

极端降雨事件下城市病原微生物与抗生素抗性基因的时空响应: 以2021年郑州特大暴雨为例

刘焱帆¹, 陈二杰¹, 姚东良¹, 王璟媛¹, 李华², 吴新军², 刘毅¹, 秦红灵¹, 朱宝利^{1*}

1. 中国科学院亚热带农业生态研究所, 长沙 410125

2. 桃源县农业农村局, 常德 415799

* 联系人, E-mail: baoli.zhu@isa.ac.cn

2025-06-05 收稿, 2025-07-18 修回, 2025-08-11 接受, 2025-08-11 网络版发表

国家自然科学基金(42177104)资助

摘要 极端降雨事件通常会加剧城市环境中病原菌及抗生素抗性基因(antibiotic resistance genes, ARGs)的传播风险, 但其驱动机制与长期生态效应仍不明晰. 本研究整合qPCR定量检测、宏基因组测序及Spearman相关性分析, 系统揭示特大暴雨后病原菌和ARGs的时空分异规律. 宏基因组鉴定出30种病原微生物(25种细菌和5种真菌), 其中水体机会致病菌丰度显著提升(>30%); qPCR定量显示医院区域铜绿假单胞菌特征基因(*oprI*)丰度增加超过168倍($P<0.05$), ARGs绝对丰度较其他区域高1~2个数量级($P<0.05$). ARGs呈现“时间滞后效应”, 暴雨一年后水体中*sulI*与*intl-1*基因丰度反超即时水平47~116倍($P<0.05$). 整合子基因*intl-1*作为ARGs传播载体, 与*sulI*、*ermB*、*tetM*基因丰度呈强正相关($r>0.71$, $P<0.01$), 而铵态氮($\text{NH}_4^+\text{-N}$)与溶解性有机碳(dissolved organic carbon, DOC)通过协同调控微生物代谢活性($r=0.62\sim0.78$)驱动ARGs跨生态位迁移. 值得注意的是, 暴雨后城市霍乱、痢疾等发病率与前后两年同一时期内无显著变化($P>0.05$), 说明多级卫生防控的成效. 本研究系统解析了极端降雨事件后病原菌和ARGs的时空分布特征, 揭示了气候事件与医疗活动的双重影响, 为“*One Health*”框架下的风险管控提供科学依据.

关键词 极端降雨, 病原微生物, 抗生素抗性基因, 时空分异, 环境

全球气候变暖导致极端降雨事件频发, 其引发的洪涝灾害已成为威胁人类健康与生态安全的重大挑战. IPCC第六次评估报告^[1]明确指出, 目前全球地表平均温度较工业化前已上升约1°C, 未来极端天气事件的强度与频率将持续加剧^[2]. 研究表明, 温度升高0.5~2°C可显著增加极端降雨的发生概率^[3~6], 而洪涝灾害不仅直接破坏基础设施, 更通过污染扩散、病原微生物传播及抗生素抗性基因的转移, 对公共卫生安全构成潜在威胁^[7]. 例如, 洪涝后水源污染与卫生条件恶化可导致感染性腹泻发病率提升2~5倍^[8~11], 皮肤软组织感染风险显著增加^[12~16], 并与呼吸道疾病及耐药性感染事件密切相关^[17~19]. 值得注意的是, 洪涝期间环境介质中

ARGs的扩散可能进一步加剧抗生素耐药性危机, 但目前这一过程的作用机制尚不清晰.

近年来, 环境耐药组学研究揭示了ARGs在农业土壤^[20]、水体沉积物^[21,22]及医疗废水^[23,24]中的分布特征, 并发现整合子基因(如*intl-1*)通过水平基因转移(horizontal gene transfer, HGT)驱动ARGs传播的关键作用^[25,26]. 然而, 城市内涝作为一种特殊生境, 其复杂的环境扰动(如污水倒灌、垃圾渗滤液混合)可能显著改变ARGs的赋存状态与传播路径. 现有研究存在以下局限: 其一, 尽管洪涝灾害已被证实可短期内显著提升环境中ARGs与病原微生物的丰度, 但多数研究聚焦于洪涝后病原微生物的短期暴发和ARGs短时间内丰度的

引用格式: 刘焱帆, 陈二杰, 姚东良, 等. 极端降雨事件下城市病原微生物与抗生素抗性基因的时空响应: 以2021年郑州特大暴雨为例. 科学通报, 2026, 71: 2485–2497

Liu Y, Chen E, Yao D, et al. Spatio-temporal responses of urban pathogenic microorganisms and antibiotic resistance genes under extreme rainfall events: a case study of the severe rainstorm in Zhengzhou in 2021 (in Chinese). Chin Sci Bull, 2026, 71: 2485–2497, doi: [10.1360/CSB-2025-5046](https://doi.org/10.1360/CSB-2025-5046)

变化^[27,28]，对洪涝后病原微生物和ARGs残留风险缺乏长期追踪，且对它们的时空分布特征及其与城市功能分区的关联缺乏系统解析；其二，环境因子(如营养盐、有机碳)如何通过调控微生物群落结构间接影响ARGs的扩散仍不明确；其三，医院、居民区等高敏感区域在极端降雨后是否成为ARGs的“热点区”尚未得到实证支持。这些科学盲区严重制约了城市洪涝灾害后耐药性风险的精准评估与防控策略的制定。

郑州市作为中国特大城市与交通枢纽，2021年“7·20特大暴雨”事件^[29]导致的城市内涝为解答上述问题提供了典型研究场景。本研究突破传统灾后卫生评估的单一视角，从环境扰动、微生物响应、ARGs传播多维度构建分析框架，系统解析极端降雨事件后病原菌和ARGs的时空分异规律及驱动机制。通过对比不同功能区域(医院、居民区、商业区等)的环境介质(土壤、积水)样本，结合整合子基因与关键环境因子的协同分析，本研究有望揭示城市内涝中病原菌和ARGs扩散的复合途径，阐明高风险区域的耐药性传播特征。研究成果不仅可为极端天气事件下的公共卫生风险预警提供理论依据，还将为城市功能分区规划与耐药性污染靶向治理提供科学支撑，对推动气候适应型健康城市建设具有重要意义。

1 材料与方法

1.1 样品采集与理化性质测定

本研究于2021年7月23日郑州特大暴雨事件后，沿郑州市金水河流域系统布设采样点，涵盖医院(土样10个，水样8个)、居民区(土样12个，水样9个)、城市绿地

(土样9个，水样4个)、交通干道(土样11个，水样9个)及河道断面(土样8个，水样7个)等典型城市功能区，并在新乡市原阳县选择农区对照点(土样18个，水样13个)。共采集土壤样品68个(城市50个，农区18个)及水体样品58个(城市39个，农区13个)，并于一年后的同一时期采集同点位样品作为对照。所有样品经冰盒运输至实验室后分两部分保存：4℃冷藏样品用于理化分析，-80℃超低温冻存样品用于分子生物学研究。

土壤铵态氮(NH₄⁺-N)和硝态氮(NO₃⁻-N)含量采用2 mol/L KCl浸提-连续流动分析法测定(LY/T 1228-2015)，溶解性有机碳(DOC)采用TOC分析仪(Shimadzu TOC-L)测定，具体操作参照《土壤农化分析》(第三版)中的方法进行^[30]。

1.2 DNA提取与实时荧光定量PCR

土壤微生物基因组DNA采用Chen等人^[31]的方法进行提取，水体样品经0.22 μm聚碳酸酯滤膜(Millipore)富集微生物后，使用DNeasy PowerWater试剂盒(QIAGEN, 德国)进行提取。DNA纯度和浓度通过Nano-Drop 2000检测，浓度稀释至4~6 ng/μL。

实时荧光定量PCR在LightCycler 480 II系统(Roche, 瑞士)上进行，采用10 μL反应体系：Premix Ex Taq 5 μL(Takara)，正反向引物各0.4 μL(10 μmol/L)，模板DNA 1 μL，ddH₂O 3.2 μL。目标基因包括：(1) 微生物标记基因：16S rRNA(总细菌)、23S rRNA(肠球菌)、*cpa*(产气荚膜梭菌)、*rcsA*(肺炎克雷伯菌)、*oprI*(铜绿假单胞菌)；(2) 抗生素抗性基因：*sulI*(磺胺类)、*tetM*(四环素类)、*ermB*(大环内酯类)及*intl-1*(整合子)。各基因引物序列^[32-39]见表1。扩增程序按照Premix Ex Taq™

