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环境介质中的抗生素及其微生物生态效应

俞 慎[1,*],王 敏[1,2],洪有为[1]
(1. 中国科学院城市环境研究所,城市环境与健康重点实验室,厦门 361021; 2. 中国科学院研究生院,北京 100049)

摘要:环境介质中的抗生素因存在浓度较低被称为微量污染物,其对生态系统和人类健康的影响已逐步得到认知。长期以来,抗生素被用于人和畜禽细菌性感染疾病的治疗。然而,随着集约化养殖业的发展,抗生素被添加于饲料中来预防畜禽和鱼虾的养殖疾病。因此,环境介质中抗生素种类和含量随着畜禽和水产养殖业的快速发展逐年增加。综述了环境中抗生素的来源、残留浓度及其环境微生物生态学效应。医用、兽用抗生素和人畜粪便的农用是抗生素进入环境的主要来源,其在不同环境介质中残留浓度不一:地表水含量为 μg/L,土壤含量为 μg/kg,沉积物含量为 μg/kg—mg/kg 之间。抗生素进入土壤、水和沉积物等环境介质,经吸附-解吸、迁移和降解等过程重新分配,其降解方式主要有水解、光解和生物降解。残留抗生素已证实可影响环境介质中微生物的生物量、活性和群落结构,并诱导产生抗性基因,但对生态系统服务及其功能的干扰和影响尚有待进一步研究。

关键词:抗生素;环境介质;微生物效应;微生物群落;抗性基因

Antibiotics in environmental matrices and their effects on microbial ecosystems

YU Shen[1,*], WANG Min[1,2], HONG Youwei[1]

1 *Key Laboratory of Urban Environment and Health, Institute of Urban Environment, Chinese Academy of Sciences, Xiamen* 361021, *China*

2 *Graduate University of Chinese Academy of Sciences, Beijing* 100049, *China*

Abstract: The potential risks of antibiotics in the environment have been increasingly recognized in their influence on ecosystem stability (directly affecting the microbial ecosystem) and human health. Abtibiotics occur at a trace level (micro-pollution) in environmental matrices such as waste water, surface water, groundwater, sediments and soils. Although they were initially used against microbial infections of humans and domestic animals, antibiotics are now widely used as growth promoters in agricultural production (e.g. poultry, livestock, and fish farming). Given the overuse or misuse for non-therapeutic purposes, in particularly with the rapid increase in food animal production, the types and concentrations of antibiotics in environmental matrices have dramatically increased. This review summarizes our knowledge of antibiotic sources and residual concentrations in the environment (water, soil, and sediment) and their adverse effects on microbial communities and functions. Antibiotics are released into the environment after uses in human and veterinary medical treatments and in animal husbandry and fish farming, and via applications of contaminated manures or slurry as fertilizers to agriculture soils. Six groups of massively produced antibiotics have been detected in environmental matrices (especially in urban sediment, water, and sludge), including macrolides, fluoroquinolones, sulfonamides, tetracyclines, penicillins, and others (like trimethoprim). Residual concentrations of antibiotics vary with environmental matrix type: with trace level found in surface water (μg/L), levels at μg/kg in soils, and higher concentrations ranging from μg/kg to mg/kg in sediments. Residual concentrations of antibiotics in sediments depend on type, discharge amount, sediment properties, and other environmental factors. Antibiotics are redistributed in the environment matrices via processes of sorption-desorption, transport, and degradation, etc. Environmental factors, such as clay content, organic matter, and iron oxides in soil and

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* **通讯作者** Corresponding author. E-mail: syu@iue.ac.cn

