

目次

“大气十条”实施期间南京市 PM _{2.5} 化学组成与来源的演变特征	陈培林, 郭蓉, 王勤耕 (1)
河南省北部区域霾污染过程中城市和农村点位 PM _{2.5} 组分差异	王申博, 王玲玲, 范相阁, 王楠, 马双良, 张瑞芹 (11)
廊坊市秋冬季大气细颗粒物污染特征及来源解析	朱淑贞, 佟洁, 鲍丰, 孙浩 (20)
天津市采暖季不同气团来向 PM _{2.5} 中重金属污染特征及健康风险评价	李立伟, 邓小文, 肖致美, 元洁, 杨宁, 郭小龙, 白宇 (30)
基于多属性决策方法的太原市冬季街道尘土中潜在有害元素关键来源解析	邓文博, 刘文娟 (38)
北京市 PM _{2.5} -O ₃ 复合污染数值响应解析	刘添强 (48)
长三角区域人为源活性挥发性有机物高分辨率排放清单	田俊杰, 丁祥, 安静宇, 李曼, 王鑫, 黄成 (58)
南京北郊工业乡村混合区秋季边界层 VOCs 垂直分布特征	王泰, 朱彬, 施双双, 安俊琳, 唐贵谦, 徐家平 (66)
广西柳城县 VOCs 组分特征、来源及其对臭氧生成的敏感性	吴影, 莫招育, 吴琴琴, 陆嘉晖, 毛敬英, 陈雪梅, 栗少丽, 覃纹, 刘慧琳, 韦敏 (75)
城市臭氧污染特征与高影响气象因子:以苏州为例	何琰, 林惠娟, 曹舒娅, 宋璟璐, 孙伟, 熊宇 (85)
华北平原周县人为源氨排放清单及分布特征	康嘉慧, 孟凡磊, 刘学军, 许稳 (94)
WRF 模式最优参数化方案在不同空气质量模式中的应用	杨景朝, 蒋兴文, 伯鑫, 王刚, 冯勇 (104)
西安市春季生物气溶胶的分布特征和健康影响	魏军强, 杨柳, 沈振兴, 王秀茹 (118)
青岛近海不同天气下生物气溶胶中细菌浓度及存活率分布特征	魏文淑, 祁建华, 常成 (127)
中国沉积物多环芳烃的时空分布及驱动因子	黄柱良, 蔡家伟, 王儒威 (138)
长江口近岸地区抗生素抗性基因与微生物群落分布特征	徐秋鸿, 刘曙光, 娄厦, Larisa Dorzhieva Radnaeva, Elena Nikitina, Makhinov Aleksei Nikolavich, Araruna José Tavares, 金字辰, 李鑫 (158)
人类活动影响下的高原湿地四环素类抗生素抗性基因赋存与微生物群落共现性	秦荣, 喻庆国, 刘振亚, 王行 (169)
我国东南地区饮用水源地多种农药的赋存特征及健康风险评估	何姝, 董慧岭, 任南琪 (180)
珠海市中部主要供水水库沉积物重金属时空分布与风险评价	王思瑞, 张坤峰, 昌盛, 张茉莉, 付青 (189)
苏州水网地区河道底泥的重金属分布特征与污染风险	郑敏慧, 白冬锐, 张涛, 陈坦, 王洪涛, 杨婷, 张冰, 金军 (198)
长三角典型城郊流域生物可降解性有机质的分布及影响因素	吴文雨, 马菁晨, 杨磊, 李敏, 唐剑锋 (210)
过水性湖泊水质长期演变趋势及驱动因素:以骆马湖为例	黄雪滢, 高鸣远, 王金东, 王明明, 陈思恩, 龚志军, 王腊春, 蔡永久 (219)
渭河微塑料污染现状与风险评价	山泽萱, 张妍, 张成前, 时鹏, 张鑫 (231)
不同颜色聚碳酸酯塑料对附着藻类生长和群落结构的影响	王梦雪, 尹思成, 王振方, 陈锦贤, 张玮, 王丽卿 (243)
苦草叶表附和和水体浮游细菌群落多样性格局及其影响因素	张梅婷, 刘晋仙, 苏嘉贺, 柴宝峰 (252)
基于 16S rRNA 测序技术的青藏高原河流细菌群落多样性	璩伟卿, 张博美, 黄雪, 任泽, 高红凯 (262)
基于 eDNA 的硅藻群落时空异质性及生态健康评价	姜山, 张颜, 李飞龙, 张效伟 (272)
三峡库区澎溪河河段间水华程度差异及其机制	罗晓佼, 张钊, 黄伟, 胡鹏飞, 谭炳圆, 张磊 (282)
自然降雨下蔬菜地土壤侵蚀及氮素流失特征	宁嘉丽, 黄艳芸, 李桂芳, 陈钊柱, 王坚桦 (293)
绿色、蓝色和蓝-绿屋顶径流水质特征	章孙逊, 张守红, 闫婧, 王恺, 杨航, 王任重远, 张文龙, 李华林 (303)
基于地理探测器的山西省 2000 ~ 2020 年 NPP 时空变化特征及驱动力分析	邵嘉豪, 李晶, 闫星光, 马天跃, 张瑞 (312)
2000 ~ 2020 年西南地区植被 NDVI 时空变化及驱动机制探究	徐勇, 戴强玉, 黄雯婷, 盘钰春, 郑志威, 郭振东 (323)
青海湖周边地区表层土壤重金属含量和抗性基因丰度及相关性	胡石磊, 瞿剑里, 章丽, 赵美蓉 (336)
四川盆地典型农耕地土壤重金属含量、污染及其影响因素	刘属灵, 吴梅, 刘志远, 刘双燕, 刘永林, 赵家宇, 刘怡 (347)
宁夏引黄灌区农田土壤重金属生态风险评价及来源解析	陈林, 马琨, 马建军, 王金保, 李虹, 贾彪, 倪细炉, 马进鹏, 梁翔宇 (356)
铜冶炼场周边土壤重金属污染特征与风险评价	彭驰, 刘旭, 周子若, 姜智超, 郭朝晖, 肖细元 (367)
西南地区典型土壤酸化特征及其与重金属形态活性的耦合关系	凌云, 刘汉燧, 张小婷, 魏世强 (376)
外源 Cd 在不同类型土壤中的稳定化特征	王港, 余海英, 黄化刚, 张路, 左洪菊 (387)
基于有效硒的富硒土壤阈值及有效硒的影响因素	王莹, 马彦斌, 王泽晶 (395)
基于成土母质分区的土壤-作物系统重金属累积特征与健康风险评价	陈子万, 许晶, 侯召雷, 彭敏, 杨帆, 陈杰, 徐永强, 杨树云, 李家云, 于林松 (405)
贵州省旱地土壤和玉米 As 含量特征及其种植安全性评估	黄凤艳, 周浪, 宋波, 虎瑞, 吴勇, 王佛鹏, 张云霞 (415)
象草与苦楝/构树间作修复矿区重金属污染土壤潜力	王小慧, 肖细元, 郭朝晖, 彭驰, 王小燕 (426)
1 株高耐性肠杆菌的筛选及对铜、砷同步钝化	尹雪斐, 刘玉玲, 伍德, 黄薪铭, 张朴心, 铁柏清 (436)
黄土丘陵区人工刺槐林土壤有机碳矿化特征及其与有机碳组分的关系	朱玉帆, 刘伟超, 李佳欣, 苏玉博, 简俊楠, 杨改河, 任成杰, 冯永忠, 任广鑫, 王晓妍, 韩新辉 (444)
设施农业土壤磷素累积迁移转化及影响因素	方兵, 陈林, 王阳, 祝亚飞, 王瑞, 宋桂芳, 刘俊, 杨斌, 张世文 (452)
优化秸秆管理提高玉米农田碳氮效率与经济效益	王良, 钱欣, 高英波, 张慧, 刘开昌, 陈国庆, 李宗新 (463)
缓控释肥深施对黏性土壤麦田氮素去向的影响	侯朋福, 薛利祥, 袁文胜, 曹帅, 刘颖多, 薛利红, 杨林章 (473)
黄河下游冲积平原轮作休耕农田土壤真菌群落结构与功能	南镇武, 刘柱, 孟维伟, 代红翠, 徐杰, 王娜, 刘灵艳, 王旭清, 刘开昌 (482)
红壤区退化林地表土真菌群落结构对土壤改良措施的响应	管鸿智, 黄荣珍, 王金平, 朱丽琴, 邹显花, 姬绍晖, 林丽靖, 房焕英, 杨梦佳, 廖迎春 (494)
半干旱-亚湿润干旱沙区樟子松根内真菌群落结构和功能时空动态特征	赵珮杉, 郭米山, 高广磊, 丁国栋, 张英, 任悦 (502)
基于 QMEC 分析的青藏高原不同类型冰川前缘地土壤微生物功能潜力	张洁洁, Anders Priemé, 陈显轲, 周汉昌, 张沁唯, 庄绪亮, 秦翔, 庄国强, 马安周 (512)
中国主粮作物生物炭产量效应的 Meta 分析	于滨杭, 姬建梅, 王丽学, 刘静, 高欢, 刘丹 (520)
生物炭影响抗生素在土壤中环境行为的 Meta 分析	李经涵, 张建强, 夏丽琼, 郑世界, 杨红薇, 何杨 (531)
不同农作物秸秆原料制备生物炭特性及重金属浸出行为	李家康, 邱春生, 赵佳奇, 王晨晨, 刘楠楠, 王栋, 王少坡, 孙力平 (540)
中国县城碳排放时空演变与异质性	宋苑震, 曾坚, 王森, 梁晨 (549)
近 20 年重庆市主城区碳排放的时空动态演进及其重心迁移	向书江, 杨春梅, 谢雨琦, 王丹, 王子芳, 高明 (560)
中国 1991 ~ 2018 年突发环境事件时空特征及影响因素	余光辉, 王非凡, 刘贤赵, 李文慧, 向云波 (572)
季铵盐抗菌剂在环境中的迁移转化行为及其毒性效应	张利兰, 覃存立, 钱瑶, 易美玲 (583)
《环境科学》征订启事(29) 《环境科学》征稿简则(57) 信息(443, 481, 530)	

