西藏特有鱼类黑斑原鮡不同组织微生物群落特征及致病性研究[1]

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摘要：为深入了解健康与病死黑斑原鮡不同组织微生物群落特征及致病性，本研究对健康和病死黑斑原鮡的不同组织进行了微生物的培养同时进行了 16S rRNA 测序，系统地分析了健康和病死黑斑原鮡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，健康和病死黑斑原鮡皮肤和鳃在病理分析上存在一定差异；健康和病死黑斑原鮡皮肤菌群之间 α 多样性指数存在显著差异（P<0.05）；健康和病死黑斑原鮡鳃菌群在主坐标分析（PCoA）上存在显著差异（P<0.05）；健康和病死黑斑原鮡肠道、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（LEfSe）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。综上，气单胞属可能是主要致病菌之一，其结果可为系统了解黑斑原鮡不同组织菌群结构、健康养殖中疾病的定向防控提供科学依据。

关键字：黑斑原鮡；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*

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Abstract: To deeply understand the characteristics and pathogenicity of microbial communities in different tissues of healthy and diseased *Glyptosternum maculatum*, in this study, microorganisms from different tissues of healthy and diseased *Glyptosternum maculatum* were cultivated, and 16S rRNA sequencing was conducted. The histological differences, microbial community characteristics, and pathogenicity of different tissues of healthy and diseased *Glyptosternum maculatum* were systematically analyzed. The results indicated that there were certain differences in pathological analysis between the skin and gills of healthy and diseased *Glyptosternum maculatum*. There was a significant difference in the α diversity index between the skin microbial communities of healthy and diseased *Glyptosternum maculatum* (P < 0.05). There was a significant difference in the principal coordinate analysis (PCoA) of the gill microbial communities of healthy and diseased *Glyptosternum maculatum* (P < 0.05). The dominant bacterial species in the intestines, skin, and gills of both healthy and diseased *Glyptosternum maculatum* were mainly Firmicutes, Bacteroidetes, and Proteobacteria. The results of OTUs clustering analysis demonstrated that Chloroflexi, Desulfovibrionaceae, Actinobacteria, and Myxococcota had higher abundances in different tissues of dead fish, while Halobacterot had a higher abundance in different tissues of healthy fish. The differential analysis (LEfSe) revealed that *Shewanella* was only distributed in the intestines and had a relatively higher abundance in healthy fish. The abundance of *Aeromonas* in different tissues of dead fish was higher than that of healthy fish. In conclusion, *Aeromonas* might be one of the main pathogenic bacteria. These results can provide a scientific basis for systematically understanding the microbial community structure of different tissues of *Glyptosternum maculatum* and for targeted disease prevention and control in healthy aquaculture.

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