

目次

加速能源转型与产业结构调整的环境健康协同效益评估:以京津冀鲁地区为例	杨玺, 孙奕生, 常世彦, 李胜悦, 郑昊天, 王书肖, 张希良 (3627)
基于不同电力需求的中国减排降碳协同增效路径	向梦宇, 王深, 吕连宏, 张楠, 白梓函 (3637)
城市碳达峰碳中和行动评估方法与应用	张保留, 白梓函, 张楠, 吕连宏, 阳平坚 (3649)
基于可解释性机器学习的城市 O ₃ 驱动因素挖掘	董佳奇, 胡冬梅, 闫雨龙, 彭林, 张辉辉, 牛月圆, 段小琳 (3660)
基于响应曲面法的臭氧生成敏感性分析	朱禹寰, 陈冰, 张雅茹, 刘晓, 李光耀, 舍静, 陈强 (3669)
基于 WRF-CMAQ/ISAM 模型的榆林市夏季 O ₃ 来源解析	王伊凡, 仝纪龙, 陈羽翔, 林鑫, 刘永乐, 敖丛杰, 刘浩天 (3676)
基于轻量级梯度提升机的南京大气臭氧浓度预测	朱珈莹, 安俊琳, 冯悦政, 贺婕, 张玉欣, 王俊秀 (3685)
2022 年广东省冬季一次臭氧污染过程的气象成因及潜在源区分析	李婷苑, 陈靖扬, 龚宇, 沈劲 (3695)
夏季对流层臭氧辐射强迫对华北地区天气和空气质量的影响	杜楠, 陈磊, 廖宏, 朱佳, 李柯 (3705)
气象、本地光化学生成和外围传输对长沙市 2018~2020 年臭氧污染趋势变化影响的识别	杨俊, 杨雷峰, 丁华, 谢丹平, 刘妍妍, 余涛, 吕明, 袁自冰 (3715)
2000~2021 年成渝城市群 PM _{2.5} 时空变化及驱动机制多维探测	徐勇, 郭振东, 郑志威, 戴强玉, 赵纯, 黄雯婷 (3724)
基于 GTWR-XGBoost 模型的四川省 PM _{2.5} 小时浓度估算	吴迪, 杜宁, 王莉, 吴宇宏, 张少磊, 周彬, 张显云 (3738)
2013~2021 年邢台 PM _{2.5} 重污染过程输送和增长特性	江琪, 盛黎, 靳雨晨, 王继康, 尤媛, 王飞 (3749)
基于高分辨率在线观测数据分析上海市城区秋冬季大气有机气溶胶化学特征及污染来源	朱书慧 (3760)
机动车尾气碳质气溶胶排放因子及其稳定碳同位素特征	于鸣媛, 王谦, 付明亮, 戈畅, 谢峰, 曹芳, 章炎麟 (3771)
沈阳工业区夏季 VOCs 组成特征及其对二次污染形成的贡献	关璐, 苏枫枫, 库盈盈, 胡建林, 于兴娜 (3779)
疫情管控期间深圳市城区 VOCs 的变化特征及减排效果评估	云龙, 林楚雄, 李成柳, 邱志诚, 古添发, 李光程, 张明棣, 郭健锋 (3788)
西安市冬季道路扬尘中有机质组成特征及其氧化潜势	王擎雯, 陈庆彩, 王超, 王瑞鹤, 刘国瑞, 李豪, 李艳广 (3797)
淮北孙疃矿区地表尘中多环芳烃类化合物的污染特征及致癌风险评价	徐振鹏, 钱雅慧, 洪秀萍, 罗钟庚, 高秀龙, 梁汉东 (3809)
雄安建设初期白洋淀水质时空差异及其对降雨和土地利用的响应	王子铭, 杨丽虎, 宋献方 (3820)
流域尺度污染溯源模拟-优化防控方法:以铜陵市顺安河流域为例	刘国王辰, 陈磊, 李佳奇, 张钰晨, 赵奕欣, 刘妍琪, 沈珍瑶 (3835)
南昌市浅层地下水水质评价及监测指标优化	郑紫吟, 储小东, 徐金英, 马志飞 (3846)
闪电河流域“三水”氢氧同位素特征及水体转换分析	杨丽娜, 贾德彬, 高瑞忠, 苏文旭, 卢方园, 郝玉胜 (3855)
金沙江丰富类和稀有类浮游真核微生物的分布特征与影响因素	燕炳成, 崔戈, 孙胜浩, 王沛芳, 王超, 吴程, 陈娟 (3864)
嘉陵江不同干扰断面河道沉积物细菌群落多样性	竹兰萍, 张拓, 李佳宁, 王佳颖, 郭伟亮, 徐飞, 张富斌 (3872)
水库水深变化对不同浮游微生物群落及网络互作关键种的影响	王洵, 廖琴, 王沛芳, 袁秋生, 胡斌, 邢小蕾, 徐浩森 (3881)
典型工业区地下水细菌群落多样性特征与环境因子响应初探	吴建强, 张书源, 王敏, 陈敏, 叶文娟, 熊丽君, 黄沈发 (3892)
太湖流域肥料施用策略调整对典型作物系统氮磷流失的影响	俞映倬, 王逸之, 杨根, 杨林章, 段婧婧, 韩雪梅, 薛利红 (3902)
基于机器学习的长江流域农田氮径流流失负荷估算	张有福, 潘哲祺, 陈丁江 (3913)
千岛湖地区上梧溪流域地表径流非点源氮污染分类识别	俞珂, 严璇, 唐张轩, 张方方, 何圣嘉, 姜培坤 (3923)
沱江和涪江水系干支流氮磷营养盐的空间分布特征	李子阳, 周明华, 徐鹏, 陈露, 刘祥龙, 林洪羽, 江南, 任兵, 张博文 (3933)
外秦淮河底泥污染及疏浚效果	张沐, 任增谊, 张曼, 赵琼, 尹洪斌 (3945)
新污染物多环芳烃衍生物的来源、分布与光化学行为	葛林科, 王子宇, 曹胜凯, 车晓佳, 朱超, 张蓬, 马宏瑞 (3957)
镉砷在针铁矿界面共吸附的相互作用机制	苏子贤, 刘赛红, 管玉峰, 陶亮 (3970)
环糊精键合 Fe-TAML 催化剂的制备及其活化 H ₂ O ₂ 氧化水中有机微污染物	刘清泉, 蔡本哲, 蔡喜运 (3978)
Co(II) 活化过一硫酸盐降解氨基三甲膦酸的性能及反应机制	朱敬林, 汪舒 (3990)
微塑料诱导下污泥造粒潜能变化及微生物富集特征	谢晴帆, 俞楠, 张妮, 谢周云, 单珂欣, 吴亦馨, 唐力, 夏静芬, 杨国靖 (3997)
中国农田土壤 Cd 累积分布特征及概率风险评价	王静, 魏恒, 潘波 (4006)
渝东南典型地质高背景区土壤重金属来源解析及污染评价	蒋玉莲, 余京, 王锐, 王佳彬, 李瑜, 余飞, 张云逸 (4017)
基于 PMF 模型的农田土壤重金属源暴露风险综合评价:以浙江省某电子垃圾拆解区为例	方嘉, 何影, 黄乃涛, 支裕优, 傅伟军 (4027)
乌鲁木齐市郊农田土壤及农作物中多环芳烃的污染特征及风险评价	范悦, 曹双瑜, 艾力江·努尔拉, 于芸云江·吗米提敏, 阿不都艾尼·阿不里, 谢宣宣, 古丽斯坦·阿不都拉, 刘河疆 (4039)
荒漠绿洲土壤抗生素抗性基因分布特征及驱动机制	黄福义, 周曙仡, 苏建强, 朱永官 (4052)
近 15 年我国土壤抗生素污染特征与生物修复研究进展	赵晓东, 乔青青, 秦宵睿, 李晓晶, 李永涛 (4059)
改性生物炭修复砷镉复合污染土壤研究进展	吕鹏, 李莲芳, 黄晓雅 (4077)
沼液还田对土壤-作物系统重金属累积的影响:Meta 分析	赵奇志, 杨志敏, 孔凡靖, 熊海灵, 朱康文, 陈玉成 (4091)
两种铁改性生物炭对微碱性砷镉污染土壤的修复效果	梁欣冉, 何丹, 郑墨华, 付庆灵, 胡红青, 朱俊 (4100)
秸秆离田对土壤 Cd 生物有效性及水稻 Cd 积累的影响	王子钰, 周航, 周坤华, 谭文韬, 蒋毅, 唐棋, 伍港繁, 辜娇峰, 曾鹏, 廖柏寒 (4109)
秸秆与脱硫石膏配施改良黄河三角洲盐碱地的理化性质	赵惠丽, 于金艺, 刘涛, 王丽, 赵英 (4119)
基于环境 DNA 的复合污染土壤生物评价和胁迫诊断	黄湘云, 钟文军, 刘训杰, 毕婉娟, 钱林皓, 张效伟 (4130)
地质高背景区土壤-玉米重金属综合质量评价	张传华, 王钟书, 刘力, 刘燕 (4142)
浙江省蔬菜生产系统重金属污染生态健康风险	张述敏, 刘翠玲, 杨桂玲, 邓美华 (4151)
生物炭配施磷肥对土壤养分、酶活性及紫花苜蓿养分吸收的影响	刘鑫裕, 王冬梅, 张泽洲, 张鹏, 樊桐桐 (4162)
低密度聚乙烯微塑料对空心菜生长和生理特征的影响	周颖, 蒋文婷, 刘训悦, 朱高荻, 唐荣贵, 章海波, 蔡延江 (4170)
沼液施用对麦茬口期土壤微生物群落结构特征及功能的影响	乔宇颖, 奚辉, 李娜, 陈喜靖, 沈阿林, 喻曼 (4179)
大同铅锌尾矿不同污染程度土壤细菌群落分析及生态功能特征	刘泽勋, 庄家尧, 刘超, 郑康, 陈玲 (4191)
马尾松采伐迹地火烧黑炭对土壤有机碳组分和碳转化酶活性的影响	姚智, 焦鹏宇, 吴晓生, 严强, 刘先, 胡亚林, 王玉哲 (4201)
《环境科学》征订启事(3648) 《环境科学》征稿简则(3659) 信息(3714, 4150, 4178)	

