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大量抗生素在自然水体中积累会造成严重的污染,抗生素残留被视为新兴的“伪持久性”环境污染物。这些污染物不但导致细菌病原体中抗生素耐药性的传播,还会对水生生态系统产生负面影响。抗生素污染已成为环境和公共卫生领域的重大挑战之一。2023 年生态环境部公布了《重点管控新污染物名单(2023 年版)》,将抗生素作为新污染物重点严格管控。李华教授团队的综述文章以黄河流域为研究对象,系统梳理了水环境中抗生素与抗性基因的污染特征、迁移规律及风险机制,为流域污染防治提供了重要的科学依据。

流域抗生素及抗性基因研究进展及黄河流域研究展望

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摘要: 抗生素以其极低浓度即可特异性地抑制或影响微生物的生存、发育和生长, 凭借其卓越的特性, 已成为医学、农业及畜牧业中举足轻重的组成部分。然而, 抗生素的广泛应用亦引发了一系列环境健康与生态安全的潜在风险。本文通过全面检索“地表水”“地下水”“河流”“湖泊”“海洋”“悬浮物”“沉积物”“抗生素”及“抗生素抗性基因”等关键词, 对水环境中抗生素与抗性基因的研究对象进行了详尽的统计分析。同时, 本文还就抗生素的检测技术、归趋路径、来源解析、风险评估, 以及抗生素抗性基因的来源分析、检测方法、抗性机制和传播机制等研究现状进行了简要的概述。此外, 本文还对黄河流域抗生素与抗生素抗性基因的时空差异进行了初步分析, 并在此基础上, 对黄河流域抗生素与抗性基因的治理研究提出了前瞻性的展望。期望通过本文的研究, 能够为相关领域的学者和决策者提供有价值的参考, 共同推动抗生素与抗性基因治理研究的深入发展。

关键词: 水环境; 抗生素; 抗性基因; 黄河流域

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Research progress on antibiotics and resistance genes in river basins and research prospects in the Yellow River basin

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Abstract: Antibiotics can specifically inhibit or affect the survival, development and growth of microorganisms at extremely low concentrations. With their excellent properties, they have become an important part in medi-

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cine, agriculture and animal husbandry. However, the widespread use of antibiotics has also caused a series of potential risks to environmental health and ecological security. By comprehensively retrieving keywords such as "surface water" "groundwater" "river" "lake" "ocean" "suspended matter" "sediment" "antibiotics", and "antibiotic resistance genes", this paper conducts a detailed statistical analysis of the research objects of antibiotics and resistance genes in the water environment. At the same time, this paper also gives a brief and comprehensive overview of the current research status of antibiotic detection techniques, fate paths, source analysis, risk assessment, as well as the source analysis, detection methods, resistance mechanisms and transmission mechanisms of antibiotic resistance genes. In addition, this paper preliminarily analyzes the spatiotemporal differences of antibiotics and resistance genes in the Yellow River basin and also puts forward, on this basis, a forward-looking prospect for the governance research of antibiotics and resistance genes. It is expected that the research can provide valuable references for the related scholars and decision-makers in this fields in order to promote jointly the in-depth development of the research in antibiotics and resistance genes.

Key words: water environment; antibiotics; resistance genes; the Yellow River

0 引言

抗生素(ANTs)是一种能够以极低的浓度特异性地抑制或影响微生物的生存、发育和生长的化合物,被广泛应用于细菌感染的治疗和预防^[1-2]。由于其优异的特性,抗生素已成为医学、农业和畜牧业中的重要部分^[2]。然而,抗生素在治疗疾病和促进畜牧生产的发展的同时也带来了环境健康和生态安全的风险^[4-5]。动物和人体无法充分吸收和代谢抗生素,大量剩余的会排入环境中^[6]。抗生素在不同环境中的半衰期存在差异,在生物体内相对较短,在自然环境中相对较长。此外,由于抗生素的使用量与排放量大,容易在环境中出现“假持久性”现象,成为高频检出的新污染物^[7]。

一方面,抗生素的广泛应用提高了人们的健康水平,但另一方面,过量使用的问题也愈发普遍^[8]。大量抗生素通过地表物质循环进入水环境^[9-11]。残留的抗生素会持续存在于水环境中,影响甚至损害水中的微生物群落和水生生物^[3-12]。而且,这些抗生素会通过食物链参与循环,给人类健康和生态系统带来较高风险^[13-14]。另外,环境中抗生素的长期残留还会诱导产生抗性基因(ARGs)以及耐药菌(ARB)^[15],给全球健康带来严重威胁。

近年来,抗生素的环境问题逐渐引起了关注。我国水环境中检测出的抗生素约有68种,污染物浓度通常在ng/L到 $\mu\text{g/L}$ 之间^[16]。与国外相比,我国抗生素的检出浓度和频率都偏高^[15,17-21],主要河流、湖泊和水库中普遍出现抗生素类的污染^[22-27]。全球每年排放的抗生素数量庞大^[28],水生环境容易受到生活废水、医疗废水和农业径流等污染源的影响^[29]。

研究表明,抗生素对水生环境造成危害,影响了微藻^[30-33]、甲壳类^[34-35]、鱼类^[34,36-37]甚至两栖动物^[38]的营养水平,一些降解产物也表现出相同或更强毒性^[39]。迄今为止,几乎所有种类的抗生素及其相关抗药基因均出现在各种水环境中^[3,40-41]。

1 水环境中抗生素与抗生素抗性基因的研究现状

1.1 水环境中的抗生素

本综述深入分析了Web of Science核心合集数据库(访问地址:<https://www.webofscience.com/>)中关于水环境中抗生素的文献数据。通过系统检索“地表水”“地下水”“河流”“湖泊”“海洋”“悬浮物”“沉积物”及“抗生素”等关键词,我们获得了迄今为止共计36 586篇相关文献的详尽统计。

具体来看,这些文献涵盖了多个水环境领域:地表水中的抗生素研究文献数量最多,达到18 718篇;地下水、河流、湖泊、海洋、悬浮物及沉积物中的抗生素研究文献量则分别为87、6 242、4 852、2 465、150和4 072篇。这一庞大的文献数据基础,不仅反映了学术界对水环境中抗生素问题的高度关注,也揭示了不同水环境领域研究热度的差异。

值得一提的是,最早关注水环境中抗生素问题的研究可追溯至1943年,当时已有学者发表了关于地表水中抗生素的研究成果。而相对较晚,直至2003年,才出现关于悬浮物与地下水中抗生素的文献。这一时间线清晰地展示了学术界对不同水环境领域抗生素问题的关注演变过程。

通过对2000年以来的文献数据分析(图1),可以发现学术界对流域中抗生素的研究关注度显著

提升,甚至呈现倍数增长。具体来看,2000年至2008年间相关研究数量较少,但自2009年起,文献数量开始大幅增加,并于2023年达到峰值,全年发表文献达4736篇。尽管2024年文献量有所下降,但整体趋势表明该领域仍受到持续且深入地关注。

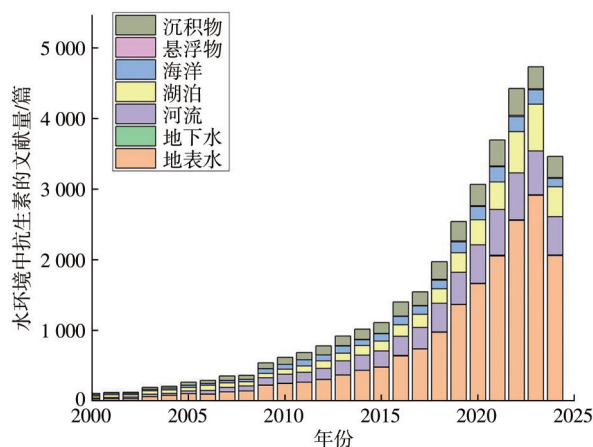


图1 2000年至2024年水环境中抗生素的文献量/篇

Figure 1 The number of literatures on antibiotics in the water environment from 2000 to 2024

