

目次

气候变化对中国夏季臭氧影响	胡安琪, 谢晓栋, 龚康佳, 侯宇晖, 胡建林 (1801)
基于 EOF 分解和 KZ 滤波的 2019~2021 年中国臭氧时空变化及驱动因素分析	王浩琪, 张裕芬, 罗忠伟, 王艳阳, 戴启立, 毕晓辉, 吴建会, 冯银厂 (1811)
华北工业城市夏季大气臭氧生成机制及减排策略	郑镇森, 姜建平, 张国涛, 李丽明, 徐勃, 杨文, 白志鹏 (1821)
2015~2020 年中国城市 PM _{2.5} -O ₃ 复合污染时空演变特征	牛笑笑, 钟艳梅, 杨璐, 易嘉慧, 慕航, 吴倩, 洪松, 何超 (1830)
2015~2021 年京津冀及周边地区 PM _{2.5} 和臭氧复合污染时空特征分析	宋小涵, 燕丽, 刘伟, 贺晋瑜, 王亚晨, 黄同林, 李园园, 陈敏, 孟静静, 侯战方 (1841)
2000~2020 年中国典型经济区 PM _{2.5} 时空变化及其与植被景观格局的关系	徐勇, 李欣怡, 黄雯婷, 郭振东, 盘钰春, 郑志威, 戴强玉 (1852)
北京市核心区冬春季大气离子沉降量特征及来源解析	赵宇, 李贝贝, 黄玉虎, 梁静, 杨洪玲, 秦建平, 朱玲 (1865)
南京近郊农田大气颗粒物及金属干沉降输入特征	刘翠英, 靳浩, 樊建凌 (1873)
西安冬季 PM _{2.5} 中不同极性水溶性有机物的污染特征及氧化潜势	罗玉, 黄沙沙, 张甜, 孙健, 沈振兴 (1882)
机动车源和民用燃料源颗粒物中有机碳和元素碳的排放特征	王红磊, 刘思略, 孙杰娟, 刘煥武, 赵天良, 裴宇僊, 可玥, 武自豪, 刘诗云 (1890)
伊犁河谷核心区春季 PM _{2.5} 组分特征及来源解析	谷超, 徐涛, 马超, 伊布提哈尔·加帕尔, 郭丽瑶, 李新琪, 杨文 (1899)
基于高分辨率网格的郑州市城镇居民 PM _{2.5} 暴露浓度与健康风险变化评估	李媛, 徐艺斐, 袁明浩, 苏方成, 王申博, 王克, 张瑞芹 (1911)
基于多源数据融合的河南省建材行业排放清单	刘晓, 胡京南, 王红梅, 杨丽, 张皓 (1924)
开封市城区冬季大气挥发性有机物污染特征及来源解析	施雨其, 郑凯允, 丁玮婷, 刘金平, 陈洪光, 高光, 王玲玲, 王楠, 马双良, 郑瑶, 谢绍东 (1933)
2020 年和 2021 年南京城区臭氧生成敏感性和 VOCs 来源变化分析	陆晓波, 王鸣, 丁峰, 喻义勇, 张哲海, 胡崑 (1943)
北京市城区夏季大气 VOCs 变化特征及臭氧生成潜势	张蕊, 孙雪松, 王裕, 王飞, 罗志云 (1954)
青岛市臭氧污染与非污染期间 VOCs 化学特征及来源解析	贾智海, 顾瑶, 孔翠丽, 宋江邦, 孟赫, 石来元, 吴建会, 刘保双 (1962)
基于总过氧自由基观测研究合肥市西郊夏季 O ₃ 生成特征	俞辉, 韦娜娜, 徐学哲, 刘芊芊, 姚易辰, 赵卫雄, 张为俊 (1974)
“大气十条”政策的节能降碳效果评估与创新中介效应	李少林, 王齐齐 (1985)
北京市减污降碳协同控制情景模拟和效应评估	俞珊, 张双, 张增杰, 翟艳芝, 刘桐坤 (1998)
基于不同排放清单的长三角人为 CO ₂ 排放模拟	马心怡, 黄文晶, 胡凝, 肖薇, 胡诚, 张弥, 曹畅, 赵佳玉 (2009)
武汉汉江水源水质变化趋势及风险分析	卓海华, 姜保峰, 徐杰, 陈洁, 陈杰, 兰秀薇, 范文重, 欧阳雪姣, 兰静 (2022)
长江武汉段水源地典型抗生素及抗性基因污染特征与生态风险评价	李柏林, 张贺, 王俊, 沙雪妮, 陈晓飞, 卓海华 (2032)
陕北矿区典型河流多环芳烃的赋存特征、来源及毒性风险分析	吴喜军, 董颖, 赵健, 刘静, 张亚宁 (2040)
典型湖泊有机聚集体时空特征及驱动因子	谢贵娟, 龚伊, 朱富成, 刘昌利, 卢宝伟, 邓辉, 汤祥明 (2052)
桂林市不同功能型公园水体微塑料的分布特征及风险评估	李沛钊, 吴莉, 黄菲菲, 林才霞, 舒小华, 张倩 (2062)
长江流域浮游植物群落的环境驱动及生态评价	张静, 胡愈圻, 胡圣, 黄杰 (2072)
环境异质性对三峡库区支流香溪河附石硅藻群落的影响及驱动作用	纪璐璐, 赵璐, 欧阳添, 杨宋琪, 郑保海, 杜雨欣, 李玉鑫, 李佳欣, 施军琼, 吴忠兴 (2083)
武汉市 3 种类型湖泊浮游植物群落特点及关键影响因素	张浩坤, 闵奋力, 崔慧荣, 彭雪, 张心怡, 张淑烟, 李竹栖, 葛芳杰, 张璐, 吴振斌, 刘碧云 (2093)
重金属污染对不同生境中微生物群落结构的影响	何一凡, 肖新宗, 王佳文 (2103)
毫清河水体细菌群落的结构和分布特征	王森, 陈建文, 张红, 李君剑 (2113)
微塑料暴露对小棒指软珊瑚 (<i>Sinularia microclavata</i>) 共附生细菌群落结构和功能的影响	刘敏, 车文学, 曾映旭, 边伟杰, 吕淑果, 穆军 (2122)
上海市从源头到龙头的饮用水新型污染物分布特征及健康风险评价	严棋 (2136)
铝改性生物炭对水体低浓度氟的吸附特性	刘艳芳, 高玮, 刘蕊, 尹思婕, 张妙雨, 刘晓帅, 李再兴 (2147)
典型雌激素在微塑料上的吸附特征及位点能量分布	刘姜艳, 郑密密, 胡嘉梧, 柳玉荣, 贺德春, 潘杰 (2158)
面向工业园区废水臭氧氧化深度处理性能评价的模型污染物选择与评估	辛勃, 单超, 吕路 (2168)
基于地理探测器和多源数据的耕地土壤重金属来源驱动因子及其交互作用识别	张宏泽, 崔文刚, 刘绥华, 崔瀚文, 黄月美 (2177)
基于 APCS-MLR 和 PMF 模型的煤矸山周边耕地土壤重金属污染特征及源解析	马杰, 沈智杰, 张萍萍, 刘萍, 刘今朝, 孙静, 王玲灵 (2192)
基于蒙特卡罗模拟的铅锌冶炼厂周边农田土壤重金属健康风险评估	黄剑波, 姜登登, 温冰, 王磊, 石佳奇, 周艳 (2204)
基于 BP 神经网络预测北京市加油站周边土壤多环芳烃含量	马赛炎, 魏海英, 马瑾, 刘奇缘, 吴颐杭, 屈雅静, 田雨欣, 赵文浩 (2215)
石家庄市土壤中喹诺酮类抗生素时空分布及其风险评估	赵鑫宇, 陈慧, 赵波, 宋圆梦, 卢梦淇, 崔建升, 张璐璐, 李双江 (2223)
典型黑色岩系地质高背景区土壤和农产品重金属富集特征与污染风险	邓帅, 段佳辉, 宁墨兔, 谭林, 蒲刚, 陈际行, 齐小兵, 蒋尚智, 谢桃园, 刘意章 (2234)
岩溶区不同母质土壤 Cd 地球化学特征及玉米籽实 Cd 含量预测	戴亮亮, 徐宏根, 巩浩, 彭志刚, 肖凯琦, 吴欢欢, 许青阳, 郭军, 汤媛媛, 张俊 (2243)
龙岩市不同利用类型土壤及农作物 Pb、Cd 和 As 污染风险与贡献分析	王蕊, 陈楠, 张二喜 (2252)
小麦籽粒镉含量影响因素 Meta 分析和决策树分析	刘娜, 张少斌, 郭欣宇, 宁瑞艳 (2265)
黄土高原次生林演替过程土壤有机碳库及其化学组成响应特征	刘涵宇, 刘颖异, 张琦, 封伦, 高起乾, 任成杰, 韩新辉 (2275)
短期氮磷添加对祁连山亚高山草地土壤呼吸组分的影响	江原, 甘小玲, 曹丰丰, 赵传燕, 李伟斌 (2283)
黄河源区斑块退化高寒草甸土壤微生物多样性对长期封育的响应	杨鹏年, 李希来, 李成一, 段成伟 (2293)
不同海拔箭筈锦鸡儿根际和非根际土壤细菌群落多样性及 PICRUSt 功能预测	李媛媛, 徐婷婷, 艾喆, 魏庐璐, 马飞 (2304)
模拟酸雨及氮沉降对马尾松林土壤细菌群落结构及其多样性的影响	王楠, 钱少郁, 潘小承, 陈一磊, 白尚斌, 徐飞 (2315)
磷石膏和碱蓬对盐渍化土壤水盐及细菌群落结构的影响	刘月, 杨树青, 张万峰, 姜帅 (2325)
菌渣与化肥肥施对稻田土壤微生物群落组成及多样性的影响	耿和田, 王旭东, 石思博, 叶正钱, 周文晶 (2338)
增氧对不同秸秆还田稻田田面水养分动态及温室气体排放的影响	胡锦涛, 薛利红, 钱聪, 魏利祥, 曹帅 (2348)
外源褪黑素对胁迫下水稻幼苗生长和抗氧化系统的影响	储玉檀, 李颜, 黄益宗, 保琼莉, 孙红羽, 黄永春 (2356)
面向 2035 的节能与新能源汽车全生命周期碳排放预测评价	付佩, 兰利波, 陈颖, 郝卓, 邢云翔, 蔡旭, 张春梅, 陈轶嵩 (2365)
农田土壤微塑料分布、来源和行为特征	薄录吉, 李冰, 张凯, 马荣辉, 李彦, 王艳芹, 孙斌, 刘月岩 (2375)
农田土壤除草剂污染的修复技术研究进展	胡芳雨, 安婧, 王宝玉, 徐明恺, 张惠文, 魏树和 (2384)
我国黑土地农田土壤除草剂残留特征研究及展望	李睿, 吴秋梅, 赵归梅, 胡文友, 田康, 黄标, 吴祥为, 刘峰, 赵玉国, 赵永存 (2395)
《环境科学》征订启事(1910)	《环境科学》征稿简则(1984)
信息	(2167, 2191, 2324)