表 1 本研究选取的病原菌和抗生素抗性基因及其引物
Table 1 The pathogenic bacteria and their primers selected in this study

监测内容	目标基因	定量方法	正向引物5'→3'	反向引物5'→3'	参考文献	
病原菌	肠球菌	23S rRNA	SYBR green	GAGAAATTCCAAACGAACCTTG	CAGTGCTCTACCTCCATCATT	[32]
	产气荚膜梭菌	<i>cpa</i>	SYBR green	AAGAACTAGTAGCTTACATATCAACTA	TTTCCTGGGTTGTCCATTTC	[33]
	肺炎克雷伯菌	<i>rcsA</i>	SYBR green	GGATATCTGACCAGTCGG	GGGTTTTGCGTAATGATCTG	[34]
	铜绿假单胞菌	<i>oprI</i>	SYBR green	ATGAACAACGTTCTGAAATTCTCTGCT	CTTGCGGCTGGCTTTTCCAG	[35]
抗性基因	大环内酯类	<i>erm B</i>	SYBR green	GATACCGTTTACGAAATTGG	GAATCGAGACTTGAGTGTGC	[36]
	磺胺类	<i>sulI</i>	TaqMan	CCGTTGGCCTTCCTGTAAAG	TTGCCGATCGCGTGAAGT	[37]
				FAM-CAGCGAGCCTTGCGGCGG-TAMRA		
	四环素	<i>tetM</i>	TaqMan	GGTTTCTCTTGGATACTTAAATCAATCR	CCAACCATAYAATCCTTGTTTCRC	[38]
			JOE-ATGCAGTTATGGARGGGATACGCTA	TGGY-BHQ-1		
整合子基因	<i>intl-1</i>	TaqMan	GCC TTG ATG TTA CCC GAG AG	GAT CGG TCG AAT GCG TGT	[39]	
			FAM-ATTCTTGCCGTGGTTCTGGGTT	TT-BHQ1		

(Takara, China)或SYBR Green Premix Pro Taq HS qPCR Kit说明书中给定程序进行。标准曲线采用梯度稀释的质粒标准品($10^6 \sim 10^{10}$ copies/ μL)建立, 扩增效率控制在90%~110%, $r^2 > 0.95$ 。目标基因检出限设定为CT值>35的样本视为未检出(ND)。

1.3 宏基因组分析

本研究选取2021年极端降雨事件后和2022年同一时期的绿地、农田和河流样本各3个(共18个样本)进行宏基因组测序分析。原始测序数据使用fastp软件(v0.23.2)进行质量控制, MEGAHIT(v1.2.9)进行组装。使用组装后的contigs, 形成一个非冗余基因组, 采用DIAMOND(v2.1.6)与PHI-base病原菌数据库(v4.12)和CARD抗生素抗性基因数据库(v3.2.6)进行比对。相关基因丰度定量分析使用CoverM(v0.6.1)完成, 通过将质控后的clean reads比对至非冗余基因组, 计算每个基因的TPM(transcripts per million)值。

1.4 数据统计分析

数据通过Shapiro-Wilk正态性检验(显著性水平 $\alpha=0.05$)评估环境参数与抗生素抗性基因丰度的数据分布特征, 针对非正态分布的基因丰度数据实施以10为底的对数转换预处理。采用单因素方差分析(one-way ANOVA)结合最小显著性差异法(LSD)进行采样点间的差异性检验, 统计显著性阈值设定为 $P < 0.05$ 。运用Spearman相关性分析法探究微生物群落结构特征与环境因子间的相互作用关系。所有统计分析均在R环境(v4.2.0)中完成, 使用ggplot2(v3.4.0)进行数据可视化。

2 结果与分析

2.1 极端暴雨对病原指示菌丰度的时空影响

qPCR定量分析显示(图1), 2021年特大暴雨事件对土壤中病原菌标志性基因丰度的影响具有显著种属和空间异质性。肠球菌属(23S rRNA)、产气荚膜梭菌

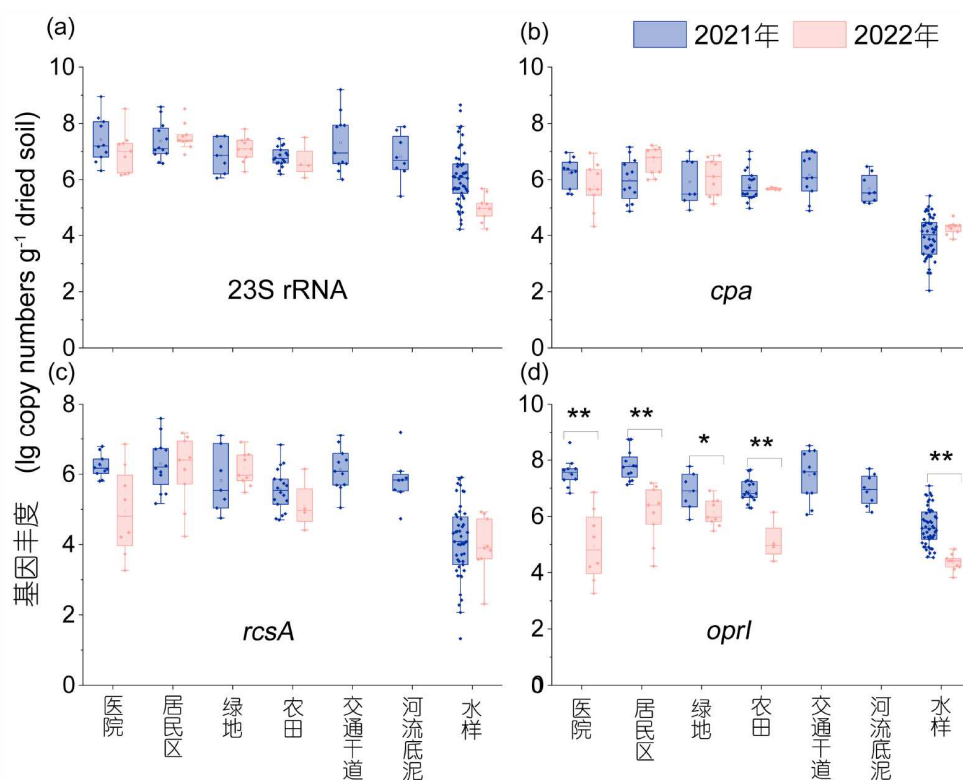


图1 (网络版彩色)暴雨后肠球菌属、产气荚膜梭菌、肺炎克雷伯菌、铜绿假单胞菌的生物标志物23S rRNA(a)、cpa(b)、rcsA(c)、oprI(d)基因绝对丰度变化。*和**为显著($P \leq 0.05$)或极显著($P \leq 0.01$)差异

Figure 1 (Color online) Changes in the absolute abundance of 23S rRNA (a), cpa (b), rcsA (c), oprI (d) genes for *Enterococcus* spp., *Clostridium perfringens*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* after the rainstorm. * and ** indicate significant ($P \leq 0.05$) or highly significant ($P \leq 0.01$) differences

(*cpa*)及肺炎克雷伯菌(*rcsA*)的丰度在暴雨后(2021年)与对照年(2022年)间无显著差异($P>0.05$), 其lg拷贝数分别稳定在6.99~7.22、5.77~6.24和4.95~6.23 g^{-1} 干土/ mL^{-1} 水。然而, 铜绿假单胞菌(*oprI*)的丰度在暴雨后升高最为显著($P<0.05$), 为 7.55 ± 1.04 lg拷贝数 g^{-1} 干土/ mL^{-1} 水, 比对照年的 5.32 ± 1.17 增加了160多倍。空间分布模式进一步揭示, 医院和居民区暴雨后(2022年)铜绿假单胞菌*oprI*基因丰度显著高于其他区域(绿地和农田等, $P<0.05$), 为病原菌富集的热点区域。

2.2 抗生素抗性基因对极端降水的响应特征

特大暴雨事件显著改变了研究区域内抗生素抗性基因的空间分布格局与动态特征(图2)。医院区域三种ARGs(磺胺类*sulI*、四环素类*tetM*、大环内酯类*ermB*)及整合子*intl-1*在暴雨后的绝对丰度达到峰值, 分别为7.55、8.69、7.60和8.13 lg拷贝数 g^{-1} 干土/ mL^{-1} 水, 较灾后一年显著升高28~176倍($P<0.05$)。除*ermB*外, 其余三种ARGs在居民区的丰度也较灾后一年同一时期增