基于 QMEC 分析的青藏高原不同类型冰川前缘地土壤微生物功能潜力

张洁洁^{1,2,3,4}, Anders Priemé^{4,5}, 陈显轲^{1,2,3}, 周汉昌^{1,6}, 张沁唯^{1,6}, 庄绪亮^{1,7}, 秦翔⁸, 庄国强^{1,6*}, 马安周^{1,6*}

(1. 中国科学院生态环境研究中心, 北京 100085; 2. 中国科学院大学中丹学院, 北京 101400; 3. 中国-丹麦科研教育中心, 北京 101400; 4. Department of Biology, University of Copenhagen, Universitetsparken 15, DK-2100, Copenhagen, Denmark; 5. Center for Permafrost (CENPERM), University of Copenhagen, Øster Voldgade 10, DK-1350, Copenhagen, Denmark; 6. 中国科学院大学资源与环境学院, 北京 101408; 7. 中国科学院青藏高原研究所, 北京 100101; 8. 中国科学院西北生态环境资源研究院冰冻圈科学国家重点实验室, 祁连山冰川与生态环境综合观测研究站, 兰州 730000)

摘要: 微生物通过多种功能代谢过程主导着因气候变暖裸露的冰川前缘地土壤元素的地球化学循环。以青藏高原的海洋型冰川、亚大陆型冰川和极大陆型冰川的前缘地土壤为研究对象, 分析不同类型冰川前缘地土壤的微生物功能特征。依次选择玉龙冰川、天山乌鲁木齐1号冰川和老虎沟12号冰川作为三类冰川的典型代表, 采用高通量功能基因芯片(QMEC)检测土壤微生物的功能基因特征。结果表明, 在三类冰川前缘地土壤中, 半纤维素降解基因和还原型乙酰辅酶A途径相关的碳固定基因丰度最高, 三者主要的氮功能基因和氨化作用有关, 磷、硫功能基因则主要与有机磷矿化过程和硫酸化过程相关。其中, 水热条件较好的海洋型冰川的微生物功能基因的种类与丰度最高, 其次为环境较为干燥的极大陆型冰川。三类冰川前缘地土壤的微生物功能基因结构的显著差异, 证实了地理环境差异对微生物功能特征的影响, 也为不同类型冰川前缘地土壤微生物的功能及其介导的元素地球化学循环研究提供了基础。

关键词: 青藏高原; 冰川类型; 前缘地土壤; 微生物功能基因; 高通量功能基因芯片(QMEC)

中图分类号: X172 文献标识码: A 文章编号: 0250-3301(2023)01-0512-08 DOI: 10.13227/j.hjxx.202203184

QMEC-based Analysis of the Soil Microbial Functional Potentials across Different Tibetan Plateau Glacier Forelands

ZHANG Jie-jie^{1,2,3,4}, Anders Priemé^{4,5}, CHEN Xian-ke^{1,2,3}, ZHOU Han-chang^{1,6}, ZHANG Qin-wei^{1,6}, ZHUANG Xu-liang^{1,7}, QIN Xiang⁸, ZHUANG Guo-qiang^{1,6*}, MA An-zhou^{1,6*}

(1. Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing 100085, China; 2. Sino-Danish College, University of Chinese Academy of Sciences, Beijing 101400, China; 3. Sino-Danish Center for Education and Research, Beijing 101400, China; 4. Department of Biology, University of Copenhagen, Universitetsparken 15, DK-2100, Copenhagen, Denmark; 5. Center for Permafrost (CENPERM), University of Copenhagen, Øster Voldgade 10, DK-1350, Copenhagen, Denmark; 6. College of Resources and Environment, University of Chinese Academy of Sciences, Beijing 101408, China; 7. Institute of Tibetan Plateau Research, Chinese Academy of Sciences, Beijing 100101, China; 8. Qilian Shan Station of Glaciology and Ecologic Environment, State Key Laboratory of Cryospheric Science, Northwest Institute of Eco-environment and Resources, Chinese Academy of Sciences, Lanzhou 730000, China)

Abstract: Soil microorganisms dominate the biogeochemical cycles of elements in glacier forelands, which continue to expand due to the climate warming. We analyzed the soil microbial functional characteristics among three types of glacier forelands on the Tibetan Plateau: Yulong Glacier (Y), a temperate glacier; Tianshan Urumqi Glacier No. 1 (T), a sub-continental glacier; and Laohugou Glacier No. 12 (L), a continental glacier. Here, soil microbial functional genes were quantified using quantitative microbial element cycling technology (QMEC). We found that, in the three glacier forelands, the abundances of soil microbial functional genes related to hemicellulose degradation and reductive acetyl-CoA pathway were highest compared with other carbon-related functional genes. The main nitrogen cycling genes were involved in ammonification. The functional genes of the phosphorus cycle and sulfur cycle were related to organic phosphate mineralization and sulfur oxidation. Furthermore, the soils of the temperate glacier foreland with better hydrothermal conditions had the most complex microbial functional gene structure and the highest functional potentials, followed by those of the soils of continental glacier foreland with the driest environment. These significant differences in soil microbial functional genes among the three types of glacier forelands verified the impacts of geographic difference on microbial functional characteristics, as well as providing a basis for the study of soil microbial functions and biogeochemical cycles in glacier forelands.

Key words: Tibetan Plateau; glacier types; glacier foreland soil; microbial functional gene; quantitative microbial element cycling (QMEC)

收稿日期: 2022-03-21; 修订日期: 2022-05-08

基金项目: 第二次青藏高原综合科学考察研究项目(2019QZKK0307, 2019QZKK0402); 国家重点研发计划项目(2018YFA0901204); 中国科学院科技服务网络计划项目(KFJ-EW-STS-140)

作者简介: 张洁洁(1997~), 女, 硕士研究生, 主要研究方向为微生物生态, E-mail: jiejiezhang90@163.com

* 通信作者, E-mail: gqzhuang@rcees.ac.cn; azma@rcees.ac.cn

冰川消退带来大量的前缘地裸露土壤,伴随着一系列的演替现象如土壤发育、微生物演替变化和植被定殖等^[1~3]. 微生物作为冰川前缘地生命活动的主要承担者^[4~6]在冰川前缘地的土壤发育及各元素的生物地球化学循环中发挥着重要的作用^[7~9]. 作为先锋者,微生物通过各种功能代谢活动如固碳、固氮、硝化作用、氨化作用和磷酸水解作用等介导着前缘地土壤碳、氮、磷等元素的循环流动,改善着前缘地土壤的营养环境^[1,7,10~12]. 而不同的地理环境,其水热条件和初始养分储量的不同均会影响微生物的功能潜力,进而影响土壤发育与生态系统演替^[13~15].

中国是世界上中低纬度地带冰川规模最大且数量最多的国家,冰川总面积为51 766.08 km²,其冰川多分布于青藏高原地区^[16,17]. 由于气候变暖,82%以上的冰川处于消退状态,且各冰川的退缩规模和比例各不相同,存在显著的区域差异^[18]. 基于冰川的发育条件与物理性质,中国的冰川可分为3种类型,分别为极大陆型冰川、亚大陆型冰川和海洋型冰川,其水热条件差异显著^[19,20]. 海洋型冰川受到季风气候影响,夏季降水充沛,消退也较为明显;而极大陆型冰川的年均降水量最低,最为干燥,其年均温度也低于0℃^[21,22]. 目前,许多研究多关注于不同冰川前缘地土壤的微生物群落结构^[23~27],而缺乏对其土壤微生物功能潜力的报道.

随着高通量基因组学技术的不断发展,功能基因的检测成为了解微生物群落基因多样性与功能代谢潜力的有效手段^[28~30]. 高通量功能基因芯片(quantitative microbial element cycling, QMEC)能通过检测71个与碳、氮、磷、硫循环相关的微生物功能基因对微生物的功能特征和代谢潜力进行表征^[31]. 因此,本文基于QMEC技术,选取3个典型的冰川前缘地土壤作为研究对象,依次为玉龙冰川(海洋型冰川)、天山乌鲁木齐1号冰川(亚大陆型冰川)和老虎沟12号冰川(极大陆型冰川),研究不同类型的冰川前缘地土壤微生物功能特征与代谢潜力,以加深人们对地理区域差异下的不同微生物功能特征的认识.

1 材料与方法

1.1 研究区概况

玉龙冰川(Y)位于青藏高原东南部,横断山以南(26°59'~27°17'N, 100°04'~100°15'E),是欧亚大陆上离赤道最近的典型的温带海洋型冰川^[32]. 其海拔5 596 m,冰川面积为11.61 km²,整个冰川退缩成东、西两支. 该冰川年均温度为1.62℃,因季风气

候影响,伴有充沛降水,年降水量可达930 mm^[33]. 天山乌鲁木齐1号冰川(T),位于天山北坡中部(43°06'N, 86°49'E),是典型的亚大陆型冰川,其年平均温度为-4.12℃,最高温度出现在7月约5.3℃^[22]. 根据大西沟气象观测站的监测数据显示,在1981~2010年间,其年均降水量为478.1 mm,月平均相对湿度为57.5%^[24]. 1993年前该冰川整体退缩速度为4.5 m·a⁻¹,随后逐步消退成东、西两支^[34]. 老虎沟12号冰川(L),是青藏高原地区最大的极大陆型冰川,位于西祁连山北坡(39°26'N, 96°32'E),海拔5 481 m,年均气温为-11.8℃,为典型的大陆性气候^[35]. 受西风影响,降水主要集中在夏末至初秋时期,年均降水量为390 mm. 在1960~2015年,该冰川末端退缩402.96 m,年均退缩速率达7.3 m·a⁻¹,其冰川长度也缩减了9.7 km^[36]. 3个冰川的地理位置如图1.