金沙江丰富类和稀有类浮游真核微生物的分布特征与影响因素

燕炳成^{1,2}, 崔戈^{1,2}, 孙胜浩^{1,2}, 王沛芳^{1,2}, 王超^{1,2}, 吴程³, 陈娟^{1,2*}

(1. 河海大学浅水湖泊综合治理与资源开发教育部重点实验室, 南京 210098; 2. 河海大学环境学院, 南京 210098; 3. 中国电建集团昆明勘测设计研究院有限公司, 昆明 650051)

摘要: 浮游真核微生物通常由少数丰富类和大量稀有类组成,二者在维持水生生态系统健康稳定方面具有重要作用。目前对大型筑坝河流中这两类真核微生物的生物地理分布模式所知甚少。以我国西南梯级水电开发河流金沙江为研究区域,对比分析丰富类和稀有类浮游真核微生物在不同河段的分布特征,解析影响两类微生物空间分布的主导因素。结果表明,相比上游自然河段,金沙江浮游真核微生物的 α 多样性在梯级大坝河段显著升高,稀有类的 α 多样性增长比高于丰富类。浮游真核丰富类和稀有类微生物的群落组成在不同河段间存在显著差异,其中 *Vermamoeba* 属等优势属的相对丰度在两河段间同样存在明显差异。影响丰富类和稀有类浮游真核微生物群落组成的关键地化因子有海拔和 pH 等,两类微生物群落相似性与地理距离和环境异质性均符合距离衰减关系,其群落构建均受扩散限制和环境筛选共同影响;方差分解分析和偏 Mantel 检验结果显示扩散限制是影响丰富类和稀有类分布的主要驱动因素。研究结果为我国西南缺资料区水电开发河流中微生物的地理分布模式和生态响应提供数据支持。

关键词: 浮游真核微生物; 稀有类; 地理分布模式; 扩散限制; 金沙江

中图分类号: X172 文献标识码: A 文章编号: 0250-3301(2023)07-3864-08 DOI: 10.13227/j.hjxx.202207269

Distribution Characteristics and Influencing Factors of Abundant and Rare Planktonic Microeukaryotes in Jinsha River

YAN Bing-cheng^{1,2}, CUI Ge^{1,2}, SUN Sheng-hao^{1,2}, WANG Pei-fang^{1,2}, WANG Chao^{1,2}, WU Cheng³, CHEN Juan^{1,2*}

(1. Key Laboratory of Integrated Regulation and Resource Development on Shallow Lakes, Ministry of Education, Hohai University, Nanjing 210098, China; 2. College of Environment, Hohai University, Nanjing 210098, China; 3. Kunming Engineering Corporation Limited, Power China, Kunming 650051, China)

Abstract: Planktonic microeukaryotes are usually composed of a few abundant species and a large number of rare species, which play an important role in maintaining the health and stability of aquatic ecosystems. At present, little is known about the biogeographical distribution patterns of these two groups of microeukaryotes in large damming rivers. This study analyzed the distribution patterns of abundant and rare planktonic microeukaryotes and the dominant factors affecting their spatial distributions in the Jinsha River, one of the largest rivers in southwestern China that is strongly regulated by cascade dams. The results showed that the alpha diversity of planktonic microeukaryotes in the Jinsha River was higher in the cascade dam reach than that in the upstream natural reach, and the increase in alpha diversity of rare species was larger than that of rich species. There were significant differences in microbial community composition among different river sections, and the relative abundances of the dominant genera such as *Vermamoeba* shared by them were also significantly different between the two river sections. The results of distance decay analysis revealed that the geographic distribution patterns of rare and abundant taxa were jointly influenced by environmental heterogeneity and dispersal limitation, and the results of variance decomposition analysis and partial Mantel further indicated that dispersal limitation was the dominant ecological process. The results provided data support for the distribution and ecological response of microorganisms in rivers in the areas lacking data in Southwest China.

Key words: planktonic microeukaryotes; rare taxa; biogeographic pattern; dispersal limitation; Jinsha River

真核微生物形态大小各异,分布广泛,具有高度的多样性,在生物地球化学循环和能量流动方面发挥着重要作用^[1,2]。多数微生物通常由少数丰富类和大量稀有类组成,丰富类是生态系统中生物量的主要贡献者,而稀有类则是维持生态系统多样性和稳定性的重要类群^[3,4]。研究丰富类和稀有类的分布特征与影响因素对认识水域生态系统的功能具有重要意义^[4]。环境筛选(与环境异质性相关)和扩散限制(与地理距离相关)是影响微生物群落构建的关键生态学过程^[5]。这两个过程在微生物群落构建中通常共同发挥作用,但在不同生态系统或环境介质中,各自的作用强度不同^[6]。已有河流微生物生

态学相关研究重点解析了浮游细菌的沿程生态演替规律和群落建成机制^[7,8],但丰富类和稀有类浮游真核微生物在大型河流的地理分布模式及影响因素仍不甚了解。

金沙江是我国西南地区最重要的大型河流之一,也是微生物信息资料缺乏区^[9]。由于金沙江等西南河流的自然环境条件复杂,同时受到水电开发

收稿日期: 2022-07-29; 修订日期: 2022-09-14

基金项目: 国家重点研发计划项目(2022YFC3203902); 国家自然科学基金项目(52022028, 52279061, 92047201, 92047303)

作者简介: 燕炳成(1995~),男,硕士研究生,主要研究方向为河流微生物生态学, E-mail: ml5195890577@163.com

* 通信作者, E-mail: chenjuanm@hhu.edu.cn

等强人类活动影响,是典型的生态脆弱区^[10,11].已有研究以细菌为主要微生物类群,开展了西南河流微生物的初步普查,重点阐释了澜沧江等河流中浮游细菌的群落组成及时空变化规律^[12~14].然而,目前对西南河流浮游真核微生物信息仍十分匮乏,其对梯级水电开发的响应更不清楚.解析金沙江浮游真核微生物的地理分布模式,对于补充西南缺资料区数据信息、认识西南河流的生物生境特征及响应规律具有重要意义.本研究利用 18S rRNA 基因扩增子测序技术,对比分析丰富类和稀有类浮游真核微生物在不同河段的分布特征,解析影响两类微生物空间分布的主导因素,以期为我国西南河流微生物的分布规律和生态响应提供数据支持.

1 材料与方法

1.1 样品采集与地化因子测定

研究区域范围覆盖金沙江干流河长 2 279 km,海拔范围为 3 441 ~ 250 m.共布设 49 个采样点(图 1),包括上游河段采样点共 13 个(N1 ~ N13),其中 N13 位于梨园(LY)水库变动回水区以外,不受水库蓄水影响;中下游河段采样点共 36 个(LY.1 至 CJD).金沙江上游主要为自然流态河段,定名为“上游自然河段”;中下游人类活动的影响主要是梯级大坝的建设,定名为“梯级大坝河段”.

于 2019 年 9 月进行现场观测和水体样品采集.使用 GPSMAP 62s(Garmin, KS, USA)现场记录每个采样点的经度、纬度和海拔,使用便携式 HQ40d 多参数水质分析仪(Hach, CO, USA)测量水温

(*T*)、电导率(*Ec*)、pH 值和溶解氧(*DO*);使用便携式 2100P 浊度仪(Hach, CO, USA)现场测定水体浊度.在每个采样点采集 3 份表层水样,共获得 147 份水样.采集的水样分两部分,一部分水样用 0.22 μm 孔径的聚碳酸酯滤膜过滤收集浮游微生物;另一部分水样运送回实验室,参照 Xue 等^[15]的方法,测定水样的 pH、电导率(*Ec*)、总有机碳(*TOC*)、硝氮(NO_3^-)、氨氮(NH_4^+)、有效磷(*AP*)、总氮(*TN*)和总磷(*TP*)等理化指标.采样点信息及水体理化性质数据已在 Chen 等^[6]研究中详细列出.