加最高达75倍($P<0.05$)。另外, *ermB*在绿地和农田丰度也显著高于一年后水平($P<0.05$), 提示城市不同功能类型区域对特定抗性基因的环境行为可能具有筛选作用。

进一步研究发现, 整合子基因*intl-1*与*sul-1*的丰度呈现显著协同升高趋势($r^2=0.79$, $P<0.01$), 表明水平基因转移可能在暴雨后ARGs的扩散中起关键作用。值得注意的是, 水环境中ARGs的动态表现出明显的时间滞后效应: 暴雨一年后*sulI*和*intl-1*的丰度反超暴雨后即时水平47~116倍($P<0.05$), 造成该结果的原因之一可能与抗性基因通过宿主菌的适应性存活或遗传元件稳定性维持有关, 可产生长期的生态效应。

2.3 病原菌与抗生素抗性基因的生态位分化特征

基于16S rRNA基因标准化分析, 微生物群落在不同功能分区中表现出显著的生态位特异性分布特征。在病原菌层面, 水体环境中条件致病菌标志基因(肠球菌属23S rRNA基因和铜绿假单胞菌*oprI*基因)的相对

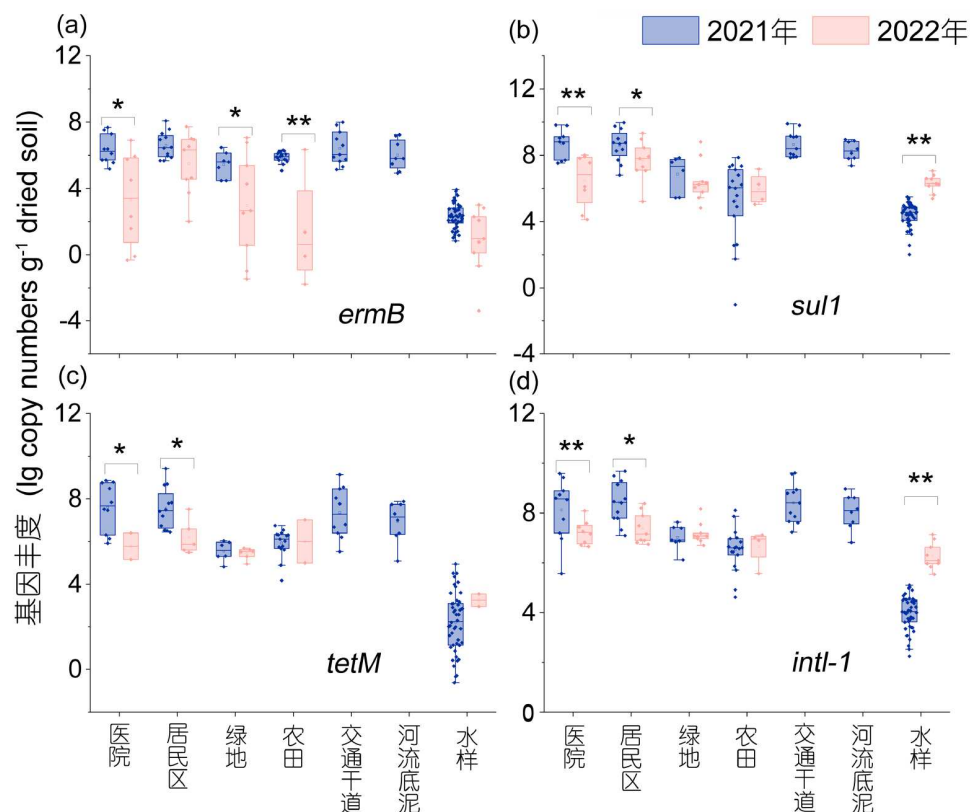


图2 (网络版彩色)暴雨后抗生素抗性基因*ermB*(a)、*sulI*(b)、*tetM*(c)及*intl-1*(d)绝对丰度变化。*和**为显著($P\leq 0.05$)或极显著($P\leq 0.01$)差异
Figure 2 (Color online) Changes in the absolute abundance of antibiotic resistance genes *ermB* (a), *sulI* (b), *tetM* (c) and *intl-1* (d) after the rainstorm. * and ** indicate significant ($P\leq 0.05$) or highly significant ($P\leq 0.01$) differences

丰度显著富集, 分别达到12.34%和21.10%, 较居民区(5.17%, $P<0.05$)与绿地(2.32%, $P<0.05$)高2.4~9.1倍, 表明水体流动性可能通过促进生物膜形成增强条件致病菌的定殖能力(图3)。

在ARGs分布层面, 医院功能区作为主要富集热点, 其*tetM*、*sul1*和*intl-1*基因的相对丰度分别达0.13%、0.89%和0.50%, 较绿地功能区(0.002%、0.16%和0.10%)高1~2个数量级($P<0.05$), 提示高强度医疗活动(如抗生素使用)通过持续选择压力驱动ARGs的累积。值得注意的是, 尽管水体中条件致病菌丰度最高, 但ARGs(*tetM*、*sul1*和*intl-1*)的相对丰度却处于所有功能区最低水平, 表明水体的强流动性可能通过物理稀释作用抑制ARGs的垂直传播, 同时加速耐药基因的水平扩散衰减(图4)。

2.4 宏基因组分析极端暴雨对病原菌和抗性基因丰度的影响

基于宏基因组测序分析, 本研究在三种典型生境(绿地、农田和水体)中共鉴定出30种具有较高相对丰度的病原微生物, 其中细菌占优势(25种), 真菌类5种(图5(a))。极端降雨事件对不同生境中病原菌群落的影响

呈现显著差异($P<0.05$): 水体生态系统中病原菌总丰度较对照年显著提升19.12%($P=0.003$), 其中机会致病菌(如*Pseudomonas cichorii*、*Candida albicans*)增幅尤为显著($>30\%$); 相比之下, 陆生生态系统(绿地和农田)的病原菌群落结构保持相对稳定, 仅部分兼性致病菌(如*Ralstonia solanacearum*、*Vibrio cholerae*)呈现显著增长趋势($P<0.05$)。这一分布特征提示, 极端降水可能通过水文连通性促进水环境中条件致病菌的富集与扩散。

在抗生素抗性基因方面, 研究检测到25种ARGs(图5(b))。定量分析显示, 极端降雨事件导致三类生境中ARGs总丰度均显著升高($P<0.01$), 其中水环境的ARGs负荷增加最为显著(22.79%)。极端降雨后, 水体生态系统中9类ARGs: 氨基糖苷类(aminoglycoside)、青霉素 β -内酰胺类(penicillin beta-lactam)、糖肽类(glycopeptide)、酰胺醇类(phenicol)、二氨基嘧啶类(diaminopyrimidine)、磺胺类(sulfonamide)、双环霉素类(bicyclomycin-like)、夫西地酸类(fusidane)、四环素类(tetracycline)等抗生素抗性基因的丰度增幅均超过30%($P=0.001$)。农田生态系统中大环内酯类(macrolide)和双环霉素类(bicyclomycin-like)抗生素抗性基因丰度

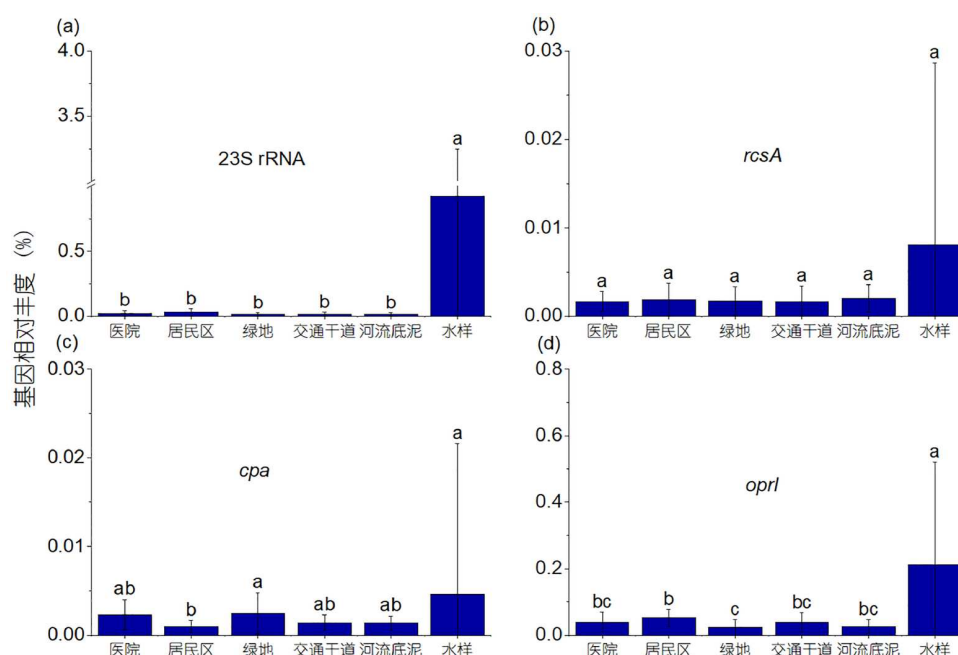


图3 (网络版彩色)暴雨后城市土壤样品肠球菌属、肺炎克雷伯菌、产气荚膜梭菌、铜绿假单胞菌的生物标志物23S rRNA(a)、*rscA*(b)、*cpa*(c)、*oprI*(d)基因相对丰度变化。a, b代表显著性差异水平
Figure 3 (Color online) Changes in the relative abundance of 23S rRNA (a), *rscA* (b), *cpa* (c), *oprI* (d) genes for *Enterococcus* spp, *Klebsiella pneumoniae*, *Clostridium perfringens*, and *Pseudomonas aeruginosa* in urban soil samples after the rainstorm. Different lowercase letters (a, b) indicate significant differences