亳清河水体细菌群落的结构和分布特征

王森^{1,2}, 陈建文¹, 张红¹, 李君剑^{1*}

(1. 山西大学黄土高原研究所, 太原 030006; 2. 山西农业大学资源环境学院, 太原 030006)

摘要: 城镇生活和工业生产均会对水生环境中细菌群落的结构和分布产生影响。亳清河是黄河小浪底水库的重要支流, 流经铜尾矿库和城镇, 为了厘清亳清河水体中的细菌群落结构和分布特征, 通过采集亳清河沿线具有空间代表性的水体样品, 分析亳清河水体中细菌群落的多样性特征, 探讨了其与重金属等环境因子的响应关系。结果表明, 亳清河下游细菌群落丰富度和多样性高于上游, 表现出先降后升的趋势, 在汇入小浪底水库之前达到峰值, 在铜尾矿库及其附近水体中具有最低的群落丰富度和多样性; 变形菌门 (Proteobacteria)、放线菌门 (Actinobacteriota)、拟杆菌门 (Bacteroidota)、厚壁菌门 (Firmicutes) 和不动杆菌属 (*Acinetobacter*)、*Limnohabitans*、假单胞菌属 (*Pseudarthrobacter*)、黄杆菌属 (*Flavobacterium*) 分别是亳清河水体中的主要优势菌门和主要优势菌属; 不动杆菌属在城镇水体中具有最高的相对丰度, 其与 TC 显著正相关; 黄杆菌属与 As 具有共现性且显著正相关, As 对亳清河流域致病菌的传播可能具有促进作用。研究结果对多因素影响下的水体健康评估具有重要意义。

关键词: 细菌群落结构; 分布特征; 铜尾矿库; 重金属; 亳清河

中图分类号: X172 文献标识码: A 文章编号: 0250-3301(2023)04-2113-09 DOI: 10.13227/j.hjxx.202204179

Structure and Distribution Characteristics of Bacterial Community in Boqing River Water

WANG Sen^{1,2}, CHEN Jian-wen¹, ZHANG Hong¹, LI Jun-jian^{1*}

(1. Institute of Loess Plateau, Shanxi University, Taiyuan 030006, China; 2. College of Resources and Environment, Shanxi Agricultural University, Taiyuan 030006, China)

Abstract: The structure and distribution of bacterial communities should be influenced by urban and industrial activities. The Boqing River, which flows through towns and a copper tailing reservoir, is an important tributary of Xiaolangdi Reservoir in South Shanxi. In order to clarify the structure and distribution characteristics of the bacterial community in the Boqing River, we collected water samples along the Boqing River. The diversity characteristics of bacterial communities were analyzed, and their relationships with environmental factors were also explored. The results showed that the abundance and diversity of the bacterial community were higher in the downstream than that in the upstream of the river. Both of the parameters first decreased and then increased along the river. The lowest and highest bacterial abundance and diversity existed in the copper tailing reservoir and the site adjacent to the Xiaolangdi Reservoir, respectively. Proteobacteria, Actinobacteriota, Bacteroidota, and Firmicutes were dominant taxa at the bacterial phylum level in the river, and *Acinetobacter*, *Limnohabitans*, *Pseudoarthrobacter*, and *Flavobacterium* were dominant taxa at the genus level. *Acinetobacter* had the highest relative abundance in urban water of the river, which was significantly positively correlated with TC. *Flavobacterium* was significantly correlated with As. Considering its co-occurrence with As, we speculated that As might contribute to the spread of pathogenic bacteria in the study area. The results of this study were of great importance for the assessment of aquatic health under a complex environment.

Key words: bacterial community structure; distribution characteristics; copper tailing ponds; heavy metals; Boqing River

细菌群落对环境变化的响应是一个很重要的生态问题^[1]。在水生环境中, 细菌群落具有生态功能指示和水体自净的重要作用, 其群落结构及分布也会随着水生环境的变化而改变^[2]。由于细菌群落对生存环境变化的敏感性, 细菌群落的生物量、多样性指数和优势分布常被用来指示污染生态系统中的水体质量和变化^[3,4]。

随着农林牧渔和工矿业等生产活动的发展, 重金属污染已成为影响水生环境中细菌群落结构与组成的重要因素^[5]。这是由于重金属会使细胞内的蛋白质失去活性, 影响细胞呼吸和能量交换^[6], 从而阻碍细菌的新陈代谢和生物活性。Bhagat 等^[7]发现革兰氏阴性菌的形态随水体中重金属 Ni 和 Cd 含量的升高发生改变, 细胞表面变得更加黏稠或粗糙。在重金属污染的水体中, 细菌群落的丰度和多样性受到环境梯度或地理距离、河流深度以及营养物质等

多种环境因素的影响^[8-10], 其中, 重金属对细菌群落结构的影响甚至高于营养物质所形成的选择压力^[11]。有研究发现, 铜尾矿库中的细菌群落组成更易受到 As、Pb 和 Zn 的毒害作用^[12]。然而, 这些研究或针对环境中的特定菌群进行探讨, 或针对受重金属影响较大的局部区域进行调查, 而对流经有尾矿库与城镇的河流中细菌群落特征的研究较少。

亳清河是山西省垣曲县境内的第二大河流, 属于黄河的一级支流。河流发源于垣曲西北部矿山, 流经尾矿库和城镇, 汇入小浪底水库, 区域特征鲜明。本文通过对亳清河细菌群落特征和重金属污染状况的测定分析, 旨在探究: ①亳清河中细菌群落的分布

收稿日期: 2022-04-14; 修订日期: 2022-07-06

基金项目: 国家自然科学基金项目 (U1910207)

作者简介: 王森 (1992~), 男, 硕士研究生, 主要研究方向为微生物生态学, E-mail: 1077206885@qq.com

* 通信作者, E-mail: lijunjian@sxu.edu.cn

特征及其与重金属之间的响应关系;②引起细菌群落结构空间分异的驱动因子.本研究对黄河流域生态文明建设具有重要意义.

1 材料与方法

1.1 研究区概况

亳清河(35°05'~35°20'N,111°33'~111°51'E)位于山西省南部运城市垣曲县境内,向东南流贯垣曲县汇入黄河小浪底水库,全长48 km,流域总面积1128 km²,流域人口170 000人.该区域属暖温带

大陆季风性气候,年降雨量780 mm,年均温14℃,无霜期大于200 d,四季分明.流域上游建有十八河铜尾矿库,库容 1.25×10^8 m³.

1.2 水样采集方法

2020年11月,选择亳清河典型位置进行水体样本采集(表1和图1).采用便携式水样采集器在每个样点采集河流表层水(0~50 cm)2 L,每样点3个重复,并保存于无菌水样采集袋中,及时放入4℃车载冰箱保存,立即运回实验室进行下一步分析.