sediment, and pH, dissolved organic carbon (DOC), and cations, have been found to influence movement of antibiotics in environmental matrices. Degradation processes for environmental residual antibiotics include hydrolysis, photolysis, and biodegradation. Biodegradation is a ubiquitous process for antibiotics degradation in environmental matrices while hydrolysis is the typical process for antibiotics degradation in water. The movement and degradation processes of environmental residual antibiotics are predominantly determined by the type of antibiotic, with multiple processes usually contributing to their redistribution and degradation. Adverse effects of environmental residual antibiotics were revealed, including reducing microbial biomass and activity, altering microbial community structure and diversity (especially functional microbial community, such as nitrifiers and denitrifiers), changing microbially-mediated ecological processes (such as nitrification and denitrification), and inducing antibiotic resistant microbial community in contaminated environments. Antibiotic resistance genes for tetracycline, chloramphenicol, vancomycin, erythromycin, sulfonamides, methicillin, and β-lactams have been well studied in environmental matrices. Antibiotic resistant genes have also been identified in pathogens due to long term overuse or misuse of antibiotics, such as the super bacteria (MRSA), and have led to major public health concerns. Further studies of the disturbances and influences of antibiotics on ecosystem functions and services (including public human health) as well as effects of multiple contaminations of antibiotics with heavy metals and other organic pollutants in environmental matrices are required. The type and chemical structure of antibiotics should be taken into account for understanding their ecosystem disturbances while high-throughput quantitative analytical methods are under development.

Key Words: antibiotics; environmental matrix; microbial response; microbial community; resistant genes

与重金属、化学肥料、农药、多环芳烃和多氯联苯等污染物所引起环境问题的认知相比,抗生素的环境行为和生态效应仅在近年来才受到国内外学者关注。近年来在世界各地发现了多药物抗性超级致病微生物[1-3]。除了用于人类和动物细菌性感染疾病的治疗,抗生素也被作为促长剂和饲料添加剂在集约化畜牧业和养殖业中大量应用。摄入人体和动物体内未被代谢的抗生素经不同途径进入环境,导致水体(水和沉积物)和土壤等环境介质抗生素及其代谢活性产物浓度逐渐提高。进入环境介质的抗生素可引起包括抑制有益微生物的活性,干扰生态系统物质循环和能量流动,影响植物、动物和微生物的生长和健康等相关的环境问题,对生态系统稳定构成潜在性的风险。环境残留抗生素可诱导致病微生物产生抗性基因,而耐药致病菌对人类健康威胁巨大,尤其是具有多药物抗性的超级致病菌(*Staphylococcus aureus*, MRSA)[3]。

1 环境抗生素的来源及残留

1.1 环境抗生素的来源

自然环境介质中的微生物是抗生素的产生者[4]。比如,放线菌类和链霉菌等可产生不同的抗生素,包括β-内酰胺类、链霉素、氨基糖苷类抗生素等[5]。自然环境介质中抗生素产生及其抗生现象属于微生物自然防御机制。但是自然界环境微生物产生的抗生素浓度非常低,而目前环境抗生素残留主要来自工业生产的医用抗生素和兽用抗生素,通过医院污水废物、使用者粪便、畜禽与水产养殖废水废物以及生产企业的工业废水废料排放、垃圾渗滤液污染、粪便农用等多种途径进入环境。

医用抗生素是水体环境中抗生素的主要来源[6]。抗生素类药物在医院的使用较为频繁和集中,病人未完全代谢的抗生素经排泄进入医院污水系统中,医院废水抗生素浓度可达到 μg/L。比如,瑞典某一医院废水中检测出多种抗生素:环丙沙星 3.6—101.0 μg/L,磺胺甲恶唑 0.4—12.8 μg/L,氧氟沙星 0.2—7.6 μg/L,甲氧苄氨嘧啶 0.6—7.6 μg/L,强力霉素 0.6—6.7 μg/L[7]。而医药企业污水废料也是环境抗生素的重要来源,但其类型和浓度尚未有报道。

兽用抗生素是环境介质中抗生素的另一重要来源,主要来自于集约化的畜禽养殖业。以美国为例,按其抗生素类兽药每年用量约 11000t 计算,每年从养殖业流入环境的抗生素就达到 6600—9900t[8]。现今的集约

化水产养殖也大量使用抗生素。土霉素、喹酸和喹诺酮类是在鱼类养殖中经常使用的抗生素[9]。水产养殖废水通常未作处理与自然水体直接交换,因而引起自然水体(水和沉积物)抗生素浓度增加。据估计,水产养殖中使用的抗生素至少有75%进入自然水体并在底泥中形成蓄积性污染[10]。

畜禽粪便农用则是抗生素进入土壤的最主要途径。因粪便农用途径进入土壤的抗生素估计每年达每公顷数百克[11]。另外,喷洒抗生素防治水果、蔬菜和观赏性植物细菌性病害是抗生素进入土壤的另一重要途径。此类抗生素包括土霉素、氟苯尼考、沙拉沙星、红霉素、磺胺类中的甲氧苄氨嘧啶等[12]。