1.1.1 抗生素的检测与归趋

由于抗生素性质各异且种类繁多,不同介质中样品的提取方法也各不相同。水体样品通常采用固相萃取柱进行富集和洗脱,这种方法操作简便且有机溶剂消耗少,因而在水环境抗生素研究中广泛应用^[42-44]。对于固体中的抗生素,则多使用EDTA-McIlvaine溶液超声提取,随后通过固相萃取小柱(HLB)小柱萃取,再进行浓缩和定容^[45-48]。

抗生素在水相与沉积相之间的迁移和转化过程会影响其持久性和稳定性^[49-50]。为深入研究其分布和迁移行为,研究者常用分配系数(K_p)表征化合物的分配状态^[15,47,51-52]。这一参数对抗生素迁移过程的解析具有重要意义^[53-55]。研究表明,中国水体中抗生素的分配系数差异显著,其中喹诺酮类(QNs)和大环内酯类(MLs)普遍较高^[46,48,53,56],四环素类(TCs)也表现出较高的分配系数^[46,52-53,56],而磺胺类(SAs)和氯霉素类(CAs)则相对较低^[46,48,56]。这种差异不仅与抗生素的化学性质有关,还受流量、季节变化、水体温度等环境因素的影响^[57-58]。传统 K_p 计算通常基于Kow(辛醇-水分配系数)^[15,59],但实际研究中 K_p 受多种因素影响,常表现出较大波动^[45-46,53]。

抗生素在流域水环境中的分配系数受多种因素影响,包括沉积物的机械组成、酸碱度、有机碳含量、金属含量和离子强度等环境因子和抗生素自身性

质^[48,52-53,56]。一些研究通过回归分析建立了抗生素分配系数与沉积物理化性质之间的线性模型^[60],发现沉积物性质对某些抗生素的分配影响显著,而其他抗生素的分配则更易受环境因素干扰,导致模型准确性较低^[53]。此外,通过拟合logKoc(标准化分配系数)与logKow和分子量,研究发现 K_p 与logKow及分子量呈线性关系^[52]。然而,这些模型通常仅关注沉积物的部分参数^[49,54-55,58],而实际环境中水体的理化因子对抗生素分配同样具有重要影响。

1.1.2 抗生素的来源解析

确定抗生素的来源对于评估其危害和制定治理策略至关重要。早期研究通过分析抗生素的用途,使用相关性分析法以及主成分分析法(PCA)进行定性源解析^[4,61-62]。随着研究的不断进展,对来源的分析要求逐渐提高,除定性外,定量也受到越来越多的关注。正矩阵因式分解(PMF)受体模型、Unmix和化学质量平衡(CMB)模型是比较常用的定量模型^[63]。CMB法有对原配置文件的需求^[64],Unmix模型需依赖大量的样本分析来揭示来源信息^[65]。相比之下,正矩阵因式分解受体模型在计算过程中要求考虑源贡献结果的非负性与变量的不确定性,使其结果可信度更高^[4,66]。此外,PMF可以对每种污染源类型的贡献进行定量^[67-69],因此获得了广泛的应用^[70]。

PMF模型早期主要用于大气污染的源解析^[71-72]。近年来,PMF模型在污染物来源解析研究中得到了广泛应用^[73]。Yu等使用PMF2和PMF3模型对长江口多环芳烃的时空分布进行了分析^[4,74]。Men等使用PMF2、PMF3模型分析了北京市污染物的来源解析问题^[75],近年来,PMF模型已广泛应用于流域抗生素来源解析研究中,Wang等人通过PMF分析了汾河中抗生素的污染来源,结果表明汾河的抗生素污染主要有6个来源,其中制药废水贡献最大(30%),其次是牲畜排放(22%),并且不同来源的耐药风险差异显著^[76]。

1.1.3 抗生素的风险评估

随着抗生素残留造成的危害越来越大^[77],如何评估抗生素带来的风险显得尤为重要。生态风险评估是一种对有毒污染物可能造成的生态危害进行量化和评估的关键技术,其中,熵值法(RQs)在研究中被广泛应用,该方法常用于评估单一化学物质的毒理效应^[78]。在评价抗生素的生态风险时,也常使用风险熵值法^[79],根据RQs的不同值来划分风险等级:RQs<0.1表示低风险,0.1—1.0表示中风险,

而 $RQs > 1.0$ 则表示高风险。不同季节的抗生素生态风险差距悬殊,寒冷季节的风险较高^[7,52,62]。目前,研究主要聚焦于抗生素对水生生物的毒性效应,不同种类的抗生素与不同生物之间的毒性差异显著^[10,81-82]。

预测无效应浓度(PNEC)是地表水生态安全风险评估的阈值^[22,83],PNEC 值与风险水平直接相关^[84-86],目前有多种方法用于计算推导 PNEC 值,如物种敏感性分布(SSD)法^[87]和评估因子(AF)法^[88]。AF 法是一种常用的手段,它根据对低等水生生物的毒性数据进行计算^[89-90],可能导致其评价结果有其缺陷。SSD 法近年来广泛应用于计算基准值,该方法通过整合多种物种在相同污染物暴露条件下的毒性数据,运用物种敏感度分布曲线对污染物在特定浓度下对生物的危害比例进行估算^[14,23],尽管在抗生素的应用上还相对较少,但它提供了一种更为全面的风险评估方法。

1.2 水环境中的抗性基因

抗生素的输入和残留会对水体中的微生物施加选择性压力^[91],从而加速抗生素耐药菌和 ARGs 的增殖、传播和积累^[24,92]。本综述针对水环境中抗性基因的文献量展开了统计工作。经检索,总共获取到 8 549 篇相关文献。其中,河流中的 ARGs 研究文献量最多,达到 2 650 篇,地表水、地下水、湖泊、海洋、悬浮物以及沉积物中的抗性基因文献量分别为 2 547、23、944、731、42 和 1 612 篇。相较于抗生素相关文献,抗性基因的文献量有所减少,仅为抗生素文献量的 23%。

在这些文献中,最早发表的关于水环境中 ARGs 的研究是 1984 年针对地表水与河流中的 ARGs 开展的研究。而关于悬浮物中抗性基因的文献发表时间较晚,数量也最少,于 2009 年才得以发表。由此可见,学者们较早将关注点放在地表水与河流中的 ARGs 上,对悬浮物中 ARGs 的研究起步相对较晚。

本综述还对 2000 年以来的抗性基因相关文献量进行了统计与研究(图 2)。从图中能够看出,自 2000 年起,人们对流域中抗性基因的关注先是上升后趋于下降。2000 年至 2008 年期间,人们针对流域中 ARGs 的研究相对匮乏。自 2009 年起,有关流域中 ARGs 的文献量显著上升,这一趋势十分明显。整体而言,其趋抗生素的趋势相似,但 ARGs 研究在 2022 年达到最多的 1 156 篇文献的高峰后,文献量开始出现下降。

