杨礼震,刘天琪,王禄禄,等.养猪废水处理工艺对耐药基因迁移影响研究进展[J].华中农业大学学报,2022,41(4):1-9.
DOI:10.13300/j.cnki.hnlkxb.2022.04.001

主持人语: 我国畜牧业每年生产1.5亿多t肉蛋奶,在保障肉食品供给、提高人民生活质量做出巨大贡献的同时,也产生约38亿t畜禽养殖废弃物,若处理不当,将造成较大的环境污染。在习总书记"宁要绿水青山,不要金山银山;绿水青山就是金山银山"的绿色发展理念指引下,国家出台了一系列治理畜牧业养殖污染的政策法规并投入大量资金,经过近几年的攻坚克难,农业面源污染得到了有效治理,生态环境明显好转,但全面实现养殖废弃物的资源化和高值化利用还有很长的路要走。主要表现在生物转化技术还不成熟、处理成本居高不下、产品利用率不高、产品多元化有待提升等问题。因此,开展畜禽养殖废弃物高效生物转化调控机制研究和废弃物高值资源化利用新产品研发是当务之急,本刊特组织"畜禽养殖废弃物资源化利用"专题,刊发综述和研究论文共15篇,内容涉及畜禽养殖废弃物肥料化、饲料化、能源化,臭气净化,以及碳氮减排等资源化利用和无害化处理技术与应用,以期抛砖引玉,引发更多讨论和重视。

养猪废水处理工艺对耐药基因迁移影响研究进展

杨礼震,刘天琪,王禄禄,曹芸芸,周文兵,肖乃东,蔡建波

华中农业大学资源与环境学院/生猪健康养殖省部共建协同创新中心,武汉 430070

摘要 生猪养殖是环境中抗生素耐药基因(antibiotic resistance genes,ARGs)的重要来源之一,而养猪废水的排放是ARGs进入环境的主要渠道。目前,养猪废水中ARGs排放所导致的环境效应尚不明晰,同时,不同养猪废水处理工艺对于ARGs去除的相关研究尚处于起始阶段,需要进行更加深入、细致的研究,以及探索减少养猪废水中ARGs丰度的养殖废水处理方法。本文综述了养猪场内ARGs从产生到进入环境的过程以及当前ARGs污染情况和研究现状,从不同的污水处理法(厌氧生物处理法、好氧生物处理法、物理化学法、人工湿地法)出发,重点介绍养猪场污水处理工艺中ARGs的分布和去除效果,认为物理化学法是消减养猪废水中ARGs污染问题最具前景的处理方式。最后,基于目前养猪废水处理工艺在去除ARGs存在的不足,提出了优化处理工艺措施并强化各工艺间ARGs监测的可行性建议。

关键词 抗性基因; 抗生素; 基因迁移; 养猪废水; 养猪场; 处理工艺

中图分类号 X713 **文献标识码** A **文章编号** 1000-2421(2022)04-0001-09

为预防动物疾病和保证动物产品稳产高产,畜禽养殖业广泛使用抗生素。然而,抗生素的使用会使细菌产生耐药基因,养殖废弃物是导致环境中抗生素及耐药基因污染的重要来源之一。到2050年,预计全世界每年将有1 000万人因抗生素耐药性而死亡,卫生部门经济负担将高达100万亿美元[1]。我国是世界上最大的生猪生产国,养猪场每年产生大量含抗生素耐药基因(antibiotic resistance genes,ARGs)的废水[2]。污水处理系统是养猪场必不可少的环保设施,然而,当前养猪场污水处理系统多为降低有机物(化学需氧量)、氨氮等污染物而设计,对于残留ARGs的污染问题尚未引起足够关注[3]。

生猪肠道中微生物受到抗生素压力胁迫发生基

收稿日期:2022-03-31
基金项目:国家重点研发计划项目(2018YFF0213503-1)
杨礼震,E-mail:yanglizhenylz@163.com
通信作者:蔡建波,E-mail:jbcai@mail.hzau.edu.cn

因突变而产生的ARGs,可通过水平基因转移和垂直基因转移2种方式促使细菌耐药性发生转移,导致ARGs类环境问题不断产生[4]。含ARGs的废水进入到污水处理系统后可随废水排出进入水、空气和土壤环境中,进而通过呼吸作用和食物链对人类产生危害。养猪场内抗生素转移传递方式如图1所示。不同类型的抗生素以及污水处理方式使得细菌中抗生素耐药性有所差异。携带ARGs的可移动遗传元件也可在动物和人类之间的不同肠道微生物群之间进行传播[5]。在复杂环境体系中,细菌间会相互影响,如一些敏感细菌可与耐药细菌相互作用而共存[6]。因此,水样环境越复杂越难以调查废水中ARGs的作用方式。笔者针对养猪废水处理工艺中ARGs污染问题,结合国内外最新文献报道,阐述生猪养殖场内ARGs污染情况,介绍养猪废水处理工艺的几种关键方法,以期为养猪废水处理工艺去除ARGs提供技术参考,促进我国生猪养殖绿色可持续发展。

1 生猪养殖场耐药基因的产生

1.1 生猪肠道内抗生素及抗性基因的产生

在生猪养殖过程中,抗生素的长期使用,导致ARGs的出现和耐药菌的增加。生猪肠道微生物群作为ARGs的潜在储存库已逐渐引起人们关注[7]。生猪肠道微生物能维持宿主代谢稳态,保障多种生理、神经和免疫功能。生猪肠道微生物相互作用会影响微生物群落的功能和结构,如真菌可以影响细菌生长,噬菌体能够调节细菌的多样性,但目前关于ARGs的研究主要集中于细菌,对真菌、病毒等微生物的研究则相对较少[8]。为了促进生猪生长,常在饲料中添加抗生素,饲料中抗生素添加剂量一般在2.5~125 mg/kg[9],然而30%~90%的抗生素不能被生猪肠道吸收而被直接以粪便排出,同时ARGs也随着耐药菌一起排出并进入环境,从而进一步对ARGs的产生造成选择性压力[10]。