抗生素也经集污系统进入污水处理厂。然而,现代污水处理技术很难将抗生素类微量污染物完全去除。在污水处理厂出水中检出了包括红霉素、磺胺甲恶唑等多种抗生素[13]。因此,污水处理厂也是环境介质中抗生素的来源之一[14]。

1.2　环境抗生素残留

水、沉积物和土壤是三大重要的环境介质,也是各种污染物的源汇载体。Gros 等[15]在不同水体(包括市政污水、河水、湖水甚至地下水)中检出了30多种抗生素。磺胺类和氟喹诺酮类是水体中常见的抗生素,其次是大环内酯类。磺胺类和氟喹诺酮类抗生素—磺胺甲恶唑和环丙沙星在生活污水较为常见,但农业径流可检测到磺胺二甲嘧啶;大环内酯类阿奇霉素和泰乐菌素则在生活污水和农业径流中都存在[13]。相对于城市生活污水和甲鱼养殖场废水,养猪场废水中抗生素的检出种类最多,其浓度也最高;磺胺类抗生素在3种废水中检出频率最高,包括磺胺甲恶唑、磺胺二甲嘧啶和磺胺甲氧嘧啶[16]。沉积物和土壤是吸附累积抗生素的重要环境介质[17]。医用和兽用抗生素在沉积物中可被大量检出,包括四环素、磺胺类和大环内脂类抗生素等[18]。集约式水产养殖区水体(水和沉积物)中抗生素含量普遍偏高,沉积物土霉素含量可高达285 mg/kg[19]。

根据有限的研究表明(表1),不同环境介质中抗生素残留浓度差异较大:水体为痕量残留(μg/L);土壤残留含量一般为μg/kg(粪便农用的土壤含量相对较高,可达到mg/kg);沉积物残留含量受抗生素结构、用量和环境条件不同而差异较大,通常在μg/kg—mg/kg之间。

表1　文献报道的环境抗生素残留浓度

Table 1　Reported concentrations of residual antibiotics in different environmental matrices

类别 Group of antibiotics	抗生素 Antibiotics	环境介质 Environmental matrix	质量浓度 Concentration
大环内脂类 Macrolides	红霉素 Erythromycin	河水[20]	0.62 μg/L
		城市污泥[22]	43.0 μg/kg
		城市河流沉积物[22]	125.6 μg/kg
	罗红霉素 Roxithromycin	河水[20]	0.19 μg/L
		城市污泥[22]	26.5 μg/kg
		城市河流沉积物[22]	105.0 μg/kg
	克拉霉素 Clarithromycin	河水[20]	0.19 μg/L
		城市污泥[22]	12.2 μg/kg
		城市河流沉积物[22]	6.8 μg/kg
氟喹诺酮类 Fluoroquinolones	氧氟沙星 Ofloxacin	污水处理厂出水[21]	0.65 μg/L
	诺氟沙星 Norfloxacin	医院废水[26]	0.09 μg/L
		污水处理厂进水[26]	0.06 μg/L
		污水处理厂出水[26]	0.03 μg/L
		自然污染土壤[23]	9.8 mg/kg
	环丙沙星 Ciprofloxacin	污水处理厂出水[21]	0.24 μg/L
		自然污染土壤[23]	5.8 mg/kg
磺胺类 Sulfonamides	磺胺二甲嘧啶 Sulfma-ethazine	城市污泥[22]	12.3 μg/kg
		城市河流沉积物[22]	21.3 μg/kg
		农业流域沉积物[24]	0.82 μg/kg

续表

类别 Group of antibiotics	抗生素 Antibiotics	环境介质 Environmental matrix	质量浓度 Concentration
	磺胺甲恶唑 Sulfam-ethoxazole	河水[20]	0.48 μg/L
		农业流域沉积物[24]	0.04—0.15μg/kg
		养虾池底泥[25]	820.5 mg/kg
四环素类 Tetracyclines	土霉素 Oxytetracycline	河水[20]	0.08 μg/L
青霉素类 Penicillins	阿莫西林 Amoxicillin	医院废水[26]	0.09 μg/L
		污水处理厂进水[26]	1.4 μg/L
其它 Others	甲氧苄氨嘧啶 Trimethoprim	河水[20]	0.12 μg/L
		城市河流沉积物[23]	34.6 μg/kg
		养虾池底泥[25]	734.6 mg/kg