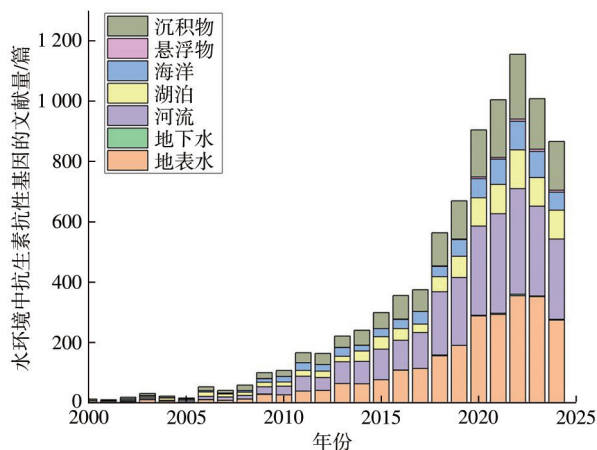


图 2 2000 年至 2024 年水环境中抗生素抗性基因的文献量/篇

Figure 2 The number of literatures on ARGs in the water environment from 2000 to 2024

1.2.1 抗性基因的检测

环境中 ARGs 的检测对于研究其在环境中的分布与传播模式至关重要。目前,环境介质中 ARGs 的研究方法主要分为两类。

第一类检测方法主要包含两种技术路径^[25]:其一是基于传统微生物培养的生物抑制法,其二是运用分子生物学原理的现代检测技术^[93]。传统细菌培养法通过选择合适的培养基对环境介质中的细菌进行培养和分离,利用抗生素药敏试验获得 ARB,并通过平板计数法计算其数量,以分析样本微生物群落中 ARB 的丰度及分布特征^[94]。尽管传统培养法在细菌耐药性研究中发挥了重要作用,但由于操作复杂、通量低且可培养细菌数量极少,可能导致对环境 ARB 总量的判断产生误差,从而影响对其抗性水平的评估^[95]。

第二类研究方法主要依托分子生物学技术,涵盖了多种检测手段,如 PCR 及其衍生技术^[96-97],包括 qPCR 和 HT-qPCR 等^[98-99],此外还涉及宏基因组学分析^[100]等。这些分子生物学技术因不需要进行细菌培养,操作简便且准确性高,被广泛用于 ARGs 的研究中。PCR 与其衍生技术虽能揭示水环境中部分抗生素抗性基因及可培养微生物群落的信息,但其检测范围有限,难以全面反映 ARGs 和微生物群落的整体特征^[95,101]。宏基因组学可以直接进行提取并克隆微生物群落的 DNA,实现了对基因组的全面分析^[102],并且克服了引物可用性有限、扩增过程中的偏差及环境样品中酶抑制剂导致的假阴性结果等问题^[101],提供环境介质中 ARGs 的全面特征。

1.2.2 抗性基因的抗性机制与传播机制

细菌对抗生素的耐药性机制主要分为两类:固有抗性和获得性抗性。固有抗性是指细菌因自身结构或功能特性对特定抗生素产生的抗性能力^[103]。获得性抗性是指细菌还可以通过染色体基因突变和水平基因转移获得的抗性能力^[104]。其抗性机制主要包括以下四类^[105-106]。

(1)外排泵:通过外排泵将抗生素排出细胞^[107]。

(2)灭活:通过酶促反应水解或修饰抗生素结构,使其失去活性^[108]。

(3)修饰靶点:通过改变药物靶点,使抗生素无法结合。

(4)改变细胞膜通透性:下调膜孔蛋白表达,降低外膜通透性,阻止亲水性抗生素进入细胞^[109]。

ARGs的传播途径主要包括垂直基因转移(VGT)和水平基因转移(HGT)^[26,110-113]。VGT通过细胞分裂将基因从亲代传递至子代^[110],HGT通过可移动基因元件(如质粒、整合子和转座子)实现基因在不同微生物间的传播^[27,111],主要途径包括接合、转导和转化^[28,114-115]。这一过程促进了ARGs在多种微生物间的交换,甚至传播至致病菌^[116-120],导致抗性基因在环境中的广泛扩散。

1.3 环境因子与抗生素及抗性基因的关系

研究表明,微生物群落、抗生素的残留以及温度、酸碱度、溶解氧、碳、氮、磷等环境因子抗生素都会影响ARGs在环境中的生长生存和传播^[29,117]。抗生素的过量生产和使用形成了选择性压力,这是促使ARGs发生水平基因转移的关键因素^[121-123]。环境因子可能通过改变ARB群落结构,进而影响ARGs的传播。此外,选择性压力的增强加速了细菌获取ARGs的过程,从而进一步推动了ARGs的扩散^[99,117,124-125]。

2 黄河流域研究现状与展望

2.1 研究现状

黄河流域抗生素浓度总体呈现出显著的空间差异。在人口密集、经济发达的城市河段,抗生素种类和浓度均较高^[126-127]。而在上游人口稀少、工农业活动较少的区域,抗生素浓度则相对较低^[138]。这种空间分布特征与抗生素抗性基因的分布模式密切相关^[127-128]。这种空间分布特征与抗生素抗性基因的分布模式密切相关^[127,129-130]。为高抗生素使用量为微生物产生和传播抗性基因提供了更多机会^[131-132]。

此外,抗生素浓度还表现出季节性变化^[133]。雨

季时,地表径流将土壤和污水中的抗生素带入黄河,导致水体中抗生素浓度上升^[134]。旱季则因河流流量减少,抗生素稀释作用减弱,浓度可能维持或小幅度升高,抗生素ARGs的丰度也会随之波动^[135]。夏季温度升高,微生物代谢活动增强,可能增加基因水平转移的频率,从而提升ARGs丰度^[136-138]。寒冷季节微生物活动减缓,抗性基因丰度则相对较低^[131]。

2.2 展望

黄河流域作为中国的主要河流之一,对抗生素和抗性基因的流域性污染防控具有重要意义,可以通过以下几个方面的研究,从而加强黄河流域抗生素的管控。

(1)深入研究抗性机制:需要进一步深入研究黄河流域耐药性产生的分子机制。例如,探究不同种类抗生素在黄河流域特定微生物中的作用靶点,以及微生物如何通过基因调控来产生抗性。这有助于更精准地预测抗性基因的产生和传播,为抗生素与抗性基因的管控提供理论依据。

(2)多介质环境研究:加强对黄河流域抗生素和抗性基因在多介质环境中的交互作用研究。目前的研究多集中在单一介质,而实际上它们在不同介质之间存在复杂的交换和转化关系。例如,研究抗生素在水体和土壤之间的迁移转化过程中,抗性基因的传播规律以及对不同介质中生物群落的影响。

(3)长期生态风险评估:开展黄河流域抗生素和抗性基因的长期生态风险评估。由于它们对生态系统的影响是一个周期比较长的过程,需要建立长期监测体系,评估其对生态系统的影响。

参考文献:

- [1] LUO Y, XU L, RYSZ M, *et al.* Occurrence and Transport of Tetracycline, Sulfonamide, Quinolone, and Macrolide Antibiotics in the Haihe River Basin, China[J]. *Environmental Science & Technology*, 2011, 45(5): 1827-1833.DOI:10.1021/es104009s.
- [2] LIU X, LU S, GUO W, *et al.* Antibiotics in the aquatic environments: A review of lakes, China[J]. *Science of the Total Environment*, 2018, 627: 1195-1208. DOI:10.1016/j.scitotenv.2018.01.271.
- [3] 赵英姿,徐振,颜冬云,等.大环内酯类抗生素在土壤中的迁移转化与毒性效应分析[J].土壤,2014,46(01): 23-28.DOI:10.13758/j.cnki.tr.2014.01.004
- [4] WU M, QUE C, TANG L, *et al.* Distribution, fate, and risk assessment of antibiotics in five wastewater treatment plantss in Shanghai, China[J]. *Environmen-*