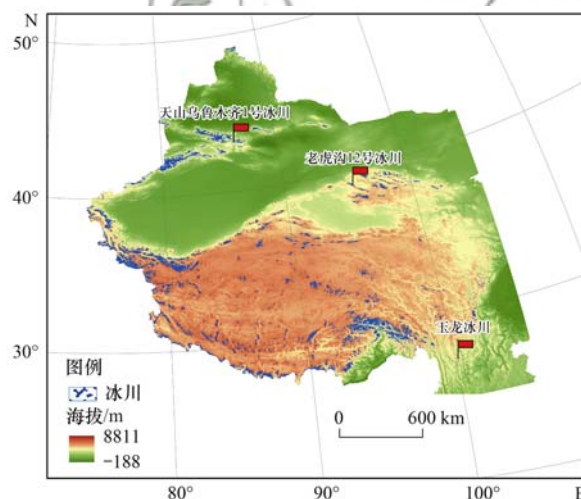


图1 3个冰川的地理位置分布示意

Fig. 1 Geographic locations of three glaciers

1.2 样品采集

分别于2018年8月、2018年11月和2020年11月前往Y、T和L采集其冰川最前端的前缘地裸露表层土壤(0~20 mm),每个采样点设置3个重复. 采集土壤样品并筛去大颗粒后过2 mm筛网,将每个样本分为两部分以便随后的理化性质和生物分子信息的检测,低温运输至实验室中保存. 用于分析理化性质的样品保存于-4℃冰箱中,另一份样品则保存于-20℃冰箱中以分析相关的微生物分子信息.

1.3 土壤理化性质的测定

土壤有机碳(SOC)和总氮(TN)由元素分析仪(Vario Macro cube, Elementar, Germany)通过燃烧法测定. DOC、NH₄⁺-N和NO₃⁻-N通过浸提法由总有机碳分析仪(Vario TOC, Elementar, Germany)与流动分析仪(SEAL-AA3, Germany)测定. 土壤总磷

(TP)由钼锑抗分光光度法测定;土壤含水率与田间持水率采用烘干法测定;土壤 pH 由 pH 计测定土壤水溶液获得.

1.4 土壤样品 DNA 的提取与 QMEC 检测

利用 PowerSoil DNA Isolation Kit (MOBIO Laboratories, Carlsbad, CA USA)从土壤样品中提取 DNA,提取流程参照产品说明书.使用 Qubit 4.0 (Thermo Fisher Scientific, Waltham, USA)和 NanoDrop 2000 (Thermo Scientific, Wilmington, DE, USA)检测 DNA 的浓度与纯度.采用基于高通量荧光定量 PCR (qPCR)的功能基因芯片 (QMEC)解析微生物的功能特征,以 16S rRNA 基因为内参基因,检测和量化与碳氮硫磷元素循环相关的 71 个功能基因^[31].采用 SmartChip RealTime PCR 系统 (WaferGen Biosystems, USA)进行 qPCR 反应与荧光信号检测.每个样品均设置 3 个技术重复与阴性对照.当阴性对照无扩增、扩增效率在 1.8~2.2 范围内且 Ct 值小于 31 时,判定该基因检测信号为阳性可用于后续的数据分析,并通过 Ct 值与 16S rRNA 基因的拷贝数,计算获得各基因在每克干土中的拷贝数^[37,38].

1.5 数据分析

利用 R 语言 (R 4.0.5) 进行数据分析.土壤理化性质和功能基因丰度的方差齐性检验通过 car 包实现,随后利用 agricolae 包的 LSD (the fisher's least significant difference) 方法进行显著性差异检验.通过

heatmap 包绘制热图以表征土壤微生物功能基因丰度,并采用 vegan 包进行土壤微生物功能基因特征的不相似性检验.采用 ggplot2 包完成数据的可视化.

2 结果与分析

2.1 三类冰川前缘地土壤的理化性质

三类冰川前缘地土壤的基础理化性质见表 1. 所有土壤样本均为碱性, pH 值均高于 8. 其中极大陆型冰川 L 的 pH 值最高 (8.68 ± 0.19), 且土壤含水率最低仅 0.01% 左右. 亚大陆型冰川 T 的土壤含水率和田间持水率最高分别达 (11.58 ± 0.01)% 和 (22.81 ± 2.04)%. 海洋型冰川 Y 的土壤水分条件和 T 相近, 其 pH 值最低为 8.25, 且 Y 的 $\omega(\text{SOC})$ 显著高于 T 与 L, 为 (101.17 ± 2.64) $\text{g} \cdot \text{kg}^{-1}$. 极大陆型冰川 L 的 $\omega(\text{SOC})$ 次之, 但仍较为匮乏, 约为 22.21 $\text{g} \cdot \text{kg}^{-1}$. T 的 $\omega(\text{SOC})$ 最低, 但其 $\omega(\text{DOC})$ 最高, 分别比 Y 和 L 高约 30 $\text{mg} \cdot \text{g}^{-1}$ 和 18 $\text{mg} \cdot \text{g}^{-1}$. T 与 Y 的氮资源含量 (TN、 $\text{NH}_4^+ - \text{N}$ 和 $\text{NO}_3^- - \text{N}$) 相近, 且显著低于 L, 但三者的氮资源均较低, L 的 $\omega(\text{TN})$ 也仅 0.22 $\text{g} \cdot \text{kg}^{-1}$. 三类冰川前缘地土壤的磷元素含量也较低, $\omega(\text{TP})$ 在 L 土壤中为 (0.66 ± 0.03) $\text{g} \cdot \text{kg}^{-1}$, 在 T 中为 (0.59 ± 0.01) $\text{g} \cdot \text{kg}^{-1}$, 但在 Y 处仅 0.06 $\text{g} \cdot \text{kg}^{-1}$. 因 Y 的碳含量相对较为丰富, 而氮、磷含量相对较低, 其 C/N 值和 C/P 值最高, 分别达到 811.45 与 4 091. 相对而言, T 的 C/N 值和 C/P 值均最低, 分别为 42.15 和 20.52.

表 1 冰川前缘地土壤的基础理化性质汇总¹⁾

Table 1 Soil physicochemical properties of glacier forelands

采样点	Y	T	L
pH	$8.25 \pm 0.14\text{b}$	$8.48 \pm 0.06\text{ab}$	$8.68 \pm 0.19\text{a}$
含水率/%	$10.22 \pm 0.01\text{a}$	$11.58 \pm 0.01\text{a}$	$0.01 \pm 0.00\text{b}$
田间持水率/%	$21.49 \pm 1.14\text{a}$	$22.81 \pm 2.04\text{a}$	$14.90 \pm 4.80\text{b}$
$\omega(\text{SOC})/\text{g} \cdot \text{kg}^{-1}$	$101.17 \pm 2.64\text{a}$	$4.71 \pm 0.12\text{c}$	$22.21 \pm 0.52\text{b}$
$\omega(\text{DOC})/\text{mg} \cdot \text{kg}^{-1}$	$12.74 \pm 0.51\text{c}$	$41.22 \pm 2.04\text{a}$	$23.33 \pm 2.35\text{b}$
$\omega(\text{TN})/\text{g} \cdot \text{kg}^{-1}$	$0.15 \pm 0.01\text{b}$	$0.13 \pm 0.00\text{b}$	$0.22 \pm 0.06\text{a}$
$\omega(\text{NH}_4^+ - \text{N})/\text{mg} \cdot \text{kg}^{-1}$	$0.47 \pm 0.02\text{b}$	$0.49 \pm 0.00\text{b}$	$0.87 \pm 0.11\text{a}$
$\omega(\text{NO}_3^- - \text{N})/\text{mg} \cdot \text{kg}^{-1}$	$0.12 \pm 0.01\text{b}$	$0.08 \pm 0.01\text{b}$	$1.54 \pm 0.20\text{a}$
$\omega(\text{TP})/\text{g} \cdot \text{kg}^{-1}$	$0.06 \pm 0.00\text{c}$	$0.59 \pm 0.01\text{b}$	$0.66 \pm 0.03\text{a}$
C/N	$811.45 \pm 61.16\text{a}$	$42.15 \pm 0.70\text{b}$	$124.60 \pm 38.11\text{b}$
C/P	$4\,091.85 \pm 213.08\text{a}$	$20.52 \pm 0.54\text{b}$	$87.49 \pm 1.91\text{b}$

1) Y: 玉龙冰川; T: 天山乌鲁木齐 1 号冰川; L: 老虎沟 12 号冰川; SOC: 土壤有机碳; DOC: 溶解性有机碳; TN: 总氮; $\text{NH}_4^+ - \text{N}$: 铵态氮; $\text{NO}_3^- - \text{N}$: 硝态氮; TP: 总磷; C/N: 碳氮比; C/P: 碳磷比; 不同小写字母表示差异显著 ($P < 0.05$); 数值为平均值 $\pm$ 标准差 ($n = 3$)

2.2 三类冰川前缘地土壤的微生物功能基因

对冰川前缘地土壤样品进行 71 个功能基因检测, 包括 36 个碳循环基因、22 个氮循环基因、8 个磷循环基因和 5 个硫循环基因. 在海洋型冰川 Y、亚大陆型冰川 T 和极大陆型冰川 L 的前缘地土壤中检测信号呈阳性的功能基因数分别为 65、48 和 53 个.