表1 采样点介绍

Table 1 Introduction of sample sites

采样点	样点介绍	东经	北纬
S1	刘家庄村西北方向,发源地	111°33'57.36"	35°20'02.49"
S2	瓦舍水库,新城镇东北方	111°42'18.34"	35°20'32.65"
S3	十八河尾矿库入口	111°37'49.30"	35°17'20.97"
S4	十八河尾矿库内部	111°37'43.00"	35°17'12.96"
S5	十八河尾矿库出水口	111°39'31.76"	35°15'42.21"
S6	位于新城镇中部	111°39'23.27"	35°17'28.77"
S7	离主城区约2 km,国道附近	111°39'57.39"	35°15'59.56"
S8	流入皋落乡前	111°40'19.17"	35°15'41.66"
S9	流经长直乡前,附近有一污水处理厂	111°41'03"	35°14'49"
S10	长直乡和王茅镇的交界处	111°45'32.41"	35°11'21.68"
S11	王茅镇出口	111°48'55.36"	35°08'21.22"
S12	古城入口	111°49'33.51"	35°07'24.87"
S13	由此汇入小浪底水库	111°51'50.95"	35°05'56.501"

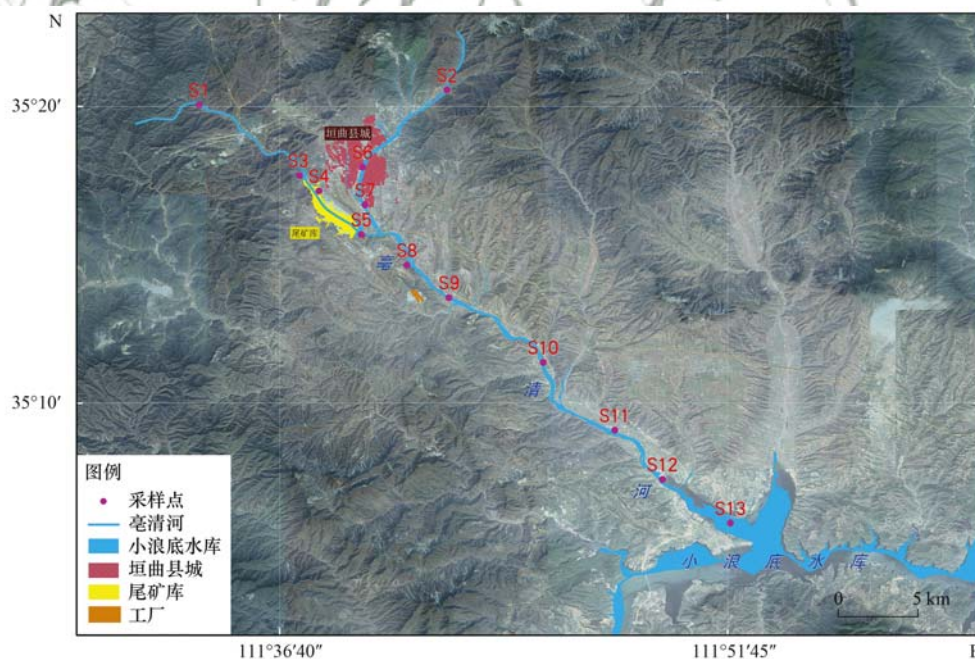


图1 亳清河采样点位置

Fig. 1 Location of sampling sites in Boqing River

1.3 样品预处理与各项指标测定方法

采用全自动凯式定氮仪(Kjeltec 8400,丹麦FOSS)测定水体总氮(TN);采用CNS元素分析仪(vario ISOTOPE select,德国Elementar)测定水中总

碳(TC);使用原子吸收分光光度计(NexION 350D,美国PerkinElmer)测定Cu、Zn、Pd和Cd的含量;使用电感耦合等离子体质谱仪(200 Series AA,美国Agilent)测定水中Hg、Cr和As的含量.

1.4 DNA 抽提、PCR 扩增和 Illumina MiSeq 测序

从采集的每个水样中分取 500 mL, 经 0.2 μm 的聚碳酸酯膜过滤, 收集浮游微生物, 装于 2 mL 的 EP 管中, 封存在 -80°C 的冰箱中. 根据 FastDNA[®] Spin Kit for Soil (MPBiomedicals, 美国) 试剂盒说明书步骤抽提样品中的微生物群落总 DNA, 采用 1% 的琼脂糖凝胶电泳检测 DNA 所提取的质量, 使用 NanoDrop2000 测定 DNA 浓度和纯度; 使用 338F (5'-ACTCCTACGGGAGGCAGCAG-3') 和 806R (5'-GGACTACHVGGGTWTCTAAT-3') 作为引物对 16S rRNA 基因进行扩增. 扩增程序为: 95°C 预变性 3 min, 27 个循环(95°C 变性 30 s, 55°C 退火 30 s, 72°C 延伸 30 s), 72°C 稳定延伸 10 min. PCR 反应体系为: $5 \times$ TransStartFastPfu 缓冲液 4 μL , $2.5 \text{ mmol} \cdot \text{L}^{-1}$ dNTPs 2 μL , 上游引物 ($5 \mu\text{mol} \cdot \text{L}^{-1}$) 0.8 μL , 下游引物 ($5 \mu\text{mol} \cdot \text{L}^{-1}$) 0.8 μL , TransStartFastPfu DNA 聚合酶 0.4 μL , 模板 DNA 10 ng, ddH₂O 补足至 20 μL . 每个样本 3 个重复. 将同一样本的 PCR 产物混合后使用 2% 琼脂糖凝胶回收 PCR 产物, 利用 AxyPrep DNA Gel Extraction Kit (AxygenBiosciences, Union City, CA, 美国) 进行回收产物纯化, 2% 琼脂糖凝胶电泳检测, 并用 Quantus[™] Fluorometer (Promega, 美国) 对回收产物进行检测定量. 使用 NEXTflex[™] Rapid DNA-Seq Kit (Bioo Scientific, 美国) 进行建库. 最后在 Illumina 公司的 MiSeq PE300/NovaSeq PE250 平台进行测序(上海美吉生物医药科技有限公司), 获得 OTU 信息和种属鉴定.

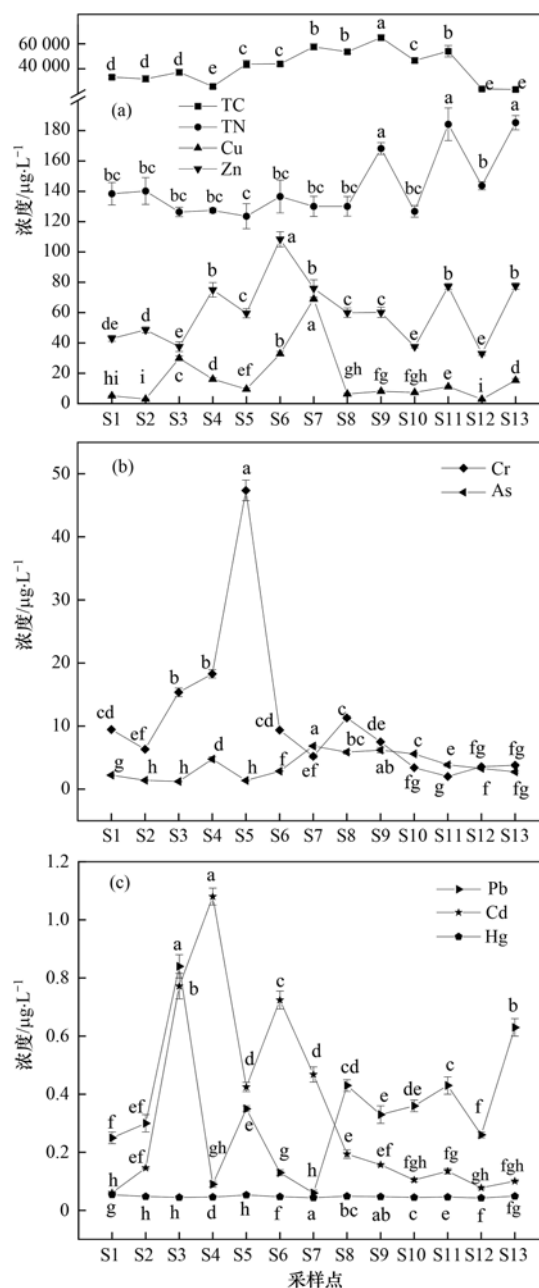
1.5 数据处理方法

采用 One-way ANOVA 分析毫清河水体理化性质在不同样点之间的差异性, 并用 Tukey 进行多重比较; 采用 Spearman 相关系数检验细菌群落多样性指数、优势菌属与环境因子间的相关性; 热图可视化利用 R (软件包) 完成; 网络分析可视化通过 Gephi(0.9.2) 实现.

2 结果与分析

2.1 毫清河水体理化性质

TC 浓度在 S9 处最高(图 2), 显著高于其他样点($P < 0.05$); TN 浓度在 S9、S11 和 S13 处显著高于其他样点($P < 0.05$). 重金属 Cr 在 S5 处的含量最高, 显著高于其他样点($P < 0.05$); Cd 在 S3 和 S4 处的含量最高, 显著高于其他样点($P < 0.05$); As 在 S7 处最高, 显著高于其他样点($P < 0.05$); 有 3 种重金属的最低值出现在 S12 处, 分别是 Cu、Zn 和 Hg. 除 Hg 外, 其他所有重金属的最高值均集中在 S3 ~ S7 处, 其中 Cu 和 As 都在 S7 处最高, Zn 的最



不同小写字母表示两样点间差异显著($P < 0.05$),

TN 和 TC 分别表示总氮和总碳

图 2 毫清河水体理化性质

Fig. 2 Water physico-chemical characteristics at each sampling site in Boqing River

高含量位于 S6 处, 且显著高于其他样点($P < 0.05$).

2.2 细菌群落特征

2.2.1 细菌群落结构

在本次调查采集的 13 个样点中, 共得到细菌有效序列信息 604 951 条, 单个样点序列信息在 26 528 ~ 51 886 条之间, 通过与数据库进行分类学分析, 共得到 3 261 个 OTU, 分属 43 个门, 929 个属. 流域中共有优势菌门(相对丰度大于 1%) 14 个[图 3(a)], 按照相对丰度高低依次为变形菌门(Proteobacteria,

30.16% ~ 83.79%)、放线菌门 (Actinobacteriota, 2.91% ~ 42.61%)、拟杆菌门 (Bacteroidota, 3.75% ~ 24.08%)、厚壁菌门 (Firmicutes, 0% ~ 11.34%)、蓝细菌门 (Cyanobacteria, 0.12% ~ 8.09%)、绿弯菌

门 (Chloroflexi, 0% ~ 7.90%) 等. 丰度最高的前 3 种类群在各样本群落中占比为 77.73% ~ 96.41%. 变形菌门在 S5、S6 和 S7 处的相对丰度较高, 而放线菌门在 S11、S12 和 S13 处的相对丰度较高.