- tal Science and Pollution Research*, 2016, 23 (18): 18055-18063. DOI: 10.1007/s11356-016-6946-0.
- [5] LIU Y, CAI D, LI X, *et al.* Occurrence, fate, and risk assessment of antibiotics in typical pharmaceutical manufacturing and receiving water bodies from different regions[J]. *Plos One*, 2023, 18(1): e0270945. DOI: 10.1371/journal.pone.0270945.
- [6] ZHANG G, LIU X, LU S, *et al.* Occurrence of typical antibiotics in Nansi Lake's inflowing rivers and antibiotic source contribution to Nansi Lake based on principal component analysis-multiple linear regression model [J]. *Chemosphere*, 2020, 242: 125269. DOI: 10.1016/j.chemosphere.2019.125269.
- [7] CHEN H, JING L, TENG Y, *et al.* Characterization of antibiotics in a large-scale river system of China: Occurrence pattern, spatiotemporal distribution and environmental risks[J]. *Science of the Total Environment*, 2018, 618: 409-418. DOI: 10.1016/j.scitotenv.2017.11.054.
- [8] GROSSMAN Z, DEL TORO S, HADJIPANAYIS A, *et al.* Antibiotic prescribing for upper respiratory infections: European primary paediatricians' knowledge, attitudes and practice[J]. *Acta Paediatrica*, 2012, 101(9): 935-940. DOI: 10.1111/j.1651-2227.2012.02754.x.
- [9] LIANG X, CHEN B, NIE X, *et al.* The distribution and partitioning of common antibiotics in water and sediment of the Pearl River Estuary, South China[J]. *Chemosphere*, 2013, 92(11): 1410-1416. DOI: 10.1016/j.chemosphere.2013.03.044.
- [10] DONG D, ZHANG L, LIU S, *et al.* Antibiotics in water and sediments from Liao River in Jilin Province, China: occurrence, distribution, and risk assessment[J]. *Environmental Earth Sciences*, 2016, 75(16): 1202. DOI: 10.1007/s12665-016-6008-4.
- [11] 张焱, 王静. 水环境抗生素残留及其生态与健康影响[J]. *湖北医药学院学报*, 2019, 38(06): 609-614. DOI: 10.13819/j.issn.2096-708X.2019.06.023.
- [12] REDDY B, DUBEY S K. River Ganges water as reservoir of microbes with antibiotic and metal ion resistance genes: High throughput metagenomic approach [J]. *Environmental Pollution*, 2019, 246: 443-451. DOI: 10.1016/j.envpol.2018.12.022.
- [13] BIALK-BIELINSKA A, STOLTE S, ARNING J, *et al.* Ecotoxicity evaluation of selected sulfonamides[J]. *Chemosphere*, 2011, 85(6): 928-933. DOI: 10.1016/j.chemosphere.2011.06.058.
- [14] 王林芳. 汾河流域典型抗生素污染特征及归趋研究[D]. 太原: 山西大学, 2021.
- [15] SIEDLEWICZ G, BIALK-BIELINSKA A, BORECKA M, *et al.* Presence, concentrations and risk assessment of selected antibiotic residues in sediments and near-bottom waters collected from the Polish coastal zone in the southern Baltic Sea - Summary of 3 years of studies [J]. *Marine Pollution Bulletin*, 2018, 129(2): 787-801. DOI: 10.1016/j.marpolbul.2017.10.075.
- [16] ZAINAB S M, JUNAID M, XU N, *et al.* Antibiotics and antibiotic resistant genes (ARGs) in groundwater: A global review on dissemination, sources, interactions, environmental and human health risks[J]. *Water Res*, 2020, 187: 116455. DOI: 10.1016/j.watres.2020.116455.
- [17] KOLPIN D W, FURLONG E T, MEYER M T, *et al.* Pharmaceuticals, hormones, and other organic wastewater contaminants in U.S. streams, 1999—2000: a national reconnaissance [J]. *Environmental science & technology*, 2002, 36(6): 1202-1211.
- [18] LINDSEY M E, MEYER T M, THURMAN E M. Analysis of trace levels of sulfonamide and tetracycline antimicrobials in groundwater and surface water using solid-phase extraction and liquid chromatography/mass spectrometry [J]. *Analytical chemistry*, 2001, 73(19): 4640-4646. DOI: 10.1021/ac010514w.
- [19] CASTIGLIONI S, FANELLI R, CALAMARI D, *et al.* Methodological approaches for studying pharmaceuticals in the environment by comparing predicted and measured concentrations in River Po, Italy [J]. *Regulatory toxicology and pharmacology: RTP*, 2004, 39(1): 25-32. DOI: 10.1016/j.yrtph.2003.10.002.
- [20] NGOC HAN T, LAN H, LONG DUC N, *et al.* Occurrence and risk assessment of multiple classes of antibiotics in urban canals and lakes in Hanoi, Vietnam [J]. *Science of the Total Environment*, 2019, 692: 157-174. DOI: 10.1016/j.scitotenv.2019.07.092.
- [21] FERREIRA DA SILVA B, JELIC A, LOPEZ-SERNA R, *et al.* Occurrence and distribution of pharmaceuticals in surface water, suspended solids and sediments of the Ebro river basin, Spain [J]. *Chemosphere*, 2011, 85(8): 1331-1339. DOI: 10.1016/j.chemosphere.2011.07.051.
- [22] LIU S, LI X, LOU S, *et al.* Occurrence of sulfonamides and tetracyclines in the coastal areas of the Yangtze River (China) Estuary [J]. *Environmental Science and Pollution Research*, 2023, 30(56): 118567-118587. DOI: 10.1007/s11356-023-30698-z.
- [23] ZHANG Y, LI J, WU T, *et al.* Characteristics of antibiotic resistance genes and microbial community dis-

