不足的，亟待开展栖息地修复改良工作，为濒危水生动物重建自然繁衍的家园，才能解决物种拯救难题。

关键词：珍稀濒危；栖息地修复；长江鲟；人类活动；种群重建

A pressing need for restoring habitats for endangered aquatic species in the Yangtze River: Practical insights gained from reshaping the natural breeding behavior of the Yangtze sturgeon

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Abstract: The biodiversity crisis in the Yangtze River has attracted global attention. Against the backdrop of the ongoing major conservation efforts for the Yangtze River, the restoration of aquatic biological resources in the river is generally improving. However, some endangered species with unique life histories, high habitat demands, and severely depleted resources remain difficult to reverse their endangered status. Taking the "wildly extinct" Yangtze sturgeon (*Acipenser dabrynus*) as an example, based on years of research breakthroughs and after constructing and clarifying the natural reproduction demand model for the Chinese sturgeon, in 2023, successful controlled reproduction in natural waters was achieved through the creation of a new-type spawning nest. In 2024, there was another breakthrough in technology for restoring spawning grounds in natural waters for the Yangtze sturgeon, achieving successful natural reproduction in the restored spawning grounds. These achievements have laid a solid theoretical and practical foundation for the reconstruction of wild populations of the Yangtze

Key words: rare and endangered species; Yangtze sturgeon; habitat restoration; rehabilitation

稻-罗氏沼虾轮作模式对复垦土壤理化性质及养分供应的影响

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摘要: 为研究新构建的稻-罗氏沼虾轮作种养系统对复垦土壤理化性质、养分供应能力及微生物多样性的影响, 以客观综合评价新建稻虾综合种养系统经济和生态综合效益。本研究通过现场采样和室内化学指标分析, 测定了稻沼虾轮作种养模式三个不同生产阶段(放虾前、收虾后和收稻后)的两个土层(0-20cm 和 20-40cm)处土壤的物理性质、还原性物质及全量和速效养分。结果显示: 收虾后和收稻后>2mm 土壤团聚体占比自上而下显著增加($P<0.05$), 土壤容重、0.25-2mm 和<0.25mm 的土壤团聚体占比均大于放虾前; 收虾后 20-40cm 土壤还原性指标显著大于 0-20cm ($P<0.05$), 收虾后和收稻后有机还原性物质、 Fe^{2+} 和 Mn^{2+} 含量显著大于放虾前 ($P<0.05$); 0-20cm 土壤全量和速效养分均高于 20-40cm, 土壤有机质、全量和速效养分含量顺序依次为收虾后>收稻后>放虾前。

关键词: 稻-罗氏沼虾; 土壤物理性质; 还原性物质含量; 土壤养分;

Effects of a new rice-macrobrachium rosenbergii crop rotation model on reclaimed soil physicochemical properties and nutrient supply

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Abstract : To investigate the impacts of the newly established rice-macrobrachium rosenbergii rotation system on reclaimed soil physicochemical properties and nutrient supply capacity, and finally in order to objectively evaluate the comprehensive economic and ecological benefits of this system. This study examined the physical properties, reducing substances, total and available nutrients of soil layers (0-20cm and 20-40cm) at three different production stages (before shrimp stock, after shrimp harvest, and after rice harvest) using field sampling, and laboratory chemical analysis. The results indicated a significant increase in the proportion of >2mm soil aggregates from top to bottom after shrimp and rice harvesting ($P<0.05$). Soil bulk density, 0.25-2mm, and <0.25mm soil aggregates were all higher compared to those before shrimp stock. The soil reducing index in the 20-40cm layer after shrimp harvest was significantly higher than that in the 0-20cm layer ($P<0.05$). Additionally, the levels of organic reducing substances, Fe^{2+} , and Mn^{2+} after shrimp and rice harvest were significantly higher than

Key words:: Rice-macrobrachium rosenbergii rotation; Soil physical properties; Reducing substance content; Soil nutrients

缢蛏养殖对蟹-虾混养系统浮游生物粒径结构及其碳代谢特征的影响

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摘要: 浮游生物粒径结构及其碳代谢特征对水生生态系统至关重要。滤食性贝类是重要的水产经济物种, 其生理活动会显著影响养殖系统群落结构, 但关于其对浮游生物粒径结构影响的研究仍十分有限。本研究在蟹-虾系统中混养了 4 个不同密度缢蛏, 对不同养殖系统大型、小型、微型、微微型浮游生物的叶绿素 a (Chl-a) 含量、总初级生产力(GPP)、净初级生产力(NPP)和呼吸进行了测定。结果显示, 微微型浮游生物是养殖系统呼吸的主要贡献者, 微型浮游生物对 Chl-a 和 GPP 起重要作用。微型浮游生物 NPP 在各个系统中均为正值, 而微微型浮游生物 NPP 为负值。高密度混养组大型、小型和微型浮游生物的呼吸、Chl-a、GPP 和 NPP 显著低于低密度组, 而微微型浮游生物 Chl-a 和碳代谢特征在缢蛏高低密度混养系统中呈相反趋势。本研究表明, 缢蛏混养主要通过影响微型浮游生物而显著降低浮游生物总量和代谢强度, 并且使浮游生物群落小型化。

关键词: 混养系统; 滤食性贝类; 浮游生物粒径结构; 碳代谢特征

Effects of razor clam farming on the size fraction structure of plankton and their carbon metabolism in a polyculture system

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Abstract: The size fraction structure and carbon metabolism of plankton are critical to aquatic ecosystem functions. Filter-feeding bivalves are important co-culture species in aquaculture, however, research on their impact on plankton size fraction is limited. In this study, razor clams were stocked in a crab-shrimp polyculture system at four densities (PMS1, PMS2, PMS3, PMS4). Chl-a, GPP, NPP, and respiration were measured for macro-, micro-, nano-, and picoplankton. Results showed that picoplankton were the primary contributors to respiration, and nanoplankton played a key role in Chl-a and GPP. Nanoplankton had positive NPP across systems, while picoplankton showed negative. In high-density clam groups (PMS3, PMS4), respiration, Chl-a, GPP and NPP of macro-, micro-, and nanoplankton were significantly lower compared to low-density groups (PMS1, PMS2), while picoplankton showed the opposite trend. Co-culturing razor clams significantly decreased plankton biomass and metabolism, particularly impacting nanoplankton, and led to plankton community miniaturization in the system.

Key words: Polyculture systems; Filter-feeding bivalve; Size-fractioned plankton; Carbon metabolism

珠海外伶仃人工鱼礁稳定性研究

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摘要: 摘要: 人工鱼礁对投放海域的生态具有重大而深远的影响,为探明不同外观结构礁体的稳定性和沉降量,根据珠海外伶仃海域的水文、地质条件,选取了两种礁体开展研究工作,一种为箱型框架结构(3.0 m×3.0 m×4.0 m),另一种为梯形框架结构,横截面为梯形(上底宽 0.5 m、下底宽 3.5 m),底面为正方形(3.5 m×3.5 m)。在 4 种流速(0.4、1.2、1.5、2.0 m·s⁻¹)条件下,对两种礁体的水流力、抗滑抗倾稳定性、地基承载力和沉降量等特性进行了计算。结果表明,在流速 1.2 m·s⁻¹时,两种礁体的抗滑移和抗倾覆系数分别为 1.57、4.10 和 2.19、5.72,均不会发生滑移和倾覆翻滚,地基承载力和沉降量也满足要求,能发挥应有的效果;

关键词: 人工鱼礁; 稳定性; 沉降; 外伶仃

Research on the stability of artificial reef in Zhuhai Wailingding

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Abstract: Abstract: Artificial reefs have significant and far-reaching impacts on the ecology of sea areas where they are released. Based on the hydrological and geological conditions of Zhuhai Wailingding, two types of reefs were selected for research work, to investigate the stability and settlement of reef structures with different appearances. One is a box frame structure (3.0 m × 3.0 m × 4.0 m), and the other is a trapezoidal frame structure, with a trapezoidal cross-section (upper bottom width of 0.5 m, lower bottom width of 3.5 m) and a square bottom surface (3.5 m × 3.5 m). The characteristics of water flow force, anti-sliding and anti-overturning stability, foundation bearing capacity, and settlement of two types of reefs were calculated under four flow velocities (0.4, 1.2, 1.5, 2.0 m·s⁻¹). The results showed that at the velocity of 1.2 m·s⁻¹, the anti-sliding and anti-overturning coefficients of the two types of reefs were 1.57, 4.10 and 2.19, 5.72, respectively, and none of them will be slipped, overturned and rolled. The bearing capacity and settlement of the foundation also met t

Key words: artificial reefs; Stability; Settlement; Wailingding

蛋白核小球胞内、外物质对生物絮团培养中水质、絮团形成和微生物组成的影响

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摘要: 生物絮团技术 (BFT) 是一种通过调控水体中碳氮比促进微生物絮团形成的技术, 广泛应用于水质净化和水产养殖中, 添加微藻促进生物絮团的形成已被证实。本研究利用蛋白核小球藻, 探讨了蛋白核小球藻的胞内物质 (IPS) 和胞外分泌物 (EPS) 对生物絮团形成、水质及微生物群落组成的影响。通过分离和处理蛋白核小球藻的培养液、藻细胞、胞内物质、胞外分泌物及细胞碎片参与生物絮团的培养, 研究结果表明蛋白核小球藻的各组分对总氮都有一定的去除率, 胞外分泌物组去除率最高可达到 80%。而蛋白核小球藻胞内物质对生物絮团形成具有显著的促进作用, 且其效果优于其他处理组。16srDNA 测序结果展示各组微生物群落结构的变化, 蛋白核小球藻胞内物质不仅能够提供充足的营养物质促进微生物生长, 还通过增加系统中优势菌群 (如黄杆菌属和申氏杆菌属) 的相对丰度促进絮团形成并增强絮团稳定性。这些发现对于理解微藻与细菌在生物絮团形成中的应用有重要意义。

关键词: 微藻; 胞外分泌物; 胞内物质; 氮转化; 生物絮团

Effects of intracellular and extracellular substances of *Chlorella pyrenoidosa* on water quality, floc formation, and microbial composition in biofloc systems

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Abstract: Biofloc technology, widely used in water purification and aquaculture, enhances microbial floc formation by adjusting the carbon-to-nitrogen ratio. While microalgae addition has been shown to boost biofloc formation, the specific contributing components remain unclear. This study isolated components of *Chlorella pyrenoidosa*—algal cells, extracellular secretions, intracellular substances, and cell fragments—to assess their impacts on biofloc formation, water quality, and microbial communities. The findings revealed that *C. pyrenoidosa*'s IPS significantly promoted biofloc formation, outperforming other components. These substances not only supplied nutrients to foster microbial growth but also increased the dominance of key bacterial genera like *Flavobacterium* and *Shinella*, thus enhancing floc stability. All microalgal components contributed to nitrogen reduction, with EPS demonstrating an 80% removal efficiency. These results highlight the importance of understanding the interactions between microalgae and bacteria in biofloc systems, with implications for water treatment applications.