1.2 DNA 提取和高通量测序

使用 PowerWater DNA 提取试剂盒(MoBio, CA, USA)提取水样中微生物 DNA,具体方法参照试剂盒说明书.根据 Xue 等^[15]的方法,选取带 barcode 的特异性引物 528F(5'-GCGGTAATTCAGCTCCAA-3')和 706R(5'-AATCCRAGAATTTCACCTCT-3'),对 18S rRNA 基因的 V4 高变区进行 PCR 扩增.参照 Liu 等^[16]的方法构建基因文库,将各样品的 PCR 产物以等量(mol)混合,使用 Illumina MiSeq PE250 平台(Illumina, San Diego, CA, USA)进行双端测序.使用 QIIME2(v. 1.8.0)平台切除序列的引物片段,弃去未匹配引物的序列.使用 DADA2 算法对原始数据进行质量过滤,将过滤后的高质量序列按照 100% 的相似性聚类成扩增子序列变异体(ASV).选择每个 ASV 中出现频数最高的序列,在 Silva 数据库中采用 RDP 分类器对 ASV 代表序列进行比对注释.最后以序列最少的样本为标准将 ASV 均一化处理,最大限度消除由于测序量不同而导致的偏差.参照 Zhang 等^[17]的方法,从测序得到的真核生物数据集中排除了后生动物等多细胞动物的 ASVs.参照 Mo 等^[18]的方法,将平均相对丰度大于 0.1% 的 ASV 界定为丰富类,将平均相对丰度小于 0.001% 的 ASV 界定为稀有类.

1.3 数据分析

使用 R 3.5.1 软件的“vegan”程序包进行以下分析:①计算样品的浮游真核微生物 α 多样性指数(ACE 指数和 Shannon 指数);②基于样品间 Bray-Curtis 距离计算浮游真核微生物的 β 多样性,并采用非度量多维尺度分析(NMDS)可视化不同样品间真核微生物的群落结构差异;③使用相似性分析(ANOSIM)方法检测各样品间群落组成差异的显著性;④进行 Mantel 检验,分析单个环境因素或地理因素与浮游真核微生物群落相似性的相关性;⑤基于欧式距离计算环境差异性矩阵,用于距离衰减分析;⑥通过方差分解分析(VPA)计算地理距离和环境因素对浮游真核微生物群落结构变异的解释率,

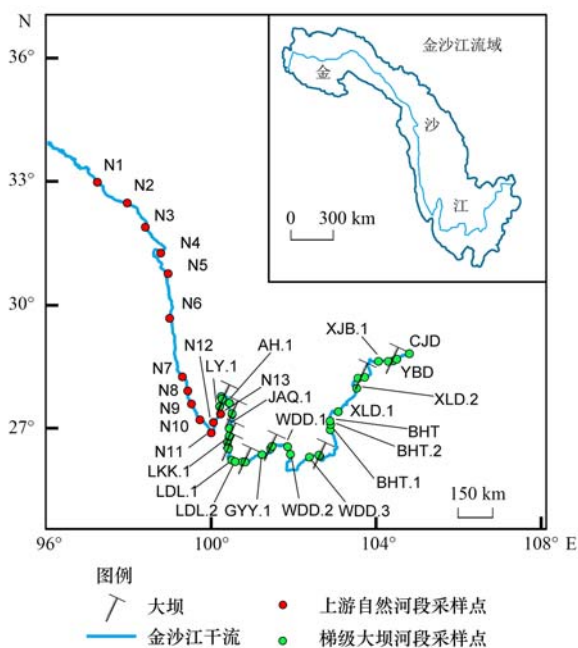


图 1 金沙江 49 个采样点位分布示意

Fig. 1 Distribution of the 49 sampling sites along the Jinsha River

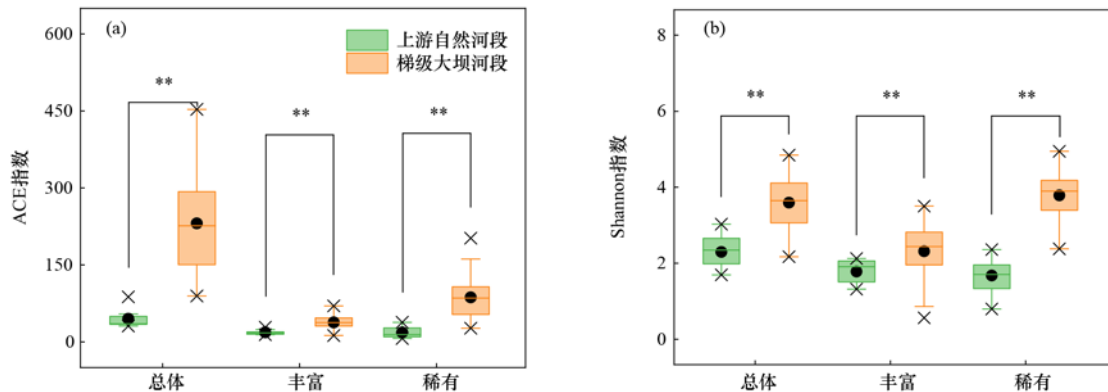
其中基于地理距离的空间变量使用主轴邻距法(PCNM)进行计算;⑦用偏 Mantel 检验确定所有的环境因素或地理距离的共同作用与群落结构是否显著相关. 利用 PASSAGE2 软件 (www.passagesoftware.net) 对群落相似性、地理距离和环境差异性矩阵进行线性化.

2 结果与分析

2.1 浮游真核微生物的 α 多样性

如图 2 所示, α 多样性 (ACE 指数和 Shannon

指数) 分析结果表明, 浮游真核微生物总体、丰富类和稀有类的 α 多样性在不同河段间 (上游自然河段和梯级大坝河段) 存在显著差异性 (ACE 指数: $P < 0.01$; Shannon 指数: $P < 0.01$). 相比上游自然河段, 梯级大坝河段总体、丰富类和稀有类的 ACE 指数平均值分别增加了 412%、104% 和 374% [图 2(a)], Shannon 指数平均值分别增加了 56.5%、30.0% 和 126% [图 2(b)]. 稀有类 ACE 指数和 Shannon 指数平均值在梯级大坝河段的增加幅度均高于丰富类.



箱体内的横线表示数据中值, 实心圆表示数据平均值, 叉号表示数据最大值和最小值; ** 表示 $P < 0.01$

图 2 金沙江浮游真核微生物的 ACE 指数和 Shannon 指数

Fig. 2 ACE index and Shannon index of planktonic microeukaryotes in the Jinsha River

2.2 浮游真核微生物的群落组成

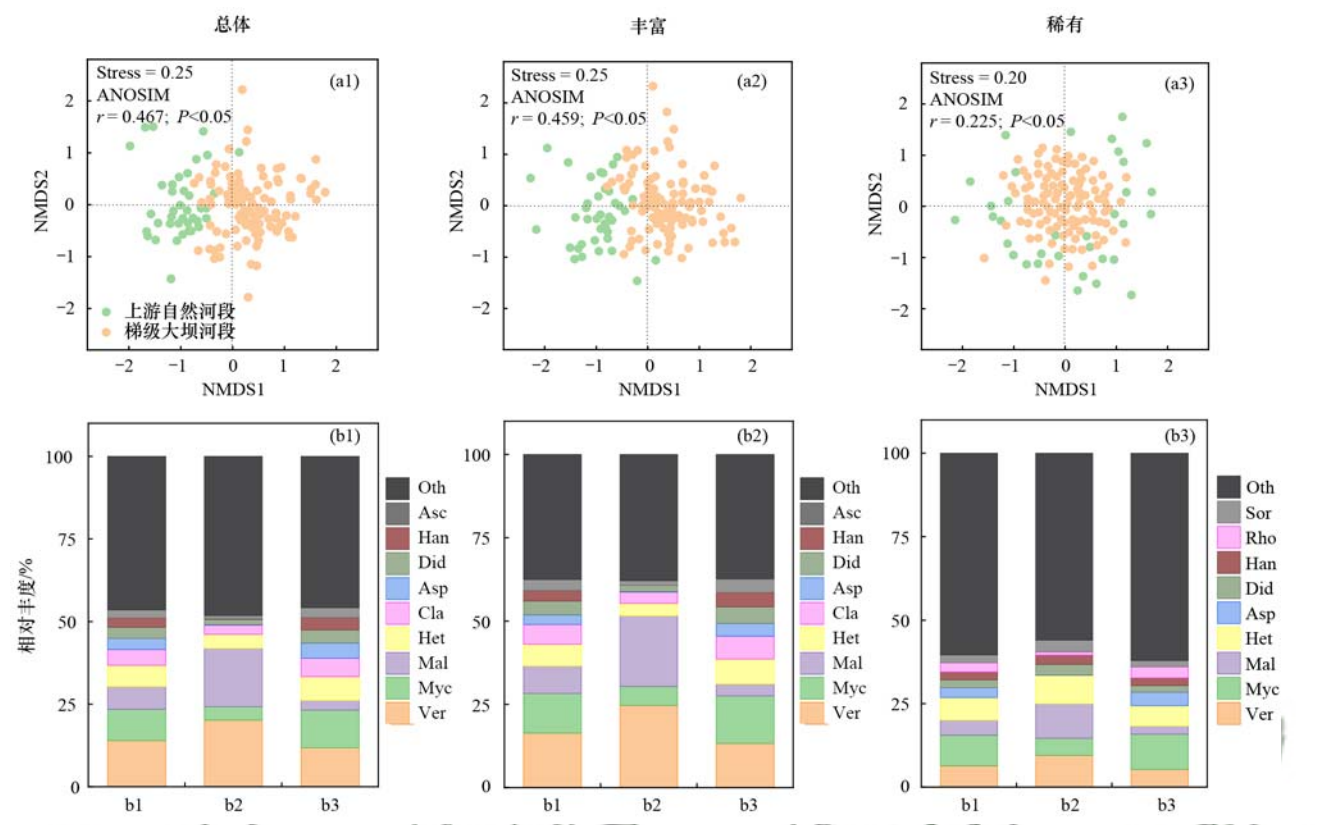
浮游真核微生物总体、丰富类和稀有类的 NMDS 分析结果如图 3(a) 所示, 总体和丰富类的上游自然河段 (N1 ~ N9) 和多数梯级大坝河段 (AH. 1 至 CJD) 样点明显分开, 而稀有类的梯级大坝河段样点相比上游自然河段分布较为聚集. ANOSIM 分析结果显示, 总体、丰富类和稀有类浮游真核微生物的群落组成在两个河段间均呈现出显著差异 ($P < 0.05$), 稀有类 ($r = 0.225$) 在河段间的差异性小于丰富类 ($r = 0.459$).