- tribution in Wanfeng Lake, upper Pearl River, China[J]. *Environmental Science and Pollution Research*, 2023, 30 (35): 83214-83230. DOI: 10.1007/s11356-023-28158-9.
- [24] ZHAO J, HOU S, ZHANG H, *et al.* Spatiotemporal variations and priority ranking of emerging contaminants ANT in nanwan reservoir: A case study from the agricultural region in huaihe river basin in China[J]. *Journal of Environmental Management*, 2024, 368: 122195. DOI: 10.1016/j.jenvman.2024.122195.
- [25] YIN Z. Distribution and ecological risk assessment of typical antibiotics in the surface waters of seven major rivers, China[J]. *Environmental Science-Processes & Impacts*, 2021, 23 (8): 1088-1100. DOI: 10.1039/d1em00079a.
- [26] WANG W, WANG H, ZHANG W, *et al.* Occurrence, distribution, and risk assessment of antibiotics in the Songhua River in China[J]. *Environmental Science and Pollution Research*, 2017, 24(23): 19282-19292. DOI: 10.1007/s11356-017-9471-x.
- [27] LU P, FANG Y, BARVOR J B, *et al.* Review of Antibiotic Pollution in the Seven Watersheds in China[J]. *Polish Journal of Environmental Studies*, 2019, 28(6): 4045-4055. DOI: 10.15244/pjoes/99061.
- [28] MICHAEL I, RIZZO L, MCARDELL C S, *et al.* Urban wastewater treatment plants as hotspots for the release of antibiotics in the environment: A review[J]. *Water Research*, 2013, 47(3): 957-995. DOI: 10.1016/j.watres.2012.11.027.
- [29] NNADOZIE C F, ODUME O N. Freshwater environments as reservoirs of antibiotic resistant bacteria and their role in the dissemination of antibiotic resistance genes[J]. *Environmental Pollution*, 2019, 254 (PB): 113067. DOI: 10.1016/j.envpol.2019.113067.
- [30] SENDRA M, MORENO-GARRIDO I, BLASCO J, *et al.* Effect of erythromycin and modulating effect of CeO₂ NPs on the toxicity exerted by the antibiotic on the microalgae *Chlamydomonas reinhardtii* and *Phaeodactylum tricomutum* [J]. *Environmental Pollution*, 2018, 242 (PA): 357-366. DOI: 10.1016/j.envpol.2018.07.009.
- [31] WANG Z, CHEN Q, ZHANG J, *et al.* Long-term exposure to antibiotic mixtures favors microcystin synthesis and release in *Microcystis aeruginosa* with different morphologies[J]. *Chemosphere*, 2019, 235: 344-353. DOI: 10.1016/j.chemosphere.2019.06.192.
- [32] SEOANE M, RIOBOO C, HERRERO C, *et al.* Toxicity induced by three antibiotics commonly used in aquaculture on the marine microalga *Tetraselmis suecica* (Kylin) Butch [J]. *Marine Environmental Research*, 2014, 101: 1-7. DOI: 10.1016/j.marenvres.2014.07.011.
- [33] LEE S, KIM C, LIU X, *et al.* Ecological Risk Assessment of Amoxicillin, Enrofloxacin, and Neomycin: Are Their Current Levels in the Freshwater Environment Safe? [J]. *Toxics*, 2021, 9 (8): 196. DOI: 10.3390/toxics9080196.
- [34] ISIDORI M, LAVORGNA M, NARDELLI A, *et al.* Toxic and genotoxic evaluation of six antibiotics on non-target organisms[J]. *The Science of the total environment*, 2005, 346(1-3): 87-98. DOI: 10.1016/j.scitotenv.2004.11.017.
- [35] FERREIRA C S G, NUNES B A, HENRIQUES-ALMEIDA J M D M, *et al.* Acute toxicity of oxytetracycline and florfenicol to the microalgae *Tetraselmis chuii* and to the crustacean *Artemia parthenogenetica* [J]. *Ecotoxicology and environmental safety*, 2007, 67(3): 452-458. DOI: 10.1016/j.ecoenv.2006.10.006.
- [36] YANG C, SONG G, LIM W. A review of the toxicity in fish exposed to antibiotics[J]. *Comparative Biochemistry and Physiology C-Toxicology & Pharmacology*, 2020, 237: 108840. DOI: 10.1016/j.cbpc.2020.108840.
- [37] XU Y, LUO L, CHEN J. Sulfamethoxazole induces brain capillaries toxicity in zebrafish by up-regulation of VEGF and chemokine signalling[J]. *Ecotoxicology and Environmental Safety*, 2022, 238: 113620. DOI: 10.1016/j.ecoenv.2022.113620.
- [38] HUANG H, LIU Z, YANG H, *et al.* Acute and Chronic Toxic Effects of Chloramphenicol, Erythromycin and Tetracycline on the Early Life Stage of Amphibian (*Xenopus tropicalis*) [J]. *Asian Journal of Chemistry*, 2013, 25 (18): 10293-10295. DOI: 10.14233/ajchem.2013.15283.
- [39] BAUMANN M, WEISS K, MALETZKI D, *et al.* Aquatic toxicity of the macrolide antibiotic clarithromycin and its metabolites[J]. *Chemosphere*, 2015, 120: 192-198. DOI: 10.1016/j.chemosphere.2014.05.089.
- [40] GUO X, SONG R, LU S, *et al.* Multi-Media Occurrence of Antibiotics and Antibiotic Resistance Genes in East Dongting Lake [J]. *Frontiers in Environmental Science*, 2022, 10: 866332. DOI: 10.3389/fenvs.2022.866332.
- [41] SINGH R, SINGH A P, KUMAR S, *et al.* Antibiotic resistance in major rivers in the world: A systematic review on occurrence, emergence, and manage-

- ment strategies [J]. *Journal of Cleaner Production*, 2019, 234: 1484-1505. DOI: 10.1016/j.jclepro.2019.06.243.
- [42] 闫先收. 小清河流域典型抗生素分布、来源及风险评价[D]. 济南: 山东师范大学, 2018.
- [43] 徐晖. 上海地区水体中抗生素类药物的检测及其环境行为研究[D]. 上海: 上海大学, 2015.
- [44] DUJUAN Z, LIUSISI X, WANGYAN C. Antibiotics in the coastal water of the South Yellow Sea in China: Occurrence, distribution and ecological risks [J]. *Science of the Total Environment*, 2017, 595: 521-527. DOI: 10.1016/j.scitotenv.2017.03.281.
- [45] BAI Y, MENG W, XU J, *et al.* Occurrence, distribution and bioaccumulation of antibiotics in the Liao River Basin in China [J]. *Environmental Science-Processes & Impacts*, 2014, 16 (3): 586-593. DOI: 10.1039/c3em00567d.
- [46] HU Y, YAN X, SHEN Y, *et al.* Antibiotics in surface water and sediments from Hanjiang River, Central China: Occurrence, behavior and risk assessment [J]. *Ecotoxicology and Environmental Safety*, 2018, 157: 150-158. DOI: 10.1016/j.ecoenv.2018.03.083.
- [47] XU J, ZHANG Y, ZHOU C, *et al.* Distribution, sources and composition of antibiotics in sediment, overlying water and pore water from Taihu Lake, China [J]. *Science of the Total Environment*, 2014, 497: 267-273. DOI: 10.1016/j.scitotenv.2014.07.114.
- [48] ZHOU L J, LI J, ZHANG Y, *et al.* Trends in the occurrence and risk assessment of antibiotics in shallow lakes in the lower-middle reaches of the Yangtze River basin, China [J]. *Ecotoxicology and Environmental Safety*, 2019, 183: 109511. DOI: 10.1016/j.ecoenv.2019.109511.
- [49] ZHOU J L, FILEMAN T W, EVANS S, *et al.* The partition of fluoranthene and pyrene between suspended particles and dissolved phase in the Humber Estuary: a study of the controlling factors [J]. *Science of the Total Environment*, 1999, 243: 305-321. DOI: 10.1016/S0048-9697(99)00404-0.
- [50] MASKAOUI K, ZHOU J L. Colloids as a sink for certain pharmaceuticals in the aquatic environment [J]. *Environmental Science and Pollution Research*, 2010, 17(4): 898-907. DOI: 10.1007/s11356-009-0279-1.
- [51] KIM S C, CARLSON K. Temporal and spatial trends in the occurrence of human and veterinary antibiotics in aqueous and river sediment matrices [J]. *Environmental Science & Technology*, 2007, 41(1): 50-57. DOI: 10.1021/es060737+.
- [52] CHEN K, ZHOU J L. Occurrence and behavior of antibiotics in water and sediments from the Huangpu River, Shanghai, China [J]. *Chemosphere*, 2014, 95: 604-612. DOI: 10.1016/j.chemosphere.2013.09.119.
- [53] ZHAO S, LIU X, CHENG D, *et al.* Temporal-spatial variation and partitioning prediction of antibiotics in surface water and sediments from the intertidal zones of the Yellow River Delta, China [J]. *Science of the Total Environment*, 2016, 569: 1350-1358. DOI: 10.1016/j.scitotenv.2016.06.216.
- [54] YANG J F, YING G G, ZHAO J L, *et al.* Simultaneous determination of four classes of antibiotics in sediments of the Pearl Rivers using RRLC-MS/MS [J]. *Science of the Total Environment*, 2010, 408 (16): 3424-3432. DOI: 10.1016/j.scitotenv.2010.03.049.
- [55] ZHOU L J, YING G G, ZHAO J L, *et al.* Trends in the occurrence of human and veterinary antibiotics in the sediments of the Yellow River, Hai River and Liao River in northern China [J]. *Environmental Pollution*, 2011, 159(7): 1877-1885. DOI: 10.1016/j.envpol.2011.03.034.
- [56] CHEN L, LI H, LIU Y, *et al.* Distribution, residue level, sources, and phase partition of antibiotics in surface sediments from the inland river: a case study of the Xiangjiang River, south-central China [J]. *Environmental Science and Pollution Research*, 2020, 27(2): 2273-2286. DOI: 10.1007/s11356-019-06833-0.
- [57] ADAMEK E, BARAN W, SOBCZAK A. Assessment of the biodegradability of selected sulfa drugs in two polluted rivers in Poland: Effects of seasonal variations, accidental contamination, turbidity and salinity [J]. *Journal of Hazardous Materials*, 2016, 313: 147-158. DOI: 10.1016/j.jhazmat.2016.03.064.
- [58] LIAO X, ZOU R, LI B, *et al.* Biodegradation of chlortetracycline by acclimated microbiota [J]. *Process Safety and Environmental Protection*, 2017, 109: 11-17. DOI: 10.1016/j.psep.2017.03.015.
- [59] LU J, WU J, ZHANG C, *et al.* Occurrence, distribution, and ecological-health risks of selected antibiotics in coastal waters along the coastline of China [J]. *Science of the Total Environment*, 2018, 644: 1469-1476. DOI: 10.1016/j.scitotenv.2018.07.096.
- [60] 全浩玉, 朱恺彧, 兰宇宇, 等. 黄河三角洲湿地表层沉积物中典型抗生素的分布特征和生态风险评估 [J]. *海洋与湖沼*, 2023, 54(04): 1028-1038. DOI: 10.11693/hyh20221200333.
- [61] LIU K, YIN X, ZHANG D, *et al.* Distribution, sources, and ecological risk assessment of quinotone