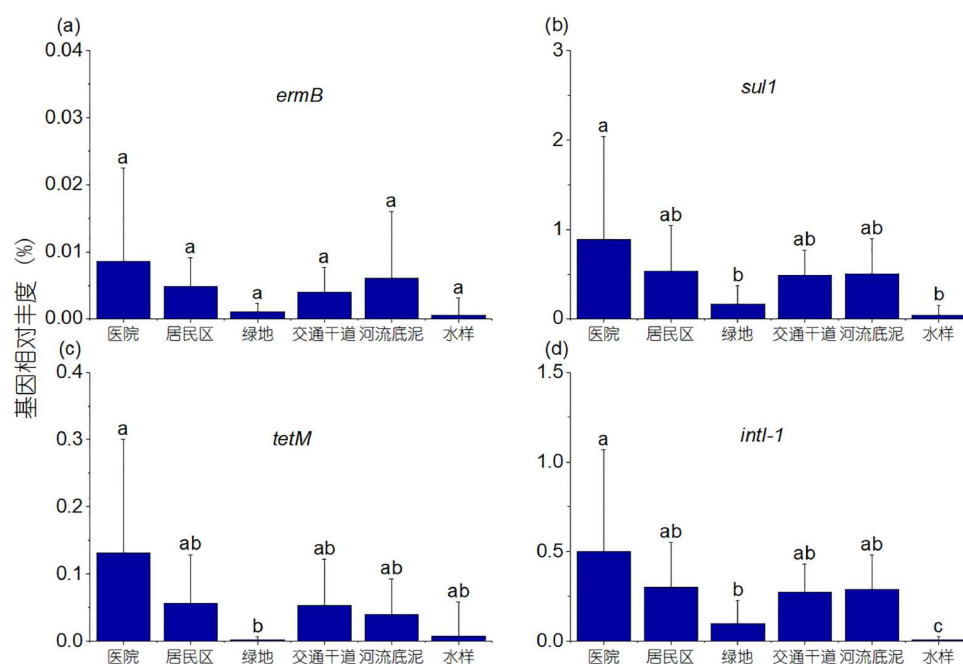


图 4 (网络版彩色)暴雨后抗生素抗性基因*ermB*(a)、*sul1*(b)、*tetM*(c)及*intl-1*(d)相对丰度变化。a, b代表显著性差异水平

Figure 4 (Color online) Changes in the relative abundance of antibiotic resistance genes *ermB* (a), *sul1* (b), *tetM* (c) and *intl-1* (d) after the rainstorm. Different lowercase letters (a, b) indicate significant differences

也呈现相似增长趋势。这些数据表明, 极端气候事件加速ARGs在环境中的传播扩散, 对公共卫生安全构成潜在威胁。

2.5 环境因子与病原微生物及抗生素抗性基因的相互关系

通过Spearman相关性分析(图6)发现铵态氮($\text{NH}_4^+\text{-N}$)、硝态氮($\text{NO}_3^-\text{-N}$)和溶解性有机碳(DOC)浓度是关键驱动因子, 铵态氮($\text{NH}_4^+\text{-N}$)和溶解性有机碳(DOC)与暴雨后土壤样品病原菌标志基因及ARGs均呈显著正相关($P<0.05$)。硝态氮($\text{NO}_3^-\text{-N}$)与肠球菌属23S rRNA基因和铜绿假单胞菌*oprI*基因及ARGs基因的丰度呈显著负相关($P<0.05$), 与肺炎克雷伯菌*rcaA*基因、产气荚膜梭菌*cpa*基因的丰度无相关性($P>0.05$)。抗生素抗性基因*ermB*、*sul1*和*tetM*之间以及与*intl-1*基因均存在显著的正相关性($P<0.05$), 病原菌基因与ARGs间同样存在较强的协同关系($P<0.05$), 揭示了病原菌与抗性基因共选择的潜在机制。

值得注意的是, 郑州市2020、2021、2022年7~8月肠道传染病发病数统计结果表明(表2), 极端降雨并没有增加霍乱、痢疾等肠道传染病的爆发, 揭示现代城

市公共卫生体系在多重暴露风险中的缓冲能力——即使环境病原体载量增加, 应急管控仍能有效阻断耐药菌群向易感人群的传播链。

3 讨论

3.1 极端降水驱动医院源耐药基因扩散与公共卫生防控成效

本研究发现, 尽管极端降水事件导致医院周边环境中的抗生素抗性基因及条件致病菌(如铜绿假单胞菌)的丰度显著升高, 但郑州市2020~2022年同期的肠道传染病发病率并未出现统计学显著波动($P>0.05$)。这一现象可能归因于多重公共卫生防控机制的有效协同作用。首先, 医院感染控制体系(如暴雨期间的强化消毒程序)与城市排水系统的快速应急响应, 可能阻断了病原体从环境向人体的暴露途径^[40]。其次, 耐药基因的环境丰度升高并不直接等同于致病性增强——铜绿假单胞菌等条件致病菌的临床感染需突破宿主免疫屏障, 而环境菌株的毒力因子表达常处于抑制状态^[41~43]。此外, 郑州市推行的抗菌药物使用分级管理制度(2020年实施)可能通过减少临床广谱抗生素的选择压力, 降低了