Key words: Microalgae; Extracellular secretion; Intracellular substances; Nitrogen transformation; Biofloc system

基于美国哈德逊河条纹鲈的鱼类产卵策略的年代际变化研究

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摘要：了解产卵行为对于评估鱼类种群的生产力和对开发和气候变化的脆弱性至关重要。利用哈德逊河生物监测计划 (HRBMP) 收集的鱼类浮游生物数据，我们评估了条纹鲈的产卵行为，条纹鲈是哈德逊河口 (HRE) 中一种具有高生育力的多次产卵溯河物种。我们开发了三个新的产卵最佳指数：热最佳指数、时间最佳指数和空间最佳指数。我们的结果表明，条纹鲈喜欢在两个特定且不同的时间段在特定温度范围产卵，但产卵地点在 HRE 的广泛地区。鲈鱼的产卵行为随着时间的推移发生了变化，在 1985 年和 1998 年发生了两次转变，导致在更普遍的策略下，有三个不同的时期采用不同的产卵策略。这些变化，包括最佳产卵温度范围变窄以及空间和时间产卵行为多样性降低，可能会对种群的稳定性和生殖弹性产生负面影响。研究表明，长期监测鱼卵的发生和丰度对于了解鲈鱼的长期产卵策略非常重要，并强调了在渔业管理中考虑产卵行为的重要性。

关键词：条纹鲈，产卵策略，产卵行为，时空变化

Decadal-scale changes in fish spawning strategies: a case study of striped bass in the Hudson River

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Abstract: Understanding spawning behavior is critical in evaluating the productivity and vulnerability of fish populations to exploitation and climate change. Using the ichthyoplankton data collected in a long-term monitoring program, we evaluated the spawning behavior of *Morone saxatilis*. We developed three novel spawning optimum indices: the Thermal Optimum Index, the Temporal Optimum Index, and the Spatial Optimum Index. Our results showed that striped bass prefer to spawn at certain temperature ranges during two specific and distinct time periods but in extensive locations in the HRE. We also found that the striped bass spawning behavior had changed over time, with two shifts occurring in 1985 and 1998. These changes, including a narrower range of optimal spawning temperatures and reduced diversity in spatial and temporal spawning behavior, may negatively impact the population's stability and reproductive resilience.

Key words: striped bass, spawning temperature optima, spatio-temporal spawning behavior

腊者水电站开发对多依河鱼类多样性和群落组成变化的影响

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摘要： 本研究旨在分析腊者水电站建设对多依河鱼类多样性及其群落结构造成的影响。通过对比建设前后所采集的鱼类样本，研究结果表明，水电站的建设显著降低了多依河鱼类的多样性。具体而言，鱼类种类及数量均有所减少，特别是某些特定物种的栖息地受到破坏，导致其数量显著降低。此外，鱼类群落结构亦发生了显著变化，优势物种的构成发生了转变，生态链的稳定性受到了挑战。进一步的研究指出，水电站的蓄水和水流调节对鱼类的繁殖和栖息行为产生了不利影响。基于这些发现，建议在水电站开发过程中，应加强水生生态系统的保护措施，并合理规划运营管理，以减少对鱼类多样性和生态平衡的负面影响。

关键词： 腊者水电站, 多依河, 鱼类多样性, 群落组成, 生态影响

Effect of development of Lazhi hydropower Station on fish diversity and community composition changes in Doyi River

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Abstract: The purpose of this study is to analyze the influence of rahe hydropower station construction on the fish diversity and its community structure in Duoyi River. By comparing the fish samples collected before and after the construction, the results showed that the construction of hydropower stations significantly reduced the diversity of fish in the Doyi River. Specifically, both fish species and fish numbers have decreased, especially in the habitat destruction of certain specific species, resulting in a significant decrease in their numbers. In addition, the fish community structure has also changed significantly, the composition of the dominant species has changed, and the stability of the ecological chain has been challenged. Further research pointed out that the water storage and flow regulation of hydropower station adversely affected the reproduction and habitat behavior of fish. Based on these findings, it is suggested that during the development of hydropower stations, the protection measures of aquatic ecosystems should be strengthened, and the operation management should be rationally planned to reduce the negative impact on fish diversity and ecological balance.

Key words: Lahe hydropower station, Duoyi River, fish diversity, community composition, ecological impact

水产品保鲜和加工技术研究进展

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渤海大学

摘要：介绍了我国水产业现状、水产品保鲜和加工技术发展趋势、水产品预制菜加工关键技术、励建荣研究团队在水产品保鲜和加工方面的技术成果。

关键词：水产品保鲜，水产品加工，水产品预制菜加工，关键技术

Research progressing of fresh preservation and processing technology of aquatic products

Jianrong Li
Bohai University

Abstract: The presentation introduces the research progressing of fresh preservation and processing technology of aquatic products in China.

Key words: aquatic products, fresh preservation, processing technology.

假单胞菌响应磷虾壳氟胁迫的分子机制解析 与代谢工程改造

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摘要：南极磷虾 (*Euphausia superba*) 产量巨大，但因高值转化技术缺乏，其加工副产物磷虾壳常被大量丢弃。基于假单胞菌 (*Pseudomonas putida*) 的微生物细胞工厂能够进行多种高值产品的生物合成，为废弃物质的高值化提供了一条新型高效途径。然而，磷虾壳中的高浓度氟会严重抑制假单胞菌的细胞生长，进而阻碍了磷虾壳发酵生产高价值产品——中链聚羟基脂肪酸酯 (mcl-PHA)。本研究本项目拟通过转录组分析探明假单胞菌响应磷虾壳氟胁迫的转录谱变化，并根据转录组分析结果对该菌株进行遗传改造。值得注意的是，工程菌株 KT21 的细胞生长显著增加了 33.7 倍，能够发酵磷虾壳用于 mcl-PHA 的生物合成，与对照菌株相比，mcl-PHA 产量增加了 40.3 倍。这项研究增进了我们对恶臭假单胞菌如何应对来自磷虾壳的氟胁迫的理解，并提供了耐氟菌株，实现了磷虾壳至 mcl-PHA 的高效转化。

关键词：恶臭假单胞菌；南极磷虾壳；氟；中链长度聚羟基脂肪酸酯；代谢工程

Enhancing fluoride tolerance of *Pseudomonas putida* for the production of medium-chain-length polyhydroxyalkanoates from Antarctic krill shell waste

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Abstract : Antarctic krill shell waste (AKSW), a byproduct of Antarctic krill processing, has substantial quantity but low utilization. Utilizing microbial-based cell factories, with *Pseudomonas putida* as a promising candidate, offers an ecofriendly and sustainable approach to producing valuable bioproducts from renewable sources. However, the high fluoride content in AKSW impedes the cell growth of *P. putida*. This study aims to investigate the transcriptional response of *P. putida* to fluoride stress from AKSW and subsequently conduct genetic modification of the strain based on insights gained from transcriptomic analysis. Notably, the engineered strain KT21 exhibited a remarkable 33.7-fold increase in cell growth, capable of fermenting AKSW for medium-chain-length-polyhydroxyalkanoates (mcl-PHA) biosynthesis, achieving a 40.3-fold increase in mcl-PHA yield compared to the control strain. This research advances our understanding of how *P. putida* responds to fluoride stress from AKSW and provides fluorine-tolerant strains that serve as excellent platforms for producing mcl-PHA through AKSW.

Key words:: *Pseudomonas putida*, Antarctic Krill Shell Waste (AKSW), Fluoride, Medium-chain-length-polyhydroxyalkanoates (mcl-PHA), Metabolic Engineering

水产品预制菜的研究开发与创新发展

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摘要: 随着消费者对方便、快捷加工食品需求的不断增长, 以及新冠疫情引起生活方式的改变, 水产品预制菜越来越得到广大消费者的亲睐。水产原料独有的营养功能特性和加工适性使其可以广泛用于即热、即烹、即配等预制菜的开发, 但其特有的腥味、质构及易腐败特性, 要求在加工和贮藏过程中采用适当的预处理技术、风味和品质改良与保持技术以及贮藏技术来保持预制菜产品的品质。影响水产品预制菜质量安全的主要因素包括生物性危害、化学性危害和物理性危害, 因此在原料采收阶段、加工过程、冷链运输过程的质量控制技术及管理控制体系是保障产品质量安全的重要手段。水产品预制菜未来将会向着营养、健康、美味、方便和多元化方向发展。

关键词: 水产品预制菜; 原料特性; 加工技术; 质量安全

Research advances on processing and quality safety control technology of aquatic pre-made products