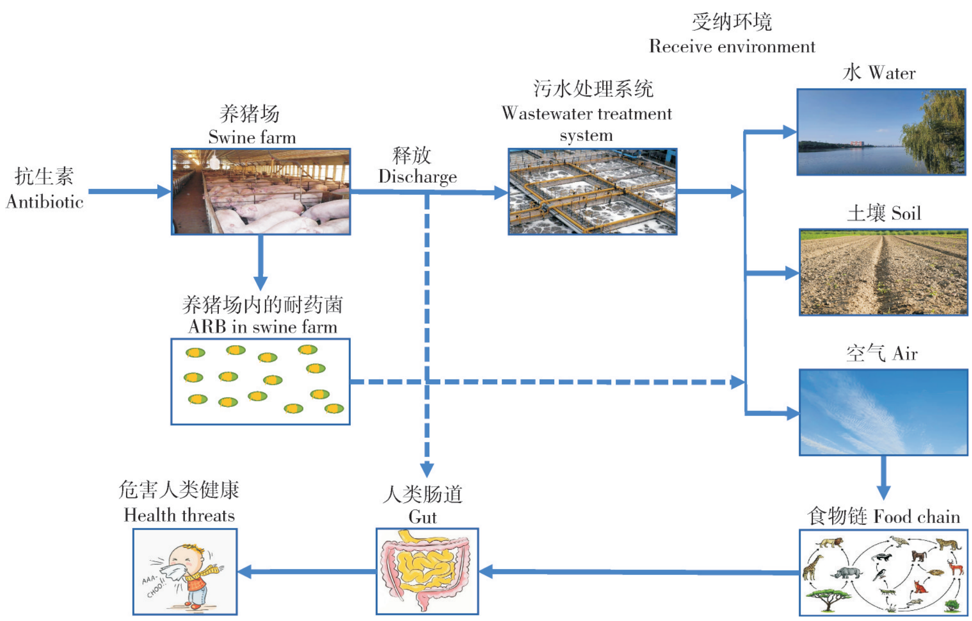

图1 抗生素在养猪场内传播路径

Fig.1 Transmission routes of antibiotics in swine farms

国内很多学者在生猪肠道中检测出ARGs[11],在生猪肠道中含有大量微生物菌群,其数量超过宿主细胞。抗生素的使用会使生猪肠道内微生物群发生紊乱,例如,在生猪保育期和生长期使用抗生素会导致肠道微生物生态失调,与对照组相比,使用泰乐菌素的生猪肠道中乳酸杆菌和醋杆菌属占有较大的丰度[12-13]。生猪肠道微生物群中的病原体,具有向人类传播抗生素耐药性潜力[12,14]。针对复杂的肠道微生物群,消减生猪养殖系统中ARGs丰度可从以下几个方面入手:从源头控制并且加强用药监督;在饲料中添加抗生素替代品(如益生元、有机酸、抗菌肽和杆菌肽)改善肠道健康,使生猪保持良好的肠道菌群;通过接种疫苗,刺激宿主利用自然防御系统产生免疫力来保障成本和免疫疾病[12,15-16]。

1.2　生猪养殖环境中抗生素及抗性基因分布

养猪场废水的排放导致环境中ARGs丰度和多样性增加，进而影响地表水和土壤中微生物生态[3]。养猪废水的抗生素含量与饲料、喂养模式、养猪场的规模以及养猪场的地理位置有关。生猪肠道吸收抗生素的能力较差，抗生素常以粪便形式进入生猪养殖环境[17]。猪粪中富集的抗生素，如土霉素含量高达5 175.3 μg/kg，远高于饲料中的含量(152.7 μg/kg)[18]。

养猪废水中的ARGs，除了环境中已经携带ARGs的微生物，其余均来源于养猪场内生猪体内的微生物。生猪养殖环境中残留抗生素又会造成选择性压力，诱导微生物发生突变，使不含ARGs的微生物产生耐药性。养猪场内的ARGs的分布如表1所示，在养猪场内能够检测到大量的ARGs，其中主要是四环素类ARGs(*tetO*、*tetM*、*tetC*和*tetQ*)和磺胺类ARGs(*sul1*和*sul2*)。ARGs广泛分布于猪舍的各个位置，甚至地下水中也能检测到ARGs的存在。在丰度方面，Gao等[19]调查养猪场内井水耐药基因丰度，其平均值高达5.27×10^{7} copies/L。这些耐药基因会随着废水水平基因转移到受纳环境中。Mu等[20]调查了北方某养猪场附近的土壤，发现磺胺类ARGs(1.3×10^{9}～2.6×10^{9} copies/g)在ARGs中最普遍，占总样本约70%。养猪场空气中生物气溶胶也含有大量致病菌和潜在ARGs宿主，这些生物气溶胶可远距离传播到外部环境，对公众健康带来重大潜在风险[21]。

生活在养猪场环境中的工人肠道微生物菌群失调风险较高，可能影响人体健康。据报道，相对于肉鸡养殖场，生猪养殖户粪便中ARGs含量更高[22]。生猪养殖废弃物的不规范处理和排放将导致周围水、土壤和大气等环境受到严重污染。特别是ARGs这种不同于其他化学污染物的特殊污染物，一旦产生，很难控制和清除，并且ARGs在养猪环境中具有可持久性、会在环境中发生迁移和转化，具有比抗生素更严重的危害性。