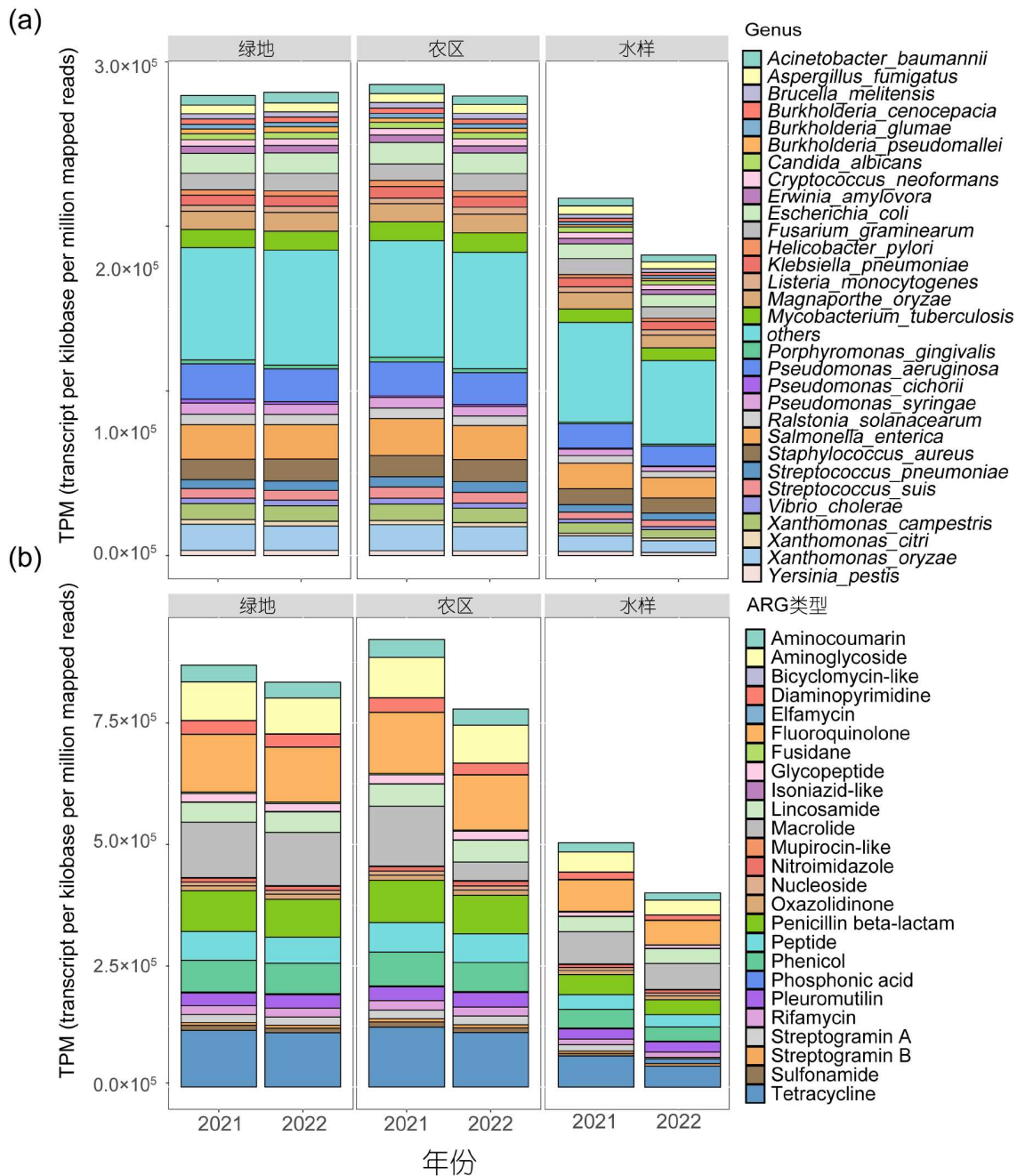


图 5 (网络版彩色)不同样品中病原菌(a)和抗性基因(b)丰度差异图

Figure 5 (Color online) Differences in abundance of pathogenic bacteria (a) and antibiotic resistance genes (b) across different samples

耐药菌株的竞争优势^[44,45].

值得注意的是, 本研究结果与其他国家和地区耐药菌暴发案例^[46–48]形成鲜明对比, 提示气候背景^[49]公共卫生基础设施的交互作用至关重要. 郑州市作为中国中部特大城市, 其医疗废水处理厂普遍配备三级处理工艺(活性炭吸附+紫外消毒), 可去除>99%的活体细

菌^[50], 而季风区其他发展中国家常面临污水处理能力不足的瓶颈. 这印证了联合国环境署提出的“*One Health*”框架中工程干预的关键作用^[51]. 此外, 疾控部门在暴雨季前开展的针对性监测(如医院周边水体NDM-1基因筛查)和公众健康教育(如接触洪水后消毒指引), 可能进一步阻断了环境到人类的传播链.

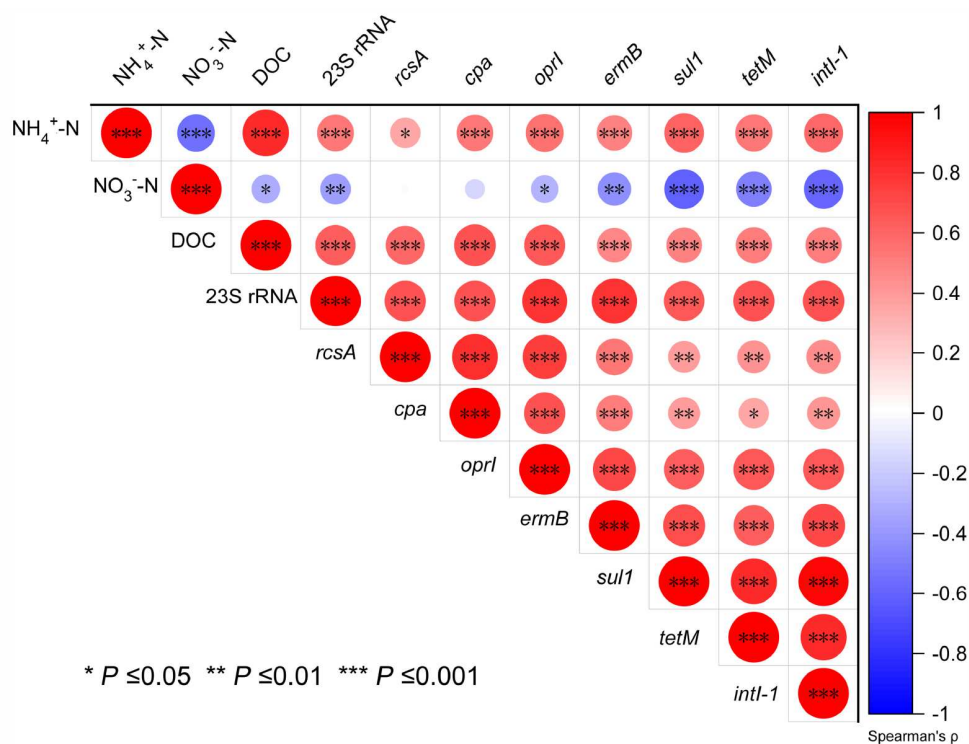


图 6 (网络版彩色)暴雨后土壤样品土壤理化性质, 抗生素抗性基因与病原微生物基因之间Spearman相关性热图

Figure 6 (Color online) Spearman correlation heatmap between soil physicochemical properties, antibiotic resistance genes, and pathogenic microbial genes in soil samples after the rainstorm

3.2 宏基因组视角下极端降雨对病原菌-抗性基因组的级联效应

宏基因组分析揭示, 极端降雨对水体微生物组的扰动最为显著, 水体中病原菌总丰度增加19.12% ($P=0.003$), 其中铜绿假单胞菌(*P. aeruginosa*)和白色念珠菌(*C. albicans*)等机会致病菌增幅超过30%. 这种“生物放大器”效应可能是由于水文连通性促进医院和居民区病原菌向水体的汇集. Okafor和Nwodo^[52]的研究也发现医疗废水排放点检测到了铜绿假单胞菌*oprI*基因; 其次, 洪水导致沉积物再悬浮, 使原本埋藏的病原菌重新进入水柱^[53], 水体DOC浓度骤升创造富营养化环境^[54], 暴雨后与碳代谢相关的KEGG通路丰度显著提升($P<0.05$), 为病原菌增殖提供能量基础. 水生系统是病原菌扩散的“加速器”, 需重点关注医院-水体连通带的监测.

宏基因组检测到的9类ARGs暴雨后在水体环境激增, 呈现级联扩散特征. Lee等人^[55]通过Contig拼接发现, 67.3%的*sul1*基因与*intl1*整合子位于同一支架(scaf-

folds)上, 且该比例在暴雨后显著升高. 本研究qPCR定量分析也发现*intl-1*与*sul1*基因呈现显著协同升高, 证实水平基因转移是ARGs扩散的关键驱动力. 另外, 水环境中ARGs的动态表现出明显的时间滞后效应: 暴雨一年后*sul1*和*intl-1*的丰度反超暴雨后即时水平47~116倍, 揭示了抗性基因在环境中的复杂动态特征. 这可能是由于极端降水初期通过物理冲刷导致部分耐药菌死亡, 但存活菌株在环境选择压力下可通过群体感应等机制重建种群^[56,57]; 此外, 暴雨后水体营养物质(如DOC)的持续输入可能创造新的生态位, 促进携带ARGs的菌群重建, 这一过程与Di等人^[58]在河口生态系统的观测结果相符. 值得注意的是, 该滞后效应主要出现在流动性强的水体环境, 暗示水文特征对ARGs动态的关键调控作用. 水环境中ARGs的时间滞后效应可能表明ARGs滞留风险被低估, 当前洪涝灾害后对ARGs多集中于灾后的即时检测, 而ARGs风险峰值可能迟滞至灾后1~2年才显现, 忽视滞后效应会导致对灾后抗生素抗性基因污染程度和风险的误判^[59]. 同时洪涝频率因气候变化逐渐增加^[60], ARGs时间滞后效应可考虑建立模型,

表 2 郑州市2020~2022年7~8月肠道传染病发病数统计^{a)}
Table 2 Statistics on the number of intestinal infectious disease cases in Zhengzhou during July–August 2020–2022

年份	病种	7月发病数(人)	8月发病数(人)
2020年	霍乱	0	0
	痢疾	39	23
	伤寒+副伤寒	0	1
	甲肝	1	0
	戊肝	2	1
	手足口病	146	2442
	合计	188	2467
2021年	霍乱	0	0
	痢疾	31	16
	伤寒+副伤寒	0	1
	甲肝	0	3
	戊肝	4	3
	手足口病	1014	233
	合计	1049	256
2022年	霍乱	0	0
	痢疾	28	20
	伤寒+副伤寒	0	0
	甲肝	0	2
	戊肝	7	3
	手足口病	2221	2193
	合计	2256	2218

a) 数据来源: 郑州市卫生健康委员会

以预测未来灾害后耐药基因库的扩散规律, 评估长期生态健康风险. 这一发现对公共卫生管理具有重要启示, 建议建立至少1~2年的ARGs追踪机制并建立相关模型以准确评估长期风险.