三类冰川前缘地土壤的 16S rRNA 基因的拷贝数 (以干土计) 在 $2.07 \times 10^7 \sim 6.81 \times 10^7 \text{ copies} \cdot \text{g}^{-1}$ 范围内, 其中 Y 最高, L 次之, 但三者间不存在显著性差异. 基于此, 可计算各功能基因的拷贝数, 发现除基因 *lig*、*korA*、*nifH*、*hao*、*nirS1*、*nirS2*、*dsrA* 和 *dsrB* 外, 其余功能基因在 Y 中的丰度最高, 如丰度热图 2. 同时, 基

于三类冰川前缘地土壤的功能基因矩阵的 Bray-Curtis 距离进行不相似性检验,结果如表 2. 3 种检验的 P 值均小于 0.05,说明三类冰川前缘地土壤的微生物功能基因结构存在显著性差异.

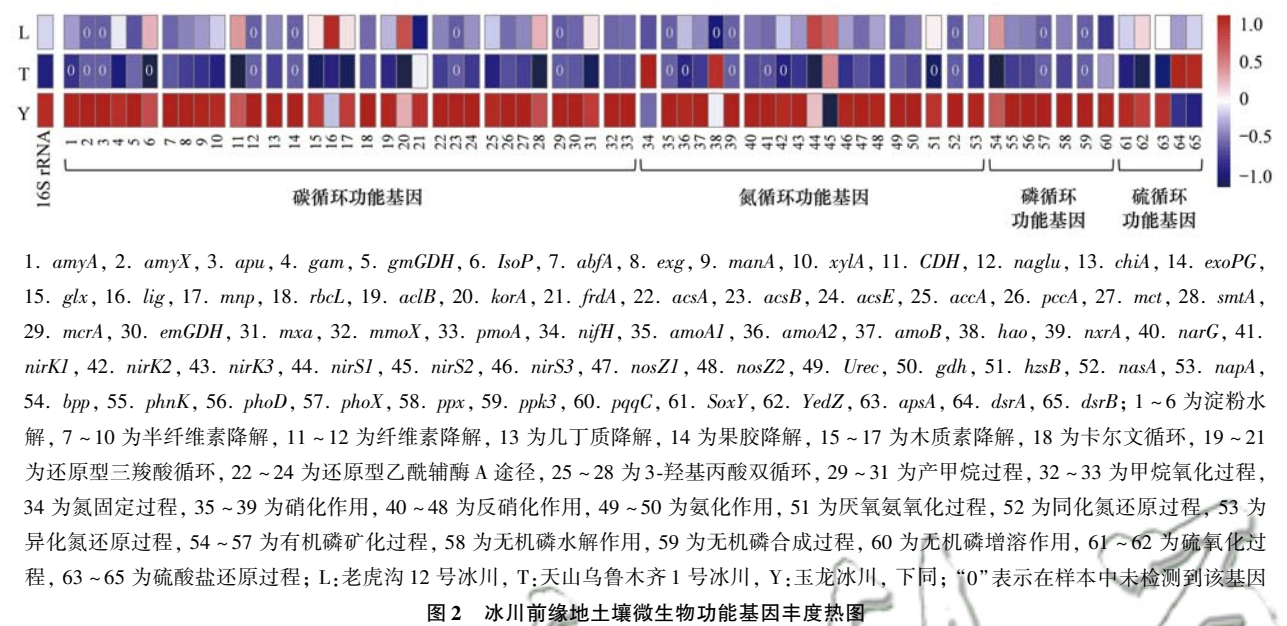


Fig. 2 Heatmap of absolute copy number of microbial functional genes in the glacier forelands

表 2 基于 Bray-Curtis 距离的三类冰川前缘地土壤微生物功能基因的不相似性检验¹⁾

Table 2 Dissimilarity test based on Bray-Curtis distance of microbial functional genes among three types of glacier forelands¹⁾

不相似性检验	差异解释度	P 值
MRPP	$\delta = 0.432$	0.014
Anosim	$R = 0.490$	0.023
PERMANOVA	$R^2 = 3.605$	0.009

1) MRPP (multiple response permutation procedure): 多响应置换检验, 其 δ 值大于 0 说明组间差异大于组内差异; Anosim (analysis of similarities): 相似性分析, 其 R 值大于 0 说明组间差异显著; PERMANOVA (permutational MANOVA): 置换多因素方差分析, 其 R^2 越大说明组间差异越显著; P 值小于 0.05 表示统计具有显著性

2.2.1 土壤碳循环微生物功能基因特征

在三类冰川前缘地土壤的碳循环功能基因中, 碳固定基因的丰度最高, 其次为碳降解基因. 海洋型冰川 Y 的前缘地土壤碳功能基因丰度显著高于其他两种类型冰川 (如图 3), 其中碳固定基因丰度为 $81.07 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$, 分别为 T ($9.37 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$) 和 L ($24.37 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$) 的 8.65 倍和 3.33 倍; 碳降解基因丰度为 $17.15 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$, 而 T 和 L 分别仅为 $1.63 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$ 和 $6.98 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$. 三类冰川前缘地土壤中与甲烷相关的功能基因丰度在 $0.65 \times 10^5 \sim 9.59 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$ 之间, 涵盖基因 *mmoX*、*pmoA*、*emGDH* 和 *mxs*, 在 Y 中还检测到 *mcrA* 基因.

检测到的碳固定基因可表征 4 种固碳途径, 分别为卡尔文循环 (calvin cycle, CBB 循环)、还原型三羧酸循环 (reductive tricarboxylic acid cycle, rTCA

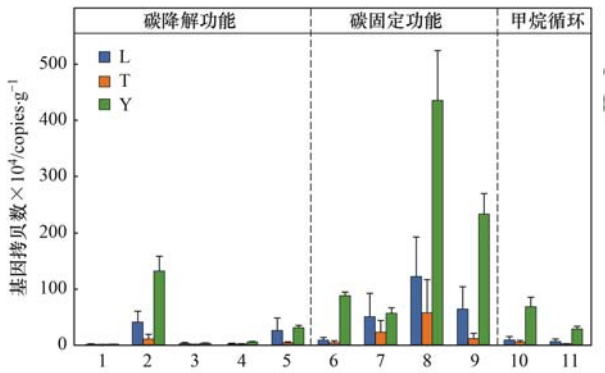


图 3 冰川前缘地土壤微生物碳循环功能基因丰度

Fig. 3 Absolute copy number of microbial functional gene groups of carbon cycle in the glacier forelands

循环)、还原型乙酰辅酶 A 途径 (reductive acetyl-CoA pathway, WL 循环) 和 3-羟基丙酸双循环 (3-hydroxypropionate bicycle, 3HP 循环). 三类冰川前缘地土壤中表征 WL 循环的功能基因丰度最高, 其主要表征基因为 *acsA* 和 *acsE*. 在海洋型冰川 Y 中一半以上的碳固定基因与 WL 循环相关, 其丰度为 $43.42 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$, 随后是 3HP 循环, 其基因丰度占总的碳固定基因丰度的 28.74%. T 和 L 土壤中主要的固碳基因也与 WL 循环有关, 其相对丰度分别为 60.64% 和 49.95%. 而二者的第二大潜在碳固定途径则分别为 rTCA 循环和 3HP 循环, 其基因丰度分别为 $2.24 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$ 和 6.36×10^5

$\text{copies} \cdot \text{g}^{-1}$. CBB 循环的相关基因丰度在三类冰川前缘地土壤中均较低,其与总的碳固定基因丰度的比值在 Y 中达 10.79%,而其在 T 与 L 的土壤中该比例仅 3% 左右.

三类冰川前缘地土壤的碳降解基因主要与半纤维素降解和木质素降解有关,主要表征基因为 *manA*、*xylA*、*glx*、*lig* 和 *mnp*. 其中, Y 的半纤维素降解基因丰度最高,为 $13.15 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$, 占其所有的碳降解基因丰度的 76.67%,而 T 与 L 显著低于 Y,二者的丰度为 $1.01 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$ (69.17%) 和 $4.05 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$ (57.95%). 类似地, Y 的木质素降解基因丰度最高 ($3.06 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$), 其相对丰度为 17.82%. L 土壤中的木质素降解基因丰度与 Y 相近,其为 $2.55 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$, 该相对丰度达 36.3%; 而 T 的木质素降解基因丰度最低虽仅为 $0.33 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$, 但其相对丰度也达 22.73%. 其他碳降解基因如淀粉、果糖和几丁质等的降解基因丰度则在三类冰川中均较低.

2.2.2 土壤氮循环微生物功能基因特征

海洋型冰川 Y 的氮循环功能基因最为丰富(如图 2 和图 4), 其拷贝数也最高 ($65.52 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$), 亚大陆型冰川 T 和极大陆型冰川 L 的氮循环功能基因丰度则相近,在 $11.37 \times 10^5 \sim 13.01 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$ 间. 表征氨化作用的基因 *Urec* 和 *gdh* 是三类冰川前缘地土壤中主要的氮循环功能基因,在 Y 中其丰度为 $50.35 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$, 占 Y 的总氮循环功能基因丰度的 76.85%,二者在 T 和 L 中

的相对丰度也分别达到 60.01% 和 48.34%. 反硝化基因是第二大氮功能基因,在 L 中其相对丰度达 34.57% ($4.50 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$), 在 T 中为 26.18% ($2.98 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$); 在 Y 中其相对丰度虽最低 (14.36%), 但该基因丰度依旧是三类冰川前缘地土壤中最高的,为 $9.59 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$. 表征氮固定作用的基因 *nifH* 是 T 和 L 土壤中重要的氮功能基因,其丰度分别为 $1.36 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$ 和 $1.08 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$, 分别占各自氮功能基因丰度的 11.95% 和 8.30%, 而其在 Y 土壤中的相对丰度仅为 1.67%.