图 3(b) 显示了金沙江浮游真核微生物优势属的相对丰度, 总体和丰富类的优势属相同, 主要包括 *Vermamoeba*、麦克属 (*Mychonastes*)、马拉色菌属 (*Malassezia*)、*Heteromita*、曲霉菌属 (*Aspergillus*) 和亚隔孢壳属 (*Didymella*), 这些优势属在总体和丰富类中的总相对丰度占比均高于 50%. 除与总体和丰富类共有的优势属外, 稀有类的优势属还有 *Rhogostoma* 和 *Sorodiplophrys*. 相比上游自然河段, 不同浮游真核微生物类群的 *Vermamoeba* 属和马拉色属在梯级大坝河段的相对丰度均较低; 例如, 总体、丰富类和稀有类的 *Vermamoeba* 属在梯级大坝河段的相对丰度分别为 11.8%、13.3% 和 5.3%, 明显低于上游自然河段 (总体: 20.1%; 丰

富类: 24.7%; 稀有类 9.5%). 相反, 总体、丰富类和稀有类的麦克属在上游自然河段的相对丰度分别为 4.2%、5.7% 和 5.1%, 均低于梯级大坝河段 (总体: 11.4%; 丰富类: 14.3%; 稀有类: 10.6%). 可见, 丰富类和稀有类真核微生物的主要优势属相对丰度在不同河段间表现出相似规律.

2.3 地化因子与浮游真核微生物群落组成的相关性

Mantel 分析结果显示 (表 1), 总体、丰富类和稀有类与海拔、地理距离、水温、pH、TP、DO、Ec 和 NO_3^- 等地化因子均具有显著相关性 ($P < 0.05$), 说明浮游真核微生物的群落组成可能受多种地理因素和环境因素共同影响. 海拔 (总体: $r = 0.35$; 丰富: $r = 0.35$; 稀有: $r = 0.08$)、地理距离 (总体: $r = 0.39$; 丰富: $r = 0.39$; 稀有: $r = 0.09$) 和 TP (总体: $r = 0.32$; 丰富: $r = 0.30$; 稀有: $r = 0.08$) 与浮游真核微生物群落的相关性较高, 推测为影响程度较大的地化因子. 丰富类和稀有类的影响因子也存在一定差异, 例如丰富类与 DOC 无显著相关性 ($P > 0.05$), 而稀有类与 DOC 显著相关 ($P < 0.05$); 稀有类与浊度无显著相关性 ($P > 0.05$), 但丰富类与浊度有显著相关性 ($P < 0.05$), 且稀有类的相关系数 r 值均较低.



(a) NMDS, (b) 优势属的相对丰度; Ver: *Vermamoeba* 属, Myc: *Myconastes* 麦属, Mal: *Malassezia* 马拉色菌属, Het: *Heteromita* 属, Cla: *Cladospori* 属, Asp: *Aspergillus* 曲霉菌属, Did: *Didymella* 亚隔孢壳属, Han: *Hannaella* 属, Asc: *Ascochyta* 壳二孢属, Rho: *Rhogostoma* 属, Sor: *Sorodiplaphrys* 属, Oth: others 其他; b1 表示全河段, b2 表示上游自然河段, b3 表示梯级大坝河段

图3 金沙江浮游真核微生物的 NMDS 分析和优势属的相对丰度

Fig. 3 NMDS analysis of planktonic microeukaryotes and relative abundances of their dominant genera in the Jinsha River

表1 Mantel 检验分析显示地化因子对浮游真核微生物群落的影响

Table 1 Mantel tests showing the effects of geochemical factors on planktonic micro eukaryotic community

地化因子	总体		丰富类		稀有类	
	<i>r</i>	<i>P</i>	<i>r</i>	<i>P</i>	<i>r</i>	<i>P</i>
海拔	0.35	0.001	0.35	0.001	0.08	0.001
距离	0.39	0.001	0.39	0.001	0.09	0.001
水温	0.25	0.001	0.26	0.001	0.06	0.001
浊度	0.08	0.015	0.09	0.018	0.02	0.121
DO	0.08	0.011	0.08	0.017	0.05	0.002
Ec	0.23	0.001	0.23	0.001	0.07	0.001
pH	0.24	0.001	0.23	0.001	0.06	0.002
DOC	0.07	0.021	0.05	0.118	0.04	0.020
TP	0.32	0.001	0.30	0.001	0.08	0.001
TN	0.01	0.334	0.01	0.418	-0.01	0.701
SRP	-0.05	0.891	-0.06	0.901	0.01	0.188
NH ₄ ⁺	-0.01	0.813	-0.01	0.539	0.01	0.207
NO ₃ ⁻	0.12	0.001	0.11	0.002	0.05	0.001

2.4 地理距离和环境异质性对浮游真核微生物群落组成的影响

距离衰减分析表明[图4(a)和4(b)], 总体、丰富类和稀有类浮游真核微生物的群落相似性与地理距离和环境异质性之间均存在显著的负相关关系 ($P < 0.01$), 符合距离衰减关系, 说明其群落结构受扩散限制和环境筛选共同影响. 在表征距离衰减关

系的线性回归方程中, 地理距离和环境异质性对稀有类回归方程的斜率(衰减率)分别为 0.003 和 0.005, 明显低于丰富类的 0.128 和 0.179, 说明稀有类受环境筛选和扩散限制的影响较小.

方差分解分析(VPA)结果显示[图5(a)], 丰富类和稀有类的群落差异性分别由环境异质性和地理距离共同解释了 30.6% 和 20.2%, 稀有类的未解

释率为 79.8%, 高于丰富类的 69.4%; 丰富类和稀有类分别由地理距离单独解释了 14.9% 和 10.2%, 高于环境异质性的 11.1% 和 6.66%。如图 5(b) 所示, 偏 Mantel 检验结果表明, 总体、丰富类和稀有类浮游真核群落组成受环境异质性和地理距离共同影

响 ($P < 0.05$), 且三者与地理距离 (总体: $r = 0.363$; 丰富: $r = 0.368$; 稀有: $r = 0.098$) 的相关性均高于环境异质性 (总体: $r = 0.098$; 丰富: $r = 0.073$; 稀有: $r = 0.032$), 说明扩散限制可能是影响浮游真核微生物群落的主导过程。