表1　生猪养殖环境中ARGs分布情况

Table 1　Distribution of ARGs in swine breeding environment

省(自治区) Province (Municipality)	采样位置 Sampling location	抗生素抗性基因 Antibiotic resistance genes	参考文献 References
广东省 Guangdong Province	猪舍粪便和冲洗废水 Swine farm manure and flushing wastewater	*tetA*、*tetH*、*ermE*、*sul2*、*sul1*、*tetG*	[3]
山东省 Shandong Province	猪舍粪便和冲洗废水 Swine farm manure and flushing wastewater	*tetM*、*tetO*、*tetW*、*tetC*、*tetG*、*sul1*、*sul2*	[23]
广西壮族自治区 Guangxi Zhuang Autonomous Municipality	猪舍井水 Swine farm well water	*tetC*、*tetG*、*tetH*、*tetO*、*tetW*、*tetB(P)*、*sul1*、*sul2*	[19]
广东省 Guangdong Province	猪舍粪便 Swine farm manure	*sul1*、*sul2*、*tetX*、*tetW*、*tetQ*、*tetO*、*tetL*	[5]
陕西省 Shannxi Province	猪舍粪便 Swine farm manure	*tetC*、*tetG*、*tetM*、*tetW*、*sul2*、*ermF*	[24]
四川省 Sichuan Province	猪舍室内空气 Swine farm indoor air	*aadE*、*tetW*、*ermB*、*sul1*、*tetQ*、*aadA*和*tet40*	[21]
辽宁省 Liaoning Province	猪舍附近土壤 Swine farm soil	*tetM*、*tetO*、*tetQ*、*tetW*、*sul1*、*sul2*、*qnrS*、*oqxB*、*ermB*和*ermC*	[20]

2　不同废水处理工艺的耐药基因迁移

当前我国生猪废水传统处理设施(如格栅、固液分离机、沉淀池、序列间歇式活性污泥反应器、人工湿地等)，未应用于处理抗生素耐药基因和抗生素耐药细菌(antibiotic resistant bacteria，ARB)[25]，处理后废水仍含有各种ARGs和ARB，尤其是规模化养猪场废水处理后，其ARGs需要引起足够关注。这些传统设施由于水力停留时间较短，以及生物生长和遗传交换会导致ARGs进一步增殖。大部分污水处理厂处理的废水仍存在微生物密度过高以及抗生素残留等特点，通常能检测到较高水平的β-内酰胺类、大环内酯类、多药类、四环素类、磺胺类、喹诺酮类和氨基糖苷类等常见抗生素[26-27]，这会促进基因水平转移和抗生素耐药性产生。我国养猪废水主要处理方

法为生物处理法,其次还有物理化学法和人工湿地法,这些方法对于抗生素及耐药基因的去除效率和作用机制均不同。

2.1 生物法处理抗生素及耐药基因

生物处理法是通过厌氧和好氧单独或结合使用对养猪废水进行处理,该方法可以有效处理常规污染物,如有机物(以化学需氧量(COD)形式表示)和总氮。然而,厌氧处理工艺不但不能完全去除养猪废水中的抗生素和ARGs,甚至可以为ARGs产生和转移创造有利条件[28-29]。生物处理反应器中ARGs的丰度变化受到抗生素种类、浓度和暴露时间的影响,但经过反应器后ARGs不但不会减少,甚至在抗生素暴露下大部分污泥和废水中ARGs丰度上升。厌氧处理养猪废水后,四环素类ARGs(*tetA*、*tetG*、*tetC*、*tetM*)和磺胺类ARGs(*sul1*、*sul2*)相对丰度增加[30-31]。Zhang等[29]研究发现,厌氧消化污泥中除bla_{TEM}减少外,其他类型ARGs丰度均有不同程度增加。厌氧反应器对于养猪废水ARGs去除效率较低,但可以通过提高温度、使用添加剂提高厌氧反应器中ARGs的去除率[32-34]。Tian等[34]将厌氧反应器中温度从35 ℃提升到55 ℃时,发现13个ARGs可能宿主的18个细菌属的总丰度从23.27%下降到11.92%。Sun等[32]通过在厌氧反应器中添加生物炭刺激厌氧消化过程,降低了ARGs丰度。

厌氧和好氧结合使用有助于消减废水ARGs丰度。厌氧缺氧/好氧和厌氧短程硝化反硝化能有效降低养猪废水ARGs的绝对丰度和多样性[2]。Yang等[35]在厌氧/好氧(anaerobic/oxic,A/O)过程中检测到大量的磺胺类和四环素类ARGs(10^5~10^9 copies/mL)。Sui等[36]从养猪场的A/O罐中检测到11种ARGs,包括四环素类、磺胺类和β-内酰胺类耐药基因,这些基因中*sul2*和*sul1*在厌氧池和好氧池中的丰度最高,分别达到10^9和10^8 copies/mL,并且其去除量高达$10^{3.43}$ copies/mL。结合厌氧好氧处理,我国台湾地区6个养猪场污水处理系统中ARGs平均去除率为33.30%~97.56%[37]。此外,增加水力停留时间会减少A/O处理工艺对ARGs的去除效率,Sui等[38]将养猪场废水通入序批式膜生物反应器,水力停留时间从12 d增加到30 d,其ARGs去除量从$10^{2.91}$ copies/mL减少到$10^{1.18}$ copies/mL。

传统的生物处理方法能耗高、运行成本高、剩余污泥处置困难,对于ARGs去除效率不理想,但目前国内养猪场大部分采用生物处理方法,需要研发出新技术或结合其他处理技术共同消减养猪废水中的ARGs。Li等[39]对比活性污泥法和微藻处理法中*sul1*基因的丰度,发现活性污泥法和微藻法中*sul1*丰度分别为3.06×10^7和1.73×10^6 copies/L,该微藻处理中ARGs丰度大幅度减少。因此今后可以使用微藻处理法,该方法去除ARGs更有效,且具有能量需求低、高碳中和的能量转换能力。