2.2.3 土壤磷循环和硫循环的微生物功能基因特征

在三类冰川前缘地土壤中,磷循环功能基因主要与有机磷矿化过程有关(见图 5), 其主要的功能基因有 *phoD*、*bpp* 和 *phnK*, 而具有相同功能的基因 *phoX* 则仅在 Y 中检测到(图 2). 类似地, Y 土壤中的磷循环功能基因丰度最高,为 $25.39 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$, 其中和有机磷矿化过程相关的基因的相对丰度达 84.23%, 和无机磷水解过程相关的基因 *ppx* 的丰度次之,其相对丰度为 12.56% ($3.19 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$). L 土壤中的磷循环功能基因丰度略高于 T,二者分别为 $5.33 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$ 和 $1.67 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$, 其基因也主要与有机磷的矿化和无机磷的水解有关.

与硫循环相关的基因 *SoxY*、*YedZ*、*apsA*、*dsrA* 和 *dsrB* 均可在三类冰川前缘地土壤中检测到(图 2). 在 Y 和 L 土壤中硫循环功能基因主要和硫的氧化过程有关(图 5), 其基因丰度分别为 7.66×10^5

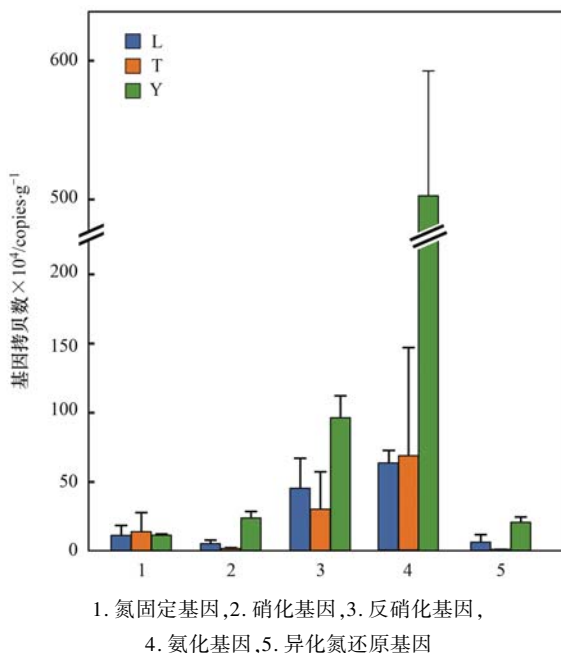


图 4 冰川前缘地土壤微生物氮循环功能基因丰度

Fig. 4 Absolute copy number of microbial functional gene groups of nitrogen cycle in the glacier forelands

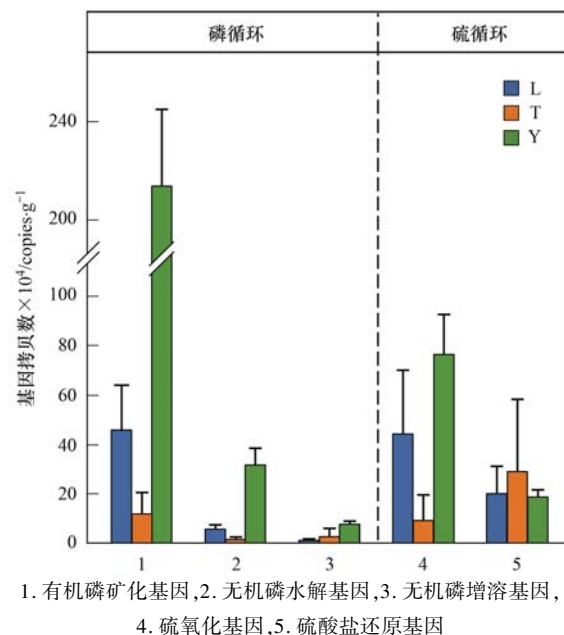


图 5 冰川前缘地土壤微生物磷、硫循环功能基因丰度

Fig. 5 Absolute copy number of microbial functional gene groups of phosphorus and sulfur cycles in the glacier forelands

$\text{copies} \cdot \text{g}^{-1}$ (80.17%) 和 $4.44 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$ (68.59%). 而在 T 中, 硫酸盐还原功能基因较为丰富(图 5), 该基因丰度占其硫循环基因总丰度的 75.67% ($2.92 \times 10^5 \text{ copies} \cdot \text{g}^{-1}$).

3 讨论

基于高通量微阵列技术的微生物功能基因芯片, 是研究环境微生物介导的各种生物地球化学循环的高效便利的手段, 不仅能表征微生物的功能基因特征, 也能通过基因丰度表征其功能潜力^[28~31, 39, 40]. Brankatschk 等^[41]发现土壤时间序列中与碳矿化相关的功能基因如 *chiA* 的丰度呈上升趋势, 且与酶活性显著相关. Chen 等^[30]还发现微生物功能基因丰度是影响呼吸、反硝化和硝化等土壤过程速率的主导因素. 同时 Xiang 等^[42]发现碳氮硫磷功能基因丰度与微生物的多样性存在显著正相关关系, 表明功能基因丰度的高低在一定程度上可暗示其微生物群落结构的复杂性. 海洋型冰川 Y 中检测到的功能基因数(65 个)显著高于亚大陆型冰川 T(48 个)与极大陆型冰川 L(53 个), 同时其各个微生物功能基因类群的丰度, 如碳固定基因、碳降解基因、反硝化基因、氨化基因和磷矿化基因等也高于其他两类冰川, 暗示海洋型冰川的前缘地土壤微生物群落结构更为复杂, 其介导的元素生物地球化学循环也更为活跃. 这与海洋型冰川前缘地土壤发育速度最快, 且在几十年后演替为森林生态系统的研究结果相一致^[43].

这三类冰川前缘地土壤的微生物碳固定基因丰度均高于碳降解基因, 与冰川前缘地土壤碳含量相对匮乏的现象相符合, 表明冰川前缘地土壤微生物可能具有较高的固碳潜力^[1, 10, 44, 45]. 在三类冰川前缘地土壤中表征 WL 途径的相关碳固定基因丰度最高, 这可能与微生物代谢重要的中间体乙酰辅酶 A 有关^[46, 47]. L 和 Y 的第二大潜在固碳途径是 3HP 循环, 而 T 为 rTCA 循环, 这可能由二者不同的微生物群落与土壤环境导致^[10, 48]. 此外, L 和 T 中不同微生物固碳途径的基因丰度相对比例更加均匀, 这与 L 和 T 土壤的 C/N 值和 C/P 值低于 Y 呈现出的显著碳营养的限制相一致, 暗示其对碳营养的迫切需求, 故存在更多的潜在固碳途径以缓解碳的限制. 同时, 功能基因的丰度也可间接表征微生物的功能潜力和相关物质的含量^[30, 49], 如 Dai 等^[50]发现土壤多糖组分的含量与降解淀粉的功能基因丰度呈正相关关系, 木质素单体和酚类物质的含量也与降解木质素的功能基因丰度呈正相关关系. 因此, 冰川前缘地土壤中丰富的半纤维素降解基因暗示其可能具有更

高的半纤维素降解能力和半纤维素碳化合物含量, 这与文献[8]的研究结果一致. 木质素降解基因在 L 和 T 土壤中的碳降解基因总丰度中占比较高, 而木质素的微生物可利用性一般低于纤维素^[50], 这可能说明这两类冰川前缘地土壤的碳化合物比海洋型冰川 Y 的更难以降解, 也暗示其微生物可能具有更强的降解难降解碳化合物的能力.

微生物通过固氮作用、氨化作用、硝化作用与反硝化作用和有机磷矿化作用等过程介导着土壤中的氮、磷循环^[51, 52]. 三类冰川前缘地土壤的 *nifH* 基因丰度相似, 其最高的基因丰度出现在 T 土壤中, 这与其 $\omega(\text{TN})$ 较低相一致, 暗示其氮需求及较高的固氮潜力. 与氨化作用相关的功能基因是三类冰川前缘地土壤中主要的氮功能基因, 表明三类冰川前缘地土壤的微生物氨化作用潜力较强. 而微生物的氨化作用可能使得土壤氮以 N_2 、 N_2O 或 NO 形式流失, 同时反硝化过程与硝化过程也被证实与土壤氮流失密切相关^[53, 54]. 海洋型冰川 Y 的前缘地土壤中与氨化作用、反硝化作用及硝化作用相关的微生物功能基因丰度显著高于其他两种类型冰川, 其 TN 、 $\text{NH}_4^+ - \text{N}$ 和 $\text{NO}_3^- - \text{N}$ 含量也较低, 暗示其氮素代谢能力较强且具有较高的氮周转速率. 类似地, Y 土壤中的磷功能基因也显著高于其他两种冰川, 说明其较高的磷素代谢能力, 这可能也是其 TP 含量较低的原因之一.

4 结论

(1) 三类冰川前缘地土壤的微生物功能基因结构存在显著差异, 其中海洋型冰川(Y)的前缘地土壤微生物功能基因种类与丰度均最高, 其次为极大陆型冰川(L).

