

研究报告

## 鳊塘浮游生物DNA序列多样性、水质和疾病的关系

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**摘要** 应用RAPD技术研究了鳊塘水生生态系统中浮游生物群落 $\alpha$ -多样性, 分析了浮游生物群落DNA序列丰富度与水质和疾病发生之间的关系, 探讨了池塘养殖密度和短周期、小密度、高投饵量养殖方式对浮游生物群落DNA序列丰富度及水质的影响. 结果表明: 1) 鳊塘浮游生物群落DNA序列丰富度与水质综合指数呈显著负相关关系 ( $P < 0.01$ ); 2) 池塘高密度养殖会造成浮游生物丰富度降低和水质综合指数升高; 3) 短周期、小密度、高投饵量的养殖模式对环境的损伤较大; 4) 浮游生物群落DNA指纹01矩阵和水质理化因子样品聚类分析表明, 发病塘在水质理化因子和浮游生物群落上具有相似性, 为鳊疾病预报模型的建立奠定了基础.

**关键词** [鳊](#) [RAPD](#) [浮游生物群落多样性](#) [理化因子](#) [养殖密度](#) [疾病](#)

分类号

## Relationships among planktons DNA sequence diversity, water quality and fish diseases in *Siniperca chuatsi* ponds

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### Abstract

By using random amplified polymorphic DNA (RAPD) technique, this paper studied the  $\alpha$ -diversity of plankton communities and its relationships with water quality and fish diseases in 7 *Siniperca chuatsi* ponds, as well as the effects of stocking density and a new culture model on the diversity and water quality. The results showed that there was a significant negative correlation between the DNA sequence diversity of plankton communities and water quality index, and high stocking density decreased the DNA sequence diversity and increased the water quality index. The new culture model with short culture period, low stocking density and high feeding stuff input had a greater damage on the water environment. Hierarchical cluster analysis indicated that there existed similarities in the DNA sequences of plankton communities and the physicochemical properties of water bodies in the ponds with fish diseases, which provided a possibility to predict the diseases occurrence in *Siniperca chuatsi* ponds.

**Key words** [Siniperca chuatsi](#); [RAPD](#); [plankton community diversity](#); [physicochemical factors](#); [stocking density](#); [disease](#)

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