- antibiotics in the surface sediments from Jiaozhou Bay wetland, China[J]. *Marine Pollution Bulletin*, 2018, 129(2): 859-865. DOI: 10.1016/j.marpolbul.2017.10.010.
- [62] LIN H, CHEN L, LI H, *et al.* Pharmaceutically active compounds in the Xiangjiang River, China: Distribution pattern, source apportionment, and risk assessment[J]. *Science of the Total Environment*, 2018, 636: 975-984. DOI: 10.1016/j.scitotenv.2018.04.267.
- [63] 曹胜男, 杨中智. 大气颗粒物源解析技术研究进展[J]. 新乡医学院学报, 2016, 33(11): 1007-1010. DOI: 10.7683/xyxyxb.2016.11.019.
- [64] KE L, LIU W, WANG Y, *et al.* Comparison of PM_{2.5} source apportionment using positive matrix factorization and molecular marker-based chemical mass balance[J]. *Science of the Total Environment*, 2008, 394(2-3): 290-302. DOI: 10.1016/j.scitotenv.2008.01.030.
- [65] HENRY R C. Duality in multivariate receptor models[J]. *Chemometrics and Intelligent Laboratory Systems*, 2005, 77(1-2): 59-63. DOI: 10.1016/j.chemolab.2005.04.001.
- [66] HUSTON R, CHAN Y C, CHAPMAN H, *et al.* Source apportionment of heavy metals and ionic contaminants in rainwater tanks in a subtropical urban area in Australia[J]. *Water Research*, 2012, 46(4): 1121-1132. DOI: 10.1016/j.watres.2011.12.008.
- [67] FRIE A L, DINGLE J H, YING S C, *et al.* The Effect of a Receding Saline Lake (The Salton Sea) on Airborne Particulate Matter Composition[J]. *Environmental Science & Technology*, 2017, 51(15): 8283-8292. DOI: 10.1021/acs.est.7b01773.
- [68] MEN C, LIU R, XU L, *et al.* Source-specific ecological risk analysis and critical source identification of heavy metals in road dust in Beijing, China[J]. *Journal of Hazardous Materials*, 2020, 388: 121763. DOI: 10.1016/j.jhazmat.2019.121763.
- [69] PAATERO P, TAPPER U. Positive matrix factorization: A non-negative factor model with optimal utilization of error estimates of data values[J]. *Environmetrics*, 1994, 5(2): 111-126. DOI: 10.1002/env.3170050203.
- [70] WANG X, ZONG Z, TIAN C, *et al.* Combining Positive Matrix Factorization and Radiocarbon Measurements for Source Apportionment of PM_{2.5} from a National Background Site in North China[J]. *Scientific Reports*, 2017, 7(1): 1-10. DOI: 10.1038/s41598-017-10762-8.
- [71] LEE E, CHAN C K, PAATERO P. Application of positive matrix factorization in source apportionment of particulate pollutants in Hong Kong[J]. *Atmos Environ*, 1999, 33(19): 3201-3212. DOI: 10.1016/S1352-2310(99)00113-2.
- [72] LARSEN R K, BAKER J E. Source apportionment of polycyclic aromatic hydrocarbons in the urban atmosphere: A comparison of three methods[J]. *Environ Sci Technol*, 2003, 37(9): 1873-1881. DOI: 10.1021/es0206184.
- [73] 徐浩, 杨龙誉. 受体模型及其在大气颗粒物来源解析中的应用[J]. 四川环境, 2015, 34(01): 138-145. DOI: 10.14034/j.cnki.schj.2015.01.026.
- [74] YU W, LIU R, WANG J, *et al.* Source apportionment of PAHs in surface sediments using positive matrix factorization combined with GIS for the estuarine area of the Yangtze River, China[J]. *Chemosphere*, 2015, 134: 263-271. DOI: 10.1016/j.chemosphere.2015.04.049.
- [75] MEN C, LIU R, XU L, *et al.* Source-specific ecological risk analysis and critical source identification of heavy metals in road dust in Beijing, China[J]. *Journal of Hazardous Materials*, 2020, 388: 121763. DOI: 10.1016/j.jhazmat.2019.121763.
- [76] WANG Y F, WANG L F, LIU R M, *et al.* Source-specific risk apportionment and critical risk source identification of antibiotic resistance in Fenhe River basin, China[J]. *Chemosphere*, 2022, 287(P1): 131997. DOI: 10.1016/j.chemosphere.2021.131997.
- [77] 王琦. 鸡源粪肠球菌噬菌体分离及生物学特性研究[D]. 邯郸: 河北工程大学, 2022.
- [78] 雷炳莉, 黄圣彪, 王子健. 生态风险评估理论和方法[J]. 化学进展, 2009, 21(2): 350-358.
- [79] SANDERSON H, BRAIN R A, JOHNSON D J, *et al.* Toxicity classification and evaluation of four pharmaceuticals classes: antibiotics, antineoplastics, cardiovascular, and sex hormones[J]. *Toxicology*, 2004, 203(1-3): 27-40. DOI: 10.1016/j.tox.2004.05.015.
- [80] 黄鹏宇. 水中抗生素高通量快速检测技术研究及应用[D]. 武汉: 武汉科技大学, 2019.
- [81] 吴志刚. 水体中典型喹诺酮类抗生素生态毒性效应研究[D]. 石家庄: 河北科技大学, 2014.
- [82] 李霞, 陈菊芳, 吕颂辉, 等. 苯丙醇类抗生素对蛋白核小球藻生长的影响[J]. 暨南大学学报(自然科学与医学版), 2012, 33(03): 294-299. DOI: 10.3969/j.issn.1000-9965.2012.03.016.
- [83] 李霁, 周俊丽, 曹莹, 等. 荧蒽的淡水沉积物预测无效应浓度推导及生态风险评估[J]. 环境化学, 2015, 34(04): 664-670. DOI: 10.7524/j.issn.0254-6108.