(2) 三类冰川前缘地土壤中碳循环功能基因主要和固碳途径 WL 循环、半纤维素降解有关, 氮循环功能基因主要和氨化作用有关, 磷、硫循环功能基因则主要分别与有机磷矿化过程和硫氧化过程相关.

致谢: 在野外采集样品过程中, 中国科学院祁连山冰冻圈与生态环境综合观测研究站秦翔站长及甘肃盐池湾国家级自然保护区管理局工作人员给予了大量的帮助, 在此一并表示衷心的感谢.

参考文献:

- [1] Donhauser J, Frey B. Alpine soil microbial ecology in a changing world[J]. FEMS Microbiology Ecology, 2018, 94(9), doi: 10.1093/femsec/fiy099.
- [2] Bockheim J G, Gennadiyev A N, Hartemink A E, et al. Soil-forming factors and Soil taxonomy[J]. Geoderma, 2014, 226-227: 231-237.

- [3] Edwards A, Cook S. Microbial dynamics in glacier forefield soils show succession is not just skin deep[J]. *Molecular Ecology*, 2015, **24**(5): 963-966.
- [4] Frey B, Rime T, Phillips M, *et al.* Microbial diversity in European alpine permafrost and active layers [J]. *FEMS Microbiology Ecology*, 2016, **92**(3), doi: 10.1093/femsec/fiw018.
- [5] Gyeong H, Hyun C U, Kim S C, *et al.* Contrasting early successional dynamics of bacterial and fungal communities in recently deglaciated soils of the maritime Antarctic [J]. *Molecular Ecology*, 2021, **30**(17): 4231-4244.
- [6] Lazzaro A, Hilfiker D, Zeyer J. Structures of microbial communities in alpine soils: seasonal and elevational effects[J]. *Frontiers in Microbiology*, 2015, **6**, doi: 10.3389/fmicb.2015.01330.
- [7] Zeng J, Lou K, Zhang C J, *et al.* Primary succession of nitrogen cycling microbial communities along the deglaciated forelands of Tianshan Mountain, China[J]. *Frontiers in Microbiology*, 2016, **7**, doi: 10.3389/fmicb.2016.01353.
- [8] Fernández-Martínez M A, Pointing S B, Perez-Ortega S, *et al.* Functional ecology of soil microbial communities along a glacier forefield in Tierra del Fuego (Chile) [J]. *International Microbiology*, 2016, **19**(3): 161-173.
- [9] Li Q W, Liu Y, Gu Y F, *et al.* Ecoenzymatic stoichiometry and microbial nutrient limitations in rhizosphere soil along the Hailuoguo Glacier forefield chronosequence[J]. *Science of the Total Environment*, 2020, **704**, doi: 10.1016/j.scitotenv.2019.135413.
- [10] 陈玉莹, 张志好, 刘勇勤. 冰川生态系统固碳微生物研究进展[J]. *微生物学报*, 2020, **60**(9): 2012-2029.
- Chen Y Y, Zhang Z H, Liu Y Q. Research progress of carbon fixation microorganisms in glaciers [J]. *Acta Microbiologica Sinica*, 2020, **60**(9): 2012-2029.
- [11] Bai Y, Xiang Q J, Zhao K, *et al.* Plant and soil development cooperatively shaped the composition of the *phoD*-harboring bacterial community along the primary succession in the Hailuoguo Glacier chronosequence[J]. *mSystems*, 2020, **5**(4), doi: 10.1128/mSystems.00475-20.
- [12] Jiang Y L, Lei Y B, Qin W, *et al.* Revealing microbial processes and nutrient limitation in soil through ecoenzymatic stoichiometry and glomalin-related soil proteins in a retreating glacier forefield[J]. *Geoderma*, 2019, **338**: 313-324.
- [13] Lazzaro A, Brankatschk R, Zeyer J. Seasonal dynamics of nutrients and bacterial communities in unvegetated alpine glacier forefields[J]. *Applied Soil Ecology*, 2012, **53**: 10-22.
- [14] Sanyal A, Antony R, Samui G, *et al.* Microbial communities and their potential for degradation of dissolved organic carbon in cryoconite hole environments of Himalaya and Antarctica [J]. *Microbiological Research*, 2018, **208**: 32-42.
- [15] Wietrzyk-Pelka P, Rola K, Szymański W, *et al.* Organic carbon accumulation in the glacier forelands with regard to variability of environmental conditions in different ecogenesis stages of High Arctic ecosystems[J]. *Science of the Total Environment*, 2020, **717**, doi: 10.1016/j.scitotenv.2019.135151.
- [16] 王宗太, 苏宏超. 世界和中国的冰川分布及其水资源意义[J]. *冰川冻土*, 2003, **25**(5): 498-503.
- Wang Z T, Su H C. Glaciers in the world and China: distribution and their significance as water resources[J]. *Journal of Glaciology and Geocryology*, 2003, **25**(5): 498-503.
- [17] Guo W Q, Liu S Y, Xu J L, *et al.* The second Chinese glacier inventory: data, methods and results[J]. *Journal of Glaciology*, 2015, **61**(226): 357-372.
- [18] Ma A Z, Zhang J J, Liu G H, *et al.* Cryosphere microbiome biobanks for mountain glaciers in China [J]. *Sustainability*, 2022, **14**(5), doi: 10.3390/su14052903.
- [19] 施雅风, 郑本兴, 姚檀栋. 青藏高原末次冰期最盛时的冰川与环境[J]. *冰川冻土*, 1997, **19**(2): 97-113.
- Shi Y F, Zheng B X, Yao T D. Glaciers and environments during the Last Glacial Maximum (LGM) on the Tibetan Plateau [J]. *Journal of Glaciology and Geocryology*, 1997, **19**(2): 97-113.
- [20] 施雅风, 任炳辉, 谢自楚. 三十年来我国冰川学研究的进展[J]. *冰川冻土*, 1979, **1**(2): 1-6.
- [21] 李开明, 陈世峰, 康玲芬, 等. 中国大陆型冰川和海洋型冰川变化比较分析——以天山乌鲁木齐河源1号冰川和玉龙雪山白水河1号冰川为例[J]. *干旱区研究*, 2018, **35**(1): 12-19.
- Li K M, Chen S F, Kang L F, *et al.* Variation of continental glacier and temperate glacier in China: a case study of glacier No. 1 at the headwaters of the Urumqi River and Baishui Glacier No. 1 [J]. *Arid Zone Research*, 2018, **35**(1): 12-19.
- [22] 牟建新, 李忠勤, 张慧, 等. 中国西部大陆性冰川与海洋性冰川物质平衡变化及其对气候响应——以乌源1号冰川和帕隆94号冰川为例[J]. *干旱区地理*, 2019, **42**(1): 20-28.
- Mu J X, Li Z Q, Zhang H, *et al.* Mass balance variation of continental glacier and temperate glacier and their response to climate change in western China: taking Urumqi Glacier No. 1 and Parlun No. 94 Glacier as examples [J]. *Arid Land Geography*, 2019, **42**(1): 20-28.
- [23] Mapelli F, Marasco R, Fusi M, *et al.* The stage of soil development modulates rhizosphere effect along a high arctic desert chronosequence[J]. *The ISME Journal*, 2018, **12**(5): 1188-1198.
- [24] 王愉琬, 马安周, 种国双, 等. 模拟升温对冰川前缘地微生物种群的影响[J]. *环境科学*, 2020, **41**(6): 2918-2923.
- Wang Y W, Ma A Z, Chong G S, *et al.* Effect of simulated warming on microbial community in glacier forefield [J]. *Environmental Science*, 2020, **41**(6): 2918-2923.
- [25] Górniak D, Marszałek H, Kwaśniak-Kominek M, *et al.* Soil formation and initial microbiological activity on a foreland of an Arctic glacier (SW Svalbard) [J]. *Applied Soil Ecology*, 2017, **114**: 34-44.
- [26] Kwon H Y, Jung J Y, Kim O S, *et al.* Soil development and bacterial community shifts along the chronosequence of the midtre løvénbreen glacier foreland in svalbard [J]. *Journal of Ecology and Environment*, 2015, **38**(4): 461-476.
- [27] Kazemi S, Hatam I, Lanoil B. Bacterial community succession in a high-altitude subarctic glacier foreland is a three-stage process [J]. *Molecular Ecology*, 2016, **25**(21): 5557-5567.
- [28] Yu L L, Luo S S, Xu X, *et al.* The soil carbon cycle determined by GeoChip 5.0 in sugarcane and soybean intercropping systems with reduced nitrogen input in South China [J]. *Applied Soil Ecology*, 2020, **155**, doi: 10.1016/j.apsoil.2020.103653.
- [29] Yan B S, Sun L P, Li J J, *et al.* Change in composition and potential functional genes of soil bacterial and fungal communities with secondary succession in *Quercus liaotungensis* forests of the Loess Plateau, western China [J]. *Geoderma*, 2020, **364**, doi: 10.1016/j.geoderma.2020.114199.
- [30] Chen Q L, Ding J, Li C Y, *et al.* Microbial functional attributes, rather than taxonomic attributes, drive top soil respiration, nitrification and denitrification processes [J]. *Science of the Total Environment*, 2020, **734**, doi: 10.1016/j.