2.2 物理化学法处理抗生素及耐药基因

养猪废水常用的物理化学法有消毒、膜分离、絮凝或芬顿氧化等。养猪废水处理中的消毒技术常使用紫外线消毒和氯消毒。紫外线消毒机制主要分为直接和间接2种机制,直接机制是紫外线直接穿透细胞壁、细胞膜和细胞质被核酸吸收;间接机制是细胞内的光敏物质吸收紫外线产生活性氧,氧化细胞膜、细胞质和核酸,从而杀灭细菌。理论上紫外线消毒是一种去除ARGs的可行方案,但在养猪废水处理系统使用紫外线对ARGs去除效率较差[40]。如Ferro等[41]使用紫外线/H_2O_2体系处理ARGs,240 min后其丰度仅从初始5.1×10^4 copies/mL减少到4.3×10^4 copies/mL。同时有研究表明,去除ARGs所需紫外线的剂量约为常规污水处理厂处理废水所需紫外线剂量的2倍[42-43]。氯消毒是通过次氯酸分子氧化水中污染物,从而达到降解的效果,但也不能彻底去除养猪废水中的ARGs,Mao等[44]检测了中国北方的2个污水处理厂出水口处ARGs丰度,发现经过氯消毒处理后,出水中依然存在相当浓度的ARGs(10^3~10^6 copies/L)。而对于膜分离的处理方法,对ARGs去除效率较高,Liang等[45]对养猪废水进行超滤和二级反渗透的集成膜过滤,通过过滤可减少99.79%的ARGs(从3.01×10^8 copies/mL降低到6.45×10^5 copies/mL)。电化学消毒方法中的电凝法和电芬顿法也可以用于ARGs的去除,其通过铁或铝阳极在电解池中氧化生成混凝剂,并与细菌或污染物形成絮状沉淀物。Chen等[46]利用连续电絮凝和电芬顿法对细胞内和细胞外ARGs的去除量分别为$10^{2.49}$和$10^{3.23}$ copies/mL。此外,还可以利用金属能破坏细胞结构的机理,进而去除养猪场内ARGs,Zhang等[47]发现养猪废水ARGs丰度为$10^{5.78}$~$10^{8.77}$ copies/mL,废水通过mFe/nCu工艺处理在60 min内ARGs去除量为$10^{2.4}$ copies/mL,并且该工艺去除ARGs的原理是杀灭细菌和破坏ARGs

结构和功能，该过程对于ARGs的去除是永久不可逆的。

由此可见，减少养猪废水中ARGs，不能只使用简单的消毒方式，还应找出高效便捷的处理措施，使其处理方式达到最优状态。膜分离方法和金属破坏细胞方法虽然去除效率较高，但是所需成本高昂并且二次污染问题严重，与前2种方法相比，电化学方法尽管耗能较高，但它是最具有前瞻性、环保性的方法，是一种很好的用于去除ARGs的化学方法。

2.3　人工湿地处理抗生素及耐药基因

湿地技术是一种自然过程，具有运行和维护费用低廉的优点，自20世纪60年代以来被用于各种污水处理中，最初人们利用植被覆盖的天然湿地来处理农村或畜禽养殖污水，现已发展为利用人工模拟生态系统建造污水处理系统[48-49]。不同类型湿地对抗生素去除效率不同，例如，水面人工湿地对养猪废水中磺胺甲嘧啶（1.5 g/L）的去除率为40%，水平潜流人工湿地对其去除率为59%，垂直潜流人工湿地对其去除率为87%；而流入四环素（0.86 g/L）时，水面人工湿地对其去除率为92%，水平潜流人工湿地对其去除率为92%，垂直潜流人工湿地对其去除率为99%[50]。四环素和磺胺类抗生素的去除率不同是因为其物理化学性质不同。Carvalho等[51]在微观层面上评估人工湿地对抗生素的降解，芦苇的种植与否对四环素的降解率的影响有显著性差异。虽然不同模式下的人工湿地对抗生素的去除效率不同，但均主要通过吸附作用进行去除。

ARGs的去除受到人工湿地中植物、基质、微生物等组分的影响[52-53]。通过复合型立式流人工湿地对养猪场废水中的四环素类抗生素及耐药基因，去除率分别为95.0%和95.1%[54]。Liu等[55]通过添加火山石的垂直流人工湿地对四环素类ARGs去除率达到50%。Chen等[56]将混合人工湿地与人工曝气相结合，对ARGs特别是四环素类和磺胺类ARGs，去除效率达到97.8%～99.1%，具有比传统污水处理厂中更高的ARGs去除率。Abou-kandil等[57]研究表明，凝灰岩填充芦苇、凝灰岩填充芦苇-香蒲和砾石填充人工湿地对污染物中的总ARGs去除能力分别为89.9%～94.7%、74.3%～76.9%和79.7%～85.3%。最近研究发现，底物系统（沸水、砾石、红砖和牡蛎壳）不同，ARGs去除效率也不同，其中砾石对于ARGs去除效率（48%）高于其他基质体系（34%～45%）[58]。因此，采用人工湿地处理养猪废水中ARGs需要选择合适的基质体系，或将人工湿地与人工曝气相结合，或与其他生物处理技术相结合，以获得高效的去除效率。

3　养猪废水受纳环境ARGs差异分析

ARGs从动物养殖场向周围环境的传播已引起国内外学者广泛关注。养猪场的污水处理系统能够去除一部分ARGs，然而大多数抗生素和ARGs会在出水中残留，不同养殖规模、受纳环境及季节影响ARGs的检出。研究发现，在养猪场附近的水域中检测到抗生素的存在，例如，Zhou等[59]研究发现，广西某养猪场周边环境中，包括地下水、泻湖废水、沉积物中均发现抗生素的残留，其中在泻湖废水中检测到17种抗生素，其存在的质量浓度在4.36～8 600 ng/L。ARGs还能在不同介质中传播，具有比抗生素更严重的危害性[60]。ARGs会随生猪养殖场排放的废水进入到受纳水体（湖泊、河流、井水和地下水）和农田中[61-62]。Fagervold等[63]证实，有机物的输入可驱动河流中微生物群落的迁移，养猪废水会影响受纳河流中ARGs丰度，废水中高浓度营养物质和抗生素能促使受纳河流中细菌群落发生转移。

