Journal of Biosciences and Medicines, 2025, 13(5), 400-421
https://www.scirp.org/journal/jbm
ISSN Online: 2327-509X
ISSN Print: 2327-5081

Distribution Characteristics of Antibiotic Resistance Genes in Chinese Livestock, Poultry, and Aquaculture Farms

Xixi Hou, Dong Ding, Mengyue Liu, Haitao Yuan, Jinzhao Long, Yuefei Jin, Fang Liu, Haiyan Yang, Jingyuan Zhu*, Shuaiyin Chen*, Guangcai Duan

College of Public Health, Zhengzhou University, Zhengzhou, China
Email: *yuanzhu@zzu.edu.cn, *sychen@zzu.edu.cn

How to cite this paper: Hou, X.X., Ding, D., Liu, M.Y., Yuan, H.T., Long, J.Z., Jin, Y.F., Liu, F., Yang, H.Y., Zhu, J.Y., Chen, S.Y. and Duan, G.C. (2025) Distribution Characteristics of Antibiotic Resistance Genes in Chinese Livestock, Poultry, and Aquaculture Farms. *Journal of Biosciences and Medicines*, **13**, 400-421.
https://doi.org/10.4236/jbm.2025.135031

Received: January 24, 2025
Accepted: May 27, 2025
Published: May 30, 2025

Abstract

Farms are hotspots for antibiotic resistance genes (ARGs) due to the high density of animal breeding, nutrient enrichment, and the frequent use of antibiotics. However, limited information is available regarding the corresponding ARGs associated with animal farms. Here, the distribution characteristics of ARGs in different farms were summarized, providing a comprehensive overview of the spectrum of ARGs found in livestock, poultry, and aquaculture farms. A search across *Pubmed*, *Web of Science*, and *Embase* databases was conducted to identify relevant papers on farm ARGs, resulting in 1955 non-duplicated articles. Through manual extraction, 103 papers were included for further analysis. A total of 1627 kinds of ARGs were reported, of which the top three genes were sulfonamide ARGs (*sul1 and sul2*) and tetracycline ARGs (*tetM*). In livestock, poultry, and aquaculture farms, sulfonamide ARGs (*sul1* and *sul2*) were the most frequently reported types. Tetracycline ARGs (*tetO*, *tetQ*, *tetW*, and *tetM*) and macrolide-lincomycin-streptomycin B (MLSB) ARGs (*ermB*) were the main ARGs in livestock farms. In poultry farms, tetracycline ARGs (*tetA*, *tetC*, *tetG*, and *tetM*) and MLSB ARGs (*ermB*) were the main ARG subtypes. In addition, *tetB*, *tetX*, and *floR* were commonly reported in aquaculture farms. The ARG subtypes shared by different farms were tetracyclines (*tetA*, *tetC*, *tetG*, *tetM*, *tetO*, *tetQ*, *tetW*, *tetX*, and *tetT*), sulphonamides (*sul1*, *sul2*, and *sul3*), MLSBs (*ermB*, *ermC*, and *ermF*), beta-lactamases (*blaTEM*, and *blaOXA-1*), multidrugs (*acrA*, *acrB*, and *floR*), quinolones (*qnrA*, *qnrS*, and *oqxB)*, aminoglycosides (*aadA1*, *aadA*, and *aadE*), chloramphenicol (*fexA*), and others (*cfr*). ARG contamination was prevalent in all regions, with the most ARG subtypes reported in studies on pig farms and Eastern China. Among environmental media, animal feces and aquatic water were the main source and reservoir of ARGs. In this study, the distribution law of

ARGs in farms from different regions of China was described, the distribution characteristics of different ARGs in different species were compared, and the transmission risk of ARGs was assessed from the perspective of possible transmission routes. The findings have important scientific implications to optimize antimicrobial strategies and deepen the understanding on the spread of ARGs on farms.