2 抗生素的环境化学行为

和其它有机污染物一样,进入土壤、水和沉积物等环境介质的抗生素通过吸附、迁移和降解等一系列物理、化学和生物学过程在环境介质间发生再分配。

2.1 吸附-解吸和迁移

吸附-解吸和迁移是抗生素在环境介质间的重要物理化学过程,决定了抗生素在环境介质中的再分配过程。土壤和沉积物及其组成成分是抗生素重要的吸附剂。抗生素在环境固相介质上的吸附-解吸行为决定了液相抗生素的浓度(或者生物有效性),也决定抗生素在环境介质中的迁移(速率和模式)、生物学效应及其降解速率。环境介质吸附抗生素的能力与介质理化特性、抗生素性质(空间构型和官能团)及环境因子有关[27]。同时,土壤和沉积物对抗生素的吸附被认为是消减其环境效应的一个重要过程[28]。

不同于其它有机污染物,抗生素是一类具有多个离子型官能团的离子型极性有机化合物,存在多级解离,其不同价态离子具有较强的亲水性。离子型官能团类型和数量可能决定了抗生素在环境介质上的吸附能力[29]。粘土矿物、土壤及活性污泥对抗生素的吸附强度依次为:四环素类 > 大环内酯类和氟喹诺酮类 > 磺胺类[17]。四环素类和喹诺酮类抗生素具有较多的羧基、羰基和酰胺基等极性官能团使其与环境介质有很强的亲和力,大环内酯类抗生素因含有较少的极性官能团与环境介质的吸附作用较弱,而含有苯胺基和酰胺基的磺胺类抗生素与环境介质的吸附作用很弱。氨基糖苷类和 β-内酰胺类抗生素与环境介质吸附作用的研究相对较少。氨基糖苷类由氨基糖与氨基环醇通过氧桥连接而成,此类化合物具有较强的极性。氨基糖苷类的氨基在酸性条件下由于质子化作用带正电荷,正电荷可促进其吸附在带负电荷的土壤中的粘土矿物上,而 β-内酰胺类极性较强,土壤对此类抗生素的吸附能力较弱[17]。与金属阳离子结合性比较强的抗生素在环境固相介质中易累积,且具有较为持久的潜在毒性[30]。比如,四环素、氟喹诺酮类和大环内酯类等抗生素能和金属离子(Ca^{2+}、Mg^{2+}、Fe^{3+} 或 Al^{3+})形成络合物,使其在环境介质中较稳定存在[6]。

土壤和沉积物以及粘土矿物对抗生素的吸附行为(吸附容量和强度)受环境因子的调控。以四环素为例,pH 和离子强度的增加会降低粘土对其的吸附量,Ca^{2+} 和 K^{+} 存在的条件下粘土对四环素的吸附能力则增强;而腐殖质则因占据粘土表面吸附位点而降低粘土对四环素的吸附,尤其降低了抗生素向粘土矿物内层的扩散吸附[31]。章明奎等[32]发现长江和珠江三角洲地区农业土壤对泰乐菌素和土霉素的吸附容量不但与土壤粘粒含量相关,而且与有机质和氧化铁含量呈正相关。

粘粒矿物和有机质组分是抗生素在土壤和沉积物中的主要吸附位点,抗生素在土壤和沉积物中的吸附是两者共同作用的结果。研究表明,有机质导致土壤对土霉素的吸附曲线呈非线性,并影响其吸附容量和强度,且对褐土的影响要大于红壤[33]。而有机质对沉积物吸附抗生素的影响则因抗生素种类而异。氟苯尼考在沉积物去除有机质前后其吸附系数变化不大[34],但四环素在沉积物去除有机质后吸附系数降低 80% 以上[35];然而,两者吸附系数都随 pH 和盐度的增加而降低[34-35]。水溶性有机质(DOM)对蒙脱石吸附抗生素具