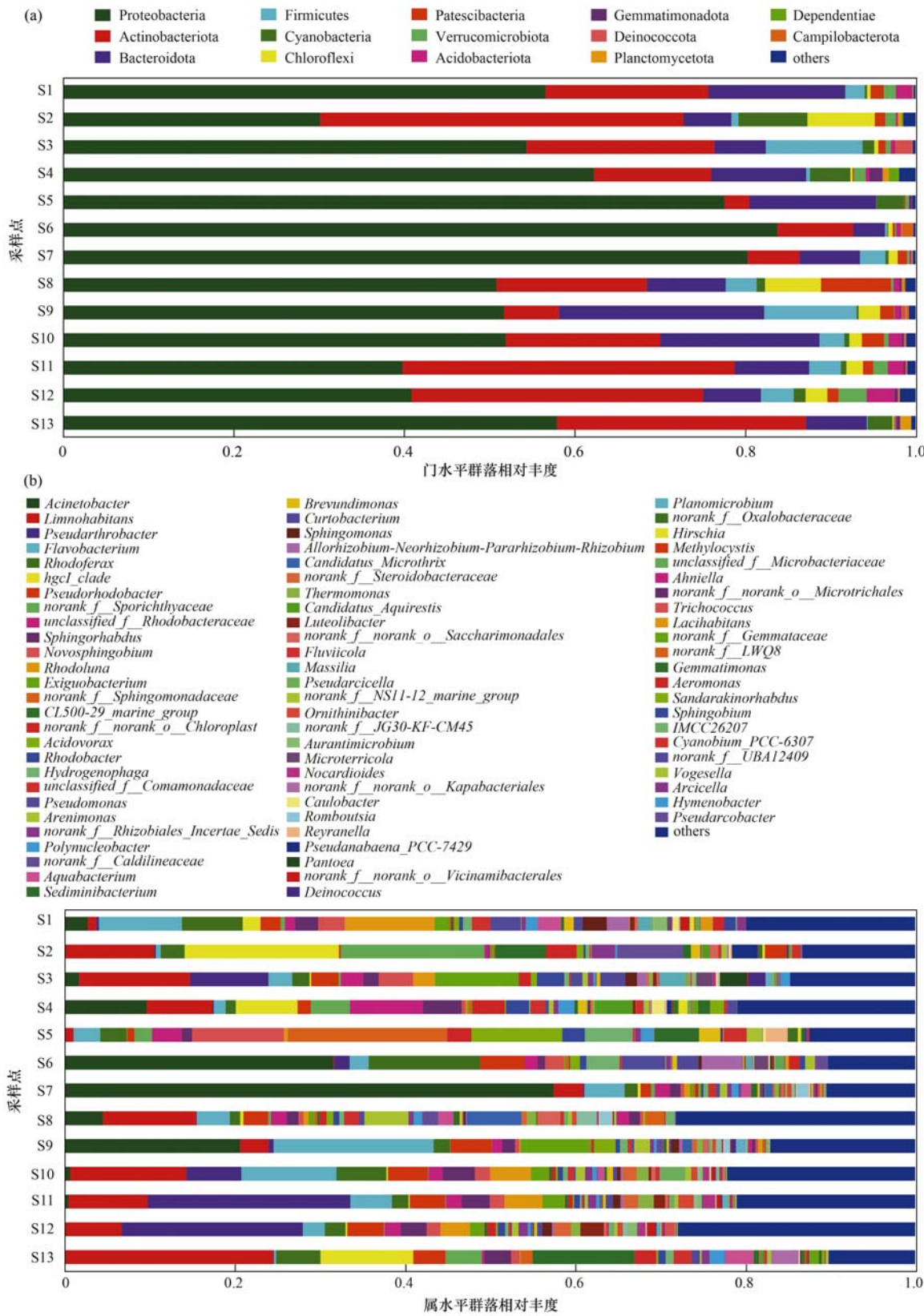


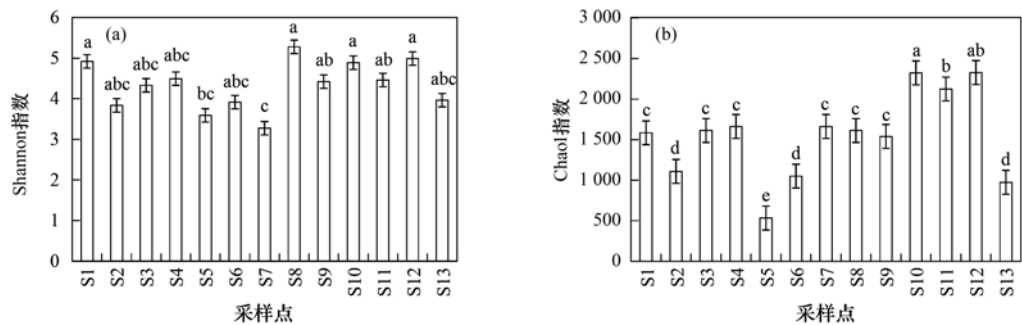
图3 亳清河水体中门、属水平细菌群落结构
Fig. 3 Bacterial community structure of Boqing River

亳清河细菌群落中的优势菌属(相对丰度大于1%)共有76种[图3(b)].其中*Limnohabitans*和黄杆菌属(*Flavobacterium*)在所有样点均为优势菌群,*Limnohabitans*的相对丰度在S13处占比最高,黄杆菌属在S9处的相对丰度最高;不动杆菌属(*Acinetobacter*)在S6和S7处相对丰度占比显著高于其他样点;假单胞菌属(*Pseudarthrobacter*)在S11和S12处的相对丰度显著高于其他样点.

2.2.2 细菌多样性与丰富度

细菌群落 Shannon 指数在 S7 处最低,在 S8 处

最高[图4(a)].沿着河流的方向,细菌群落丰富度指数 Chao1 表现出先降后升的趋势,Chao1 指数在 S5 处最低,显著低于其他样点($P < 0.05$),在 S12 处最高[图4(b)].整条河细菌群落丰富度最低的区域是 S5、S6 和 S13 处,丰富度最高的区域是 S10 ~ S12 处,细菌群落多样性最低的样点集中在 S5 ~ S7 处.且随着河流的走势,各样点间细菌的 α 多样性和丰富度变化趋势一致. Shannon 指数在 S5 和 S7 处最低,且与多样性最高的 S1、S8、S10 和 S12 处有显著性差异($P < 0.05$).



不同的字母表示两样点间差异显著 ($P < 0.05$)

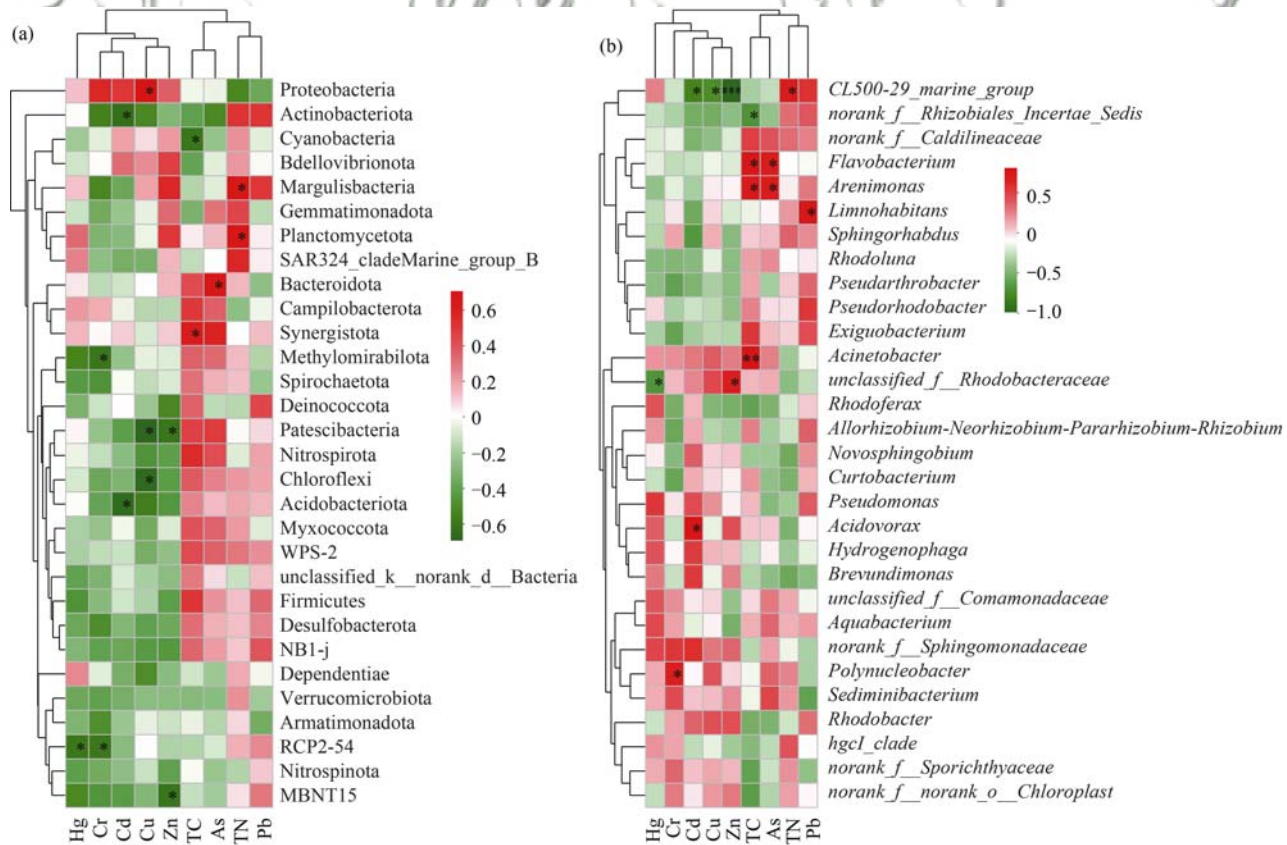
图4 亳清河细菌群落的多样性和丰富度

Fig. 4 Relative abundance and diversity of bacterial community structure in Boqing River