3.3 环境因子协同驱动病原菌与ARGs的共选择效应

本研究发现铵态氮与溶解性有机碳是驱动暴雨后土壤中病原菌标志基因及ARGs富集的关键环境因子. Spearman相关性分析表明, $\text{NH}_4^+\text{-N}$ 和DOC与所有检测的病原菌基因及ARGs均呈显著正相关($P<0.05$), 这与Zhang等人^[61]提出的“富营养化-微生物代谢耦合”机制一致. $\text{NH}_4^+\text{-N}$ 可能通过激活病原菌的铵同化途径(如谷氨酰胺合成酶活性上调)促进其增殖^[62], 而DOC作为微生物代谢的优先底物, 可显著增强抗性菌群的竞争适应性^[63,64]. 值得注意的是, 硝态氮与肠球菌属23S rRNA基因和铜绿假单胞菌*oprI*基因及ARGs基因丰度呈显著负相关关系($P<0.05$), 这可能与反硝化作用导致的快速转化有关^[65,66], 但其本身并不代表能直接抑制这些微生物, 而硝态氮与肺炎克雷伯菌*rcaA*基因、产

气荚膜梭菌*cpa*基因的丰度无相关性($P>0.05$), 这可能与病原微生物对氮源代谢偏好性差异有关^[67], 后续有待更多的研究证明这一结论. 上述病原菌与ARGs基因丰度与其土壤理化性质之间的相关性差异暗示氮素形态的差异对病原菌和ARGs的传播具有选择性调控作用.

研究进一步揭示了ARGs与病原菌基因间的协同进化关系. *ermB*、*sulI*和*tetM*基因之间以及与整合酶基因*intI-1*的显著正相关性($P<0.01$), 表明整合子介导的水平基因转移可能在多药抗性传播中起核心作用^[68]. 病原菌基因与ARGs的强协同关系($P<0.01$)提示共选择压力机制的存在: 一方面, 病原菌可通过外排泵系统同时抵抗抗生素和宿主免疫攻击^[69]; 另一方面, 抗生素与消毒剂(如暴雨径流中季铵盐类污染物)的复合暴露可能通过共同耐药靶点(如*ermB*核糖体甲基化酶)驱动协同选择^[70–72]. 这些发现为“One Health”框架下病原菌与抗性基因共进化理论提供了新的环境证据, 并提示污染治理需同步控制营养盐输入和消毒剂滥用, 以阻断ARGs-病原菌协同传播的级联效应.

4 结论

本研究通过宏基因组和qPCR等分析揭示了极端暴雨事件对城市环境中病原菌与抗生素抗性基因分布的时空动态及关键环境驱动因子。宏基因组检测到水体机会致病菌(如*Pseudomonas cichorii*)丰度显著提升(>30%), qPCR则精准量化了铜绿假单胞菌(*oprI*基因)在医院的特异性富集(暴雨后提升丰度增加两个数量级)。宏基因组分析鉴定出25类ARGs, 其中水体环境中9类抗生素抗性基因(如氨基糖苷类、 β -内酰胺类)丰度

增幅超过30%, qPCR定量进一步证实ARGs存在“时间滞后效应”, 灾后一年水体中*sulI*和*intl-1*基因丰度反超即时水平47~116倍。整合子介导的水平基因转移是核心扩散途径(*intl-1*与*sulI*协同性 $r^2=0.79$), 且 NH_4^+-N 和DOC与微生物增殖显著相关。尽管环境病原体载量增加, 城市公共卫生体系有效阻断了暴雨后胃肠道传染疾病的爆发。研究结果为极端气候事件下的微生物安全防控提供了多维度科学依据, 支撑“One Health”框架下的环境与微生物互作理论。

参考文献

- Calvin K, Dasgupta D, Krinner G, et al. Climate Change 2023: synthesis report. Contribution of working groups I, II and III to the sixth assessment report of the intergovernmental panel on climate change. IPCC, Geneva, Switzerland. First. Technical Report, Intergovernmental Panel on Climate Change (IPCC), 2023
- Zhou B T, Qian J. Changes of weather and climate extremes in the IPCC AR6 (in Chinese). Adv Clim Change Res, 2021, 17: 713–718 [周波涛, 钱进. IPCC AR6报告解读: 极端天气气候事件变化. 气候变化研究进展, 2021, 17: 713–718]
- Wu J, Shi Z G, Jie X N, et al. Sensitivity of global extreme precipitation to different climate forcings: a PDRMIP multimodel study (in Chinese). Chin Sci Bull, 2024, 69: 2093–2106 [武洁, 石正国, 解小宁, 等. 全球极端降水对不同外强迫的敏感性响应: 基于PDRMIP模拟试验. 科学通报, 2024, 69: 2093–2106]
- Yu R, Zhai P, Chen Y. Facing climate change-related extreme events in megacities of China in the context of 1.5°C global warming. Curr Opin Environ Sustainability, 2018, 30: 75–81
- Zhang W, Furtado K, Wu P, et al. Increasing precipitation variability on daily-to-multiyear time scales in a warmer world. Sci Adv, 2021, 7: eabf8021
- Fischer E M, Knutti R. Anthropogenic contribution to global occurrence of heavy-precipitation and high-temperature extremes. Nat Clim Change, 2015, 5: 560–564
- Wang Y, Wang H, Cui P, et al. Disaster effects of climate change and the associated scientific challenges (in Chinese). Chin Sci Bull, 2024, 69: 286–300 [王岩, 王昊, 崔鹏, 等. 气候变化的灾害效应与科学挑战. 科学通报, 2024, 69: 286–300]
- Zhang N, Song D, Zhang J, et al. The impact of the 2016 flood event in Anhui Province, China on infectious diarrhea disease: an interrupted time-series study. Environ Int, 2019, 127: 801–809
- Yusof N F, Hamid N, Ma Z F, et al. Exposure to environmental microbiota explains persistent abdominal pain and irritable bowel syndrome after a major flood. Gut Pathog, 2017, 9: 75
- Liu Z, Ding G, Zhang Y, et al. Identifying different types of flood-sensitive diarrheal diseases from 2006 to 2010 in Guangxi, China. Environ Res, 2019, 170: 359–365
- Luo P, Chen M, Kuang W, et al. Hysteresis effects of different levels of storm flooding on susceptible enteric infectious diseases in a central city of China. BMC Public Health, 2023, 23: 1874
- Dayrit J F, Bantanjoyo L, Andersen L K, et al. Impact of climate change on dermatological conditions related to flooding: update from the International Society of Dermatology Climate Change Committee. Int J Dermatol, 2018, 57: 901–910
- Junejo M H, Khan S, Larik E A, et al. Flooding and climate change and its effect on skin disease. J Invest Dermatol, 2023, 143: 1348–1350
- Lin P C, Lin H J, Guo H R, et al. Epidemiological characteristics of lower extremity cellulitis after a typhoon flood. PLoS One, 2013, 8: e65655
- Hiransuthikul N, Tantisirawat W, Lertutsahakul K, et al. Skin and soft-tissue infections among Tsunami survivors in Southern Thailand. Clin Infect Dis, 2005, 41: e93–e96
- Tempark T, Lueangarun S, Chatproedprai S, et al. Flood-related skin diseases: a literature review. Int J Dermatol, 2013, 52: 1168–1176
- Ziv O, Brandstaetter T, Kordeluk S. Severe acute rhinosinusitis secondary to flood related injury. Otolaryngol-head neck surg, 2024, 170: 299–300
- Mulder A C, Pijnacker R, de Man H, et al. “Sickenin’ in the rain” – increased risk of gastrointestinal and respiratory infections after urban pluvial flooding in a population-based cross-sectional study in the Netherlands. BMC Infect Dis, 2019, 19: 377
- Liu Y, Liu J, Chen F, et al. Impact of meteorological factors on lower respiratory tract infections in children. J Int Med Res, 2016, 44: 30–41
- Zheng D, Yin G, Liu M, et al. Global biogeography and projection of soil antibiotic resistance genes. Sci Adv, 2022, 8: eabq8015