有双重性: 低浓度 DOM 与抗生素在蒙脱石上发生共吸附,促进抗生素的吸附; 而高浓度 DOM 则对抗生素的增溶作用显著,使抗生素从蒙脱石上解吸下来[36]。

抗生素在土壤或沉积物剖面内的迁移受土壤或沉积物及其组成成分的吸附-解吸作用的影响,其迁移速率受土壤或沉积物性质调控。比如,在粘壤质土壤中残留的土霉素和泰乐菌素等抗生素较为稳定,不易发生迁移; 而砂质土壤残留的抗生素,特别是泰乐菌素,具有较高的迁移速率,因而具有一定的环境风险[37]。

2.2　降解

抗生素进入环境介质中除了通过吸附-解吸和迁移过程发生再分配以外,降解过程是环境抗生素重要的代谢途径。抗生素在环境介质中可发生水解、光解和生物降解等降解过程。研究表明,粪肥中抗生素降解以光解为主,土壤中主要是生物降解,而水体中 3 种降解方式都相当重要[38]。

生物降解是大部分抗生素降解的重要途径,其中以耐药菌株参与的降解作用尤为重要。但抗生素生物降解效率受其种类影响。Alexy 等[39] 在 28d 密闭瓶中模拟 18 种抗生素的降解实验表明,某些抗生素的生物降解率较低,其中苄青霉素降解 27%,氧氟沙星的降解率仅为 7.5%,而磺胺甲恶唑和甲氧苄氨嘧啶几乎没有发生降解,但苄青霉素和金霉素则被完全降解。同样,环境抗生素生物降解效率受众多环境因素的影响,尤其是受影响降解微生物生存和活性的环境因子调控,包括温度、有机和无机营养物质、供氧状况、生物量、悬浮沉积物以及环境中抗生素浓度水平等[40]。一般高氧分压会抑制抗生素降解,但抗生素浓度则决定生物降解的速率[41]。

水解是水体中抗生素主要的降解方式,β-内酰胺类、大环内酯类和磺胺类有不同程度的水解。分子结构决定了抗生素在环境介质中的降解方式。一些抗生素呈水不稳定性,易被水解,但有些抗生素则不易水解,如喹诺酮类等抗生素。温度和 pH 是影响抗生素水解的重要环境因子,与金霉素、土霉素和四环素的水解速率显著相关[42]。大环内脂和磺胺在中性 pH 条件下几乎没有降解。

同时,喹诺酮类和四环素类抗生素属光降解敏感型。抗生素光解效率决定于环境光强度和频率[43],环境因子(如土壤含水量) 也影响光解速率。目前对抗生素光降解反应过程的研究表明,某些抗生素光降解产物具有更强的毒性[44],但尚需深入研究。

然而,无论生物降解还是非生物降解过程对土壤、水和沉积物等环境介质中残留抗生素的去除都发挥着重要作用,减轻了环境抗生素的累积及其对栖息生物的负面影响,并且减少其向地表水和地下水的迁移。

3　抗生素的微生物生态学效应

基于微生物生态学的环境暴露学研究是近年来国际环境科学研究的热点,包括污染物对微生物生物量[45]、活性[46] 和群落结构[47] 影响的研究。一种化学污染物对某一生态系统中微生物(群落结构和生态功能) 的影响,可以间接地反映出该化学品对此生态系统的影响[48]。但是,目前抗生素的环境污染研究主要集中在其污染作用机制和降解机制[49],而对其环境微生物生态学效应的研究较少涉及[50-51]。由于抗生素为抗微生物药物,能直接杀死土壤、水和沉积物等环境介质中某些微生物或抑制相关微生物的生长,从而影响环境微生物群落结构和活性[50]。比如,进入土壤的抗生素可能会影响土壤生物的生存和繁殖、代谢功能和种群数量等,使生物量、群落结构和生物多样性发生改变,从而影响土壤元素生物地球化学过程和自净化能力等。

3.1　微生物群落结构

Haller 等[52] 发现抗生素对土壤微生物的生长具有持久性的影响。磺胺类(磺胺嘧啶和磺胺甲恶唑) 和四环素类(土霉素) 抗生素抑制土壤细菌和放线菌生长,使土壤微生物生物量明显下降,但能促进土壤真菌生物量增加[53]。Hammesfahr 等[54] 也证实磺胺嘧啶污染粪便对土壤微生物群落结构和细菌多样性的显著影响,使土壤细菌/真菌比例下降。抗生素污染不但对环境介质中微生物生物量和群落结构产生影响,而且也影响了参与生态系统过程的功能微生物群落,如参与氮循环的硝化细菌和反硝化细菌。Schauss 等[55] 研究发现磺胺嘧啶污染粪便的施用改变了参与土壤硝化和反硝化作用的功能微生物丰度和多样性。Costanzo 等[56] 也报道了红霉素对水体中反硝化细菌有抑制作用。