2.3 细菌群落特征与环境因子的相关性

基于环境因子和相对丰度前30的细菌门的相

关性分析发现[图5(a)],Cd与Acidobacteriota、放线菌门两种细菌显著负相关;Cu与变形菌门、



* 表示 $P < 0.05$, ** 表示 $P < 0.01$, *** 表示 $P < 0.001$

图5 门水平和属水平细菌与环境因子之间的相关性

Fig. 5 Correlations between physico-chemical characteristics and the bacterial taxa at the phylum level and genus level, respectively

Patescibacteria 和绿弯菌门这 3 种细菌显著负相关; As 与拟杆菌门显著正相关. 优势细菌门中,变形菌门和 Cu 含量显著正相关($P=0.015$),拟杆菌门与 As 显著正相关($P=0.024$),放线菌门与 Cd 也显著负相关($P=0.029$).

在属水平相对丰度前 30 的细菌中. TC 与 *norank_f_Rhizobiales_Incertae_Sedis* 显著负相关 ($P<0.05$),与菌属黄杆菌属、*Arenimonas* 显著正相关($P<0.05$),与不动杆菌属极显著正相关 ($P<0.01$) [图 5 (b)]; As 与黄杆菌属、*Arenimonas* 显著正相关($P<0.05$); TN、Pb 分别与 *CL500-29_marine_group*、*Limnohabitans* 显著正相关 ($P<0.05$). 优势属 *CL500-29-marine-*

group 与 TN、Cu、Cr、Cd 共 4 个环境因子均显著相关 ($P<0.05$),其中与 Cd 极显著相关 ($P<0.001$); 黄杆菌属、*Arenimonas* 与 TC、As 显著相关 ($P<0.05$).

丰富度和多样性指数与环境因子的相关性分析发现(表 2),在毫清水体中,Cu 同时与 Shannon 指数和 Simpson 指数均显著相关,而 Cr 和 Hg 均与 Ace、Chao1 指数显著负相关. 细菌优势属(丰度前 50)与重金属的共现性网络中共得到 57 个节点和 46 条边,平均度为 0.807,网络直径为 4,图密度为 0.014,模块度为 0.514,平均路径长度为 1.99. 共确定了 6 个关键类群(图 6),共 41 种优势菌属与其他菌属相互共存.

表 2 细菌多样性与环境因子之间的 Pearson 相关¹⁾

Table 2 Pearson correlation analysis between bacterial diversity and environmental parameters

指数	TC	TN	Cu	Zn	Cr	Pb	Cd	Hg	As
Shannon	-0.095	-0.012	-0.626 *	-0.475	-0.296	0.166	-0.298	-0.007	0.189
Simpson	0.360	-0.044	0.837 **	0.330	-0.091	-0.403	0.112	-0.334	0.324
Ace	0.031	0.078	-0.104	-0.424	-0.644 *	0.102	-0.211	-0.658 *	0.334
Chao1	0.100	0.043	-0.082	-0.407	-0.609 *	-0.056	-0.214	-0.612 *	0.478

1) * 表示 $P<0.05$, ** 表示 $P<0.01$

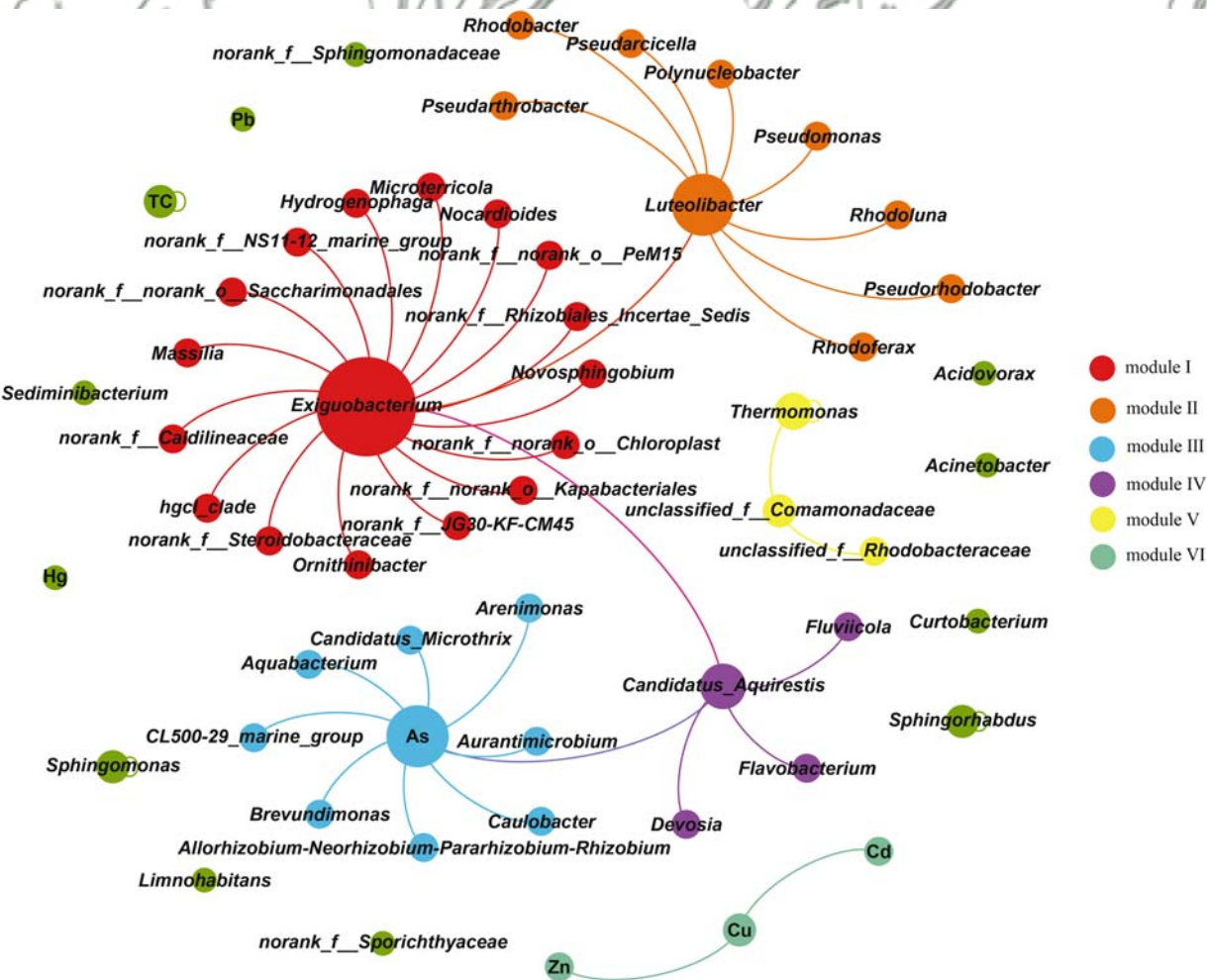


图 6 细菌优势属与重金属之间的共现性网络

Fig. 6 Network analysis between the dominant genera of bacteria and heavy metals

3 讨论

3.1 细菌多样性特征与环境因子

沿河流方向,毫清河水体的细菌 α 多样性和丰富度变化趋势一致,但各自的峰值却出现在不同的样点.在毫清河典型的金属尾矿库附近,S5 处尾矿库出口的细菌丰富度最低,可能是自尾矿库排出的废水中重金属 Cr 和 Cd 含量显著高于其他样点所致(图 2),重金属的毒性能够改变蛋白质的生物活性,从而减少了整体细菌群落的生物量^[6];同时尾矿库内 TN 和 TC 等营养物质含量较低(图 2),不能为细菌提供足够的能量供给和新陈代谢所需要的物质也加剧了这一现象^[13];另外,尾矿库内的废水还会因水库的低流速和长时间停留导致细菌死亡或者沉降,所以尾矿库出口处的细菌群落丰富度偏低^[14].细菌丰富度在 S12 处古城入口最高,这可能和多种重金属在该处含量达到最低值有关(图 2).而丰富度不是在最后汇入黄河的水库处,可能是因为黄河干流的稀释作用所致.