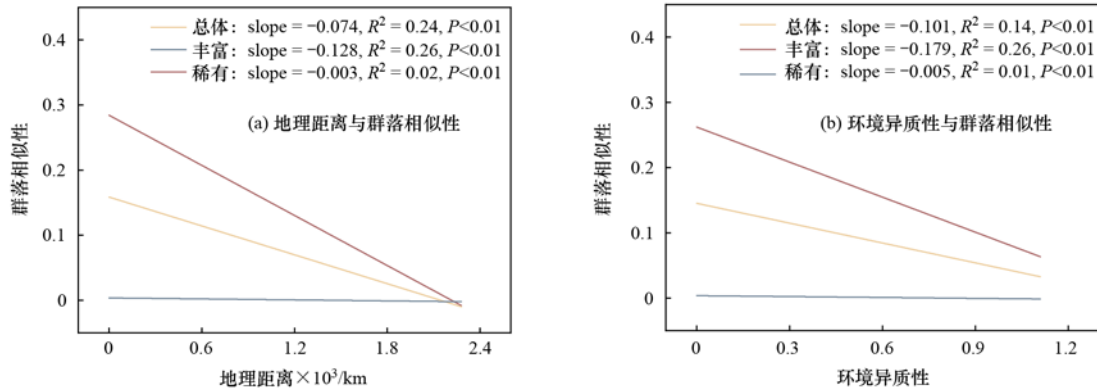
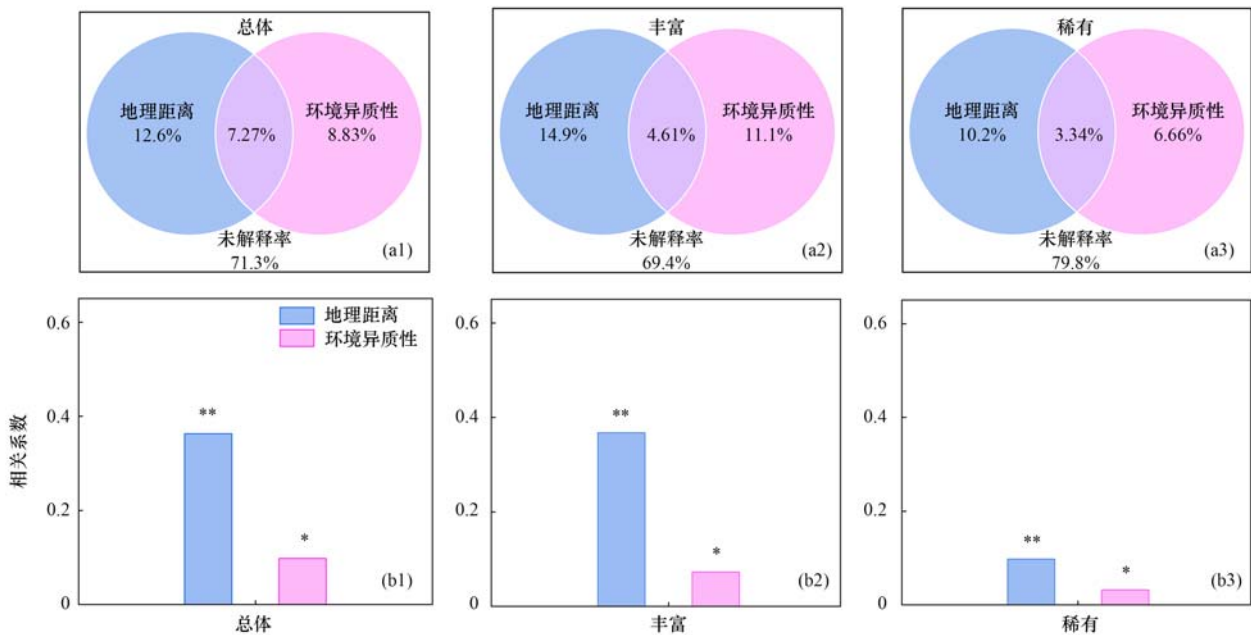


图 4 金沙江浮游真核微生物群落相似性与地理距离和环境异质性的距离衰减关系

Fig. 4 Distance decay relationships between similarity of planktonic microeukaryotic community and geographic distance and environmental heterogeneity in the Jinsha River



(a) VPA 分析, (b) 偏 Mantel 检验; ** 表示 $P < 0.01$, * 表示 $P < 0.05$

图 5 金沙江浮游真核微生物的 VPA 分析和偏 Mantel 检验

Fig. 5 VPA analysis and partial Mantel test of planktonic microeukaryotes in the Jinsha River

3 讨论

本研究中浮游真核微生物的 α 多样性表现为梯级大坝河段较上游自然河段显著增加 [图 2(a) 和 2(b)]. 这种梯级大坝河段 α 多样性的提高可能有如下 3 点原因: ①大坝的修建阻碍了河流的连通性, 使大坝前方形成新的河流汇流点, 因此微生物多样性在大坝河段显著升高^[19], 而笔者的研究结果验证了这一点; ②有文献表明携带不同微生物群落的环境介质的混合将产生新的微生物群落, 即“群落融合”^[20], 金沙江大坝蓄水后库区内水位上升, 增加了与河岸带土壤的交互作用范围, 进而将沿河土壤中的微生物物种带入水体, 这种不同环境介质的微生物群落融合, 是梯级大坝河段浮游真核微生物多样性增加的可能原因之一; ③金沙江下游水体的 TP 等营养物指标高于上游, 表明下游营养物质较上游更为丰富^[6], 基于“多个体假说”, 资源的高效获取会导致个体数量的增加^[21], 导致微生物的 α 多样性

境介质的混合将产生新的微生物群落, 即“群落融合”^[20], 金沙江大坝蓄水后库区内水位上升, 增加了与河岸带土壤的交互作用范围, 进而将沿河土壤中的微生物物种带入水体, 这种不同环境介质的微生物群落融合, 是梯级大坝河段浮游真核微生物多样性增加的可能原因之一; ③金沙江下游水体的 TP 等营养物指标高于上游, 表明下游营养物质较上游更为丰富^[6], 基于“多个体假说”, 资源的高效获取会导致个体数量的增加^[21], 导致微生物的 α 多样性

提高.同时,笔者发现浮游真核微生物稀有类的 α 多样性在梯级大坝河段的增加幅度高于丰富类.这可能与丰富类和稀有类在生态功能及环境适应性等方面的差异性有关,也支持了稀有类群是微生物多样性的主要贡献者这一观点^[22].由于稀有类较高的 α 多样性,增加了群落的功能冗余,从而提高了微生物对河流筑坝带来的变化环境的耐受能力^[15,23,24].

金沙江浮游真核微生物的群落组成在不同河段间存在显著差异[图3(a)].本研究区域覆盖2 279 km河段,海拔变幅3 191 m,沿程地形地貌从上游的高山峡谷到中下游的盆地,浮游真核微生物在河段间的空间差异特征,可能与大河流域的土地利用类型、地貌特征、海拔等地理地质因素密切相关^[25,26].如Liu等^[27]发现长江流域浮游细菌群落的空间差异与土地利用类型密切相关,同一地形的细菌群落趋向于彼此相似,而所在地形类型不同的细菌群落之间存在明显差异;Chen等^[6]发现海拔和地理距离是金沙江细菌和真菌在河段间差异性的主导驱动因素.另一方面金沙江因修建梯级大坝带来水温、pH、DO和营养盐等水体理化性质的变化^[28,29].而水温、pH、DO和营养盐等环境因素对控制水体中微生物的群落组成有重要作用^[30~32].如水温 and pH 会直接或间接影响真核微生物的生长和新陈代谢^[33,34].Mantel结果表明金沙江浮游真核微生物群落组成与海拔和地理距离等地理因素和水温、pH、DO和TP等环境因素均显著相关(表1).根据NMDS和ANOSIM的分析结果,笔者发现相比于丰富类,稀有类河段间群落组成差异性较小[图3(a)],且与多种地化因子的相关性均较低(表1).这可能与两类微生物对环境变化的敏感性有关.通常丰富类群在环境中更活跃,对环境变化高度敏感;而稀有类在环境中多数处于休眠状态,这种生态策略使其对环境变化的耐受性更强^[35,36].

金沙江浮游真核微生物的物种注释与相对丰度分析显示,麦克属和 *Vermamoeba* 属为主要优势属,均属于河流、湖泊等水域生态系统中常见的真核微生物^[37~39].其中,麦克属作为典型的绿藻纲微型生物,其有着各种潜在碳浓缩机制,为不同环境下的碳同化提供了更多的可能^[40].由于金沙江梯级大坝河段水体中的无机碳含量如碳酸根等低于上游自然河段水体^[29],而麦克属独有的高适应性碳同化能力,增强了其在碳源较为枯竭条件下的竞争能力,使其得以大量繁殖,这为麦克属在梯级大坝河段相对丰度较高的现象提供了解释. *Vermamoeba* 属是一种肉足纲的变形虫,可以作为宿主细胞支持其他微生物的生长繁殖,使其他微生物免受不利环境的干扰,而

宿主细胞往往会裂解死亡^[37].这种对其他微生物的保护机制可能是 *Vermamoeba* 属在梯级大坝河段相对丰度较低的原因.同时笔者发现稀有类的优势属相对丰度占比较丰富类有所下降,推测原因有2点:①稀有类对降水和营养波动等偶发事件有明显响应,导致部分物种在压力条件下保持低增长率;②低丰度的稀有物种在竞争中被其他丰富物种在营养物质获取等方面抑制,导致负频率依赖现象^[41].

