**附件2：会议摘要格式**

全部1.25倍行距

【题目三号，普通黑体】基于eDNA技术的长江上游珍稀特有鱼类国家级自然保护区重庆段鱼类多样性研究

【空1行】

【四号，宋体，两个字中间加空格】王 梦1 杨 鑫1 王 维2 段 聪2 刘智皓1 陈启亮1 李英文1\* 沈彦君1\*

【6号，宋体】(1. 重庆师范大学重庆市动物生物学重点实验室, 重庆 401331; 2. 重庆市珍稀特有鱼类国家级自然保护区管理处, 重庆 402260)【空1行】

【5号，宋体，500-1000字】利用环境DNA宏条形码(environmental DNA metabarcoding; eDNA metabarcoding)检测长江上游珍稀特有鱼类国家级自然保护区重庆段鱼类多样性, 探索适用于长江鱼类多样性监测和保护的新方法, 为后期长江“十年禁渔”效果评估提供一定的基础资料。研究于2021年3月在保护区重庆段共设置6个采样点, 通过水样采集、eDNA捕获及提取、PCR扩增及测序和数据库对比分析等环境DNA宏条形码标准化分析流程来检测鱼类的多样性组成。结果表明保护区重庆段6个采样点中共检测出74种鱼类(不包括未鉴定到种水平的3属), 隶属于6目16科52属, 其中国家级保护鱼类2种, 长江上游特有鱼类10种, 重庆市重点保护鱼类1种, 外来物种8种。鲤属(*Cyprinus*)、鲫属(*Carassius*)、草鱼属(*Ctenopharyngodon*)和黄颡鱼属(*Tachysurus*)在各采样点均被检测到且为优势种。各样点鱼类组成的Alpha和Beta多样性的各项指数差异不大, 表明保护区鱼类的生态结构较为均衡和稳定。总体上, 在现阶段的长江流域鱼类资源监测中, 可根据监测任务的需要, 将环境DNA技术与传统的监测方法结合使用, 用于快速调查长江流域鱼类的多样性组成及分布等。

【空2行】

【小六，中文宋体，英文新罗马】收稿日期: 2021-07-09; 修订日期: 2021-10-12

基金项目: 重庆市林业局渔业资源监测专项(02060403/202009000101); 重庆市自然科学基金面上项目(cstc2019jcyj-msxmX0157)资助

[Supported by the Special Project of Fishery Resources Monitoring of Chongqing Forestry Bureau (02060403/202009000101);

Natural Science Foundation of Chongqing (cstc2019jcyj-msxmX0157)]

作者简介: 王梦(1996—), 女, 硕士研究生; 研究方向为水域生态学。E-mail: wmyjy1123@163.com

通信作者: 李英文, 教授; E-mail: 377683289@ qq.com　沈彦君, E-mail: shenyanjun@ cqnu.edu.cn　\*共同通信作者

**【12磅，大写，粗新罗马】FISH DIVERSITY IN CHONGQING SECTION OF THE NATIONAL NATURE RESERVE FOR RARE AND ENDEMIC FISH IN THE UPPER YANGTZE RIVER BASED ON EDNA TECHNOLOGY**

【空1行】

【10磅，新罗马】WANG Meng1, YANG Xin1, WANG Wei2, DUAN Cong2, LIU Zhi-Hao1, CHEN Qi-Liang1,

LI Ying-Wen1 and SHEN Yan-Jun1

*【8磅， 新罗马，斜体】(1. Chongqing Key Laboratory of Animal Biology, Chongqing Normal University, Chongqing 401331, China; 2. Chongqing NationalNature Reserve Management Office of Rare and Endemic Fish, Chongqing 402260, China)*

【空1行】

【10磅，新罗马，500-800字】**Abstract:** The aims of this study are: (1) to detect fish diversity in Chongqing section of the national nature reserve of rare and endemic fishes in the upper Yangtze River by using environmental DNA metabarcoding (eDNA metabarcoding), (2) exploring new methods applicable to the monitoring and protection of fish diversity in the Yangtze River, (3) providing certain basic data for the evaluation of the effect of the “10-year ban on fishing in the Yangtze River” later. A total of 6 sampling points were set up in the Chongqing section of the reserve in March 2021. The fish diversity was detected by following procedures, water sample collection, eDNA capture and extraction, PCR amplification and sequencing, database comparison analysis and other environmental DNA metabarcoding standardized analysis. The results showed that 74 fish species were detected (excluding 3 genera that have not been identified at the species level), belonging to 6 orders, 16 families and 52 genera, including 2 national-level protected fish, 10 endemic fish in the upper reaches of the Yangtze River, 1 key protected fish in Chongqing, and 8 invasive species. The genus Cyprinus, Carassius, Ctenopharyngodon and Tachysurus were detected at each sampling site and became the dominant species in each site. The various indexes of Alpha and Beta diversity of fish at various points are relatively uniform, indicating that the ecological structure of fish in the reserve is relatively balanced and stable. In summary, this study showed that although environmental DNA metabarcoding cannot completely replace traditional fish resource monitoring methods, it is a good strategy to combine them to quickly investigate the diversity composition and distribution of fish species in the Yangtze River Basin.

【空1行】

**Key words:** Environmental DNA; Fish diversity; Nature reserve; Upper Yangtze River; Rare and endemic fish