在水环境中，ARGs可通过细菌或可移动遗传元件传播，废水的排放增加了受纳环境ARGs的丰度和多样性，从而影响地表水和土壤中的微生物生态。ARGs同样存在于周围河流中，如Yang等[64]在养猪场周边河流中采集水样，检测到养猪废水中的23种基因。He等[3]研究发现，养猪场出水沟处ARGs浓度高于其排放点和下游站点，并且从上游到下游呈下降趋势；ARGs的组成与对照河段的差异较大，但与养猪场废水中的ARGs的组成相似；与对照水库相比，受纳河流中的ARGs更具有多样性；而养猪废水中的ARGs也比养猪场的井水更具有多样性，养猪废水的排放会改变受纳水体的细菌群落。在丰度方面，Yuan等[65]调查了武汉某养猪场及其周围河流ARGs存在情况，发现受纳河流中ARGs的平均丰度在3.1×10^4～7.1×10^8 copies/mL。受纳环境中ARGs丰度受到季节的影响，如Ben等[23]研究发现夏季和冬季时附近湖泊的ARGs的平均相对丰度在0.094～0.170和0.021～0.059 copies/16S rRNA，冬季的丰度更高，这是因为冬季频繁使用抗生素治疗

疾病导致生猪肠道细菌的耐药水平更高。

养猪场附近的农民常将废水使用到农田以促进蔬菜的生长[66]，但这会增加农田土壤和径流中的ARGs含量[31,67]。Gao等[68]调查中国南方某养猪场，其将未处理的废水直接用于蔬菜种植农田，在该养猪场废水排放的农田中监测到17种ARGs亚型，主要是磺胺类ARGs，其次是四环素类ARGs。最终食用蔬菜可能会对人类健康构成威胁。在养猪场附近水体和土壤均能检测到ARGs，同样说明养猪废水是ARGs持续排放到环境中的一个来源，养猪废水的排放会提高受纳水体和土壤中ARGs丰度，造成环境污染。

4 展　望

生猪养殖废水是环境中ARGs的一个主要来源，受生猪养殖废水影响，各环境（水、空气、土壤）ARGs的浓度明显升高。本文重点对生猪养殖环境中ARGs从产生到进入环境的过程进行了介绍，特别是对不同养猪废水处理工艺ARGs迁移转化的差异进行了综述。在不同废水处理工艺中，生物处理方法中的厌氧工艺对于ARGs的去除率在3.5%～71%，好氧工艺甚至会增加ARGs的相对丰度，使用厌氧和好氧相结合的方式更有助于去除ARGs，而人工湿地技术去除ARGs的效率虽然高于生物处理方法，但多是吸附方式去除ARGs。基于目前的研究现状，提出未来研究的3点建议：

1）加强ARGs的源头控制、提高养猪废水处理过程中ARGs的清除效率（例如，使用益生元或优化操作条件），在保证生猪盈利能力和保护人类健康的同时，改进生猪养殖和废物管理策略，减少排放废水中ARGs的传播。

2）应强化深度处理过程。物理化学法去除ARGs具有前景性和高效性，未来ARGs的去除方法可以主要考虑物理化学法，但仍需不断优化条件以增加去除效率，同时制定养猪行业关于ARGs环境污染的相关标准，在不同工艺的污水处理环节加强对ARGs的监测。

3）建立养猪废水受纳环境ARGs预警体系，并开发出一类便携式的新型工具，其具有实用化、日常化等特性，可应用于实时测定养猪废水受纳环境中ARGs污染并提前报警。该预警体系应可防止人类因摄入含有ARGs污染的水或食物而导致抗生素耐药性在人类肠道的进一步传播。

参考文献 References

[1] TANG K，LI Z H，LI W W，et al.China's Silk Road and global health[J].The lancet，2017，390(10112)：2595-2601.

[2] YANG Y W，XING S C，CHEN Y X，et al.Profiles of bacteria/phage-comediated ARGs in pig farm wastewater treatment plants in China：association with mobile genetic elements，bacterial communities and environmental factors[J/OL].Journal of hazardous materials，2021，404：124149 [2022-03-31].https://doi.org/10.1016/j.jhazmat.2020.124149.

[3] HE L Y，YING G G，LIU Y S，et al.Discharge of swine wastes risks water quality and food safety：antibiotics and antibiotic resistance genes from swine sources to the receiving environments[J].Environment international，2016，92/93：210-219.

[4] 安新丽，苏建强.活性污泥抗生素抗性基因研究进展[J].微生物学通报，2019，46(8)：2069-2079.AN X L，SU J Q.Resistome in activated sludge：current knowledge and future directions[J].Microbiology China，2019，46(8)：2069-2079（in Chinese with English abstract）.

[5] SUN J，HUANG T，CHEN C，et al.Comparison of fecal microbial composition and antibiotic resistance genes from swine，farm workers and the surrounding villagers[J/OL].Scientific reports，2017，7(1)：4965 [2022-03-31]. https://doi. org/10.1038/s41598-017-04672-y.

[6] GALERA-LAPORTA L，GARCIA-OJALVO J. Antithetic population response to antibiotics in a polybacterial community [J/OL].Science advances，2020，6(10)：eaaz5108 [2022-03-31].https://doi.org/10.1126/sciadv.aaz5108.

[7] ACHARD C S，DUPOUY V，CAUQUIL L，et al.Early inoculation of microbial suspension in suckling piglets affects the transmission of maternal microbiota and the associated antibiotic resistance genes[J/OL].Microorganisms，2020，8(10)：1576 [2022-03-31].https://doi.org/10.3390/microorganisms8101576.

[8] PIERCE E C，MORIN M，LITTLE J C，et al.Bacterial-fungal interactions revealed by genome-wide analysis of bacterial mutant fitness[J].Nature microbiology，2021，6(1)：87-102.