- 21 Jiang H, Zhou R, Zhang M, et al. Exploring the differences of antibiotic resistance genes profiles between river surface water and sediments using metagenomic approach. *Ecotoxicol Environ Saf*, 2018, 161: 64–69
- 22 Zhang Y, Wang M, Zhou X, et al. Transmission mechanism of antibiotic resistance genes and their differences between water and sediment in the Weihe River Basin. *Environ Res*, 2024, 252: 119057
- 23 Zhu L, Yuan L, Shuai X Y, et al. Deciphering basic and key traits of antibiotic resistome in influent and effluent of hospital wastewater treatment systems. *Water Res*, 2023, 231: 119614
- 24 Wang Y, Zhang S, Yang L, et al. Spatiotemporal distribution, interactions and toxic effect of microorganisms and ARGs/MGEs from the bioreaction tank in hospital sewage treatment facility. *Sci Total Environ*, 2024, 923: 171481
- 25 Ma L, Li A D, Yin X L, et al. The prevalence of integrons as the carrier of antibiotic resistance genes in natural and man-made environments. *Environ Sci Technol*, 2017, 51: 5721–5728
- 26 Su Z G, Zhang Y, Dai T J, et al. Antibiotic resistance genes and class 1 integron in the environment: research progress (in Chinese). *Microbiol China*, 2018, 45: 2217–2233 [苏志国, 张衍, 代天娇, 等. 环境中抗生素抗性基因与 I 型整合子的研究进展. *微生物学通报*, 2018, 45: 2217–2233]
- 27 Amaral-Zettler L A, Rocca J D, Lamontagne M G, et al. Changes in microbial community structure in the wake of hurricanes Katrina and Rita. *Environ Sci Technol*, 2008, 42: 9072–9078
- 28 Saingam P, Li B, Sung S, et al. Immediate impact of hurricane lane on microbiological quality of coastal water in Hilo Bay, Hawaii. *Environ Sci Technol*, 2021, 55: 2960–2967
- 29 Liang X D, Xia R D, Bao X H, et al. Preliminary investigation on the extreme rainfall event during July 2021 in Henan Province and its multi-scale processes (in Chinese). *Chin Sci Bull*, 2022, 67: 997–1011 [梁旭东, 夏茹娣, 宝兴华, 等. 2021年7月河南极端暴雨过程概况及多尺度特征初探. *科学通报*, 2022, 67: 997–1011]
- 30 Bao S D. *Agricultural Soil Analysis* (in Chinese). Beijing: China Agriculture Press, 2000 [鲍士旦. 土壤农化分析. 北京: 中国农业出版社, 2000]
- 31 Chen Z, Luo X, Hu R, et al. Impact of long-term fertilization on the composition of denitrifier communities based on nitrite reductase analyses in a paddy soil. *Microb Ecol*, 2010, 60: 850–861
- 32 Hou A, Laws E A, Gambrell R P, et al. Pathogen indicator microbes and heavy metals in lake pontchartrain following hurricane Katrina. *Environ Sci Technol*, 2006, 40: 5904–5910
- 33 Schlegel B J, Nowell V J, Parreira V R, et al. Toxin-associated and other genes in *Clostridium perfringens* type A isolates from bovine clostridial abomasitis (BCA) and Jejunal hemorrhage syndrome (JHS). *Can J Vet Res Rev Can Rech Veterinaire*, 2012, 76: 248–254
- 34 Dong D, Liu W, Li H, et al. Survey and rapid detection of *Klebsiella pneumoniae* in clinical samples targeting the *rcsA* gene in Beijing, China. *Front Microbiol*, 2015, doi: 10.3389/fmicb.2015.00519
- 35 De Vos D, Lim Jr A, Pirnay J P, et al. Direct detection and identification of *Pseudomonas aeruginosa* in clinical samples such as skin biopsy specimens and expectorations by multiplex PCR based on two outer membrane lipoprotein genes, *oprI* and *oprL*. *J Clin Microbiol*, 1997, 35: 1295–1299
- 36 Chen J, Yu Z, Michel Jr. F C, et al. Development and application of real-time PCR assays for quantification of *erm* genes conferring resistance to *Macrolides-Lincosamides-Streptogramin B* in livestock manure and manure management systems. *Appl Environ Microbiol*, 2007, 73: 4407–4416
- 37 Heuer H, Smalla K. Manure and sulfadiazine synergistically increased bacterial antibiotic resistance in soil over at least two months. *Environ Microbiol*, 2007, 9: 657–666
- 38 Walsh F, Ingenfeld A, Zampiccoli M, et al. Real-time PCR methods for quantitative monitoring of streptomycin and tetracycline resistance genes in agricultural ecosystems. *J Microbiol Methods*, 2011, 86: 150–155
- 39 Barraud O, Baclet M C, Denis F, et al. Quantitative multiplex real-time PCR for detecting class 1, 2 and 3 integrons. *J AntiMicrob ChemoTher*, 2010, 65: 1642–1645
- 40 Vandegrift R, Bateman A C, Siemens K N, et al. Cleanliness in context: reconciling hygiene with a modern microbial perspective. *Microbiome*, 2017, 5: 76
- 41 Zhang Z, Zhang Q, Wang T, et al. Assessment of global health risk of antibiotic resistance genes. *Nat Commun*, 2022, 13: 1553
- 42 Jin Z, Li J, Ni L, et al. Conditional privatization of a public siderophore enables *Pseudomonas aeruginosa* to resist cheater invasion. *Nat Commun*, 2018, 9: 1383
- 43 Zhang M, Yu B, Fang Q, et al. Microbiome recognition of virulence-factor-governed interfacial mechanisms in antibiotic resistance and pathogenicity removal by functionalized microbubbles. *Water Res*, 2023, 242: 120224
- 44 Zhao R, Yu K, Zhang J, et al. Deciphering the mobility and bacterial hosts of antibiotic resistance genes under antibiotic selection pressure by metagenomic assembly and binning approaches. *Water Res*, 2020, 186: 116318
- 45 Medic D, Bozic Cvijan B, Bajcetic M. Impact of antibiotic consumption on antimicrobial resistance to invasive hospital pathogens. *Antibiotics*, 2023, 12: 259
- 46 Raoult D. Resistance to antibiotics of bacteria in tropical countries. *Lancet Planet Health*, 2019, 3: e238–e239