细菌多样性 Shannon 指数在新城镇出口处最低,却在刚出城市后的第一个乡镇皋落乡入口处最高.这可能是由于受到土地利用等人类活动影响^[15],农业污染使得水体富营养化^[16],河流系统带走河道周围土壤及其微生物,或者该地区有其他支流将外源细菌输入所致^[17].总体来看,毫清河流域后半段(S8~S13 处)的细菌群落 α 多样性整体高于前半段(S1~S7 处),这可能是由于随着河流的单向流动,沿途不同的土地利用方式改变了河流环境,营养物质以及新支流中的微生物会补充进入河流^[18],这就导致空间距离越大,细菌群落多样性也越高^[19,20].在十八河尾矿库出口的 S5 处、流经城市的 S6 处和城市河流出口 S7 处的细菌群落多样性和丰度均有明显下滑(图 4),水体中 Cu、Zn、Cr 和 As 的含量在这些样点处达到最高值(图 2),而能够耐受重金属环境的微生物种类相对较少,受湖库滞留作用影响,弱势菌群在长期的竞争中逐步被淘汰,从而导致细菌群落多样性明显下降^[21].

重金属含量相对较高的尾矿库和城市周边水体细菌群落多样性和丰富度较低,而乡镇等少污染的区域细菌群落多样性和丰富度相对较高(图 2 和图 4),反映了不同的地理位置可以通过影响重金属、营养成分等环境因子的分布从而影响细菌群落的结构^[21~23].

3.2 优势菌的分布与环境因子

本研究发现,毫清河水中的优势菌为变形菌门、放线菌门、拟杆菌门、厚壁菌门和蓝细菌门,这些

细菌门在受铜矿山影响的乐安河^[16]和无矿区影响的尼泊尔 Koshi 河^[24]、巴格马蒂河^[25]中均有优势分布.共现性网络分析发现(图 6),在具有共现性的 41 个细菌属中,16 个属于变形菌门,10 个属于放线菌门、6 个属于拟杆菌门,共占比 78.05%.毫清河水体中,变形菌门与 Cu 含量显著正相关(图 5),变形菌门包含了多种重金属抗性类群,如 *Pseudomonas* 属不仅具有固氮作用,同时还对重金属 Cu 具有较高抗性^[26],在这两者间能量的分配使用均表明了这类细菌较强的环境适应性.这表明微生物群落结构与环境因子之间的关系不是单一的相关,而是受多种因素综合影响所产生的结果.放线菌门与 Cd 含量显著负相关,这与太原市南沙河水体^[27]中的研究结果一致,与 TN、Pb 和 Cr 的相关性并不显著,可能是由于地缘因素所致.放线菌门的丰度及占比在矿区和离城市较近的地区(S4~S9 处)有明显的下降,但在下游 S9 处以后占比增加,这可能和尾矿库及城市产生的有机污染较重,放线菌具有分解有机物,降解有机废料的作用有关^[28].在 Ke 等^[29]对城市生活垃圾的研究中,拟杆菌门多存在于城市垃圾固废及其渗滤液中,但这一结果并未出现在本研究途经城市中心的 S6 处和城市河流出口的 S7 处中,这可能与当地城市污水处理能力较强,排污标准严格以及河流自身净化能力强、河流流速快,流量大等因素有关.

不动杆菌属、黄杆菌属和红育菌属(*Rhodoferrax*)等革兰氏阴性菌相较于革兰氏阳性菌在毫清河流域具有较高丰度.不动杆菌属是医疗环境中最主要的病原菌类群之一^[30],在新城镇中部(S6 处)和新城镇出口(S7 处)相对丰度远高于其他样点(图 3),这两个样点均位于垣曲县人民医院附近.黄杆菌属也是一种条件致病菌,发现其与重金属 As 具有共现性(图 6)且与水体中 As 含量显著相关($P < 0.01$,图 5).而革兰氏阳性菌中微小杆菌属(*Exiguobacterium*)由于其具有一定的重金属修复和分解有机物的能力^[31],从而在毫清河水体能够共现的优势属中占有重要地位(图 6).环境中的 As 会显著降低细菌群落的丰度和多样性^[32~34].在毫清河中,As 却与多种优势菌属显著正相关,这可能是由于毫清河整体 As 含量不高,少量的 As 对微生物群落产生 Hormesis 效应(毒物兴奋作用)^[35],而 Zn、Cu 和 Cd 没有与任何优势细菌共现(图 6),可能是由于过量所致. As 对毫清河细菌群落结构起着关键作用^[10],同时,As 可能对环境致病菌的传播具有促进作用,为人类健康带来潜在威胁.

4 结论

(1) 毫清河水体中, 尾矿库及其临近水体中细菌群落丰富度和多样性较低, 尾矿库中高浓度重金属和低营养的环境是引起这种分布的主要因素; 毫清河下游细菌群落丰富度和多样性高于上游, 且在汇入小浪底水库之前达到峰值, 这与沿途土壤中的营养物质、微生物以及新支流中的微生物补充有关。

(2) 变形菌门、放线菌门、拟杆菌门、厚壁菌门和不动杆菌属、*Limnohabitans*、假单胞菌属、黄杆菌属是毫清河水体中的优势类群。

(3) 优势类群中, 变形菌门与 Cu 显著正相关, 而与 TN 负相关, 表明重金属污染的环境中, 细菌可能更倾向于将能量用于对重金属的适应。同时, 微生物群落结构的形成与环境因子并非简单的相关, 而是受多因素综合影响的结果。

(4) As 在毫清河水体细菌群落的选择中起到了重要作用, 其对毫清河流域致病菌的传播具有促进作用, 为流域人类健康带来潜在威胁。

参考文献:

- [1] Liu N N, Hu H F, Ma W H, *et al.* Relationships between soil microbial diversities across an aridity gradient in temperate grasslands [J]. *Microbial Ecology*, 2022, doi: 10.1007/s00248-022-01997-8.
- [2] 陈兆进, 丁传勇, 朱静亚, 等. 丹江口水库枯水期浮游细菌群落组成及影响因素研究[J]. *中国环境科学*, 2017, **37**(1): 336-344.
- Chen Z J, Ding C Y, Zhu J Y, *et al.* Community structure and influencing factors of bacterioplankton during low water periods in Danjiangkou reservoir[J]. *China Environmental Science*, 2017, **37**(1): 336-344.
- [3] Bourhane Z, Lanzén A, Cagnon C, *et al.* Microbial diversity alteration reveals biomarkers of contamination in soil-river-lake continuum[J]. *Journal of Hazardous Materials*, 2022, **421**, doi: 10.1016/j.jhazmat.2021.126789.
- [4] Alzahrani K J. Microbiome studies from Saudi Arabia over the last 10 years: achievements, gaps, and future directions[J]. *Microorganisms*, 2021, **9**(10), doi: 10.3390/microorganisms9102021.
- [5] Wang L, Wang L A, Zhan X Y, *et al.* Response mechanism of microbial community to the environmental stress caused by the different mercury concentration in soils[J]. *Ecotoxicology and Environmental Safety*, 2020, **188**, doi: 10.1016/j.ecoenv.2019.109906.
- [6] Shuaib M, Azam N, Bahadur S, *et al.* Variation and succession of microbial communities under the conditions of persistent heavy metal and their survival mechanism[J]. *Microbial Pathogenesis*, 2021, **150**, doi: 10.1016/j.micpath.2020.104713.
- [7] Bhagat N, Vermani M, Bajwa H S. Characterization of heavy metal (cadmium and nickel) tolerant Gram negative enteric bacteria from polluted Yamuna River, Delhi[J]. *African Journal of Microbiology Research*, 2016, **10**(5): 127-137.
- [8] 何浩然. 渭河干流和秦岭北麓典型支流浮游及沉积微生物群落结构与分子生态网络研究[D]. 西安: 西安理工大学, 2020.
- He H R. Study on planktonic and sedimentary microbial community structure and molecular ecological network in the Weihe river mainstem and its typical tributaries from the northern foot of the Qinling mountains[D]. Xi'an: Xi'an University of Technology, 2020.
- [9] 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.
- [10] Zhang F, Zhang H, Yuan Y, *et al.* Different response of bacterial community to the changes of nutrients and pollutants in sediments from an urban river network[J]. *Frontiers of Environmental Science & Engineering*, 2020, **14**(2), doi: 10.1007/s11783-019-1207-3.
- [11] Zhang M Z, Wu Z J, Sun Q Y, *et al.* The spatial and seasonal variations of bacterial community structure and influencing factors in river sediments[J]. *Journal of Environmental Management*, 2019, **248**, doi: 10.1016/j.jenvman.2019.109293.
- [12] Liu J X, Li C, Jing J H, *et al.* Ecological patterns and adaptability of bacterial communities in alkaline copper mine drainage[J]. *Water Research*, 2018, **133**: 99-109.
- [13] 刘晋仙. 铜尾矿废水中微生物多样性格局及其适应机制[D]. 太原: 山西大学, 2019.
- Liu J X. Diversity patterns and adaptation mechanisms of microbial communities in copper tailings drainage[D]. Taiyuan: Shanxi University, 2019.
- [14] Luo X, Xiang X Y, Huang G Y, *et al.* Bacterial abundance and physicochemical characteristics of water and sediment associated with hydroelectric dam on the Lancang River China[J]. *International Journal of Environmental Research and Public Health*, 2019, **16**(11), doi: 10.3390/ijerph16112031.
- [15] Wang P, Zhao J, Xiao H Y, *et al.* Bacterial community composition shaped by water chemistry and geographic distance in an anthropogenically disturbed river[J]. *Science of the Total Environment*, 2019, **655**: 61-69.
- [16] Yi X S, Lin D X, Li J H, *et al.* Ecological treatment technology for agricultural non-point source pollution in remote rural areas of China[J]. *Environmental Science and Pollution Research*, 2021, **28**(30): 40075-40087.
- [17] 郭芝芝, 苏振华, 邸琰茗, 等. 北运河京津冀段河道浮游微生物群落多样性变化分析[J]. *环境科学*, 2022, **43**(2): 803-812.
- Guo Z Z, Su Z H, Di Y M, *et al.* Analysis on diversity of plankton microbial community in the Beijing-Tianjin-Hebei section of the North Canal River[J]. *Environmental Science*, 2022, **43**(2): 803-812.
- [18] Cao X F, Wang Y J, Xu Y, *et al.* Adaptive variations of sediment microbial communities and indication of fecal-associated bacteria to nutrients in a regulated urban river[J]. *Water*, 2020, **12**(5), doi: 10.3390/w12051344.
- [19] Hu Y, Cai J, Bai C R, *et al.* Contrasting patterns of the bacterial and archaeal communities in a high-elevation river in northwestern China[J]. *Journal of Microbiology*, 2018, **56**(2): 104-112.
- [20] 肖汉玉, 王鹏, 刘君政, 等. 水化学指标和空间距离对乐安江浮游细菌群落的影响[J]. *环境科学学报*, 2019, **39**(5): 1562-1571.
- Xiao H Y, Wang P, Liu J Z, *et al.* Effects of hydrochemical