[9] QIAO M，YING G G，SINGER A C，et al.Review of antibiotic resistance in China and its environment[J].Environment international，2018，110：160-172.

[10] 韩婉雪，王凤花，柏兆海，等.畜禽粪便堆放地土壤中抗生素抗性基因和细菌群落的垂直分布特征[J].中国生态农业学报（中英文），2022，30(2)：268-275.HAN W X，WANG F H，BAI Z H，et al. Vertical distribution of antibiotic resistance genes and bacterial communities in soil of livestock manure stacking site[J].Chinese journal of eco-agriculture，2022，30(2)：268-275（in Chinese with English abstract）.

[11] WEN X，MI J D，WANG Y，et al.Occurrence and contamination profiles of antibiotic resistance genes from swine manure to receiving environments in Guangdong Province Southern China[J].Ecotoxicology and environmental safety，2019，173：96-102.

[12] SAMANTA A K，JAYARAM C，JAYAPAL N，et al.Assessment of fecal microflora changes in pigs supplemented with herbal

residue and prebiotic[J/OL].PLoS One,2015,10(7):e0132961 [2022-03-31].https://doi.org/10.1371/journal.pone.0132961.

[13] LIM S K,KIM D,MOON D C,et al.Antibiotic resistomes discovered in the gut microbiomes of Korean swine and cattle[J].GigaScience,2020,9(5):1-11.

[14] WANG C L,LI P,YAN Q L,et al.Characterization of the pig gut microbiome and antibiotic resistome in industrialized feedlots in China[J/OL].mSystems,2019,4(6):e00206-e00219 [2022-03-31].https://doi.org/10.1128/msystems.00206-19.

[15] DE LANGE C F M,PLUSKE J,GONG J,et al.Strategic use of feed ingredients and feed additives to stimulate gut health and development in young pigs[J].Livestock science,2010,134(1/2/3):124-134.

[16] HOELZER K,BIELKE L,BLAKE D P,et al.Vaccines as alternatives to antibiotics for food producing animals.Part 2:new approaches and potential solutions [J/OL]. Veterinary research, 2018,49(1):70 [2022-03-31].https://doi.org/10.1186/s13567-018-0561-7.

[17] SARMAH A K,MEYER M T,BOXALL A B A.A global perspective on the use, sales, exposure pathways, occurrence, fate and effects of veterinary antibiotics (VAs) in the environment [J].Chemosphere,2006,65(5):725-759.

[18] ZHANG J Y,LU T D,CHAI Y F,et al.Which animal type contributes the most to the emission of antibiotic resistance genes in large-scale swine farms in China?[J].Science of the total environment,2019,658:152-159.

[19] GAO F Z,ZOU H Y,WU D L,et al.Swine farming elevated the proliferation of *Acinetobacter* with the prevalence of antibiotic resistance genes in the groundwater[J/OL].Environment international, 2020, 136: 105484 [2022-03-31]. https://doi. org/10.1016/j.envint.2020.105484.

[20] MU Q H,LI J,SUN Y X,et al.Occurrence of sulfonamide-,tetracycline-,plasmid-mediated quinolone- and macrolide-resistance genes in livestock feedlots in northern China[J].Environmental science and pollution research international,2015,22(9):6932-6940.

[21] YAN H L,LI Y,ZHANG Y,et al.Deciphering of microbial diversity and antibiotic resistome of bioaerosols in swine confinement buildings[J/OL].Science of the total environment,2021, 781: 147056 [2022-03-31]. https://doi. org/10.1016/j. scitotenv.2021.147056.

[22] VAN GOMPEL L,LUIKEN R E C,HANSEN R B,et al.Description and determinants of the faecal resistome and microbiome of farmers and slaughterhouse workers:a metagenome-wide cross-sectional study [J/OL]. Environment international, 2020, 143: 105939 [2022-03-31]. https://doi. org/10.1016/j. envint.2020.105939.

[23] BEN W W,WANG J,PAN X,et al.Dissemination of antibiotic resistance genes and their potential removal by on-farm treatment processes in nine swine feedlots in Shandong Province,China[J].Chemosphere,2017,167:262-268.

[24] ZHANG R R,GU J,WANG X J,et al.Contributions of the microbial community and environmental variables to antibiotic resistance genes during co-composting with swine manure and cotton stalks[J].Journal of hazardous materials,2018,358:82-91.

[25] 王荣昌,王超颖,曾旭.污水处理过程中抗生素抗性基因的检测及其水平转移机制的研究进展[J].环境化学,2017,36(12):2567-2573.WANG R C,WANG C Y,ZENG X.Detection and horizontal transfer of antibiotic resistance genes during wastewater treatment processes[J].Environmental chemistry,2017,36(12):2567-2573(in Chinese with English abstract).

[26] CHENG D L,HAO N H,GUO W S,et al.Contribution of antibiotics to the fate of antibiotic resistance genes in anaerobic treatment processes of swine wastewater: a review [J/OL]. Bioresource technology,2020,299:122654 [2022-03-31].https://doi.org/10.1016/j.biortech.2019.122654.

[27] MA Z,WU H H,ZHANG K S,et al.Long-term low dissolved oxygen accelerates the removal of antibiotics and antibiotic resistance genes in swine wastewater treatment[J].Chemical engineering journal,2018,334:630-637.

[28] PU C J,LIU H,DING G C,et al.Impact of direct application of biogas slurry and residue in fields:in situ analysis of antibiotic resistance genes from pig manure to fields[J].Journal of hazardous materials,2018,344:441-449.

[29] ZHANG J Y,CHEN M X,SUI Q W,et al.Fate of antibiotic resistance genes and its drivers during anaerobic co-digestion of food waste and sewage sludge based on microwave pretreatment [J].Bioresource technology,2016,217:28-36.