揭示微生物群落的构建和组装机制是当前微生物生态学的研究重点^[41~43].本研究发现金沙江浮游真核微生物丰富类和稀有类的群落构建受到环境筛选和扩散限制的共同作用(图4和图5).偏Mantel和VPA结果表明,相比于环境筛选,扩散限制是丰富类和稀有类真核微生物群落构建的主导驱动过程.扩散限制和环境筛选对微生物群落构建的相对贡献,与研究区域的空间尺度有关^[18,44].Wu等^[44]研究表明,真菌的地理分布模式在大区域尺度上(1 000~4 000 km)受扩散限制影响较强,而环境异质性对在较小尺度(<1 000 km)的真菌变异解释率较高.笔者在金沙江的研究区域空间距离超过2 000 km,扩散限制在大尺度空间中微生物的群落构建可能发挥主导作用.此外,河流筑坝形成的物理阻隔,导致蓄水區微生物种群的空间隔离,极大地限制了微生物沿河流的流动和扩散,提高了扩散限制对真核微生物群落构建的影响权重^[25].另一方面,根据“尺寸-可塑性”假说,扩散限制的影响会随微生物体型的增加而增加^[45].而相比细菌、古菌等微生物类群,真核微生物体型较大,这使得它们更容易受到大坝河段的扩散限制的影响^[46].同时基于VPA结果,笔者发现总体、丰富类和稀有类的未解释率均较高,且稀有类的未解释率高于丰富类.未解释率均较高的原因可能与微生物之间的相互作用、未监测到的环境因素或生物因素有关^[8,47].而稀有类比丰富类更高的未解释率,则可能是因为稀有类占据了狭窄的生态位,经常与其他物种发生相互作用,例如竞争等^[41].

4 结论

(1)金沙江浮游真核微生物的 α 多样性在梯级大坝河段显著提高,相比丰富类,稀有类的增加幅度更为明显.

(2)丰富类和稀有类浮游真核微生物群落组成在上游自然河段和梯级大坝河段之间均差异显著,且两类微生物的 *Vermamoeba* 属等优势属相对丰度在不同河段间表现出类似规律.

(3)海拔、pH等是影响丰富类和稀有类浮游真

核微生物群落组成的关键地化因子,两类微生物的地理分布受扩散限制和环境筛选共同影响,其中扩散限制是两类微生物群落构建的主导生态学过程。

参考文献:

- [1] Adl S M, Bass D, Lane C E, *et al.* Revisions to the classification, nomenclature, and diversity of eukaryotes [J]. *Journal of Eukaryotic Microbiology*, 2019, **66**(1): 4-119.
- [2] 王显, 龙健, 李娟, 等. 贵州茂兰喀斯特森林不同演替下土壤真核微生物多样性[J]. *环境科学*, 2020, **41**(9): 4314-4321.
- Wang X, Long J, Li J, *et al.* Diversity of soil eukaryotic microbes in different succession stages in Maolan karst forest of Guizhou [J]. *Environmental Science*, 2020, **41**(9): 4314-4321.
- [3] Zhao H X, Brearley F Q, Huang L L, *et al.* Abundant and rare taxa of planktonic fungal community exhibit distinct assembly patterns along coastal eutrophication gradient [J]. *Microbial Ecology*, 2023, **85**(2): 495-507.
- [4] Wu W X, Logares R, Huang B Q, *et al.* Abundant and rare picoeukaryotic sub-communities present contrasting patterns in the epipelagic waters of marginal seas in the northwestern Pacific Ocean [J]. *Environmental Microbiology*, 2017, **19**(1): 287-300.
- [5] Wang X, Wang C, Wang P F, *et al.* How bacterioplankton community can go with cascade damming in the highly regulated Lancang-Mekong River Basin [J]. *Molecular Ecology*, 2018, **27**(22): 4444-4458.
- [6] Chen J, Wang P F, Wang C, *et al.* Fungal community demonstrates stronger dispersal limitation and less network connectivity than bacterial community in sediments along a large river [J]. *Environmental Microbiology*, 2020, **22**(3): 832-849.
- [7] Wang Y, Ye F, Wu S J, *et al.* Biogeographic pattern of bacterioplanktonic community and potential function in the Yangtze River: roles of abundant and rare taxa [J]. *Science of the Total Environment*, 2020, **747**, doi: 10.1016/j.scitotenv.2020.141335.
- [8] He H R, Pan B Z, Yu K, *et al.* Determinants of bacterioplankton structures in the typically turbid Weihe River and its clear tributaries from the northern foot of the Qinling Mountains [J]. *Ecological Indicators*, 2021, **121**, doi: 10.1016/j.ecolind.2020.107168.
- [9] 崔戈, 陈娟, 王沛芳, 等. 金沙江底栖真核微生物地理分布特征及生态学机制 [J]. *环境科学*, 2023, **44**(2): 839-846.
- Cui G, Chen J, Wang P F, *et al.* Biogeographic distribution patterns and ecological mechanisms of benthic eukaryotic microorganisms in Jinsha River [J]. *Environmental Science*, 2023, **44**(2): 839-846.
- [10] Li S F, Huang X B, Lang X D, *et al.* Cumulative effects of multiple biodiversity attributes and abiotic factors on ecosystem multifunctionality in the Jinsha River valley of southwestern China [J]. *Forest Ecology and Management*, 2020, **472**, doi: 10.1016/j.foreco.2020.118281.
- [11] Gui Z H, Chen X H, He Y H. Spatiotemporal analysis of water resources system vulnerability in the Lancang River Basin, China [J]. *Journal of Hydrology*, 2021, **601**, doi: 10.1016/j.jhydrol.2021.126614.
- [12] Chen J, Wang P F, Wang C, *et al.* Distinct assembly mechanisms underlie similar biogeographic patterns of rare and abundant bacterioplankton in cascade reservoirs of a large river [J]. *Frontiers in Microbiology*, 2020, **11**, doi: 10.3389/fmicb.2020.00158.
- [13] Luo X, Xiang X Y, Huang G Y, *et al.* Bacterial community structure upstream and downstream of cascade dams along the Lancang River in southwestern China [J]. *Environmental Science and Pollution Research*, 2020, **27**(34): 42933-42947.
- [14] Wang X, Wang P F, Wang C, *et al.* Do bacterioplankton respond equally to different river regulations? A quantitative study in the single-dammed Yarlung Tsangpo River and the cascade-dammed Lancang River [J]. *Environmental Research*, 2020, **191**, doi: 10.1016/j.envres.2020.110194.
- [15] Xue Y Y, Chen H H, Yang J R, *et al.* Distinct patterns and processes of abundant and rare eukaryotic plankton communities following a reservoir cyanobacterial bloom [J]. *The ISME Journal*, 2018, **12**(9): 2263-2277.
- [16] Liu L M, Chen H H, Liu M, *et al.* Response of the eukaryotic plankton community to the cyanobacterial biomass cycle over 6 years in two subtropical reservoirs [J]. *The ISME Journal*, 2019, **13**(9): 2196-2208.
- [17] Zhang W J, Pan Y B, Yang J, *et al.* The diversity and biogeography of abundant and rare intertidal marine microeukaryotes explained by environment and dispersal limitation [J]. *Environmental Microbiology*, 2018, **20**(2): 462-476.
- [18] Mo Y Y, Zhang W J, Yang J, *et al.* Biogeographic patterns of abundant and rare bacterioplankton in three subtropical bays resulting from selective and neutral processes [J]. *The ISME Journal*, 2018, **12**(9): 2198-2210.
- [19] Wang S, Hou W G, Jiang H C, *et al.* Microbial diversity accumulates in a downstream direction in the Three Gorges Reservoir [J]. *Journal of Environmental Sciences*, 2021, **101**, doi: 10.1016/j.jes.2020.08.006.
- [20] Luo X, Xiang X Y, Yang Y H, *et al.* Seasonal effects of river flow on microbial community coalescence and diversity in a riverine network [J]. *FEMS Microbiology Ecology*, 2020, **96**, doi: 10.1093/femsec/fiaa132.
- [21] Furness E N, Garwood R J, Mannion P D, *et al.* Productivity, niche availability, species richness, and extinction risk: Untangling relationships using individual - based simulations [J]. *Ecology and Evolution*, 2021, **11**(13): 8923-8940.
- [22] Lynch M D J, Neufeld J D. Ecology and exploration of the rare biosphere [J]. *Nature Reviews Microbiology*, 2015, **13**(4): 217-229.
- [23] Timpe K, Kaplan D. The changing hydrology of a dammed Amazon [J]. *Science Advances*, 2017, **3**(11), doi: 10.1126/sciadv.1700611.
- [24] Gao Y, Zhang W L, Li Y, *et al.* Dams shift microbial community assembly and imprint nitrogen transformation along the Yangtze River [J]. *Water Research*, 2021, **189**, doi: 10.1016/j.watres.2020.116579.
- [25] Chen J, Sun S H, Wang P F, *et al.* Sedimentary microeukaryotes reveal more dispersal limitation and form networks with less connectivity than planktonic microeukaryotes in a highly regulated river [J]. *Freshwater Biology*, 2021, **66**(5): 826-841.
- [26] Hassell N, Tinker K A, Moore T, *et al.* Temporal and spatial dynamics in microbial community composition within a temperate stream network [J]. *Environmental Microbiology*, 2018, **20**(10): 3560-3572.
- [27] Liu T, Zhang A N, Wang J W, *et al.* Integrated biogeography of planktonic and sedimentary bacterial communities in the Yangtze River [J]. *Microbiome*, 2018, **6**(1), doi: 10.1186/s40168-017-0388-x.