- parameter and spatial distance on bacterioplankton community in the Le'an River[J]. *Acta Scientiae Circumstantiae*, 2019, **39**(5): 1562-1571.
- [21] 赵君, 王鹏, 徐启渝, 等. 袁河流域不同土地利用方式下河流浮游细菌群落结构特征[J]. *环境科学学报*, 2020, **40**(3): 890-900.
- Zhao J, Wang P, Xu Q Y, *et al.* Effects of land use in drainage basin on bacterioplankton communities in the Yuan River[J]. *Acta Scientiae Circumstantiae*, 2020, **40**(3): 890-900.
- [22] 汪银龙, 冯民权, 董向前. 汾河下游水体 *nirS* 型反硝化细菌群落组成与无机氮关系[J]. *环境科学*, 2019, **40**(8): 3596-3603.
- Wang Y L, Feng M Q, Dong X Q. Community composition of *nirS*-type denitrifying bacteria in the waters of the lower reaches of the Fenhe River and its relationship with inorganic Nitrogen[J]. *Environmental Science*, 2019, **40**(8): 3596-3603.
- [23] 万甜, 何梦夏, 任杰辉, 等. 渭河流域水体细菌群落的环境响应及生态功能预测[J]. *环境科学*, 2019, **40**(8): 3588-3595.
- Wan T, He M X, Ren J H, *et al.* Environmental response and ecological function prediction of aquatic bacterial communities in the Weihe River basin[J]. *Environmental Science*, 2019, **40**(8): 3588-3595.
- [24] Adhikari N P, Liu Y Q, Liu K S, *et al.* Bacterial community composition and diversity in Koshi River, the largest river of Nepal[J]. *Ecological Indicators*, 2019, **104**: 501-511.
- [25] Shrestha R G, Tandukar S, Bhandari D, *et al.* Prevalence of *Aerobacter* and other pathogenic bacteria in river water in Nepal[J]. *Water*, 2019, **11**(7), doi: 10.3390/w11071416.
- [26] Fakhar A, Gul B, Gurmani A R, *et al.* Heavy metal remediation and resistance mechanism of *Aeromonas*, *Bacillus*, and *Pseudomonas*: a review[J]. *Critical Reviews in Environmental Science and Technology*, 2020, **52**(11): 1868-1914.
- [27] 王兴华, 熊怡. 太原市南沙河水体的环境特征及其污染评价和相关性研究[J]. *山东农业科学*, 2013, **45**(3): 83-87, 90.
- Wang X H, Xiong Y. Environmental characteristics, pollution evaluation and correlation analysis of Nansha River in Taiyuan[J]. *Shandong Agricultural Sciences*, 2013, **45**(3): 83-87, 90.
- [28] 刘幸春, 王洪杰, 王亚利, 等. 府河水体及沉积物细菌群落结构分布特征及其影响因素[J]. *生态毒理学报*, 2021, **16**(5): 120-135.
- Liu X C, Wang H J, Wang Y L, *et al.* Distribution characteristics and influencing factors of bacteria community structure in water and sediments of Fuhe River[J]. *Asian Journal of Ecotoxicology*, 2021, **16**(5): 120-135.
- [29] Ke H, Li J H, Zhang X Q, *et al.* Bacterial community structure and predicted metabolic function of landfilled municipal solid waste in China[J]. *Sustainability*, 2022, **14**(6), doi: 10.3390/su14063144.
- [30] Ayoub Moubareck C, Hammoudi Halat D. Insights into *Acinetobacter baumannii*: a review of microbiological, virulence, and resistance traits in a threatening nosocomial pathogen[J]. *Antibiotics*, 2020, **9**(3), doi: 10.3390/antibiotics9030119.
- [31] Amaesan N, Kumar M S, Annapurna K, *et al.* Beneficial microbes in agro-ecology[M]. Amsterdam: Academic Press, 2020.
- [32] Li W X, Liu J, Hudson-Edwards K A. Seasonal variations in arsenic mobility and bacterial diversity: the case study of Huangshui Creek, Shimen Realgar Mine, Hunan Province, China[J]. *Science of the Total Environment*, 2020, **749**, doi: 10.1016/j.scitotenv.2020.142353.
- [33] Leon C G, Moraga R, Valenzuela C, *et al.* Effect of the natural arsenic gradient on the diversity and arsenic resistance of bacterial communities of the sediments of Camarones River (Atacama Desert, Chile)[J]. *PLoS One*, 2018, **13**(5), doi: 10.1371/journal.pone.0195080.
- [34] Huang B, Long J, Liao H, *et al.* Characteristics of bacterial community and function in paddy soil profile around antimony mine and its response to antimony and arsenic contamination[J]. *International Journal of Environmental Research and Public Health*, 2019, **16**(24), doi: 10.3390/ijerph16244883.
- [35] Sun X X, Li B Q, Han F, *et al.* Impacts of arsenic and antimony co-contamination on sedimentary microbial communities in rivers with different pollution gradients[J]. *Microbial Ecology*, 2019, **78**(3): 589-602.