[30] CHENG W X,LI J N,WU Y,et al.Behavior of antibiotics and antibiotic resistance genes in eco-agricultural system:a case study [J].Journal of hazardous materials,2016,304:18-25.

[31] SUI Q W,ZHANG J Y,CHEN M X,et al.Distribution of antibiotic resistance genes (ARGs) in anaerobic digestion and land application of swine wastewater[J].Environmental pollution,2016,213:751-759.

[32] SUN W,GU J,WANG X J,et al.Impacts of biochar on the environmental risk of antibiotic resistance genes and mobile genetic elements during anaerobic digestion of cattle farm wastewater[J].Bioresource technology,2018,256:342-349.

[33] ZHANG J Y,LIU J B,LU T D,et al.Fate of antibiotic resistance genes during anaerobic digestion of sewage sludge:role of solids retention times in different configurations[J].Bioresource technology,2019,274:488-495.

[34] TIAN Z,ZHANG Y,YU B,et al.Changes of resistome,mobilome and potential hosts of antibiotic resistance genes during the transformation of anaerobic digestion from mesophilic to thermophilic[J].Water research,2016,98:261-269.

[35] YANG Y W,WU R T,HU J X,et al.Dominant denitrifying bacteria are important hosts of antibiotic resistance genes in pig farm anoxic-oxic wastewater treatment processes [J/OL]. Environment international,2020,143:105897 [2022-03-31].https://doi.org/10.1016/j.envint.2020.105897.

[36] SUI Q W,CHEN Y L,YU D W,et al.Fates of intracellular and extracellular antibiotic resistance genes and microbial community structures in typical swine wastewater treatment processes [J/OL]. Environment international, 2019, 133: 105183 [2022-03-31].https://doi.org/10.1016/j.envint.2019.105183.

[37] TAO C W,HSU B M,JI W T,et al.Evaluation of five antibiotic

resistance genes in wastewater treatment systems of swine farms by real-time PCR[J]. Science of the total environment, 2014, 496:116-121.

[38] SUI Q W, JIANG C, ZHANG J Y, et al. Does the biological treatment or membrane separation reduce the antibiotic resistance genes from swine wastewater through a sequencing-batch membrane bioreactor treatment process[J]. Environment international, 2018, 118:274-281.

[39] LI S N, CHU Y H, XIE P, et al. Insights into the microalgae-bacteria consortia treating swine wastewater: symbiotic mechanism and resistance genes analysis[J/OL]. Bioresource technology, 2022, 349: 126892 [2022-03-31]. https://doi. org/10.1016/j.biortech.2022.126892.

[40] CHEN H, ZHANG M M. Occurrence and removal of antibiotic resistance genes in municipal wastewater and rural domestic sewage treatment systems in Eastern China[J]. Environment international, 2013, 55:9-14.

[41] FERRO G, GUARINO F, CASTIGLIONE S, et al. Antibiotic resistance spread potential in urban wastewater effluents disinfected by UV/H_2O_2 process[J]. Science of the total environment, 2016, 560/561:29-35.

[42] MCKINNEY C W, PRUDEN A. Ultraviolet disinfection of antibiotic resistant bacteria and their antibiotic resistance genes in water and wastewater[J]. Environmental science & technology, 2012, 46(24):13393-13400.

[43] RIZZO L, MANAIA C, MERLIN C, et al. Urban wastewater treatment plants as hotspots for antibiotic resistant bacteria and genes spread into the environment: a review[J]. Science of the total environment, 2013, 447:345-360.

[44] MAO D Q, YU S, RYSZ M, et al. Prevalence and proliferation of antibiotic resistance genes in two municipal wastewater treatment plants[J]. Water research, 2015, 85:458-466.

[45] LIANG C Y, WEI D, ZHANG S Y, et al. Removal of antibiotic resistance genes from swine wastewater by membrane filtration treatment [J/OL]. Ecotoxicology and environmental safety, 2021, 210: 111885 [2022-03-31]. https://doi.org/10.1016/j.ecoenv.2020.111885.

[46] CHEN L, GAO S X, LOU L P, et al. Removal of intracellular and extracellular antibiotic resistance genes from swine wastewater by sequential electrocoagulation and electro-fenton processes [J]. Environmental engineering science, 2021, 38(2):74-80.

[47] ZHANG Y H, WANG L, XIONG Z K, et al. Removal of antibiotic resistance genes from post-treated swine wastewater by mFe/nCu system[J/OL]. Chemical engineering journal, 2020, 400: 125953 [2022-03-31]. https://doi.org/10.1016/j.cej.2020.125953.

[48] COLE S. The emergence of treatment wetlands[J]. Environmental science & technology, 1998, 32(9):218A-223A.

[49] WU H M, ZHANG J, NGO H H, et al. A review on the sustainability of constructed wetlands for wastewater treatment: design and operation[J]. Bioresource technology, 2015, 175:594-601.

[50] LIU L, LIU Y H, WANG Z, et al. Behavior of tetracycline and sulfamethazine with corresponding resistance genes from swine wastewater in pilot-scale constructed wetlands[J]. Journal of hazardous materials, 2014, 278:304-310.

[51] CARVALHO P N, ARAÚJO J L, MUCHA A P, et al. Potential of constructed wetlands microcosms for the removal of veterinary pharmaceuticals from livestock wastewater[J]. Bioresource technology, 2013, 134:412-416.

[52] SONG H L, ZHANG S, GUO J H, et al. Vertical up-flow constructed wetlands exhibited efficient antibiotic removal but induced antibiotic resistance genes in effluent[J]. Chemosphere, 2018, 203:434-441.

[53] VACCA G, WAND H, NIKOLAUSZ M, et al. Effect of plants and filter materials on bacteria removal in pilot-scale constructed wetlands[J]. Water research, 2005, 39(7):1361-1373.