- [28] Chen X J, He D, Zhou L F, *et al.* Influence of hydropower stations on the water microbiota in the downstream of Jinsha River, China[J]. PeerJ, 2020, **8**, doi: 10.7717/peerj.9500.
- [29] Yuan Q S, Wang P F, Chen J, *et al.* Influence of cascade reservoirs on spatiotemporal variations of hydrogeochemistry in Jinsha River[J]. Water Science and Engineering, 2021, **14** (2): 97-108.
- [30] Wang Y M, Liu L M, Chen H H, *et al.* Spatiotemporal dynamics and determinants of planktonic bacterial and microeukaryotic communities in a Chinese subtropical river [J]. Applied Microbiology and Biotechnology, 2015, **99**(21): 9255-9266.
- [31] 杨思航, 秦泽生, 梁漫春. 不同气候类型下污水厂活性污泥中微生物群落比较[J]. 环境科学, 2021, **42**(10): 4844-4852.
- Yang S H, Qin Z S, Liang M C. Meta-analysis of microbial communities in the activated sludge of wastewater treatment plants under different climate types[J]. Environmental Science, 2021, **42**(10): 4844-4852.
- [32] Hu W G, Jin X T, Wang Y P, *et al.* Diversity of eukaryotic micro-organisms and changes in the dominant fungal taxa composition in relationship with soil environment in the Ebinur Lake wetland[J]. Biotechnology & Biotechnological Equipment, 2018, **32**(2): 408-419.
- [33] Zhang H J, Huang X L, Huang L, *et al.* Microeukaryotic biogeography in the typical subtropical coastal waters with multiple environmental gradients [J]. Science of the Total Environment, 2018, **635**: 618-628.
- [34] Tian J Q, Zhu D, Wang J Z, *et al.* Environmental factors driving fungal distribution in freshwater lake sediments across the Headwater Region of the Yellow River, China[J]. Scientific reports, 2018, **8**(1), doi: 10.1038/s41598-018-21995-6.
- [35] Zhang S, Li K X, Hu J M, *et al.* Distinct assembly mechanisms of microbial sub-communities with different rarity along the Nu River[J]. Journal of Soils and Sediments, 2022, **22**(5): 1530-1545.
- [36] Debroas D, Hugoni M, Domaizon I. Evidence for an active rare biosphere within freshwater protists community [J]. Molecular Ecology, 2015, **24**(6): 1236-1247.
- [37] Delafont V, Rodier M H, Maisonneuve E, *et al.* *Vermamoeba vermiformis*: a free-living amoeba of interest [J]. Microbial Ecology, 2018, **76**(4): 991-1001.
- [38] Shi X L, Li S N, Fan F, *et al.* *Mychonastes* dominates the photosynthetic picoeukaryotes in Lake Poyang, a river-connected lake[J]. FEMS Microbiology Ecology, 2019, **95**(1), doi: 10.1093/femsec/fiy211.
- [39] Liu Q F, Lai Z N, Wang C, *et al.* Seasonal variation of planktonic fungal community structure in the Xijiang River, China[J]. Applied Ecology and Environmental Research, 2021, **19**(3): 1925-1937.
- [40] Liu C Q, Shi X L, Wu F, *et al.* Genome analyses provide insights into the evolution and adaptation of the eukaryotic Picophytoplankton *Mychonastes homosphaera* [J]. BMC Genomics, 2020, **21**(1), doi: 10.1186/s12864-020-06891-6.
- [41] Jia X, Dini-Andreote F, Salles J F. Community assembly processes of the microbial rare biosphere [J]. Trends in Microbiology, 2018, **26**(9): 738-747.
- [42] Chen J, Wang P F, Wang C, *et al.* Dam construction alters function and community composition of diazotrophs in riparian soils across an environmental gradient [J]. Soil Biology and Biochemistry, 2019, **132**: 14-23.
- [43] 孙胜浩, 陈娟, 王沛芳, 等. 澜沧江硅藻的地理分布模式与关键驱动因素[J]. 环境科学, 2020, **41**(12): 5458-5469.
- Sun S H, Chen J, Wang P F, *et al.* Biogeographic distribution patterns of diatoms in Lancang River and their key drivers [J]. Environmental Science, 2020, **41**(12): 5458-5469.
- [44] Wu B, Tian J Q, Bai C M, *et al.* The biogeography of fungal communities in wetland sediments along the Changjiang River and other sites in China[J]. The ISME Journal, 2013, **7**(7): 1299-1309.
- [45] Farjalla V F, Srivastava D S, Marino N A C, *et al.* Ecological determinism increases with organism size[J]. Ecology, 2012, **93** (7): 1752-1759.
- [46] Lu L H, Tang Q, Li H, *et al.* Damming river shapes distinct patterns and processes of planktonic bacterial and microeukaryotic communities [J]. Environmental Microbiology, 2022, **24**(4): 1760-1774.
- [47] Chen W D, Ren K X, Isabwe A, *et al.* Stochastic processes shape microeukaryotic community assembly in a subtropical river across wet and dry seasons[J]. Microbiome, 2019, **7**(1), doi: 10.1186/s40168-019-0749-8.