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Abstract: Due to the growing demand for instant food and lifestyle change after the COVID-19, aquatic pre-made products become popular. The unique nutritional and functional characteristics and processing suitability of aquatic products make them suitable for the development of instant heat, instant cooked and ready-to-use pre-made products. However, due to their unique fishy taste, texture and perishable characteristics, appropriate pretreatment technology, flavor and quality improvement and maintenance technology as well as storage technology in the processing and storage process need to be adopted so as to improve the quality of pre-made products. The main factors affecting the quality and safety of aquatic product pre-made products include biological hazards, chemical hazards and physical hazards. Therefore, quality control technologies of aquatic pre-made products including the raw material collection, processing process and the cold chain transportation process are necessary. [Conclusion] In the future, aquatic pre-made products should be more nutritious,

Key words: Aquatic pre-made products; Material characteristics; Processing technology; Quality control technology

利用靶向蛋白质组学和可视化策略研究海参 (*Apostichopus japonicus*) 体壁中原纤维蛋白 的存在

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摘要: 原纤蛋白是结缔组织中一种重要的结构蛋白。刺参中原纤蛋白的存在仍然知之甚少, 这限制了我们对原纤蛋白在刺参微结构中的作用的理。本文旨在利用靶向蛋白质组学和可视化策略阐明刺参中原纤蛋白的存在。测定了三种不同亚型高丰度原纤蛋白的含量, 分别为 0.96、2.54 和 0.15 $\mu\text{g/g}$ (湿基)。选择原纤蛋白 (GeneBank 编号: PIK56741.1) 631-921aa 的氨基酸序列用于克隆和表达抗原。成功获得了效价大于 1:64000 的抗刺参原纤蛋白抗体。在微观尺度上观察到原纤蛋白在刺参体壁中以原纤维束的形式分散。在纳米尺度上观察到原纤蛋白存在于胶原纤维附近, 部分与胶原纤维缠绕。此外, 刺参中最主要的胶原蛋白和原纤蛋白分子的化学计量比约为 250:1。这些结果有助于理解原纤蛋白在海参微观结构中的作用。

关键词: 海参、原纤蛋白、靶向蛋白质组学、免疫定位、化学计量

Investigation of the Presence of Fibrillin in Sea Cucumber (*Apostichopus japonicus*) Body Wall by Utilizing Targeted Proteomics and Visualization Strategies

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Abstract: Fibrillin is an important structural protein in connective tissues. The presence of fibrillin in *Apostichopus japonicus* is still poorly understood. The aim of this study was to clarify the presence of fibrillin in the *A. japonicus* by utilizing targeted proteomics and visualization strategies. The contents of three different isoforms of fibrillin with high abundance were determined to be 0.96, 2.54, and 0.15 $\mu\text{g/g}$ (wet base), respectively. The amino acid sequence of fibrillin (GeneBank number: PIK56741.1, 631-921aa) was selected for cloning and expressing antigen. An anti-*A. japonicus* fibrillin antibody with a titer greater than 1:64 000 was successfully obtained. It was observed that the distribution of fibrillin in the *A. japonicus* was scattered and dispersed in the form of fibril bundles at the microscale. It further observed that fibrillin was present near collagen fibrils and some entangled outside the collagen fibrils at the nanoscale. Moreover, the stoichiometry of the most dominant collagen and fibrillin molecules in *A. japonicus* was determined to be approximately 250:1.

Key words: sea cucumber, fibrillin, targeted proteomics, immunolocalization, stoichiometry

休闲渔业游客感知价值、地点认同与行为意向关系的研究——以福建省为例

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摘要：休闲渔业作为一种新型渔业发展方式和新型休闲和旅游方式，把旅游、观光、垂钓等休闲活动与现代渔业有机结合，开辟了新的乡村旅游市场。现有对休闲渔业的研究主要侧重于休闲渔业基本理论和休闲渔业供给侧的研究，较少涉及休闲渔业游客需求方面的报道。研究基于游客对福建省休闲渔业的体验感知，依托 347 份调研问卷，从游客对休闲渔业的需求出发，借助“认知→情感→行为”的关系理论构建了休闲渔业感知价值、地点认同、行为意向的结构模型，并对“感知价值-地点认同”、“地点认同-行为意向”、“地点认同作为中介变量”之间的影响机制进行了假设设定，进行了相应的验证分析和效应检验。

关键词：休闲渔业；福建省；感知价值；地点认同；行为意向

Study on the Impact Mechanism of Recreational Fisheries Sustainable Development in Fujian Province: Perceived value, Place identity and Behavioral intention

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Abstract: As a new way of fishery development and a new way of leisure and tourism, recreational fisheries combine tourism, sightseeing, fishing and other leisure activities with modern fisheries, opening up a new rural tourism market. The current research on recreational fisheries mainly focuses on the basic theory of recreational fisheries and the supply side of recreational fisheries, and few reports involve the demand of recreational fisheries tourists. Based on tourists' experience and perception of recreational fisheries in Fujian Province, this study relies on 347 questionnaires and builds a structural model of perceived value, location identification and behavioral intention of recreational fisheries based on the relationship theory of "cognition→emotion→behavior". Moreover, the influence mechanism of "perceived value - place identity", "place identity - behavior intention" and "place identity as an intermediary variable" is hypothesized, and the corresponding verification analysis and effect test are carried out.

Key words: Recreational fisheries; Attitude theory; Perceived value; Location identification; Behavioral intention

中国快速增长的休闲渔业经济对温室气体排放的供应链影响

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摘要: 休闲渔业作为渔业重要部分, 在减少碳排放方面具有巨大潜力。尽管休闲渔业发展迅速, 但社会经济因素与碳排放之间的作用机制尚不清晰。定量评估休闲渔业的碳足迹, 对于实现中国 2030 年碳封顶目标至关重要。本研究采用投入产出分析法, 从供应链角度评估了中国休闲渔业碳排放量。结果显示, 与传统渔业生产相比, 休闲渔业产生的碳排放量较低, 2018 年至 2021 年平均为 0.5 万吨。此外, 休闲渔业的碳排放主要与其与生产和销售的上游产业的联系所驱动。研究进一步确定了影响休闲渔业碳排放的关键因素, 并提出了相应的管理策略。本研究为实现渔业的高质量发展提供科学依据, 符合中国 2030 年碳减排目标。

关键词: 休闲渔业; 供应链效应; 碳排放; 投入产出; 温室气体

Supply chain effects of China's fast growing recreational fishery economy on greenhouse gas emissions

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Abstract: As an important part of the fishery industry, recreational fisheries have great potential for reducing carbon emissions. Despite the rapid development of recreational fisheries, the mechanism of the role between socioeconomic factors and carbon emissions is unclear. Quantitatively assessing the carbon footprint of recreational fisheries is crucial for realizing China's 2030 carbon capping target. In this study, we used input-output analysis to assess the carbon emissions of recreational fisheries in China from a supply chain perspective. The results show that compared with traditional fishery production, recreational fisheries generate lower carbon emissions, averaging 0.5 million tons from 2018 to 2021. In addition, carbon emissions from recreational fisheries are mainly driven by their linkages with upstream industries for production and marketing. The study further identifies the key factors affecting carbon emissions from recreational fisheries and proposes corresponding management strategies. This study provides a scientific basis for realizing the development of fishery.

Key words: Recreational fisheries; supply chain effects; carbon emissions; input-output; greenhouse gases

中国休闲渔业发展模式略论

宁波

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摘要：休闲渔业已经成为消费者休闲放松、以渔为乐的一种文化消费途径。本文将休闲渔业业态类型划分为休闲观光型、教育研学型、休闲垂钓及采集业、观赏鱼产业，并对其主要特征及优势进行分析。梳理中国休闲渔业主要发展模式，可以划分为个体创业驱动模式、产业转型驱动模式、政策资金驱动模式以及资本融合驱动模式。中国4种休闲渔业发展模式目前存在个体创业驱动模式占比过大、产业转型驱动模式比较雷同、政策资金驱动模式有欠协调、资本融合驱动模式易走极端等问题。对此，可以通过提升个体经营竞争力、优化产业链、完善相关政策、提升资本融合度等措施推进休闲渔业发展。

关键词：休闲渔业；业态类型；发展模式

A brief discussion on the development model of recreational fishery in China

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Abstract: Recreational fishery has become a cultural consumption way for many consumers to relax and enjoy fishing. In this paper, the types of recreational fishery are divided into leisure tourism, educational type, recreational fishing and collecting industry and ornamental fish industry, and their main characteristics and advantages are analyzed. The main development models of China's recreational fishery are individual entrepreneurship driven model, industrial transformation driven model, policy fund driven model and capital integration driven model. At present, there are some problems in China's four recreational fishery development models, such as a large proportion of individual entrepreneurship driven models, similarity in industrial transformation driven models, lack of coordination in policy and funding driven models, and the tendency of capital integration driven models to go extreme. In this regard, the development of recreational fishery can be promoted by enhancing the competitiveness of self-employed businesses, optimizing the industrial chain structure, improving relevant polic

Key words:: recreational fishery; type of business format; development model

崇明岛渔文化资源结合新质生产力提质增效 的思考

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摘要：随着我国乡村振兴战略和城乡融合发展的不断推进，都市农业逐渐成为代替传统农业促进区域经济增长的主要发展模式。本文旨在探讨上海市崇明岛如何通过发掘和应用崇明岛现有渔文化资源，合理搭配新质生产力，促进渔业经济增长，进而推动都市农业发展。文章首先分析崇明岛渔文化资源以及都市农业的现状，分析崇明岛渔文化资源的发展存在的局限，然后深入探讨渔文化资源应如何与新质生产力相结合，最后提出对应的都市农业发展策略和建议，以为其他都市农业发展提供参考。

关键词：渔文化资源；新质生产力；休闲渔业；崇明岛都市农业

Thinking on improving the quality and efficiency of Chongming Island fishing culture resources combined with new quality productivity

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Abstract : With the continuous development of rural revitalization strategy and urban-rural integration, urban agriculture has gradually become the main development mode to replace traditional agriculture to promote regional economic growth. The purpose of this paper is to discuss how to promote the growth of fishery economy and the development of urban agriculture by exploring and applying the existing fishery culture resources in Chongming Island of Shanghai and rationally matching the new quality productivity. This paper first analyzes the current situation of fishery cultural resources and urban agriculture in Chongming Island, analyzes the limitations of the development of fishery cultural resources in Chongming Island, and then deeply discusses how to combine fishery cultural resources with new quality productivity. Finally, it puts forward corresponding urban agriculture development strategies and suggestions to provide reference for other urban agriculture development.