3.2 微生物活性及其生态功能

微生物群落结构的变化,尤其是功能微生物群落的消长,直接影响微生物的生态功能。Boleas 等[57] 发现四环素在浓度为 1 mg/kg 时即可显著抑制土壤脱氢酶和磷酸酶的活性,但和牲畜粪便混施时酶活性先受抑制,但抑制作用随后消失。污染土壤中四环素的平均浓度约为 0.3 mg/kg,而相关研究表明四环素浓度在 0.003—7.35 mg/kg 时对土壤微生物活性具有抑制作用[45]。而磺胺嘧啶对土壤基质诱导呼吸作用的影响随时间、剂量和土壤性质的不同有所变化[58]。

抗生素对环境微生物活性的影响也干扰微生物参与的碳、氮循环等重要生态系统过程。Kong 等[59] 发现土壤微生物的碳源利用多样性(Biolog®,或者群落功能多样性)随土霉素浓度升高显著降低。而土壤氮素循环则明显受到高浓度四环素类抗生素的抑制,例如恩诺沙星在低浓度(0.01 mg/kg 和 0.1mg/kg)时可刺激土壤氨化作用,但在浓度为 1mg/kg 时对土壤氨化作用产生抑制,并对硝化作用也显现一定的抑制作用;而在浓度为 10 mg/kg 时,强烈抑制土壤硝化作用[60]。由此可见,抗生素污染将危及土壤微生物参与的生态系统过程(比如碳、氮循环过程),但对其生态毒性和对不同环境介质中微生物生态功能的影响有待进一步研究[61]。

3.3 诱导抗药性基因

抗生素不但对环境微生物生物量、群落结构及其相关生态功能产生影响,而且抗生素能诱导环境微生物产生抗性基因,从分子遗传水平上改变环境微生物群落结构。致病致害微生物抗药性的诱导会对生态系统稳定性、多样性和健康产生表观或潜在的威胁。Pruden 等[62] 认为抗生素诱导产生的环境微生物抗药性基因也是环境污染物。研究者普遍认为抗生素对环境微生物抗药性的选择和诱导是抗生素环境效应的最重要组成[63]。抗生素在禽畜和水产养殖业中的大量使用是导致环境微生物抗性增强的重要诱因。饲料添加抗生素和养殖废水得不到处理是抗生素大量进入环境的重要途径,对致病微生物和环境微生物群落施加选择性压力,提高了抗药性基因的产生概率。具有多药抗性的超级致病细菌(*Staphylococcus aureus* 等)已经成为本世纪的医学难题[3]。表 2 中列出了在水体、沉积物及土壤中发现的已编码的各种抗药性基因,医院废水、生活污水、沉积物、畜禽粪便、污水处理厂活性污泥等成为环境抗性基因污染的主要来源。

表 2 文献报道的抗性基因

Table 2 Reported antibiotics resistant genes in environment

抗生素 Antibiotics	抗药基因 Resistant Gene	所检测的环境介质 Detected environmental matrix
四环素 Tetracycline	tet A, tet B, tet C, tet D	猪粪便、化粪池和地下水[64]、污水处理厂活性污泥[65]
	tet E, tet H, tet Z	猪粪便、化粪池和地下水[64]
	tet G, tet L, tet S, tet Y	猪粪便[64,66]、养鱼场[67]
	tet M, tet O, tet Q, tet W	土壤[68]、河流沉积物[69]、污水处理厂活性污泥[65]
氯霉素 Chloramphenicol	cat I, cat II, cat III, cat IV	海水[70]
万古霉素 Vancomycin	van A, van B	废水、饮用水[71]
红霉素 Erythromycin	erm A, erm C, erm E	土壤[68]、污水处理厂进水、饮用水[72]
	erm B, erm F	养猪场化粪池[73]、土壤[68]
磺胺类 Sulfonamides	sul I, sul II	河流沉积物[69]
甲氧西林 Methicillin	mec A	医院废水[71]
β-内酰胺类 β-Lactams	bla OXA-B, bla CARB	河口水域[74]
	bla SHV, bla TEM	养猪场化粪池[73]、河口水域[74]、土壤[68]
	amp C	废水、表水和饮用水[71]