CONTENTS

Assessing the Environmental and Health Co-benefits of Accelerated Energy Transition and Industrial Restructuring: A Case Study of the BTHS Region	YANG Xi, SUN Yi-sheng, CHANG Shi-yan, <i>et al.</i> (3627)
Synergistic Paths of Reduced Pollution and Carbon Emissions Based on Different Power Demands in China	XIANG Meng-yu, WANG Shen, LÜ Lian-hong, <i>et al.</i> (3637)
Evaluation Method and Application for Urban Carbon Peaking & Neutrality Performance	ZHANG Bao-liu, BAI Zi-han, ZHANG Nan, <i>et al.</i> (3649)
Revealing Driving Factors of Urban O ₃ Based on Explainable Machine Learning	DONG Jia-qi, HU Dong-mei, YAN Yu-long, <i>et al.</i> (3660)
Sensitivity Analysis of Ozone Formation Using Response Surface Methodology	ZHU Yu-huan, CHEN Bing, ZHANG Ya-ru, <i>et al.</i> (3669)
Analysis of O ₃ Sources in Yulin City in Summer Based on WRF-CMAQ/ISAM Model	WANG Yi-fan, TONG Ji-long, CHEN Yu-xiang, <i>et al.</i> (3676)
Atmospheric Ozone Concentration Prediction in Nanjing Based on LightGBM	ZHU Jia-ying, AN Jun-lin, FENG Yue-zheng, <i>et al.</i> (3685)
Meteorological Formation Mechanisms and Potential Sources of an Ozone Pollution Process in Winter of 2022 in Guangdong Province	LI Ting-yuan, CHEN Jing-yang, GONG Yu, <i>et al.</i> (3695)
Impact of Summer Tropospheric Ozone Radiative Forcing on Meteorology and Air Quality in North China	DU Nan, CHEN Lei, LIAO Hong, <i>et al.</i> (3705)
Identification of Impacts from Meteorology and Local and Transported Photochemical Generation on Ozone Trends in Changsha from 2018 to 2020	YANG Jun, YANG Lei-feng, DING Hua, <i>et al.</i> (3715)
Spatio-temporal Variation and Multi-dimensional Detection of Driving Mechanism of PM _{2.5} Concentration in the Chengdu-Chongqing Urban Agglomeration from 2000 to 2021	XU Yong, GUO Zhen-dong, ZHENG Zhi-wei, <i>et al.</i> (3724)
Estimation of PM _{2.5} Hourly Concentration in Sichuan Province Based on GTWR-XGBoost Model	WU Di, DU Ning, WANG Li, <i>et al.</i> (3738)
Transmission and Growth Characteristics of Severe PM _{2.5} Pollution Events from 2013 to 2021 in Xingtai, Hebei	JIANG Qi, SHENG Li, JIN Yu-chen, <i>et al.</i> (3749)
Chemical Characteristics and Source Apportionment of Organic Aerosols in Urban Shanghai During Cold Season Based on High Time-resolution Measurements of Organic Molecular Markers	ZHU Shu-hui (3760)
Emission Factors of Carbonaceous Aerosol and Stable Carbon Isotope for In-use Vehicles	YU Ming-yuan, WANG Qian, FU Ming-liang, <i>et al.</i> (3771)
Composition Characteristics of Volatile Organic Compounds and Associated Contributions to Secondary Pollution in Shenyang Industrial Area in Summer	GUAN Lu, SU Cong-cong, KU Ying-ying, <i>et al.</i> (3779)
Characteristics of VOCs and Assessment of Emission Reduction Effect During the Epidemic Lockdown Period in Shenzhen Urban Area	YUN Long, LIN Chu-xiong, LI Cheng-liu, <i>et al.</i> (3788)
Characteristics of Organic Matter Composition and Oxidation Potential in Road Dust in Winter in Xi'an	WANG Qing-wen, CHEN Qing-cai, WANG Chao, <i>et al.</i> (3797)
Contamination Characteristics and Risk Assessment of Polycyclic Aromatic Compounds in Surface Dust of Suntuan Mining Area in Huaibei	XU Zhen-peng, QIAN Ya-hui, HONG Xiu-ping, <i>et al.</i> (3809)
Spatial-temporal Variation in Water Quality and Its Response to Precipitation and Land Use in Baiyangdian Lake in the Early Stage of the Construction of Xiong'an New Area	WANG Zi-ming, YANG Li-hu, SONG Xian-fang (3820)
Simulation of Pollution Apportionment and Optimization of Control Methods in Watershed Scale: A Case Study of the Shun'an Watershed in Tongling City	LIU Guo-wangchen, CHEN Lei, LI Jia-qi, <i>et al.</i> (3835)
Evaluation of Shallow Groundwater Quality and Optimization of Monitoring Indicators in Nanchang	ZHENG Zi-yin, CHU Xiao-dong, XU Jin-ying, <i>et al.</i> (3846)
Hydrogen and Oxygen Isotopic Characteristics and Influencing Factors of "Three Waters" in Shandian River Basin	YANG Li-na, JIA De-bin, GAO Rui-zhong, <i>et al.</i> (3855)
Distribution Characteristics and Influencing Factors of Abundant and Rare Planktonic Microeukaryotes in Jinsha River	YAN Bing-cheng, CUI Ge, SUN Sheng-hao, <i>et al.</i> (3864)
Bacterial Community Diversity in Channel Sediments of Different Disturbance Sections of the Jialing River	ZHU Lan-ping, ZHANG Tuo, LI Jia-ning, <i>et al.</i> (3872)
Effects of Reservoir Water Depth on Different Plankton Communities and Keystone Species of Network Interaction	WANG Xun, LIAO Qin, WANG Pei-fang, <i>et al.</i> (3881)
Correlation Between the Diversity Characteristics of Groundwater Bacterial Community and Environmental Factors in Typical Industrial Areas	WU Jian-qiang, ZHANG Shu-yuan, WANG Min, <i>et al.</i> (3892)
Effects of Fertilizer Application Strategy Adjustments on Nitrogen and Phosphorus Loss from Typical Crop Systems in Taihu Lake Region	YU Ying-liang, WANG Yi-zhi, YANG Bei, <i>et al.</i> (3902)
Estimation of Cropland Nitrogen Runoff Loss Loads in the Yangtze River Basin Based on the Machine Learning Approaches	ZHANG Yu-fu, PAN Zhe-qi, CHEN Ding-jiang (3913)
Classification and Identification of Non-point Source Nitrogen Pollution in Surface Flow of the Shangwu River Watershed in the Qiandao Lake Region	YU Ke, YAN Yan, TANG Zhang-xuan, <i>et al.</i> (3923)
Spatial Distribution of Nitrogen and Phosphorus Nutrients in the Main Stream and Typical Tributaries of Tuojiang River and Fujiang River	LI Zi-yang, ZHOU Ming-hua, XU Peng, <i>et al.</i> (3933)
Sediment Pollution and Dredging Effect of Waqinhui River	ZHANG Mu, REN Zeng-yi, ZHANG Man, <i>et al.</i> (3945)
Critical Review on Environmental Occurrence and Photochemical Behavior of Substituted Polycyclic Aromatic Hydrocarbons	GE Lin-ke, WANG Zi-yu, CAO Sheng-kai, <i>et al.</i> (3957)
Cadmium and Arsenic Interactions During Co-adsorption onto Goethite	SU Zi-xian, LIU Sai-hong, GUAN Yu-feng, <i>et al.</i> (3970)
Preparation of Catalyst Cyclodextrin-Fe-TAML to Activate H ₂ O ₂ and Oxidize Organic Micropollutants in Water	LIU Qing-quan, CAI Ben-zhe, CAI Xi-yun (3978)
Performance and Reaction Mechanism of Co(II) Mediated Activation of Peroxymonosulfate for Degrading Nitrilotris (Methylene Phosphonic Acid)	ZHU Jing-lin, WANG Shu (3990)
Change in Granulation Potential and Microbial Enrichment Characteristics of Sludge Induced by Microplastics	XIE Qing-fan, YU Nan, ZHANG Ni, <i>et al.</i> (3997)
Accumulation Characteristics and Probabilistic Risk Assessment of Cd in Agricultural Soils Across China	WANG Jing, WEI Heng, PAN Bo (4006)
Source Analysis and Pollution Assessment of Soil Heavy Metals in Typical Geological High Background Area in Southeastern Chongqing	JIANG Yu-lian, YU Jing, WANG Rui, <i>et al.</i> (4017)
Integrated Analysis on Source-exposure Risk of Heavy Metals in Farmland Soil Based on PMF Model: A Case Study in the E-waste Dismantling Area in Zhejiang Province	FANG Jia, HE Ying, HUANG Nai-tao, <i>et al.</i> (4027)
Pollution Characteristics and Risk Assessment of Polycyclic Aromatic Hydrocarbons in Farmland Soil and Crops in the Suburbs of Urumqi	FAN Yue, CAO Shuang-yu, Nuerla Ailijiang, <i>et al.</i> (4039)
Distribution and Driving Mechanisms of Antibiotic Resistance Genes in Desert-Oasis Continuum	HUANG Fu-yi, ZHOU Shu-yidan, SU Jian-qiang, <i>et al.</i> (4052)
Characteristics of Antibiotic Contamination of Soil in China in Past Fifteen Years and the Bioremediation Technology: A Review	ZHAO Xiao-dong, QIAO Qing-qing, QIN Xiao-rui, <i>et al.</i> (4059)
Modified Biochar for Remediation of Soil Contaminated with Arsenic and Cadmium: A Review	LÜ Peng, LI Lian-fang, HUANG Xiao-ya (4077)
Effect of Biogas Slurry Return to Field on Heavy Metal Accumulation in Soil-crop System: A Meta-analysis	ZHAO Qi-zhi, YANG Zhi-min, KONG Fan-jing, <i>et al.</i> (4091)
Remediation Effect of Two Iron-modified Biochars on Slightly Alkaline Arsenic and Cadmium Contaminated Soil	LIANG Xin-ran, HE Dan, ZHENG Zhao-hua, <i>et al.</i> (4100)
Effects of Straw Removal Measure on Soil Cd Bioavailability and Rice Cd Accumulation	WANG Zi-yu, ZHOU Hang, ZHOU Kun-hua, <i>et al.</i> (4109)
Application of Desulphurized Gypsum with Straw to Improve Physicochemical Properties of Saline-alkali Land in Yellow River Delta	ZHAO Hui-li, YU Jin-yi, LIU Tao, <i>et al.</i> (4119)
Biological Evaluation and Key Stress Factor Diagnosis of Compound Contaminated Soil Based on Environmental DNA	HUANG Xiang-yun, ZHONG Wen-jun, LIU Xun-jie, <i>et al.</i> (4130)
Comprehensive Quality Assessment of Soil-Maize Heavy Metals in High Geological Background Area	ZHANG Chuan-hua, WANG Zhong-shu, LIU Li, <i>et al.</i> (4142)
Ecological Risk and Health Risk of Heavy Metal Pollution in Vegetable Production System of Zhejiang Province	ZHANG Shu-min, LIU Cui-ling, YANG Gui-ling, <i>et al.</i> (4151)
Effect of Biochar with Phosphorus Fertilizer on Soil Nutrients, Enzyme Activity, and Nutrient Uptake of <i>Alfalfa</i>	LIU Xin-yu, WANG Dong-mei, ZHANG Ze-zhou, <i>et al.</i> (4162)
Effects of Low-density Polyethylene Microplastics on the Growth and Physiology Characteristics of <i>Ipomoea aquatica</i> Forsk	ZHOU Ying, JIANG Wen-ting, LIU Xun-jie, <i>et al.</i> (4170)
Effects of Biogas Slurry Application on Soil Microbial Communities Structure and Function During Wheat-rice Stubble Period	QIAO Yu-ying, XI Hui, LI Na, <i>et al.</i> (4179)
Analysis of Soil Bacterial Community Structure and Ecological Function Characteristics in Different Pollution Levels of Lead-zinc Tailings in Datong	LIU Ze-xun, ZHUANG Jia-yao, LIU Chao, <i>et al.</i> (4191)
Effect of Fire-deposited Charcoal on Soil Organic Carbon Pools and Associated Enzyme Activities in a Recently Harvested <i>Pinus massoniana</i> Plantation Subjected to Broadcast Burning	YAO Zhi, JIAO Peng-yu, WU Xiao-sheng, <i>et al.</i> (4201)