CONTENTS

Impact of Climate Change on Summer Ozone in China	HU An-qi, XIE Xiao-dong, GONG Kang-jia, <i>et al.</i> (1801)
Spatial-temporal Variation and Driving Factors of Ozone in China from 2019 to 2021 Based on EOF Technique and KZ Filter	WANG Hao-qì, ZHANG Yu-fen, LUO Zhong-wei, <i>et al.</i> (1811)
Photochemical Mechanism and Control Strategy Optimization for Summertime Ozone Pollution in an Industrial City in the North China Plain	ZHENG Zhen-sen, DOU Jian-ping, ZHANG Guo-tao, <i>et al.</i> (1821)
Spatiotemporal Evolution Characteristics of PM _{2.5} -O ₃ Compound Pollution in Chinese Cities from 2015 to 2020	NIU Xiao-xiao, ZHONG Yan-mei, YANG Lu, <i>et al.</i> (1830)
Spatiotemporal Distribution Characteristics of Co-pollution of PM _{2.5} and Ozone over BTH with Surrounding Area from 2015 to 2021	SONG Xiao-han, YAN Li, LIU Wei, <i>et al.</i> (1841)
Spatio-temporal Variation in PM _{2.5} Concentration and Its Relationship with Vegetation Landscape Patterns in Typical Economic Zones in China from 2000 to 2020	XU Yong, LI Xin-yi, HUANG Wen-ting, <i>et al.</i> (1852)
Characteristics and Source Apportionment of Atmospheric Ion Deposition During Winter and Spring in the Core Area of Beijing	ZHAO Yu, LI Bei-bei, HUANG Yu-hu, <i>et al.</i> (1865)
Input Characteristics of Dry Deposition of Atmospheric Particulates and Metals in Farmland in the Suburb of Nanjing	LIU Cui-ying, JIN Hao, FAN Jian-ling (1873)
Pollution Characterizations and Oxidative Potentials of Water-Soluble Organic Matters at Different Polarity Levels in Winter PM _{2.5} Over Xi'an	LUO Yu, HUANG Sha-sha, ZHANG Tian, <i>et al.</i> (1882)
Emission Characteristics of Organic Carbon and Elemental Carbon in PM ₁₀ and PM _{2.5} from Vehicle Exhaust and Civil Combustion Fuels	WANG Hong-lei, LIU Si-han, SUN Jie-juan, <i>et al.</i> (1890)
Characteristics and Source Apportionment of PM _{2.5} in the Core Area of Ili River Valley in Spring	GU Chao, XU Tao, MA Chao, <i>et al.</i> (1899)
Evaluation of Changes in PM _{2.5} Exposure Concentration and Health Risk for Urban Resident in Zhengzhou Based on High Spatial Resolution Grids	LI Yuan, XU Yi-fei, YUAN Ming-hao, <i>et al.</i> (1911)
Emission Inventory of Building Material Industry in Henan Province Based on Multi-source Data Integration	LIU Xiao, HU Jing-nan, WANG Hong-mei, <i>et al.</i> (1924)
Pollution Characteristics and Source Apportionment of Atmospheric Volatile Organic Compounds in Winter in Kaifeng City	SHI Yu-qi, ZHENG Kai-yun, DING Wei-ting, <i>et al.</i> (1933)
Changes in O ₃ -VOCs-NO _x Sensitivity and VOCs Sources at an Urban Site of Nanjing Between 2020 and 2021	LU Xiao-bo, WANG Ming, DING Feng, <i>et al.</i> (1943)
Variation Characteristics and Ozone Formation Potential of Ambient VOCs in Urban Beijing in Summer	ZHANG Rui, SUN Xue-song, WANG Yu, <i>et al.</i> (1954)
Chemical Characteristics and Source Apportionment for VOCs During the Ozone Pollution Episodes and Non-ozone Pollution Periods in Qingdao	JIA Zhi-hai, GU Yao, KONG Cui-li, <i>et al.</i> (1962)
Characteristics of O ₃ Production in the Western Suburb of Hefei in Summer Based on the Observation of Total Peroxy Radical	YU Hui, WEI Na-na, XU Xue-zhe, <i>et al.</i> (1974)
Evaluation of Energy Saving and Carbon Reduction Effect of Air Pollution Prevention and Control Action Plan and Innovation Intermediary Effect	LI Shao-lin, WANG Qi-qi (1985)
Scenario Simulation and Effects Assessment of Co-control on Pollution and Carbon Emission Reduction in Beijing	YU Shan, ZHANG Shuang, ZHANG Zeng-jie, <i>et al.</i> (1998)
Simulation of Anthropogenic CO ₂ Emissions in the Yangtze River Delta Based on Different Emission Inventories	MA Xin-yi, HUANG Wen-jing, HU Ning, <i>et al.</i> (2009)
Water Quality Change Trend and Risk Analysis of Wuhan Hanjiang River Water Source	ZHUO Hai-hua, LOU Bao-feng, XU Jie, <i>et al.</i> (2022)
Pollution Characteristics and Risk Assessment of Antibiotics and Resistance Genes in Different Water Sources in the Wuhan Section of the Yangtze River	LI Bo-lin, ZHANG He, WANG Jun, <i>et al.</i> (2032)
Occurrence Characteristics, Sources, and Toxicity Risk Analysis of Polycyclic Aromatic Hydrocarbons in Typical Rivers of Northern Shaanxi Mining Area, China	WU Xi-jun, DONG Ying, ZHAO Jian, <i>et al.</i> (2040)
Spatio-temporal Characteristics of Organic Aggregates and the Driving Factors in Typical Lakes	XIE Gui-juan, GONG Yi, ZHU Fu-cheng, <i>et al.</i> (2052)
Distribution Characteristics and Risk Assessment of Microplastics in Water of Different Functional Parks in Guilin	LI Pei-zhao, WU Li, HUANG Fei-fei, <i>et al.</i> (2062)
Environmental Driving Factors and Assessment on the Aquatic Ecosystem of Periphytic Algae of Six Inflow Rivers in Yangtze River Basin	ZHANG Jing, HU Yu-xin, HU Sheng, <i>et al.</i> (2072)
Influence and Driving of Environmental Heterogeneity on the Epilithic Diatom Community in Xiangxi River, a Tributary of the Three Gorges Reservoir Area	JI Lu-lu, ZHAO Lu, OUYANG Tian, <i>et al.</i> (2083)
Characteristics of Phytoplankton Communities and Key Impact Factors in Three Types of Lakes in Wuhan	ZHANG Hao-kun, MIN Fen-li, CUI Hui-rong, <i>et al.</i> (2093)
Effects of Heavy Metal Pollution on the Structure of Microbial Communities in Different Habitats	HE Yi-fan, XIAO Xin-zong, WANG Jia-wen (2103)
Structure and Distribution Characteristics of Bacterial Community in Boqing River Water	WANG Sen, CHEN Jian-wen, ZHANG Hong, <i>et al.</i> (2113)
Effects of Microplastic Exposure on the Community Structure and Function of Symbiotic Bacteria in <i>Sinularia microclavata</i>	LIU Min, CHE Wen-xue, ZENG Ying-xu, <i>et al.</i> (2122)
Distribution Characteristics and Health Risk Assessment of Emerging Contaminants from Raw Water to Drinking Water in Shanghai	YAN Qi (2136)
Adsorption Characteristics of Fluoride in Low-Concentration Water by Aluminum and Zirconium-Modified Biochar	LIU Yan-fang, GAO Wei, LIU Rui, <i>et al.</i> (2147)
Sorption Characteristics and Site Energy Distribution Theory of Typical Estrogens on Microplastics	LIU Jiang-yan, ZHENG Mi-mi, HU Jia-wu, <i>et al.</i> (2158)
Selection and Evaluation of Model Pollutants for Performance Assessment of Advanced Treatment of Industrial Park Wastewater by Ozonation	XIN Bo, SHAN Chao, LÜ Lu (2168)
Identifying Driving Factors and Their Interacting Effects on Sources of Heavy Metal in Farmland Soils with Geodetector and Multi-source Data	ZHANG Hong-ze, CUI Wen-gang, LIU Sui-hua, <i>et al.</i> (2177)
Pollution Characteristics and Source Apportionment of Heavy Metals in Farmland Soils Around the Gangue Heap of Coal Mine Based on APCS-MLR and PMF Receptor Model	MA Jie, SHEN Zhi-jie, ZHANG Ping-ping, <i>et al.</i> (2192)
Contamination and Probabilistic Health Risk Assessment of Heavy Metals in Agricultural Soils Around a Lead-Zinc Smelter	HUANG Jian-bo, JIANG Deng-deng, WEN Bing, <i>et al.</i> (2204)
Prediction of PAHs Content in Soil Around Gas Stations in Beijing Based on BP Neural Network	MA Sai-yan, WEI Hai-ying, MA Jin, <i>et al.</i> (2215)
Spatial-temporal Distribution and Risk Assessment of Quinolones Antibiotics in Soil of Shijiazhuang City	ZHAO Xin-yu, CHEN Hui, ZHAO Bo, <i>et al.</i> (2223)
Accumulation and Pollution Risks of Heavy Metals in Soils and Agricultural Products from a Typical Black Shale Region with High Geological Background	DENG Shuai, DUAN Jia-hui, NING Mo-huan, <i>et al.</i> (2234)
Geochemical Characteristics of Cd in Different Parent Soils in Karst Area and Prediction of Cd Content in Maize	DAI Liang-liang, XU Hong-gen, GONG Hao, <i>et al.</i> (2243)
Pollution Risk and Contribution Analysis of Pb, Cd, and As in Soils and Crops Under Different Land Use Types in Longyan City	WANG Rui, CHEN Nan, ZHANG Er-xi (2252)
Influencing Factors of Cadmium Content in Wheat Grain: A Meta-analysis and Decision Tree Analysis	LIU Na, ZHANG Shao-bin, GUO Xin-yu, <i>et al.</i> (2265)
Response Characteristics of Soil Organic Carbon Pool and Its Chemical Composition During Secondary Forest Succession in the Loess Plateau	LIU Han-yu, LIU Ying-yi, ZHANG Qi, <i>et al.</i> (2275)
Effects of Short-Term Nitrogen and Phosphorus Addition on Soil Respiration Components in a Subalpine Grassland of Qilian Mountains	JIANG Yuan, GAN Xiao-ling, CAO Feng-feng, <i>et al.</i> (2283)
Response of Soil Microbial Diversity to Long-term Enclosure in Degraded Patches of Alpine Meadow in the Source Zone of the Yellow River	YANG Peng-nian, LI Xi-lai, LI Cheng-yi, <i>et al.</i> (2293)
Diversity and Predictive Functional of <i>Caragana jubata</i> Bacterial Community in Rhizosphere and Non-rhizosphere Soil at Different Altitudes	LI Yuan-yuan, XU Ting-ting, AI Zhe, <i>et al.</i> (2304)
Effects of Simulated Acid Rain and Nitrogen Deposition on Soil Bacterial Community Structure and Diversity in the Masson Pine Forest	WANG Nan, QIAN Shao-yu, PAN Xiao-cheng, <i>et al.</i> (2315)
Effects of Phosphogypsum and <i>Suaeda salsa</i> on the Soil Moisture, Salt, and Bacterial Community Structure of Salinized Soil	LIU Yue, YANG Shu-qing, ZHANG Wan-feng, <i>et al.</i> (2325)
Effects of Combined Application of Fungal Residue and Chemical Fertilizer on Soil Microbial Community Composition and Diversity in Paddy Soil	GENG He-tian, WANG Xu-dong, SHI Si-bo, <i>et al.</i> (2338)
Effects of Aeration on Surface Water Nutrient Dynamics and Greenhouse Gas Emission in Different Straw Returning Paddy Fields	HU Jin-hui, XUE Li-hong, QIAN Cong, <i>et al.</i> (2348)
Effects of Exogenous Melatonin Treatment on the Growth and Antioxidant System of Rice Seedlings Under Antimony Stress	CHU Yu-tan, LI Yan, HUANG Yi-zong, <i>et al.</i> (2356)
Life Cycle Prediction Assessment of Energy Saving and New Energy Vehicles for 2035	FU Pei, LAN Li-bo, CHEN Ying, <i>et al.</i> (2365)
Distribution, Sources, and Behavioral Characteristics of Microplastics in Farmland Soil	BO Lu-ji, LI Bing, ZHANG Kai, <i>et al.</i> (2375)
Research Progress on the Remediation Technology of Herbicide Contamination in Agricultural Soils	HU Fang-yu, AN Jing, WANG Bao-yu, <i>et al.</i> (2384)
Research Progress and Prospect of Herbicide Residue Characteristics in Black Soil Region of China	LI Rui, WU Qiu-mei, ZHAO Gui-mei, <i>et al.</i> (2395)