而抗生素抗性基因在生物中的转移主要有垂直和水平基因转移两种机制。垂直基因转移是抗性基因由亲代传递给子代,为遗传基因 DNA 自身变化的结果,具有典型的种属特异性,能够代代相传。水平基因转移(horizontal gene transfer, HGT),又称侧向基因转移,是细菌从附近其它细菌摄取抗药基因,为外界环境诱导的

遗传因子。基因水平转移可能存在 4 种机制,即抗性基因通过转导、转化、接合和转座在微生物间传播。转导是在同种细菌间由噬菌体转移抗药基因,转化则是外界环境耐药菌溶解后释放抗药基因后进入敏感菌体内。接合是细菌间的直接接触、转移抗药质粒 DNA,不仅可在同种菌之间进行,也可在属间不同菌之间进行,通过接合方式可完成对多种抗性基因的转移。转座则是抗药基因依赖细菌的染色体、噬菌体或质粒进行复制和繁殖[75-76]。

抗生素对耐药菌株抗性基因的诱导具有专一性,因此,抗生素在环境中的迁移、转化及归趋等环境行为与其所诱导的抗药性基因在环境中的传播在理论上应该具有相似性和一致性[63]。具有抗生素抗药性基因的微生物群落在环境中转移、传播和扩散,并在群落竞争中逐渐成为优势群落,从而改变自然微生物群落结构。因此,集约式水产养殖业和畜禽养殖业大量使用抗生素使水、土壤和沉积物不仅成为抗药性基因库,也成为抗药性基因扩展和演化的媒介,使得加强集约式水产养殖业和畜禽养殖业抗生素使用管理及对其抗药性基因的传播、扩散机制的研究迫在眉睫[63]。同时,环境抗生素对致病微生物(病原菌)抗药性基因的诱导以及环境抗药性基因向致病微生物转移直接威胁人类健康[50],也使得医用抗生素的有效管理、环境行为以及抗药性基因诱导和转移的研究十分迫切。

4　研究中存在的问题及展望

四环素类、大环内酯类、喹诺酮类、磺胺类和 β-内酰胺类等五大类抗生素的环境效应研究已都有所涉及[77],且抗生素的环境转归和对环境微生物及其生态学等方面的影响也进行了初步的研究。通过上述的归纳分析表明,抗生素环境效应研究有待进一步深入:

(1) 环境介质中抗生素污染是多种抗生素及其它有机无机污染物(如重金属、PCBs、PAHs 等)共存的复合污染,但已报道的研究多以单种或单类抗生素作为研究对象,多对其在环境介质(主要是土壤)中的吸附-解吸、迁移和降解(消解)等行为或过程进行研究,缺乏抗生素复合污染的环境效应研究;并且抗生素进入土壤、水和沉积物等环境介质的迁移、转化和降解过程与植物、动物及微生物生态效应耦合关系有待进一步研究;

(2) 抗生素对环境微生物生态效应的研究多集中在抗生素对微生物毒性效应上,并已明确环境抗生素降低土壤微生物生物量、改变微生物群落结构以及影响微生物活性。但尚缺乏抗生素本身性质(如官能团和空间结构等)对环境微生物群落结构、功能微生物群落结构和活性以及生态系统功能等影响的专一性及其调控机理方面的研究,抗生素低剂量和长期暴露对微生物群落结构的选择性压力机理研究尚需展开;

(3) 在分析技术上,环境抗生素残留浓度和种类的高通量、快速和准确检测方法或系统有待建立。在不同的环境介质中均发现抗生素耐药菌和抗性基因,应加强对环境抗药性基因检测方法的研究,并对耐药微生物和抗药性基因的环境生物学和生态学效应等研究领域进行积极探索;

(4) 现有的抗生素环境暴露和生态毒理效应研究尚缺少多尺度和多层次(即个体、群落和生态系统等)的研究。应加强抗生素环境生态毒理学研究,并与抗生素环境化学研究相结合,以建立环境抗生素残留预测模型、环境效应模型和生态风险评估体系,实现对抗生素环境安全性的预测预警和评价,为抗生素使用的有效管理提供依据。

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