Key words: : Fishing culture resources; New quality productivity; Recreational fisheries; Chongming Island urban agriculture

望天眼金鱼的血液和玻璃体液生理生化指标研究

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摘要：研究目的是了解望天眼金鱼（*Carassius auratus*）血液和玻璃体液生理、生化成分，并比较两者差异。采集健康望天眼金鱼血液和玻璃体液，在全自动血液分析仪中检测白和红细胞等 17 项生理指标；同时在全自动生化分析仪中检测白蛋白和 Ga2+ 等 20 项生化指标；并进行了采集血液和玻璃体液后，对望天眼金鱼后续成活率影响实验。结果显示：血液 17 项生理指标均有数值，其中红细胞为 $2.19 \times 10^{12}/L$ ，白细胞为 $62.21 \times 10^9/L$ ，血红蛋白为 $138.25 g/L$ ，未发现嗜酸性和嗜碱性粒细胞；而其玻璃体液 17 项生理指标均未显示数值，未检测到细胞；血清和玻璃体液的 20 个生化指标中，11 个指标的浓度在玻璃体液中显著比血清低；7 个指标差异不显著；而 2 个指标在玻璃体液中显著比血清高。这次试验为望天眼金鱼的健康养殖、和完善金鱼血液学的研究以及金鱼望天眼性状发育形成的机制研究提供基础数据。

关键词：望天眼金鱼；血液；玻璃体液；生理指标；生化指标

Study on Hematological and Biochemical Index of Blood and Vitreous humor in the celestial goldfish

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Abstract : The purpose of this study was to investigate the hematological and biochemical components of the blood and vitreous humor in the celestial goldfish (*Carassius auratus*). Blood and vitreous humour samples were drawn from healthy celestial goldfish. An automatic haematology analyzer was used to measure 17 physiological indicators in the blood and vitreous humour. Additionally, 20 biochemical indexes were measure by an automatic biochemical analyzer. Experiments were also conducted on the effect of blood and vitreous humour collection on the subsequent survival rate of the celestial goldfish. The results showed that the blood of the goldfish had values for 17 hematological indicators, including red blood cells (2.19×10^{12}), white blood cells (62.21×10^9), hemoglobin ($138.25 g/L$), and no eosinophils or basophils. However, no data for hematological indicators of vitreous humor were found. The levels of 11 biochemical components in the vitreous humor were lower than those in the serum, and the levels of ALT and GGT in vitreous humor were significantly higher than those in serum.

Key words:: celestial goldfish; blood; vitreous humor; hematological indicators; biochemical indicators

网衣清洗装置设计及仿真试验研究

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摘要: 针对网衣在水中易被藻类、紫贻贝等生物附着,造成水质交换不畅、溶氧降低、鱼病频发等问题,基于空化射流原理,本研究提出一种网箱网衣清洗装置。采用三维建模及仿真试验方法,开展了喷嘴网格无关性验证试验。利用 Fluent 软件建立喷嘴有限元模型,对喷嘴结构参数进行单因素试验。以气相体积分数为评价指标进行二次回归正交试验,得到喷嘴最佳参数组合为末端扩散角 35.495° 、第二段喉管半径 0.834mm 、第二段喉管收缩角 41.047° ,该参数组合下气相体积分数可达到 0.9413 。依据仿真优化结果试制网衣清洗试验台,以靶件表面粗糙度为指标开展空蚀性能试验,分析不同环境参数下的空蚀性能,确定最优环境参数为高压泵泵压 22.512MPa 、靶距 13.404mm 、夹角 17.335° ,该参数组合下靶件的最大表面粗糙度为 6.828 。研究结果为网衣清洗装置的研制和优化改进提供参考。

关键词: 渔业机械;空化射流;喷嘴;Fluent 仿真

Design and simulation test research of net clothing cleaning device

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Abstract: In view of the problems that netting is easy to be attached by algae, purple mussels and other organisms in water, resulting in poor water quality exchange, reduced dissolved oxygen, and frequent occurrence of fish diseases, based on the principle of cavitation jet, a cage netting cleaning device was proposed. Using the three-dimensional modeling and simulation test methods, the nozzle grid independence verification test was carried out. The finite element model of the nozzle was established by Fluent software, and the single-factor test of the nozzle structural parameters was carried out. The quadratic regression orthogonal test was carried out with the gas phase volume fraction as the evaluation index, and the optimal parameter combinations of the nozzle were 35.495° at the end diffusion angle, 0.834mm from the second section of the throat, and 41.047° from the second section of the throat, and the gas phase volume fraction could reach 0.9413 under the combination of these parameters. According to the simulation optimization results, the net cleaning test bench was trial-produced, and the cavitation performance test was carried out with the surface roughness of the target as the index, and the cavitation performance under different environmental parameters was analyzed, and the optimal environmental parameters were determined to be the pump pressure of the high-pressure pump 22.512MPa , the target distance of 13.404mm , and the included angle of 17.335° , and the maximum surface roughness of the target under the combination of parameters was 6.828 . The research results provide a reference for the development, optimization and improvement of net clothing cleaning equipment.

Key words:: Fishery machinery; Cavitation jets; Nozzle; Fluent emulation

基于离散延迟涡模型的 PET 网片绕流特性数值模拟

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摘要: 聚对苯二甲酸乙二酯(PET)网衣(俗称“龟甲网”)作为典型的渔用高性能网衣目前被广泛应用, 研究其绕流特性对掌握阻力特性和尾流分布至关重要。本研究基于离散延迟涡模型(IDDES)研究了 PET 网片周围流场分布与目脚尾流特性。研究结果表明, 目脚结构对网片周围流场分布产生显著影响, PET 网片的双股捻制目脚近尾流区域出现了横流现象。双股捻制目脚由于其扭曲结构影响了目脚表面限制流线, 导致目脚产生明显的 3D 分离和涡流形成长度的显著增长, 形成了更稳定的自由剪切层。这种结构的改变显著降低了近尾流中的湍流动能(TKE), 从而降低了阻力和升力波动。双股捻制目脚相比于光滑目脚阻力低了大约 10%, 湍流动能降低了 25%。此外, 探究了 PET 网片后方流速衰减情况, 在网片密实度为 0.173 时, 网片速度衰减为 94%。本研究开展了 PET 网片绕流特性研究, 为进一步优化高分子渔用高性能网衣奠定基础。

关键词: PET 网片; 数值模拟; 尾流分布; 自由剪切层; 阻力

Numerical Simulation of Flow Characteristics Around PET Net Panels Based on the Delayed Detached Eddy Simulation Model

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Abstract: Polyethylene terephthalate (PET) nets, known as "tortoise shell nets" are widely used as high-performance fishing nets. Understanding their flow characteristics is essential for analyzing drag properties and wake distribution. This research employs the Improved Delayed Detached Eddy Simulation (IDDES) method to investigate the flow field and wake characteristics around PET net panels. Results show that the net structure significantly influences the surrounding flow, with the double-stranded twisted design exhibiting transverse flow phenomena in the near-wake region. The twisted structure alters flow lines, leading to three-dimensional separation and increased vortex formation length, thus creating a more stable free shear layer. This change reduces turbulent kinetic energy (TKE) in the near-wake, resulting in approximately 10% lower drag and a 25% reduction in TKE compared to smooth nets. Additionally, velocity decay behind the net panels reaches 94% at a solidity of 0.173. This research provides a foundation for optimizing high-performance polymer fishing nets.

Key words: PET nets; numerical simulation; wake distribution; free shear layer; drag

铜合金编织网网片阻力水槽试验研究

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摘要: 铜合金编织网是目前应用于大型养殖围栏上的一种耐海水腐蚀、防海洋污损生物附着的金属网衣。通过开展不同铜丝直径及不同网目尺寸的铜合金编织网网片水阻力试验, 获得系列规格铜合金编织网网片的阻力变化规律及计算公式。试验结果为: 网片的阻力在流速变大时或迎流冲角增大时, 网片的阻力随之增加; 相同网线直径的网片在特定流速与冲角下, 其阻力随网目尺寸的增加而减小; 相同网目尺寸的网片在特定流速与冲角下, 其阻力随网线直径的增加而增大。基于试验数据得出铜合金编织网网衣在垂直流速时随流速变化的单位面积网衣阻力计算公式; 利用点状图回归分析法得出铜合金编织网在垂直流速与平行流速两种状态下的阻力系数和雷诺数的对应关系; 参考经验公式提出不同冲角下阻力系数的推导公式, 并基于试验数据给出网片平面垂直于流速及平行于流速状态下的阻力系数。本研究可为铜合金编织网网衣的受力计算以及水动力性能分析提供参考。

关键词: 铜合金编织网; 网片; 阻力; 水槽试验

Experimental research on resistance of copper alloy woven net in water tank

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Abstract: Water tank experiment studied copper alloy woven net resistance to obtain changing law. Tested at 5 trailer speeds. Resistance increased with flow velocity and attack angle. At fixed flow rate and angle, resistance decreased with mesh size but increased with wire diameter. Obtained net resistance formula using regression analysis. Analyzed resistance coefficient vs. Reynolds number under vertical and parallel flow. Proposed resistance coefficient formula under various attack angles and gave drag coefficients based on data. Study aids force calculation and hydrodynamic analysis of copper alloy woven nets.