- 2015.04.2014090701.
- [84] CHEN H, LIU S, XU X R, *et al.* Antibiotics in the coastal environment of the Hailing Bay region, South China Sea: Spatial distribution, source analysis and ecological risks[J]. *Marine Pollution Bulletin*, 2015, 95(1): 365-373.DOI:10.1016/j.marpolbul.2015.04.025.
- [85] DYER S D, VERSTEEG D J, BELANGER S E, *et al.* Comparison of species sensitivity distributions derived from interspecies correlation models to distributions used to derive water quality criteria[J]. *Environmental Science & Technology*, 2008, 42(8): 3076-3083.DOI:10.1021/es702302e.
- [86] MONTI G S, FILZMOSER P, DEUTSCH R C. A Robust Approach to Risk Assessment Based on Species Sensitivity Distributions[J]. *Risk Analysis*, 2018, 38(10): 2073-2086.DOI:10.1111/risa.13009.
- [87] STAPLES C A, WOODBURN K B, KLECKA G M, *et al.* Comparison of four species sensitivity distribution methods to calculate predicted no effect concentrations for bisphenol A[J]. *Human and Ecological Risk Assessment*, 2008, 14(3): 455-478.DOI:10.1080/10807030802074170.
- [88] LEUNG H W, MINH T B, MURPHY M B, *et al.* Distribution, fate and risk assessment of antibiotics in sewage treatment plants in Hong Kong, South China[J]. *Environment International*, 2012, 42(1): 1-9.DOI: 10.1016/j.envint.2011.03.004.
- [89] GOLET E M, ALDER A C, GIGER W. Environmental exposure and risk assessment of fluoroquinolone antibacterial agents in wastewater and river water of the Glatt Valley Watershed, Switzerland[J]. *Environmental Science & Technology*, 2002, 36(17): 3645-3651.DOI:10.1021/es0256212.
- [90] TURKDOGAN F I, YETILMEZSOY K. Appraisal of potential environmental risks associated with human antibiotic consumption in Turkey[J]. *Journal of Hazardous Materials*, 2009, 166(1): 297-308.DOI: 10.1016/j.jhazmat.2008.11.012.
- [91] 董满园. 铜绿假单胞菌群体感应抑制剂的分离与活性评价[D]. 青岛:中国海洋大学,2015.
- [92] PRUDEN A, PEI R T, STORTEBOOM H, *et al.* Antibiotic resistance genes as emerging contaminants: Studies in northern Colorado[J]. *Environmental Science & Technology*, 2006, 40(23): 7445-7450.DOI: 10.1021/es060413l.
- [93] KARKMAN A, THI THUY D, WALSH F, *et al.* Antibiotic-Resistance Genes in Waste Water[J]. *Trends in Microbiology*, 2018, 26(3): 220-228. DOI: 10.1016/j.tim.2017.09.005.
- [94] 谢静. 黄连素对污泥厌氧消化的影响与机理研究[D]. 上海:东华大学,2021.
- [95] 薛凯响, 朱晨朝, 李少华, 等. 水产养殖环境中抗生素抗性基因的检测与消除技术研究进展[J]. 分析仪器, 2024, (05): 1-7.DOI:10.3969/j.issn.1001-232x.2024.05.001.
- [96] PEI R, KIM S C, CARLSON K H, *et al.* Effect of river landscape on the sediment concentrations of antibiotics and corresponding antibiotic resistance genes (ARG) [J]. *Water research*, 2006, 40(12): 2427-2435.DOI:10.1016/j.watres.2006.04.017.
- [97] CHENG W X, CHEN H, SU C, *et al.* Abundance and persistence of antibiotic resistance genes in livestock farms: A comprehensive investigation in eastern China[J]. *Environment International*, 2013, 61: 1-7. DOI:10.1016/j.envint.2013.08.023.
- [98] ZHANG Y P, ZHANG C Q, PARKER D B, *et al.* Occurrence of antimicrobials and antimicrobial resistance genes in beef cattle storage ponds and swine treatment lagoons[J]. *Science of the Total Environment*, 2013, 463: 631-638.DOI: 10.1016/j.scitotenv.2013.06.016.
- [99] GAO P, MUNIR M, XAGORARAKI I. Correlation of tetracycline and sulfonamide antibiotics with corresponding resistance genes and resistant bacteria in a conventional municipal wastewater treatment plant[J]. *Science of the Total Environment*, 2012, 421: 173-183.DOI:10.1016/j.scitotenv.2012.01.061.
- [100] AMOS G C A, ZHANG L, HAWKEY P M, *et al.* Functional metagenomic analysis reveals rivers are a reservoir for diverse antibiotic resistance genes [J]. *Veterinary Microbiology*, 2014, 171(3-4): 441-447. DOI:10.1016/j.vetmic.2014.02.017.
- [101] 孙凌涛, 刘子述, 胡宝兰. 抗生素抗性基因检测方法发展历程及应用现状[J]. 微生物学报, 2024, 64(08): 2591-2609.DOI:10.13343/j.cnki.wsxb.20240111.
- [102] 贺纪正, 袁超磊, 沈菊培, 等. 土壤宏基因组学研究方法与进展[J]. 土壤学报, 2012, 49(01): 155-164.
- [103] 洪守强. 大肠杆菌 O157 的毒力/耐药检测及毒力表观遗传调控研究[D]. 厦门:厦门大学, 2018.
- [104] 刘小波. 食源性大肠杆菌耐药基因的鉴定及传播机制研究[D]. 咸阳:西北农林科技大学, 2018.
- [105] ALONSO A, MORALES G, ESCALANTE R, *et al.* Overexpression of the multidrug efflux pump SmeDEF impairs *Stenotrophomonas maltophilia* physiology [J]. *The Journal of antimicrobial chemotherapy*, 2004, 53(3): 432-434.DOI:10.1093/jac/dkh074.