- 47 Shears P. Epidemiology and surveillance of antimicrobial resistance in the tropics. *Trans R Soc Tropical Med Hyg*, 2001, 95: 127–130
- 48 Roberts T, Dahal P, Shrestha P, et al. Antimicrobial resistance patterns in bacteria causing febrile illness in Africa, South Asia, and Southeast Asia: a systematic review of published etiological studies from 1980–2015. *Int J Infect Dis*, 2022, 122: 612–621
- 49 MacFadden D R, McGough S F, Fisman D, et al. Antibiotic resistance increases with local temperature. *Nat Clim Change*, 2018, 8: 510–514
- 50 Knytl V, Mašin P, Vlčková V, et al. Evaluation and comparison of UV/H₂O₂ and adsorption on active carbon as a tertiary wastewater treatment for pharmaceutical removal within a small WWTP: a pilot study. *Environ Sci-Water Res Technol*, 2024, 10: 144–156
- 51 Adisasmito W B, Almuhairi S, Behraves C B, et al. One Health: a new definition for a sustainable and healthy future. *PLoS Pathog*, 2022, 18: e1010537
- 52 Okafor J U, Nwodo U U. Antibigram profile and detection of resistance genes in *Pseudomonas aeruginosa* recovered from hospital wastewater effluent. *Antibiotics*, 2023, 12: 1517
- 53 Sun W, Liu J B, Zhang J Y, et al. Pollution characteristics of pathogenic microorganisms in the sediments of Shahe Reservoir in the North Canal Basin (in Chinese). *Acta Sci Circumst*, 2021, 41: 228–238 [孙文, 刘吉宝, 张俊亚, 等. 2021. 北运河流域沙河水库沉积物中病原微生物污染特征研究. *环境科学学报*, 41: 228–238]
- 54 Kai J L, Wang J B, Huang L, et al. Seasonal variations of dissolved organic carbon and total nitrogen concentrations in Nam Co and inflowing rivers, Xizang Plateau (in Chinese). *J Lake Sci*, 2019, 31: 1099–1108 [开金磊, 王君波, 黄磊, 等. 西藏纳木错及其入湖河流溶解有机碳和总氮浓度的季节变化. *湖泊科学*, 2019, 31: 1099–1108]
- 55 Lee J, Ju F, Maile-Moskowitz A, et al. Unraveling the riverine antibiotic resistome: the downstream fate of anthropogenic inputs. *Water Res*, 2021, 197: 117050
- 56 Guo X, Wang Z, Li H, et al. Multifaceted precipitation patterns impact biocrust functionality in drylands: a cascade of variability via species replacement in soil microbiota. *Glob Ecol Biogeogr*, 2025, 34: e70061
- 57 Whiteley M, Diggle S P, Greenberg E P. Progress in and promise of bacterial quorum sensing research. *Nature*, 2017, 551: 313–320
- 58 Di Cesare A, Eckert E M, Rogora M, et al. Rainfall increases the abundance of antibiotic resistance genes within a riverine microbial community. *Environ Pollut*, 2017, 226: 473–478
- 59 Yang S H, Chen C H, Chu K H. Fecal indicators, pathogens, antibiotic resistance genes, and ecotoxicity in Galveston Bay after Hurricane Harvey. *J Hazard Mater*, 2021, 411: 124953
- 60 Zhang W, Zhou T, Wu P. Anthropogenic amplification of precipitation variability over the past century. *Science*, 2024, 385: 427–432
- 61 Zhang D, Liu F, Al M A, et al. Nitrogen and sulfur cycling and their coupling mechanisms in eutrophic lake sediment microbiomes. *Sci Total Environ*, 2024, 928: 172518
- 62 Maywald N J, Mang M, Pahls N, et al. Ammonium fertilization increases the susceptibility to fungal leaf and root pathogens in winter wheat. *Front Plant Sci*, 2022, 13: 946584
- 63 Caillon F, Schelker J. Dynamic transfer of soil bacteria and dissolved organic carbon into small streams during hydrological events. *Aquat Sci*, 2020, 82: 41
- 64 Zhang Y, Liu Y, Zhang G, et al. The effects of rice straw and biochar applications on the microbial community in a soil with a history of continuous tomato planting history. *Agronomy*, 2018, 8: 65
- 65 Wei R, Hui C, Zhang Y, et al. Nitrogen removal characteristics and predicted conversion pathways of a heterotrophic nitrification–aerobic denitrification bacterium, *Pseudomonas aeruginosa* P-1. *Environ Sci Pollut Res*, 2021, 28: 7503–7514
- 66 Li X, He H, Zhang X, et al. Distinct responses of soil fungal and bacterial nitrate immobilization to land conversion from forest to agriculture. *Soil Biol Biochem*, 2019, 134: 81–89
- 67 Xie K Z, Xu P Z, Jiang R P, et al. Combined application of inorganic and organic fertilizers improve rice yield and the abundance of soil nitrogen-cycling microbes in cold waterlogged paddy fields (in Chinese). *Plant Nutr Fert Sci*, 2016, 22: 1267–1277 [解开治, 徐培智, 蒋瑞萍, 等. 有机无机肥配施提升冷浸田土壤氮转化相关微生物丰度和水稻产量. *植物营养与肥料学报*, 2016, 22: 1267–1277]
- 68 Gillings M R, Gaze W H, Pruden A, et al. Using the class 1 integron-integrase gene as a proxy for anthropogenic pollution. *ISME J*, 2015, 9: 1269–1279
- 69 Gaurav A, Bakht P, Saini M, et al. Role of bacterial efflux pumps in antibiotic resistance, virulence, and strategies to discover novel efflux pump inhibitors. *Microbiology*, 2023, 169: 001333
- 70 Chen Z, Zhang Y, Mao D, et al. NaClO co-selects antibiotic and disinfectant resistance in *Klebsiella pneumoniae*: implications for the potential risk of extensive disinfectant use during COVID-19 pandemic. *J Hazard Mater*, 2024, 470: 134102
- 71 Zeng J, Li Y, Jin G, et al. Short-term benzalkonium chloride (C₁₂) exposure induced the occurrence of wide-spectrum antibiotic resistance in agricultural soils. *Environ Sci Technol*, 2022, 56: 15054–15063
- 72 Yang L, Wu X, Wu G, et al. Association analysis of antibiotic and disinfectant resistome in human and foodborne *E. coli* in Beijing, China. *Sci Total Environ*, 2024, 944: 173888

Summary for “极端降雨事件下城市病原微生物与抗生素抗性基因的时空响应: 以2021年郑州特大暴雨为例”

Spatio-temporal responses of urban pathogenic microorganisms and antibiotic resistance genes under extreme rainfall events: a case study of the severe rainstorm in Zhengzhou in 2021

Yanfan Liu¹, Erjie Chen¹, Dongliang Yao¹, Jingyuan Wang¹, Hua Li², Xinjun Wu², Yi Liu¹, Hongling Qin¹ & Baoli Zhu^{1*}

¹ Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha 410125, China

² Taoyuan County Bureau of Agriculture and Rural Affairs, Changde 415799, China

* Corresponding author, E-mail: baoli.zhu@isa.ac.cn

With the intensification of extreme rainfall events under global warming, flood induced public health risks, such as the spread of pathogenic microorganisms and antibiotic resistance genes (ARG) are becoming increasingly prominent. However, previous studies have mostly focused on the short-term outbreaks of pathogenic microorganisms and ARGs after floods, with limited attention to their long-term persistence, spatiotemporal distribution, and associations with urban functional zones. Additionally, the mechanism by which environmental factors indirectly influence ARGs dissemination through modulation of microbial community structure remain poorly understood. This study, centered on the Extreme Storm Event on 20 July of 2021 in Zhengzhou, employed qPCR, metagenomic sequencing, and correlation analysis to construct an integrated framework linking environmental perturbation, microbial response, and ARG transmission. The results provide a systematic depiction of the spatiotemporal dynamics of pathogens and ARGs in urban environments following the extreme rainfall.

qPCR results revealed a 168-fold increase ($P<0.05$) in the *oprI* gene of *Pseudomonas aeruginosa* in hospital-adjacent areas, where ARG abundance was one to two orders of magnitude higher than in other zones ($P<0.05$). A notable “time-lag effect” was also observed, with *sulI* and *intI-1* gene abundances in water samples one year later exceeding their immediate post-rainstorm levels by 47–116 times ($P<0.05$). Correlation analysis identified strong positive correlations between the integron gene *intI-1* and *sulI*, *ermB*, and *tetM* gene abundance ($r>0.71$, $P<0.01$), suggesting its critical role in ARG propagation. Furthermore, ammonium nitrogen ($\text{NH}_4^+\text{-N}$) and dissolved organic carbon (DOC) were found to co-regulate microbial metabolic activity, facilitating cross-niche ARG migration ($r=0.62\text{--}0.78$).

Metagenomic sequencing identified 30 pathogenic microorganisms (25 bacteria and 5 fungi) with high relative abundance across three typical habitats (green spaces, farmlands, and water bodies). In aquatic environments, the total abundance of pathogenic bacteria increased by 19.12%, with opportunistic pathogens such as *Pseudomonas cichorii* increasing by over 30%. A total of 25 ARG types were detected, and the extreme rainfall event significantly elevated the total ARG abundance across all three habitats ($P<0.01$), with the most pronounced increase (22.79%) observed in water bodies. Specifically, the abundances of 9 ARG categories (e.g., aminoglycoside and β -lactam resistance genes) increased by more than 30% ($P=0.001$) in aquatic environments. Farmland ecosystems exhibited similar trends, particularly in macrolide and bicyclomycin-like ARGs. These results indicate that extreme rainfall events may accelerate the spread and diffusion of pathogenic microorganisms and ARGs in the environment, posing a potential threat to public health security.

Despite these microbial shifts, reported incidences of urban cholera and dysentery remained stable ($P>0.05$), suggesting the effectiveness of multi-level public health interventions. Overall, this study elucidates the spatiotemporal dynamics and environmental drivers of potential pathogens and ARGs after extreme rainfall events. The findings offer critical insights for “One Health” based risk management, support functional urban zoning and targeted management of antibiotic resistance pollution, and contribute to the development of climate-resilient and health-conscious cities.

extreme rainfall, pathogenic microorganisms, antibiotic resistance genes, spatiotemporal differentiation, environment

doi: [10.1360/CSB-2025-5046](https://doi.org/10.1360/CSB-2025-5046)