Key words:: copper alloy woven net; net; resistance; water tank test

基于 Tracepro 的秋刀鱼 LED 集鱼灯水下照度研究

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摘要: 为使集鱼灯灯光得到更有效的利用, 同时减少不必要的能源损耗, 对集鱼灯进行合理配置。通过设计水箱模拟实验分析光照进入水下后的照度分布变化, 利用 Tracepro 建立理论照度模型。比较 Tracepro 拟合值与实测值发现, 模型拟合值与实测值间的线性拟合斜率系数接近于 1, 说明基于 Tracepro 建立的照度模型符合实际情况。根据模型分别计算了在 45°、60°、75° 倾角下的水下 5m 分辨率为 0.1m 的有效水体面积和体积。根据有效水体体积, 推出集鱼灯最优角度在 30-40° 之间。通过 Tracepro 为将来分析水中照度分布、LED 集鱼灯研发及渔船集鱼灯合理配置等提供理论参考。

关键词: 光诱渔业; 水下照度; 集鱼灯; Tracepro

Study on Illumination of fishing lamps Based on TracePro

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Abstract: To make more effective use of the light from fishing lamps while reducing unnecessary energy consumption, a reasonable configuration of these lamps is essential. By designing a tank simulation experiment to analyze the changes in illumination distribution after light enters underwater, a theoretical illumination model was established using Tracepro. Comparing the fitted values from Tracepro with the actual measurement values, it was found that the linear fitting slope coefficient between the model's fitted values and the actual measured values is close to 1, indicating that the illumination model based on Tracepro aligns well with real-world conditions. According to the model, the effective water volume area and volume at depths of 5 meters with a resolution of 0.1 meters were calculated for angles of incidence of 45°, 60°, and 75°. Based on the effective water volume, the optimal angle for fish-attracting lamps was determined to be between 30-40°. Through the use of Tracepro, this study provides a theoretical reference for future analysis of underwater illumination distribution, the

Key words: light attracting fishery; underwater illumination; underwater illumination; fishing lamps; Tracepro

融合多源框架信息提升渔业机器人 细粒度感知

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摘要：海洋勘探对于利用其丰富的资源至关重要。水下机器人捕获的图像存在颜色失真和对比度降低等问题。为了解决水下图像中的低照度、对比度降低和颜色偏移等问题，提出了一种基于 Transformer 和 CNN 并行融合的水下图像增强算法。实验表明，该方法可以有效地将 Transformers 的局部上下文捕获能力与 CNN 的全局特征提取能力相结合，从而提高提取特征的丰富性和准确性。为了有效地减少计算负载并减轻颜色伪影，一种新的 Transformer 模型集成了 PSNR 注意力和线性运算。通过数学方法，该方法可以将计算复杂度从 $2d^2n$ 降低到 $3dn$ ，同时提取约束特征。此外，通过利用时域和频域特征，设计了一种新的全局特征提取网络来丰富图像特征。从输入图像的傅里叶变换中提取高频和低频信息，用于融合不同骨干的特征。实验表明，该方法优化了 Transformer 和 CNN 特征的融合权重，丰富了表示特征的多样性。

关键词：水下图像增强，全局特征，局部特征，框架融合

Enhancing Fine-Grained Perception of Fishery Robots Through the Integration of Multi-Source Framework Information

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Abstract: Marine exploration is crucial for harnessing its abundant resources, yet underwater images captured by robots often suffer from color distortion and reduced contrast. To address issues such as low illumination, decreased contrast, and color shift in underwater images, a novel image enhancement algorithm based on the parallel fusion of Transformers and CNNs is proposed. Experiments demonstrate that this method effectively combines the local context-capturing ability of Transformers with the global feature extraction capability of CNNs, enhancing the richness and accuracy of feature extraction. To reduce computational load and mitigate color artifacts, a new Transformer model integrates PSNR attention and linear operations. Mathematically, this approach reduces the computational complexity from $2d^2n$ to $3dn$ while extracting constrained features. Additionally, by leveraging both time-domain and frequency-domain features, a new global feature extraction network is designed to enrich image characteristics.

Key words: Underwater image enhancement, global features, local features, framework fusion

连接方式对金枪鱼延绳钓渔具力学特性研究

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摘要：金枪鱼延绳钓渔具凭借其环境友好的特性，在海洋捕捞领域中扮演着不可或缺的重要角色。延绳钓渔具力学性能对保障和提升捕捞效率具有重要意义，尤其是不同连接方式的选择，目前对此尚缺乏足够和定量的理解。本研究主要使用拉力机，对金枪鱼延绳钓渔具在四种不同拉伸速度条件下的力学特性进行了深入研究，并对四种连接方式（单道法固定、双道法固定、圆形法固定和插眼法固定）的失效进行了详细的分析。研究结果表明：（1）插眼法和圆形固定的连接方式的聚丙烯绳力学性能优于单道固定和双道固定；（2）与没有任何连接方式的绳索相比，插眼法和圆形固定在力学特性上仅下降了5%；（3）对于直径超过2 mm的尼龙单丝，单道固定连接方式力学性能最优，能有效减少应力集中；（4）渔具中，第三段的力学性能最为薄弱，在实际作业过程中应给予重点关注。本研究有助于深入理解金枪鱼延绳钓渔具力学性能，为渔具的连接方式及安全评估提供参考。

关键词：延绳钓渔具；连接方式；破坏载荷；尼龙单丝；聚丙烯绳

Effect of Connection Methods on the Mechanical Characteristics of Tuna Longline Gear

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Abstract: Tuna longline gear is a crucial component in marine fishing. Improving the efficiency of fishing gear is highly dependent on the mechanical properties of longline fishing gear, especially the choice of connection methods, but there is still lack of sufficient and quantitative understanding. This study used tension machine to explore the static characteristics of tuna longline fishing gear by different connection methods under four stretching speeds. Then, the failure analysis of four connection types (single-fixation, double-fixation, sheet-bend and eye-splice connection) were performed in detail. The results showed that: (1) eye-splice and sheet-bend connections of polypropylene twines are better than single-fixation and double-fixation; (2) compared with the twines without connections, the mechanical characteristics of the connection twines are only reduced by 5%; (3) for nylon monofilament with a diameter exceeding 2 mm, single-fixation connection is better than other forms, which reduces stress concentration; (4) the weakest mechanical performance of the entire fishing gear occurs in the th

Key words: Longline gear; connection methods; breaking load; nylon monofilament; polypropylene twine

融合机理模型和机器视觉的斑石鲷生长预测研究

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摘要: 为了探究斑石鲷的生长规律, 本研究从幼鱼早期阶段开始, 对斑石鲷的长度、宽度和重量等生物量进行系统监测。在各个阶段生物量监测的同时, 利用关键点检测模型、图像处理和三维重建算法获取精确的鱼体形态数据。通过长期监测和数据分析, 研究斑石鲷在不同生长阶段的体长、体重及体型变化。此外, 本研究将生长数据与喂养数据相结合, 建立生长规律模型, 并使用立体视觉获得的数据对模型进行验证。实验结果表明, 立体视觉技术能够高效、准确地记录斑石鲷的生长数据, 并揭示其在不同环境条件下的生长规律。这些发现为斑石鲷的养殖管理提供了科学依据, 有助于优化养殖策略, 提高养殖效率。研究还探讨了立体视觉技术在水产养殖中的应用前景, 指出其在精准养殖、健康监测和生长评估等方面具有广泛的应用潜力。

关键词: 立体视觉; 生长规律; 生物量; 三维重建; 关键点检测

Research on growth prediction of *Maculatus maculatus* using a combination of mechanistic models and machine vision

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Abstract : In order to explore the growth law of *Porphyropleuron* at all stages, this study systematically monitored the biomass of porphyropleuron, such as length, width and weight, starting from the early stage of juvenile fish. The key point detection model, image processing and 3D reconstruction algorithm were used to obtain accurate fish body morphology data during biomass monitoring at each stage. Through long-term monitoring and data analysis, the changes of body length, body weight and body shape in different growth stages were studied. In addition, this study combined growth data with feeding data to establish a growth law model, and verified the model using data obtained from stereo vision. The experimental results show that the stereo vision technology can record the growth data efficiently and accurately, and reveal its growth law under different environmental conditions. These findings provide scientific basis for the culture management of *Porphyropomacris*, and help to optimize the culture strategy and improve the culture efficiency. The paper also discusses the application prospect

Key words:: stereovision; growth law; biomass; three-dimensional reconstruction; keypoint detection

基于可解释人工智能理论构建 VGG 模型 金枪鱼识别方法

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摘要：随着全球渔业资源的不断衰退和生态环境的日益恶化，深入理解及有效管理渔业生物信息成为当务之急。近些年，深度学习模型在海洋渔业捕捞生产领域的研究逐渐增加，但因其网络的复杂与不透明性，通常被称为“黑箱”，可能会引起监管机构与公众的担忧，可解释性研究有助于增强人们对模型的信任，对环境和社会复杂。本文针对 VGG-16 模型对金枪鱼图像的识别进行可解释性研究，利用可视化技术观察其处理图像时的特征图，对其中的颜色、纹理和边缘等特征进行分析，并使用类激活映射技术对模型认为最重要的图像区域进行识别。本文选择多个金枪鱼图像，并提取多个卷积层的对应特征图，对模型所提取的多种特征进行对比与分析，研究并提高了其可解释性。本研究初步探索揭示模型的内部工作机制，有助于改进补充模型，使其在金枪鱼识别应用中更加可靠、有效和透明，以推动渔业生物信息技术的进一步发展。

关键词：金枪鱼渔业；图像识别；可解释人工智能；特征提取

Constructing VGG Model Tuna Recognition Method Based on Interpretable Artificial Intelligence Theory

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Abstract : With the continuous decline of global fishery resources and the deterioration of the ecological environment, in-depth understanding and effective management of fishery biological information has become an urgent task. In recent years, the research of deep learning models in the field of marine fishery production has gradually increased, but due to the complexity and opacity of its network, often called the “black box”, which may cause concerns of regulatory agencies and the public, interpretable research can help to enhance people's trust in the model, the environment and social complexity. In this paper, we conduct an interpretability study on the recognition of tuna images by the VGG-16 model, using visualization techniques to observe the feature maps of the processed images, analyze the features such as color, texture, and edges, and use the class-activation mapping technique to identify the image regions that are considered to be the most important by the model. In this paper, multiple tuna images are selected and the corresponding feature maps of multiple convolutional layers are