[54] DU L, ZHAO Y Q, WANG C, et al. Removal performance of antibiotics and antibiotic resistance genes in swine wastewater by integrated vertical-flow constructed wetlands with zeolite substrate [J/OL]. Science of the total environment, 2020, 721: 137765 [2022-03-31]. https://doi.org/10.1016/j.scitotenv.2020.137765.

[55] LIU L, LIU C X, ZHENG J Y, et al. Elimination of veterinary antibiotics and antibiotic resistance genes from swine wastewater in the vertical flow constructed wetlands[J]. Chemosphere, 2013, 91(8):1088-1093.

[56] CHEN J, DENG W J, LIU Y S, et al. Fate and removal of antibiotics and antibiotic resistance genes in hybrid constructed wetlands[J]. Environment pollution, 2019, 249:894-903.

[57] ABOU-KANDIL A, SHIBLI A, AZAIZEH H, et al. Fate and removal of bacteria and antibiotic resistance genes in horizontal subsurface constructed wetlands: effect of mixed vegetation and substrate type[J/OL]. Science of the total environment, 2021, 759: 144193 [2022-03-31]. https://doi.org/10.1016/j.scitotenv.2020.144193.

[58] LIU L, LI J, XIN Y, et al. Evaluation of wetland substrates for veterinary antibiotics pollution control in lab-scale systems [J/OL]. Environmental pollution, 2021, 269: 116152 [2022-03-31]. https://doi.org/10.1016/j.envpol.2020.116152.

[59] ZHOU L J, YING G G, LIU S, et al. Simultaneous determination of human and veterinary antibiotics in various environmental matrices by rapid resolution liquid chromatography-electrospray ionization tandem mass spectrometry[J]. Journal of chromatography A, 2012, 1244:123-138.

[60] PRUDEN A. Balancing water sustainability and public health goals in the face of growing concerns about antibiotic resistance [J]. Environmental science & technology, 2014, 48(1):5-14.

[61] KRISTIANSSON E, FICK J, JANZON A, et al. Pyrosequencing of antibiotic-contaminated river sediments reveals high levels of resistance and gene transfer elements[J/OL]. PLoS One, 2011, 6(2): e17038 [2022-03-31]. https://doi. org/10.1371/journal.pone.0017038.

[62] WU N, QIAO M, ZHANG B, et al. Abundance and diversity of tetracycline resistance genes in soils adjacent to representative swine feedlots in China[J]. Environmental science & technology, 2010, 64(18):6933-6939.

[63] FAGERVOLD S K, BOURGEOIS S, PRUSKI A M, et al. River organic matter shapes microbial communities in the sediment of the Rhône prodelta[J]. The ISME journal, 2014, 8(11):2327-2338.

[64] YANG Y W, LIU Z X, XING S C, et al. The correlation between antibiotic resistance gene abundance and microbial community resistance in pig farm wastewater and surrounding rivers[J/OL]. Ecotoxicology and environmental safety, 2019, 182:109452

[2022-03-31].https://doi.org/10.1371/journal.pone.0017038.

[65] YUAN Q B, ZHAI Y F, MAO B Y, et al.Fates of antibiotic resistance genes in a distributed swine wastewater treatment plant [J].Water environment research, 2019, 91(12): 1565-1575.

[66] CHENG W X, LI J N, WU Y, et al.Behavior of antibiotics and antibiotic resistance genes in eco-agricultural system: A case study[J].Journal of hazardous materials, 2016, 304: 18-25.

[67] JOY S R, BARTELT-HUNT S L, SNOW D D, et al.Fate and transport of antimicrobials and antimicrobial resistance genes in soil and runoff following land application of swine manure slurry [J].Environmental science & technology, 2013, 47(21): 12081-12088.

[68] GAO F Z, HE L Y, HE L X, et al. Untreated swine wastes changed antibiotic resistance and microbial community in the soils and impacted abundances of antibiotic resistance genes in the vegetables[J/OL].Science of the total environment, 2020, 741: 140482 [2022-03-31]. https://doi. org/10.1016/j. scitotenv.2020.140482.

Research progress on transfer effect of antibiotic resistance gene in swine wastewater treatment process

YANG Lizhen, LIU Tianqi, WANG Lulu, CAO Yunyun, ZHOU Wenbing, XIAO Naidong, CAI Jianbo

College of Resources and Environment, Huazhong Agricultural University/
The Cooperative Innovation Center for Sustainable Pig Production Co-Sponsored
by Province and Ministry, Wuhan 430070, *China*

Abstract Antibiotic resistance genes (ARGs) in the aquatic environment have become one of the global health problems, and swine farm is one of the most important sources of ARGs in the environment, and the discharge of swine wastewater is the main channel for ARGs to enter the environment. At present, the environmental effect of ARGs from swine wastewater is not clear, the research on ARGs removal by different swine wastewater treatment processes is still in the initial stage, which needs more in-depth and detailed study to explore treatment methods that could reduce the abundance of ARGs in swine wastewater. In this paper, the process of ARGs from production to entry into the environment and the current status of ARGs pollution in swine farms were reviewed. The distribution and removal efficiency of ARGs in swine wastewater treatment processes were introduced with emphasis on different wastewater treatment methods (activated sludge method, anaerobic biological treatment method, physical and chemical method, constructed wetland method), and it was concluded that physical and chemical method is the most promising way to reduce ARGs pollution in swine farming environment. The researchers also gained insight into treatments that might reduce the amount of ARGs in swine wastewater. This paper summarized the occurrence and transmission of ARGs in the process of swine reproduction. The distribution, migration and transformation of antibiotic resistance genes in swine wastewater during different treatment processes were analyzed, and the mechanism of environmental factors affecting its transmission was elucidated. Finally, based on the shortcomings of the current pig wastewater treatment process in the removal of ARGs, the feasible suggestions of optimizing the treatment process and strengthening the monitoring of ARGs in each process were put forward.

Keywords resistance genes; antibiotics; gene migration; swine wastewater; swine farms; treatment technology

(责任编辑:赵琳琳,边书京)