- [106] 张红, 程寒飞. 水环境中氨基糖苷类抗性基因污染及研究进展[J]. 环境科学与技术, 2018, 41(10): 121-130. DOI:10.19672/j.cnki.1003-6504.2018.10.018.
- [107] 于浩森. 金黄色葡萄球菌噬菌体 Sau-p573 的分离鉴定及裂解酶 LysZB48 的重组表达与功能探究[D]. 泰安: 山东农业大学, 2022.
- [108] 伍宸旋. 潘他米丁敏化 FDA 非抗生素抑制多药耐药革兰氏阴性菌的研究[D]. 长沙: 湖南大学, 2020.
- [109] 李显志, 王浴生. 细菌包膜通透性的分子基础与细菌耐药[J]. 国外医药(抗生素分册), 1989, 10(04): 282-287+296. DOI:10.13461/j.cnki.wna.002056.
- [110] ANSARI M I, GROHMANN E, MALIK A. Conjugative plasmids in multi-resistant bacterial isolates from Indian soil[J]. *Journal of applied microbiology*, 2008, 104(6): 1774-1781. DOI:10.1111/j.1365-2672.2008.03736.x.
- [111] SORENSEN S J, BAILEY M, HANSEN L H, *et al.* Studying plasmid horizontal transfer in situ: a critical review[J]. *Nature reviews Microbiology*, 2005, 3(9): 700-710. DOI:10.1038/nrmicro1232.
- [112] 朱永官, 陈青林, 苏建强, 等. 环境中抗生素与抗性基因组的研究[J]. 科学观察, 2017, 12(6): 60-62. DOI:10.15978/j.cnki.1673-5668.201706007.
- [113] YGZA B, YI Z C, DONG Z, *et al.* Soil biota, antimicrobial resistance and planetary health[J]. *Environment International*, 2019, 131: 105059. DOI:10.1016/j.envint.2019.105059.
- [114] ABE K, NOMURA N, SUZUKI S. Biofilms: hot spots of horizontal gene transfer (HGT) in aquatic environments, with a focus on a new HGT mechanism[J]. *Fems Microbiology Ecology*, 2020, 96(5): f1aa031. DOI:10.1093/femsec/f1aa031.
- [115] WOODS L C, GORRELL R J, TAYLOR F, *et al.* Horizontal gene transfer potentiates adaptation by reducing selective constraints on the spread of genetic variation[J]. *Proceedings of the National Academy of Sciences of the United States of America*, 2020, 117(43): 26868-26875. DOI:10.1073/pnas.2005331117.
- [116] LIN Z, YUAN T, ZHOU L, *et al.* Impact factors of the accumulation, migration and spread of antibiotic resistance in the environment[J]. *Environmental Geochemistry and Health*, 2021, 43(5): 1741-1758. DOI:10.1007/s10653-020-00759-0.
- [117] ZHANG B A, QIN S, GUAN X Y, *et al.* Distribution of Antibiotic Resistance Genes in Karst River and Its Ecological Risk[J]. *Water Research*, 2021, 203: 117507. DOI:10.1016/j.watres.2021.117507.
- [118] PFEIFER E, ROCHA E P C. Phage-plasmids promote recombination and emergence of phages and plasmids[J]. *Nature Communications*, 2024, 15(1): 1545. DOI:10.1038/s41467-024-45757-3.
- [119] PIA-ITURBE A, SUAZO I D, HOPPE-ELSHOLZ G, *et al.* Horizontally Acquired Homologs of Xenogeneic Silencers: Modulators of Gene Expression Encoded by Plasmids, Phages and Genomic Islands[J]. *Genes*, 2020, 11(2): 142. DOI:10.3390/genes11020142.
- [120] GYLES C, BOERLIN P. Horizontally Transferred Genetic Elements and Their Role in Pathogenesis of Bacterial Disease[J]. *Veterinary Pathology*, 2014, 51(2): 328-340. DOI:10.1177/0300985813511131.
- [121] ZHAO W, WANG B, YU G. Antibiotic resistance genes in China: occurrence, risk, and correlation among different parameters[J]. *Environmental Science and Pollution Research*, 2018, 25(22): 21467-21482. DOI:10.1007/s11356-018-2507-z.
- [122] LI J, LI L, LI Q, *et al.* Distribution and relationship of antibiotics, heavy metals and resistance genes in the upstream of Hanjiang River Basin in Shiyan, China[J]. *Environmental Geochemistry and Health*, 2023, 45(10): 7115-7130. DOI: 10.1007/s10653-023-01683-9.
- [123] NIU Z G, ZHANG K, ZHANG Y. Occurrence and distribution of antibiotic resistance genes in the coastal area of the Bohai Bay, China[J]. *Marine Pollution Bulletin*, 2016, 107(1): 245-250. DOI: 10.1016/j.marpolbul.2016.03.064.
- [124] XU J, XU Y, WANG H M, *et al.* Occurrence of antibiotics and antibiotic resistance genes in a sewage treatment plant and its effluent-receiving river[J]. *Chemosphere*, 2015, 119: 1379-1385. DOI:10.1016/j.chemosphere.2014.02.040.
- [125] HERRIG I, FLEISCHMANN S, REGNER J, *et al.* Prevalence and seasonal dynamics of *bla*_{CTX-M} antibiotic resistance genes and fecal indicator organisms in the lower Lahn River, Germany[J]. *Plos One*, 2020, 15(4): e0232289. DOI:10.1371/journal.pone.0232289.
- [126] XU W, ZHANG G, ZOU S, *et al.* A Preliminary Investigation on the Occurrence and Distribution of Antibiotics in the Yellow River and its Tributaries, China[J]. *Water Environment Research*, 2009, 81(3): 248-254. DOI:10.2175/106143008X325719.
- [127] SU Z, WANG K, YANG F, *et al.* Antibiotic pollution of the Yellow River in China and its relationship with dissolved organic matter: Distribution and Source identification[J]. *Water Research*, 2023, 235(1): 119867. DOI:10.1016/j.watres.2023.119867.

- [128] 吴天宇. 赤水河流域水体抗生素抗性基因赋存特征及来源解析[D]. 贵阳: 贵州大学, 2022.
- [129] WANG Y, WANG L, LIU R, *et al.* Source-specific risk apportionment and critical risk source identification of antibiotic resistance in Fenhe River basin, China [J]. *Chemosphere*, 2022, 287 (P1): 131997. DOI: 10.1016/j.chemosphere.2021.131997.
- [130] WANG L, WANG Y, LI H, *et al.* Occurrence, source apportionment and source-specific risk assessment of antibiotics in a typical tributary of the Yellow River basin [J]. *Journal of Environmental Management*, 2022, 305: 114382. DOI: 10.1016/j.jenvman.2021.114382.
- [131] ZHANG S, YANG G, ZHANG Y, *et al.* High-throughput profiling of antibiotic resistance genes in the Yellow River of Henan Province, China [J]. *Scientific Reports*, 2024, 14 (1): 1-15. DOI: 10.1038/s41598-024-68699-8.
- [132] 田菲菲. 枣林日本龟蜡蚧种群数量动态变化机理研究[D]. 保定: 河北农业大学, 2004.
- [133] WU T, ZHANG Y, WANG B, *et al.* Antibiotic resistance genes in Chishui River, a tributary of the Yangtze River, China: Occurrence, seasonal variation and its relationships with antibiotics, heavy metals and microbial communities [J]. *Science of the Total Environment*, 2022, 846: 157472. DOI: 10.1016/j.scitotenv.2022.157472.
- [134] ZHANG Y, LIU L, LIU Y, *et al.* Deciphering the natural and anthropogenic drivers on the fate and risk of antibiotics and antibiotic resistance genes (ARGs) in a typical river-estuary system, China [J]. *Journal of Hazardous Materials*, 2024, 480: 136006. DOI: 10.1016/j.jhazmat.2024.136006.
- [135] WANG K, SU Z, REGUYAL F, *et al.* Seasonal occurrence of multiple classes of antibiotics in East China rivers and their association with suspended particulate matter br [J]. *Science of the Total Environment*, 2022, 853: 158579. DOI: 10.1016/j.scitotenv.2022.158579.
- [136] WEI F, XIA H, HUANG K, *et al.* Exogenous mobile genetic elements and their associated integrons drive the enrichment of antibiotic-resistant genes in the river of a valley basin city (Lanzhou, China) [J]. *Environmental Science and Pollution Research*, 2024, 31 (2): 3195-3206. DOI: 10.1007/s11356-023-31269-y.
- [137] GAO F Z, HE L Y, HU L X, *et al.* The variations of antibiotics and antibiotic resistance genes in two subtropical large river basins of south China: Anthropogenic impacts and environmental risks [J]. *Environmental Pollution*, 2022, 312: 119978. DOI: 10.1016/j.envpol.2022.119978.
- [138] LIU S, XU Q, LOU S, *et al.* Spatiotemporal distributions of sulfonamide and tetracycline resistance genes and microbial communities in the coastal areas of the Yangtze River Estuary [J]. *Ecotoxicology and Environmental Safety*, 2023, 259: 115025. DOI: 10.1016/j.ecoenv.2023.115025.



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