Key words: : Tuna fisheries; image recognition; interpretable artificial intelligence; feature extraction

仿生海豚航行器集群水动力研究

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摘要：本文基于数值模拟技术，系统分析了仿生海豚在不同队形及速度下的流体动力学特性，特别是其在水下探测中的应用潜力。通过模拟 2-4 条仿生海豚在 1-3 米每秒速度范围内的航行行为，研究了水平、垂直及线形列队下的流体阻力、升力及流场压力分布情况。分析结果表明，合理的队形编排可以有效降低个体所受阻力，并优化集群的运动效率。这不仅有助于提升仿生海豚在复杂水下环境中的长时间巡航能力，还为水下探测任务中的高效、低能耗航行提供技术支持。此外，本研究对渔业的智能化发展具有潜在应用价值，仿生海豚群游方式可用于提高水下资源探测、监控及捕捞效率，从而为可持续渔业提供创新型解决方案。通过对不同排列方式的深入分析，本文为仿生水下航行器的设计优化奠定了基础，并为未来在渔业和其他水下探测领域的应用提供了理论指导。

关键词：仿生海豚；流体动力学；数值模拟；群体游动

The Hydrodynamic Study of a Biomimetic Dolphin Vehicle Swarm

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Abstract : This study, based on numerical simulation technology, systematically analyzes the hydrodynamic characteristics of biomimetic dolphins in different formations and speeds, with a particular focus on their potential applications in underwater exploration. By simulating the movement of 2-4 biomimetic dolphins at speeds ranging from 1 to 3 meters per second, the research investigates the drag, lift, and flow field pressure distribution under horizontal, vertical, and linear formations. The analysis results show that an optimal formation arrangement can effectively reduce individual drag and enhance the overall efficiency of the swarm's movement. This not only helps improve the long-distance cruising capability of biomimetic dolphins in complex underwater environments but also provides technical support for efficient, low-energy underwater exploration tasks. Furthermore, this research has potential applications in the intelligent development of the fishing industry, where biomimetic dolphin group swimming techniques could improve the efficiency of underwater resource detection, monitoring,

Key words:: Biomimetic Dolphin; Hydrodynamics; Numerical Simulation; Group Swimming

水生生物健康监测可穿戴传感器研究

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摘要: 监测水生生物健康对维持海洋生态系统平衡和生物多样性至关重要。为及时准确评估水生生物的健康状态, 我们通过掺入液态金属 (LM, 共晶镓铟合金) 开发了一种混合角蛋白 (KE) 水凝胶, 以设计一种具有优异生物相容性、增强导电性和良好机械性能的可穿戴电子设备。所得 KELM 水凝胶可以用来监测无脊椎水生动物的微弱心跳运动以及水生脊椎动物的心跳和持续的尾部运动。它能够区分不同水生生物的心跳模式 (在本研究中为大鲵、鲟鱼和扇贝)。KELM 水凝胶具有良好的机械特性, 包括高抗拉强度 (166 kPa) 和可拉伸性 (2600%), 以及具有良好的导电性 (6.84 S m^{-1}) 和作为传感材料的灵敏度 ($\text{GF}=7.03$), 使其适用于构建高性能应变传感器。基于 KELM 水凝胶的可穿戴电子设备将其功能扩展到监测海洋生物的健康。这一创新应用为设计下一代仿生电子设备提供了新的见解, 在电子皮肤、人工智能和健康监测方面具有潜在的应用。

关键词: 海洋生物健康、水产养殖、角蛋白水凝胶、液态金属、可穿戴电子产品

Research on wearable sensors for monitoring the health of aquatic organisms

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Abstract: Monitoring the health of aquatic organisms is vital for marine ecosystem balance and biodiversity. To assess their health accurately, we developed a hybrid keratin (KE) hydrogel with liquid metal (LM, eutectic gallium-indium alloy) for a wearable electronic device with excellent biocompatibility, enhanced conductivity, and good mechanical properties. The KELM hydrogel can detect subtle heartbeat movements in invertebrates and heartbeats and tail movements in vertebrates, distinguishing patterns in giant salamanders, sturgeons, and scallops. It demonstrates high tensile strength (166 kPa), stretchability (2600%), good conductivity (6.84 S m^{-1}), and sensitivity ($\text{GF}=7.03$), making it suitable for high-performance strain sensors. This innovative wearable technology enhances marine health monitoring and provides insights for next-generation biomimetic devices, with potential applications in electronic skin, artificial intelligence, and health monitoring.

Key words: Marine inhabitants health, aquaculture, keratin hydrogel, liquid metal, wearable electronics

一种自容式多通道水下照度计的设计研究

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摘要: 精确测量水下光照对现代渔业设施装备与信息化至关重要。传统的水下光照度计受单一传感器和外部电源依赖的限制, 难以满足深海环境中长时间、高精度的测量需求。为此, 我们设计了一种基于智能 GD32 微控制器的自容式多传感器水下照度计。该设计采用自容式存储技术, 能够利用微控制器实时处理和分析来自多个传感器的数据。在性能测试阶段, 我们模拟了不同深度 (不超过 300 米) 和温度 (0-40 摄氏度) 的水下环境, 对这款水下照度计的测量范围、测量精度、响应时间、稳定性以及自供电能力进行了全面评估。通过调节配重, 该设备还能实现剖面测量, 从而进一步提高了测量的准确性。测试结果显示, 这款水下照度计在水下环境中表现出高度的可靠性和实用性。这款多功能水下照度计的应用, 为现代渔业设施装备提供了更为精确的水下光场数据, 为渔业信息化的进一步发展提供了有力支持。

关键词: 水下光照测量; 自容式多传感器照度计; 现代渔业设施装备; 渔业信息化与可持续发展

Research on the Design of a Self-Contained Multi-Channel Underwater Illuminance Meter

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Abstract: Accurate measurement of underwater illumination is vital for modern fisheries equipment and informatization. Traditional underwater illuminance meters, constrained by single sensors and dependence on external power sources, are inadequate for long-term, high-precision measurements in deep-sea environments. To address this, we have designed a self-contained multi-sensor underwater illuminance meter based on an intelligent GD32 microcontroller. This design utilizes self-contained storage technology, enabling the microcontroller to process and analyze data from multiple sensors in real-time. During performance testing, we simulated underwater environments with varying depths (up to 300 meters) and temperatures (0-40°C), comprehensively evaluating the meter's measurement range, accuracy, response time, stability, and self-powering capabilities. By adjusting the weight, the device can also achieve profile measurements, further enhancing measurement accuracy. Test results indicate that this underwater illuminance meter exhibits high reliability and practicality in underwater environments.

Key words: Underwater Lighting Measurement; Self-Contained Multi-Sensor Luminometer; Modern Fisheries Facilities and Equipment; Fisheries Informatization and Sustainable Development

重力式深水网箱系统参数化建模及应用

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摘要: 重力式深水网箱模型构建是开展网箱力学特性仿真分析的基础, 在网箱仿真过程中占据绝大部分的工作量。为解决仿真过程中网箱建模过程繁琐、效率低下的问题, 针对重力式深水网箱提出了一种参数化快速建模方案。首先根据网箱各部件特点进行参数化设计, 然后编制建模程序并开发相应的操作界面, 最终在 OrcaFlex 软件中实现重力式深水网箱模型的快速构建。工程应用实例测试表明, 该程序能大幅提高网箱建模效率, 方便开展重力式深水网箱工程计算, 研究可为多规格重力式深水网箱仿真模型的快速构建及计算分析提供借鉴。

关键词: 深水网箱; 参数化; 二次开发; OrcaFlex; 数值模拟

Parametric modeling and application of gravity deepwater cage system

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Abstract: The numerical model of gravity deepwater cage, which is the foundation for the numerical simulation analysis of mechanical characteristics of cage, undertakes the majority of the work in the cage simulation process. In order to solve the problems of tedious modeling and low efficiency in this process, we proposed a parameterized rapid modeling method for gravity deepwater cage. Firstly, each component of the cage was parameterized according to its structural characteristics. Then, the modeling program was compiled and the corresponding operation interface was developed. Finally, the rapid creation of gravity deepwater cage model was achieved in OrcaFlex. Engineering test shows that the program can improve the efficiency of cage modeling greatly and facilitate the engineering calculation of gravity deepwater cages. The study provides references for the model rapid creation and numerical analysis of gravity deepwater cages of various specifications.

Key words: Deepwater cage; Parameterization; Secondary development; OrcaFlex; Numerical simulation

基于头足类渔业知识图谱的 智能问答系统研究

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摘要：我国远洋鱿钓渔业在持续发展上面临的主要障碍是对大洋鱿鱼资源的了解、利用有限。因此，加强远洋渔业的信息化建设，特别是构建头足类资源的数据库，对于头足类渔业资源的评估、鱼类行为研究和分类学等领域显得尤为关键。本研究旨在集成头足类渔业领域的知识图谱，从而改善渔业问答服务的效果。我们采集了头足类渔业相关的知识，通过命名实体识别模型，解析渔业问句中的实体。随后采用基于 BERT-BiLSTM 的关系抽取模型进行关系抽取，构建头足类知识图谱。最后利用问句解析的结果生成查询语句，并从渔业知识图谱中获取问题的答案。通过对比实验，准确率、召回率和 F1 值均得到了提升，验证了本文智能问答系统对用户提问的理解更为准确。

关键词：头足类; 知识图谱; 渔业问答系统; 知识抽取; 深度学习; 自然语言处理

Research on intelligent Q&A system based on knowledge graph of cephalopod fisheries

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Abstract : China's pelagic squid fishery faces sustainability challenges due to inadequate understanding and use of oceanic squid resources. Enhancing fishery informatization, particularly developing a cephalopod resource database, is vital for resource assessment, fish behavior study, and taxonomy. This study focuses on integrating a knowledge graph into cephalopod fisheries to enhance fishery Q&A services. It involves collecting cephalopod-related knowledge, using a named entity recognition model for Q&A entity parsing, and a BERT-BiLSTM-based model for relationship extraction to build the knowledge graph. The system then generates query statements from parsed questions to retrieve answers from the graph. Experimental results show improved accuracy, recall, and F1 scores, confirming the system's enhanced ability to accurately interpret user queries.