- scitotenv. 2020. 139479.
- [31] Zheng B X, Zhu Y G, Sardans J, *et al.* QMEC: a tool for high-throughput quantitative assessment of microbial functional potential in C, N, P, and S biogeochemical cycling[J]. *Science China Life Sciences*, 2018, **61**(12): 1451-1462.
- [32] 苏勃, 李忠勤, 张明军, 等. 大陆型冰川与海洋型冰川物质平衡对比研究——以天山和阿尔卑斯山典型冰川为例[J]. *冰川冻土*, 2015, **37**(5): 1131-1140.
- Su B, Li Z Q, Zhang M J, *et al.* A comparative study on mass balance between the continental glaciers and the temperate glaciers: taking the typical glaciers in the Tianshan Mountains and the Alps as examples [J]. *Journal of Glaciology and Geocryology*, 2015, **37**(5): 1131-1140.
- [33] 辛惠娟, 何元庆, 牛贺文, 等. 玉龙雪山白水1号冰川近地层气象要素变化特征[J]. *冰川冻土*, 2018, **40**(4): 676-684.
- Xin H J, He Y Q, Niu H W, *et al.* Near-surface meteorological characteristics on the Baishui Glacier No. 1, Mt. Yulong [J]. *Journal of Glaciology and Geocryology*, 2018, **40**(4): 676-684.
- [34] Xu X K, Pan B L, Hu E, *et al.* Responses of two branches of Glacier No. 1 to climate change from 1993 to 2005, Tianshan, China[J]. *Quaternary International*, 2011, **236**(1-2): 143-150.
- [35] 董志文, 秦大河, 秦翔, 等. 祁连山老虎沟12号冰川积雪中飞灰颗粒物的特征[J]. *环境科学*, 2014, **35**(2): 504-512.
- Dong Z W, Qin D H, Qin X, *et al.* Characteristics of fly ash particles deposition in the snowpack of Laohugou Glacier No. 12 in western Qilian Mountains, China[J]. *Environmental Science*, 2014, **35**(2): 504-512.
- [36] Liu Y S, Qin X, Chen J Z, *et al.* Variations of Laohugou Glacier No. 12 in the western Qilian Mountains, China, from 1957 to 2015[J]. *Journal of Mountain Science*, 2018, **15**(1): 25-32.
- [37] Li H Z, Bi Q F, Yang K, *et al.* High starter phosphorus fertilization facilitates soil phosphorus turnover by promoting microbial functional interaction in an arable soil[J]. *Journal of Environmental Sciences*, 2020, **94**(8): 179-185.
- [38] Zhang Y X, Li X, Xiao M, *et al.* Effects of microplastics on soil carbon dioxide emissions and the microbial functional genes involved in organic carbon decomposition in agricultural soil[J]. *Science of the Total Environment*, 2022, **806**, doi: 10.1016/j.scitotenv. 2021. 150714.
- [39] Fan K K, Delgado-Baquerizo M, Guo X S, *et al.* Biodiversity of key-stone phylotypes determines crop production in a 4-decade fertilization experiment[J]. *The ISME Journal*, 2021, **15**(2): 550-561.
- [40] Graham E B, Knelman J E, Schindlbacher A, *et al.* Microbes as engines of ecosystem function: when does community structure enhance predictions of ecosystem processes? [J]. *Frontiers in Microbiology*, 2016, **7**, doi: 10.3389/fmicb.2016.00214.
- [41] Brankatschk R, Töwe S, Kleinedam K, *et al.* Abundances and potential activities of nitrogen cycling microbial communities along a chronosequence of a glacier forefield[J]. *The ISME Journal*, 2011, **5**(6): 1025-1037.
- [42] Xiang Q, Chen Q L, Zhu D, *et al.* Microbial functional traits in phyllosphere are more sensitive to anthropogenic disturbance than in soil[J]. *Environmental Pollution*, 2020, **265**, doi: 10.1016/j.envpol.2020.114954.
- [43] Lei Y B, Zhou J, Xiao H F, *et al.* Soil nematode assemblages as bioindicators of primary succession along a 120-year-old chronosequence on the Hailuoguo Glacier forefield, SW China [J]. *Soil Biology and Biochemistry*, 2015, **88**: 362-371.
- [44] Alfaro F D, Salazar-Burrows A, Bañales-Seguel C, *et al.* Soil microbial abundance and activity across forefield glacier chronosequence in the Northern Patagonian Ice Field, Chile[J]. *Arctic, Antarctic, and Alpine Research*, 2020, **52**(1): 553-562.
- [45] Schulz S, Brankatschk R, Dümig A, *et al.* The role of microorganisms at different stages of ecosystem development for soil formation[J]. *Biogeosciences*, 2013, **10**(6): 3983-3996.
- [46] Gagen E J, Denman S E, Padmanabha J, *et al.* Functional gene analysis suggests different acetogen populations in the bovine rumen and tammar wallaby forestomach [J]. *Applied and Environmental Microbiology*, 2010, **76**(23): 7785-7795.
- [47] Ragsdale S W. Enzymology of the Acetyl-CoA pathway of CO₂ fixation[J]. *Critical Reviews in Biochemistry and Molecular Biology*, 1991, **26**(3-4): 261-300.
- [48] 陈晓娟, 吴小红, 简燕, 等. 农田土壤自养微生物碳同化潜力及其功能基因数量、关键酶活性分析[J]. *环境科学*, 2014, **35**(3): 1144-1150.
- Chen X J, Wu X H, Jian Y, *et al.* Carbon dioxide assimilation potential, functional gene amount and rubisCO activity of autotrophic microorganisms in agricultural soils [J]. *Environmental Science*, 2014, **35**(3): 1144-1150.
- [49] Li Y, Cha Q Q, Dang Y R, *et al.* Reconstruction of the functional ecosystem in the high light, low temperature union glacier region, Antarctica[J]. *Frontiers in Microbiology*, 2019, **10**, doi: 10.3389/fmicb.2019.02408.
- [50] Dai Z M, Zang H D, Chen J, *et al.* Metagenomic insights into soil microbial communities involved in carbon cycling along an elevation climosequences [J]. *Environmental Microbiology*, 2021, **23**(8): 4631-4645.
- [51] Kuypers M M M, Marchant H K, Kartal B. The microbial nitrogen-cycling network [J]. *Nature Reviews Microbiology*, 2018, **16**(5): 263-276.
- [52] Oelmann Y, Lange M, Leimer S, *et al.* Above- and belowground biodiversity jointly tighten the P cycle in agricultural grasslands [J]. *Nature Communications*, 2021, **12**(1), doi: 10.1038/s41467-021-24714-4.
- [53] Zhou J Z, Xue K, Xie J P, *et al.* Microbial mediation of carbon-cycle feedbacks to climate warming[J]. *Nature Climate Change*, 2012, **2**(2): 106-110.
- [54] Hayatsu M, Katsuyama C, Tago K. Overview of recent researches on nitrifying microorganisms in soil[J]. *Soil Science and Plant Nutrition*, 2021, **67**(6): 619-632.