Key words: : Cephalopods; Knowledge graph; Fisheries question and answer system; Knowledge extraction; Deep learning; Natural language processing

基于深度学习的金枪鱼延绳钓渔获 图像识别技术分析

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摘要: 为了实现金枪鱼延绳钓渔获物的高效识别和分类, 改善渔业资源监测的准确性, 本研究探索了基于卷积神经网络的鱼类图像识别方法。实验采用上海海洋大学“淞航”号在中西太平洋公海调查中捕获的 3 种经济性鱼类及 10 种兼捕渔获物的图像数据, 运用单发多箱探测器 (Single shot multiBox detector, SSD) 卷积神经网络进行图像分类识别。通过将局部鱼类图像与整体图片数据集进行比较分析, 优化训练数据集, 以提升模型的分类性能。实验结果表明, 改进后的鱼类图像数据集在 SSD 模型上的分类准确率达 91.6%, 相较于原始数据集提高了 6.2%。研究表明, 利用优化后的数据集, SSD 模型能够显著提高金枪鱼延绳钓渔获物的识别准确性, 具备更好的稳定性和适应性。本研究为基于卷积神经网络的渔业资源监测提供了有效的技术路径, 尤其在提升金枪鱼延绳钓渔获物自动分类识别精度方面展现了广泛的应用潜力。

关键词: 金枪鱼延绳钓; 渔获物识别; 卷积神经网络; 数据集优化; 中西太平洋

Analysis of deep learning-based tuna longline catch image recognition technique

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Abstract: In order to achieve efficient identification and classification of tuna longline catches and to improve the accuracy of fishery resources monitoring, this study explores a fish image recognition method based on convolutional neural network. The experiments were conducted using image data of three economic fish species and ten bycatch species caught by the Song Hang of Shanghai Ocean University during the high seas survey in the western and central Pacific Ocean, and a convolutional neural network (CNN) based on a single shot multiBox detector (SSD) was used to classify and recognise the images. The results of the study were summarised in the following table. The training dataset is optimised by comparing and analysing the local fish images with the overall image dataset to improve the classification performance of the model. The experimental results show that the classification accuracy of the improved fish image dataset on the SSD model reaches 91.6%, which is a 6.2% improvement compared to the original dataset. The study shows that using the optimised dataset, the SSD model can sig

Key words: tuna longlining; catch identification; convolutional neural networks; dataset optimisation; Western and Central Pacific Ocean

基于生成对抗网络的鱼类图像识别精度提升技术研究

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摘要: 在现代渔业的发展浪潮中, 生成对抗网络 (GAN) 作为深度学习领域的明星技术, 正逐渐成为现代渔业信息化进程中不可或缺的一环, 为提高鱼类识别的准确度提供了新的解决方案。GAN 凭借其强大的图像生成与增强能力, 在渔业图像识别领域展现出显著优势。通过 GAN 技术, 我们可以有效地扩充鱼类图像数据集, 提升模型的泛化能力, 进而实现更精细、更准确的鱼类识别。在渔业资源监测、鱼群行为分析等方面, GAN 的应用显著提高了鱼类识别的准确性和时效性。GAN 还能够优化高清摄像系统和水下无人机等渔业设施的图像采集与处理流程, 进一步提升鱼类识别的精度。通过 GAN 技术, 我们能够更准确地预测渔业资源的动态变化, 为制定科学合理的渔业政策提供数据支撑。随着技术的不断进步, GAN 在渔业领域的应用前景将更加广阔, 为现代渔业的智能化管理和可持续发展提供有力支持。

关键词: 生成对抗网络 (GAN); 现代渔业; 鱼类识别; 信息化应用

Research on Enhancing Fish Image Recognition Accuracy Using Generative Adversarial Networks

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Abstract: In the wave of modern fisheries development, Generative Adversarial Networks (GANs), as a star technology in the field of deep learning, are increasingly becoming an indispensable part of the informatization process in modern fisheries, providing new solutions for improving the accuracy of fish recognition. GANs demonstrate significant advantages in the field of fisheries image recognition due to their powerful image generation and enhancement capabilities. Through GAN technology, we can effectively expand fish image datasets, enhance model generalization ability, and achieve more precise and accurate fish recognition. In areas such as fisheries resource monitoring and fish behavior analysis, the application of GANs has significantly improved the accuracy and timeliness of fish recognition. GANs can also optimize the image acquisition and processing workflows of fisheries facilities and equipment, such as high-definition camera systems and underwater drones, further enhancing the precision of fish recognition. With GAN technology, we can more accurately predict the dynamic changes in

Key words: Generative Adversarial Networks (GANs); Modern Fisheries; Fish Recognition; Informatization Application

仿生机器鱼颜色对鲤鱼视觉运动反应的影响研究

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摘要: 仿生机器鱼颜色在动物行为的诸多方面(如群体形成、维护、防御和求偶)中起着至关重要的作用。本研究基于行为实验中观察到的生理特征,探讨了仿生机器鱼颜色对鲤鱼行为的影响。通过计算机图像处理和光衰减分析,观察了不同颜色(白色、红色、蓝色、绿色和黄色)仿生机器鱼对鲤鱼数量和位置的变化影响。研究表明:(1)在淡水中可见光的衰减系数顺序为红色 > 黄色 > 绿色 > 蓝色;(2)鲤鱼对不同颜色机器鱼的反应数量变化平均值顺序为白色 > 红色 > 绿色 > 黄色 > 蓝色,鲤鱼对白色和红色机器鱼的敏感度和反应性更高;(3)不同颜色机器鱼与鲤鱼之间的距离顺序为白色 < 黄色 < 蓝色 < 绿色 < 红色,白色和黄色的机器鱼对鲤鱼的吸引力更大。因此,使用白色或黄色机器鱼可能更有效地吸引鲤鱼。

关键词: 鲤鱼; 动物行为; 视觉运动反应; 仿生机器鱼; 颜色; 图像校正

Study on the Effect of Bionic Robot Fish Color on the Optomotor Response of *Cyprinus carpio*

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Abstract: Visual selection plays a fundamental role in various aspects of animal behavior, such as colony formation, maintenance, defense, and courtship. This study investigated the effect of bionic robot fish color on carp behavior based on physiological characteristics that were observed during behavioral experiments. Through computer image processing and analysis of light attenuation, we observed changes in the number and positioning of carp with bionic robotic fish of different colors (white, red, blue, green, and yellow). The results indicated that (1) the attenuation coefficient of visible light in freshwater was red > yellow > green > blue; (2) the order of the average change in the number of carp responding to different colors of robotic fish was white > red > green > yellow > blue, and carp were more sensitive and responsive to white and red robotic fish; and (3) the order of the distances between different colors of robotic fish and carp was white < yellow < blue < green < red, and white and yellow robotic fish were more attractive to carp. Therefore, the use of white or yellow robot

Key words: *Cyprinus carpio*; animal behavior; optomotor response; bionic robot; color; image correction

基于地理相似性的中西太平洋围网鲣空间 预测与驱动因子研究

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摘要： 鲣 (*Katsuwonus pelamis*) 主要作业渔场位于中西太平洋热带海域，是金枪鱼围网捕捞中的重要资源，其资源分布与环境影响明显。地理相似性作为地理学第三定律，可以根据样本与预测点之间的地理结构相似性来进行空间预测。本文基于 WCPFC 的渔业与海洋环境数据，对渔获率与环境因子运用地理相似性模型预测鲣渔场的空间分布，并分析了不同环境因子对鲣资源分布和地理结构相似性的空间因果关系。结果表明：（1）利用地理相似性定律可以较好预测渔场的空间分布，拟合优度 R^2 为 0.72；（2）SSS、SST、NPP 对鲣资源丰度影响程度较大，其次为 SLA 和 MLD。（3）NPP 与 SST 对衡量地理结构相似性的因果关系最强。

关键词： 鲣，地理相似性，环境因子

Spatial Prediction and Driving Factors of Western and Central Pacific Purse Seine Skipjacking Based on Geographic Similarities

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Abstract : Skipjack tuna (*Katsuwonus pelamis*), whose main operating fishery is located in the tropical waters of the western and central Pacific Ocean, is an important resource in the tuna purse seine fishery, and the distribution of the resource and its environmental impacts are obvious. Geographic similarity, as the third law of geography, can be used to make spatial predictions based on the similarity of geographic structure between samples and prediction points. In this paper, based on the fishery and marine environment data from WCPFC, we applied the geographic similarity model to the catch rate and environmental factors to predict the spatial distribution of skipjack tuna fishery, and analyzed the spatial causality of different environmental factors on the distribution of skipjack tuna resources and geographic structural similarity. The results showed that: (1) the spatial distribution of the fishery could be better predicted using the law of geographic similarity, with a goodness-of-fit R^2 of 0.72; (2) SSS, SST, and NPP had a greater influence on the abundance of skipjack tuna resources,

Key words: Skipjack tuna , geographic similarity, environmental factors

金鱼不同游泳方式的水动力特性比较研究

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摘要: 本研究利用粒子图像测速技术 (PIV) 分析了幼年金鱼在三种游泳模式下的运动学与流体动力学特征: 直线游泳、冲刺-滑行和转向。结果显示, C形转向的游泳速度最高, 适合快速规避捕食者; 直线游泳最适合持续运动, 冲刺-滑行则与捕食行为相适应。涡量分析表明, 尾鳍周围的涡量是推力的主要来源, 进一步验证了涡量大小与推力之间的相关性。研究结果突显了尾鳍在游泳效率和性能中的关键作用。未来的研究应整合动物行为学、生物力学和生理学, 以加深对鱼类运动的理解, 从而为高效仿生水下机器人的设计提供指导, 并支持鱼类保护工作。

关键词: 金鱼幼鱼; 游泳行为; 涡量; 流体动力学

Comparison Study of Hydrodynamic Characteristics in Different Swimming Modes of *Carassius auratus*

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Abstract : This study utilized particle image velocimetry (PIV) to analyze the kinematic and hydrodynamic characteristics of juvenile goldfish across three swimming modes: forward swimming, burst-and-coast, and turning. The results showed that C-shaped turning exhibited the highest speed, making it suitable for rapid evasion of predators; forward swimming was optimal for sustained locomotion, while burst-and-coast swimming was associated with predatory behaviors. Vorticity analysis indicated that vorticity around the tail fin was the primary source of propulsive force, further confirming the correlation between vorticity magnitude and propulsion. The findings emphasize the crucial role of the tail fin in swimming efficiency and performance. Future research should integrate ethology, biomechanics, and physiology to deepen the understanding of fish locomotion, potentially guiding the design of efficient biomimetic underwater robots and contributing to fish conservation efforts.

Key words:: juvenile goldfish; swimming behavior; vorticity; hydrodynamics

大洋渔业资源特征原位观测技术研究

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摘要: 在全球渔业持续发展的宏观背景下, 渔业资源调查手段的变革以及资源评估的全球化已成为必然趋势。当前, 传统渔业资源探测评估技术存在诸多局限, 难以实现精准、全面的资源监测, 无法满足渔业资源管理的现实需求。本研究顺应时代潮流, 旨在解决上述问题, 设计并制作了一款新型渔业资源原位观测装备。该装备采用三组水下立体双目摄像头与成像声纳相互组合叠加的方式, 实现 360° 立体探测。通过对采集的图像信息进行处理, 并利用 YOLOV8 训练模型进行学习, 从而实现目标识别、路径跟踪以及资源评估等功能。研究表明, 此装备能够显著提高渔业资源探测的准确性与全面性, 满足渔业资源评估全球化的要求, 为大洋渔业资源的科学管理提供了强有力的技术支持, 对推动渔业可持续发展具有重要的理论价值与现实意义。

关键词: 原位观测; 资源评估; 鱼类行为; 成像声纳; 图像处理

Research on In Situ Observation Technology of Ocean Fishery Resources Characteristics

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Abstract : Currently, traditional fishery resource detection and evaluation technologies have limitations, making it difficult to achieve accurate and comprehensive resource monitoring and failing to meet the practical needs of fishery resource management. This research responds to the trend of the times. A novel in situ observation equipment for fishery resources is designed and fabricated. It combines three sets of underwater stereo binocular cameras and imaging sonars to achieve 360-degree stereo detection. Collected image information is processed and the YOLOV8 training model is utilized for learning to realize functions such as target recognition, path tracking, and resource evaluation. The results show that this equipment can significantly enhance the accuracy and comprehensiveness of fishery resource detection. It meets the requirements of globalized fishery resource assessment and provides strong technical support for the scientific management of ocean fishery resources. This research holds significant theoretical value and practical significance in promoting the sustainable development

Key words:: In situ observation; Resource assessment; Fish behavior; Imaging sonar; Image processing

浙江省设施养殖发展与对策研究

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摘要：近年来，浙江深入践行大食物观，大力发展现代设施渔业。从政策支持、技术推广两方面发力，和“十三五”末相比，设施养殖产量增长了 18.2%，亩均产值提高了 26%，六大主要设施养殖模式规模提升了 115%，设施养殖技术装备持续改善，设施养殖品种特色鲜明、效益可观，同时也存在养殖成本投入高、设施装备研发力度不足、设施用地存在一定限制等问题。下一步将以池塘设施养殖、工厂化设施养殖和深远海智能化养殖为发展重点，加大政策支持、加大资金扶持、强化科技支撑，促进设施渔业高质量发展。

关键词：浙江省、设施养殖、养殖装备

Research on the Development and Countermeasures of Facility Aquaculture in Zhejiang Province

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Abstract : In recent years, Zhejiang's in-depth practice of Great Food View, vigorously developed modern facilities aquaculture. From the policy support, technology promotion, and the 13th Five-Year Plan compared to the end of the facility aquaculture production increased by 18.2%, mu average output value increased by 26%, the scale of six major facilities aquaculture model raised by 115%, The technical equipment of aquaculture facilities continues to improve. Facility breeding varieties with distinctive characteristics and considerable benefits. At the same time, there are problems such as high investment in aquaculture costs, insufficient research and development of facilities and equipment, and certain restrictions on land for facilities. The next step will be to focus on the development of pond facility aquaculture, factory farming, and deep-sea intelligent aquaculture, increase policy support, increase financial support, strengthen scientific and technological support, and promote the high-quality development of facility aquaculture.

Key words: : Zhejiang province, facility aquaculture, aquaculture equipment

日本锦鲤池塘 — 工厂化接力养殖模式经济效益分析

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摘要：本文记录了绍兴御锦农业发展有限公司在一个完整养殖周期内，采用池塘 - 工厂化接力模式进行日本锦鲤养殖的相关流程、管理情况。该模式下日本锦鲤亩均产值 7.86 万元，亩均利润 4.43 万元。结果表明，日本锦鲤池塘 - 工厂化接力养殖模式可以获取更大经济效益。

关键词：日本锦鲤、接力养殖、经济效益

Economic Benefit Analysis of Japanese Koi Pond Factory Relay Breeding Model

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Abstract: This article records the related culture process and the culture management based on the *Cyprinus carpio* pond-factory relay culture model in a complete culture cycle adopted by Shaoxing Yujin Agricultural Development Co., Ltd. The *Cyprinus carpio* pond-factory relay culture model per mu average output value 78,600 yuan, per mu average profit 44,300 yuan. The results showed that the *Cyprinus carpio* pond-factory could obtain greater economic benefits

Key words: *Cyprinus carpio*; relay culture; economic benefit

渔业数字化发展对渔民收入影响的时空演变与收敛性分析

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摘要: 渔业数字化发展与渔民收入密切相关。首先, 本文构建了渔业数字化发展水平综合评价指标体系, 按此体系运用熵权法测算出 2011 年至 2022 年中国 30 个省(市)的渔业数字化发展水平综合得分。其次, 构建面板时空地理加权回归模型分析渔业数字化发展增收效应。最后, 分别探究沿海地区和内陆地区渔业数字化水平增收效应的空间收敛特征。研究结果表明: (1) 各地区渔业数字化发展水平总体不断提高, 沿海地区发展速度普遍快于内陆地区。(2) 渔业数字化发展增收效应显著为正, 但存在区域不平衡问题, 沿海地区和内陆地区均体现“南强北弱”的格局。(3) 空间收敛模型分析结果显示沿海和内陆地区渔业数字化发展增收效应均存在“虹吸效应”, 呈现“核心—边缘”与整体收敛并存格局。基于上述研究结果, 本文有针对性地提出相关助渔增收政策建议, 以为各地区政府决策提供相对准确、可靠的参考。

关键词: 渔民收入; 渔业数字化; 面板时空地理加权回归模型; 空间收敛性分析

Temporal and Spatial Evolution and Convergence Analysis of the Impact of Fishery Digitization Development on Fishermen's Income

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Abstract: Firstly, this paper constructs a comprehensive evaluation index system of fishery digital development level, and calculates the comprehensive score of fishery digital development level of 30 provinces (municipalities) in China from 2011 to 2022 by using entropy weight method according to this system. Secondly, the panel spatiotemporal and geographical weighted regression model is constructed to analyze the income increasing effect of fishery digital development. Finally, the spatial convergence characteristics of the income increase effect of fishery digitization level in coastal and inland areas were explored respectively. Based on the above research results, this paper puts forward relevant policy suggestions to increase fishing income, so as to provide relatively accurate and reliable reference for local governments to make decisions.

Key words: fishermen's income; digitization of fisheries; panel spatio-temporal weighted regression model; spatial convergence analysis

新质生产力赋能海洋渔业高质量发展的理论逻辑与实践路径探赜——基于马克思主义政治经济学视角的研究

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摘要：从马克思主义政治经济学的视角深入剖析，新质生产力对海洋渔业高质量发展的赋能作用蕴含着科学且严谨的理论逻辑。这一逻辑基础牢固地建立在马克思主义经典作家关于生产力的相关理论之上，并由习近平总书记在马克思主义政治经济学领域内提出的新论断，特别是新发展理念与新质生产力的创新性阐述，得到了进一步的丰富和完善。然而，在实践层面，我国海洋渔业在追求高质量发展的进程中，依然面临着诸多亟待解决的难题，其中养殖生态环境的日益严峻、捕捞作业组织化程度的不足以及海洋水产品精深加工领域的短板尤为突出。这些挑战要求我国在新发展理念的引领下，充分发挥新质生产力的赋能作用，通过采取多维度、系统性的举措，突破当前的发展瓶颈，推动海洋渔业实现高质量发展。

关键词：新质生产力；海洋渔业；高质量发展；马克思主义政治经济学

An exploration of the theoretical logic and practical path of New quality productivity enabling high-quality development of Marine fisheries ——Research based on Marxist political economy perspective

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Abstract : From the perspective of Marxist political economy, the enabling effect of new quality productivity on the high-quality development of Marine fisheries contains scientific and rigorous theoretical logic. However, in practice, China's Marine fisheries are still facing many problems to be solved in the process of pursuing high-quality development, among which the increasingly severe ecological environment of aquaculture, the lack of organization of fishing operations and the shortcomings of Marine aquatic products in the field of deep processing are particularly prominent. These challenges require China, under the guidance of the new development concept, to give full play to the enabling role of new quality productivity, through the adoption of multi-dimensional and systematic measures to break through the current development bottleneck, and promote the Marine fishery to achieve high-quality development.

Key words: : New quality productivity; Marine fisheries; High quality development; Marxist political economy