CONTENTS

Evolution of PM _{2.5} Chemical Composition and Sources in Nanjing During the Implementation of the APPCAP	CHEN Pei-lin, GUO Rong, WANG Qin-geng (1)
Differences in PM _{2.5} Components Between Urban and Rural Sites During Heavy Haze Event in Northern Henan Province	WANG Shen-bo, WANG Ling-ling, FAN Xiang-ge, <i>et al.</i> (11)
Characteristics and Source Apportionment of Atmospheric Fine Particles in Langfang in Autumn and Winter	ZHU Shu-zhen, TONG Jie, BAO Feng, <i>et al.</i> (20)
Pollution Characteristics and Health Risk Assessment of Heavy Metals in PM _{2.5} of Different Air Masses During Heating Season in Tianjin	LI Li-wei, DENG Xiao-wen, XIAO Zhi-mei, <i>et al.</i> (30)
Analysis of Critical Source of Potentially Harmful Elements in Urban Road Dust During Winter in Taiyuan Based on Multiple Attribute Decision Making Method	DENG Wen-bo, LIU Wen-juan (38)
Numerical Response Analysis of PM _{2.5} -O ₃ Compound Pollution in Beijing	LIU Tian-qiang (48)
High-resolution Emission Inventory of Reactive Volatile Organic Compounds from Anthropogenic Sources in the Yangtze River Delta Region	TIAN Jun-jie, DING Xiang, AN Jing-yu, <i>et al.</i> (58)
Vertical Distribution Characteristics of Boundary Layer Volatile Organic Compounds in Autumn in the Mixed Industrial and Rural Areas over the Northern Suburb of Nanjing	WANG Tai, ZHU Bin, SHI Shuang-shuang, <i>et al.</i> (66)
Characterization of Ambient Volatile Organic Compounds, Source Apportionment, and the Ozone-NO _x -VOC Sensitivities in Liucheng County, Guangxi	WU Ying, MO Zhao-yu, WU Qin-qin, <i>et al.</i> (75)
Characteristics of Ozone Pollution and High-impact Meteorological Factors in Urban Cities: A Case of Suzhou	HE Yan, LIN Hui-juan, CAO Shu-ya, <i>et al.</i> (85)
Emission Inventory and Distribution Characteristics of Anthropogenic Ammonia in Quzhou County, North China Plain	KANG Jia-hui, MENG Fan-lei, LIU Xue-jun, <i>et al.</i> (94)
Application of WRF Optimal Parameterization Scheme for Different Air Quality Models	YANG Jing-chao, JIANG Xing-wen, BO Xin, <i>et al.</i> (104)
Distribution Characteristics and Health Effects of Bioaerosols in Spring over Xi'an City	WEI Jun-qiang, YANG Liu, SHEN Zhen-xing, <i>et al.</i> (118)
Distribution of Bacterial Concentration and Viability in Atmospheric Bioaerosols Under Different Weather Conditions in the Coastal Region of Qingdao	WEI Wen-shu, QI Jian-hua, CHANG Cheng (127)
Spatiotemporal Distribution and Driving Factors of Polycyclic Aromatic Hydrocarbons (PAHs) in Inland Sediments of China	HUANG Zhu-liang, CAI Jia-wei, WANG Ru-wei (138)
Distributions of Antibiotic Resistance Genes and Microbial Communities in the Nearshore Area of the Yangtze River Estuary	XU Qiu-hong, LIU Shu-guang, LOU Sha, <i>et al.</i> (158)
Co-occurrence of Tetracycline Antibiotic Resistance Genes and Microbial Communities in Plateau Wetlands Under the Influence of Human Activities	QIN Rong, YU Qing-guo, LIU Zhen-ya, <i>et al.</i> (169)
Occurrence and Health Risk Assessment of Multiple Pesticides in Drinking Water Sources of Southeast China	HE Shu, DONG Hui-yu, REN Nan-qi (180)
Spatiotemporal Distribution and Pollution Risk Assessment of Heavy Metals in Sediments of Main Water Supply Reservoirs in Central Zhuhai City	WANG En-rui, ZHANG Kun-feng, CHANG Sheng, <i>et al.</i> (189)
Distribution Characteristics and Pollution Risk of Heavy Metals in River Sediment of Suzhou Water Network Area, China	ZHENG Min-hui, BAI Dong-rui, ZHANG Tao, <i>et al.</i> (198)
Distribution of Biodegradable Dissolved Organic Matter and Its Affecting Factors in a Typical Peri-urban Watershed in Yangtze River Delta	WU Wen-yu, MA Jing-sheng, YANG Lei, <i>et al.</i> (210)
Long-term Succession Patterns and Driving Factors of Water Quality in a Flood-pulse System Lake: A Case Study of Lake Luoma, Jiangsu Province	HUANG Xue-ying, GAO Ming-yuan, WANG Jin-dong, <i>et al.</i> (219)
Microplastic Pollution Status and Ecological Risk Evaluation in Weihe River	SHAN Ze-xuan, ZHANG Yan, ZHANG Cheng-qian, <i>et al.</i> (231)
Effects of Different Colored Polycarbonate Plastics on Growth and Community Structure of Periphytic Algae	WANG Meng-xue, YIN Si-cheng, WANG Zhen-fang, <i>et al.</i> (243)
Diversity Patterns and Influencing Factors of Epibiotic in <i>Vallisneria natans</i> and Planktonic Bacteria Communities	ZHANG Mei-ting, LIU Jin-xian, SU Jia-he, <i>et al.</i> (252)
Bacterial Community and Diversity of River Ecosystems on the Qinghai-Tibet Plateau Based on 16S rRNA Gene Sequencing	QU Wei-qing, ZHANG Bo-mei, HUANG Xue, <i>et al.</i> (262)
Spatial and Temporal Heterogeneity and Ecological Health Evaluation of Diatom Community Based on eDNA	JIANG Shan, ZHANG Yan, LI Fei-long, <i>et al.</i> (272)
Severity Differences and Mechanisms of Algal Blooms Among Sections in Pengxi River of the Three Gorges Reservoir	LUO Xiao-jiao, ZHANG Xing, HUANG Wei, <i>et al.</i> (282)
Characteristics of Soil Erosion and Nitrogen Loss in Vegetable Field Under Natural Rainfall	NING Jia-li, HUANG Yan-hui, LI Gui-fang, <i>et al.</i> (293)
Effects of Green, Blue, and Blue-green Roofs on Runoff Quality	ZHANG Sun-xun, ZHANG Shou-hong, YAN Jing, <i>et al.</i> (303)
Analysis of Spatiotemporal Variation Characteristics and Driving Forces of NPP in Shanxi Province from 2000 to 2020 Based on Geodetector	SHAO Jia-hao, LI Jing, YAN Xing-guang, <i>et al.</i> (312)
Spatio-temporal Variation in Vegetation Cover and Its Driving Mechanism Exploration in Southwest China from 2000 to 2020	XU Yong, DAI Qiang-yu, HUANG Wen-ting, <i>et al.</i> (323)
Heavy Metal Content and Resistance Gene Abundance and Related Properties in the Surface Soil around Qinghai Lake	HU Shi-lei, QU Jian-li, ZHANG Li, <i>et al.</i> (336)
Soil Heavy Metal Content, Pollution, and Influencing Factors in Typical Farming Area of Sichuan Basin	LIU Shu-ling, WU Mei, LIU Zhi-yuan, <i>et al.</i> (347)
Risk Assessment and Sources of Heavy Metals in Farmland Soils of Yellow River Irrigation Area of Ningxia	CHEN Lin, MA Kun, MA Jian-jun, <i>et al.</i> (356)
Characteristics and Risk Assessment of Heavy Metals in the Soil Around Copper Smelting Sites	PENG Chi, LIU Xu, ZHOU Zi-ruo, <i>et al.</i> (367)
Characteristics of Typical Soil Acidification and Effects of Heavy Metal Speciation and Availability in Southwest China	LING Yun, LIU Han-yi, ZHANG Xiao-ting, <i>et al.</i> (376)
Stabilization Characteristics of Exogenous Cd in Different Types of Soil	WANG Gang, YU Hai-ying, HUANG Hua-gang, <i>et al.</i> (387)
Threshold of Se-rich Soil Based on Available-Se and Influencing Factors of Available-Se	WANG Ying, MA Yan-bin, WANG Ze-jing (395)
Accumulation Characteristics and Health Risk Assessment of Heavy Metals in Soil-Crop System Based on Soil Parent Material Zoning	CHEN Zi-wan, XU Jing, HOU Zhao-lei, <i>et al.</i> (405)
Characteristics and Planting Safety Assessment of As Content in Dryland Soil and Maize in Guizhou Province	HUANG Feng-yan, ZHOU Lang, SONG Bo, <i>et al.</i> (415)
Potential of Intercropping <i>Pennisetum purpureum</i> Schum with <i>Melia azedarach</i> L. and <i>Broussonetia papyrifera</i> for Phytoremediation of Heavy-metal Contaminated Soil around Mining Areas	WANG Xiao-hui, XIAO Xi-yuan, GUO Zhao-hui, <i>et al.</i> (426)
Inactivation of Cd and As by an <i>Enterobacter</i> Isolated from Cd and As Contaminated Farmland Soil	YIN Xue-fei, LIU Yu-ling, WU De, <i>et al.</i> (436)
Mineralization Characteristics of Soil Organic Carbon and Its Relationship with Organic Carbon Components in Artificial <i>Robinia pseudoacacia</i> Forest in Loess Hilly Region	ZHU Yu-fan, LIU Wei-chao, LI Jia-xin, <i>et al.</i> (444)
Accumulation, Migration, and Transformation of Soil Phosphorus in Facility Agriculture and Its Influencing Factors	FANG Bing, CHEN Lin, WANG Yang, <i>et al.</i> (452)
Optimizing Straw Management to Enhance Carbon and Nitrogen Efficiency and Economic Benefit of Wheat-Maize Double Cropping System	WANG Liang, QIAN Xin, GAO Ying-bo, <i>et al.</i> (463)
Effect of Deep Fertilization with Slow/Controlled Release Fertilizer on N Fate in Clayey Soil Wheat Field	HOU Peng-fu, XUE Li-xiang, YUAN Wen-sheng, <i>et al.</i> (473)
Structure and Function of Soil Fungal Community in Rotation Fallow Farmland in Alluvial Plain of Lower Yellow River	NAN Zhen-wu, LIU Zhu, MENG Wei-wei, <i>et al.</i> (482)
Response of Topsoil Fungal Community Structure to Soil Improvement Measures in Degraded Forest of Red Soil Region	GUAN Hong-zhi, HUANG Rong-zhen, WANG Jin-ping, <i>et al.</i> (494)
Temporal and Spatial Variations in Root-associated Fungi Associated with <i>Pinus sylvestris</i> var. <i>mongolica</i> in the Semi-arid and Dry Sub-humid Desertified Regions of Northern China	ZHAO Pei-shan, GUO Mi-shan, GAO Guang-lei, <i>et al.</i> (502)
QMEC-based Analysis of the Soil Microbial Functional Potentials across Different Tibetan Plateau Glacier Forelands	ZHANG Jie-jie, Anders Priemé, CHEN Xian-ke, <i>et al.</i> (512)
Meta Analysis on Yield Effect of Biochar for Staple Crops in China	YU Bin-hang, JI Jian-mei, WANG Li-xue, <i>et al.</i> (520)
Effects of Biochar on Antibiotic Environmental Behaviors in Soil: A Meta-analysis	LI Jing-han, ZHANG Jian-qiang, XIA Li-qiong, <i>et al.</i> (531)
Properties of Biochars Prepared from Different Crop Straws and Leaching Behavior of Heavy Metals	LI Jia-kang, QIU Chun-sheng, ZHAO Jia-qi, <i>et al.</i> (540)
Spatial-temporal Evolution and Heterogeneity of Carbon Emissions at County-level in China	SONG Yuan-zhen, ZENG Jian, WANG Sen, <i>et al.</i> (549)
Spatiotemporal Dynamic Evolution and Gravity Center Migration of Carbon Emissions in the Main Urban Area of Chongqing over the Past 20 Years	XIANG Shu-jiang, YANG Chun-mei, XIE Yu-qi, <i>et al.</i> (560)
Spatiotemporal Characteristics and Influencing Factors of Environment Emergency Incident in China from 1991 to 2018	YU Guang-hui, WANG Fei-fan, LIU Xian-zhao, <i>et al.</i> (572)
Migration, Transformation, and Toxicity of Quaternary Ammonium Antimicrobial Agents in the Environment	ZHANG Li-lan, QIN Cun-li, QIAN Yao, <i>et al.</i> (583)