Keywords

Livestock, Poultry Farms, Aquaculture, Antibiotic Resistance Genes (Args), Environment, Distribution

1. Introduction

Antibiotic resistance and microbial evolution have become important causes of increased morbidity and mortality in humans and animals worldwide [1]-[3]. The annual rate of deaths directly caused by AMR is predicted to increase to 10 million by 2050, with the highest estimated deaths being in Asia [4]. Around 100,000 - 200,000 tons of antibiotics are used globally each year [5] and global consumption of veterinary antibiotics is projected to grow by 11.5% in 2030. In China, the use of veterinary antibiotics as feed additives for growth promotion has reached approximately 6000 - 8000 tons per year [6]-[8]. A survey found that the demand for antibiotics in food animals in developing countries continues to increase every year [9]. In different various habitat environments and regions, the effects of different environmental and social activities have led to differences in antibiotic residues. For example, the highest concentration of gentamycin was detected in pig manure in Shandong Province at 754.4 mg/kg, and quinolones, such as norfloxacin and enrofloxacin, were detected in eight provinces of China at 225.45 and 1420.76 mg/kg, respectively [7] [10]. Concentrations of oxytetracycline and sulphadimethoxine were detected in wastewater from nearby pig farms and rivers in Jiangsu at 72.9 and 211 μg/L, respectively [11]. The maximum concentrations of enrofloxacin and ciprofloxacin detected in chicken feces were 61.3 and 18.8 mg/kg, respectively [12]. The levels of antibiotics detected in aquaculture waters generally range from $ng \cdot L^{-1}$ levels to $\mu g \cdot L^{-1}$ levels [13].

Antibiotic resistance genes (ARGs) have emerged as a new type of environmental pollutant that poses a major threat to global public health [14] [15]. Various ARGs have been detected in farms, live poultry slaughterhouses, rivers, lakes, sewage treatment plants, municipal water supply systems, medical wastewater, and soil [16]-[22]. Considerable evidence suggested that ARGs and antibiotics are released from livestock and poultry farms into their surroundings that include water, soil and air [23]. Feces and wastewater containing ARBs can reach a wider environment through runoff and atomization [24]-[26] and then spread to humans through the food chain. ARBs and ARGs in the human body are like a "time bomb" with great destructive potential to consistently threaten residents and farm workers' health [27]. Therefore, exploring the distribution law and characteristics of ARGs in the farm environment and providing suggestions on the use of antibiotics in farms and the prevention of transmission are necessary.

The "One Health" strategy is a cross-sectoral collaborative approach to address the issue of AMR, it focuses on the health of humans, animals, and the environment from the perspective of "One Health" [28]. Therefore, the species and diversity of ARGs in the feces and surrounding environment of different species (swine, cattle, chicken, duck, and aquatic animals) were summarized in the present study. The characteristics of animal breeding and ARG pollution in different regions were compared systematically. The findings could contribute to the full understanding of ARGs in livestock, poultry, and aquaculture farms and their surrounding environment. This research aimed to provide a scientific foundation for controlling the transmission of ARGs and enhancing health management in farms.

2. Methods

2.1. Study Inclusion and Selection

The literature data for this study were searched from the core databases of *Web of Science*, *Pubmed* and *Embase* on August 26, 2023. By Using [(ARGs) OR (antibiotic resistance genes) OR (antimicrobial resistance genes) AND ((animal farms) OR (animal farms) OR (livestock)] AND (China) as the search keywords, ARG information was collected from the full texts of previously published studies searched on the three websites by artificial extraction. The inclusion criteria were as follows: 1) studies reporting the characteristics of ARGs on farms; 2) specific sampling sites, drug resistance gene detection and quantitative methods and 3) articles focusing on the analysis of major ARGs and specific ARG subtypes, with ARGs subtypes available in the attached table. The exclusion criteria were as follows: 1) lack of sampling sites and drug resistance gene testing methods; 2) repeated analysis on the same ARGs in a unified study, and 3) lack of ARG subtypes in reported farms.

2.2. Statistical Analysis and Visualization

The overall distribution of ARGs in Chinese farms was assessed on the basis of the number of reports for each ARG in a collection of 103 articles. The main ARGs present in different farms were calculated by dividing the number of literature reports on a certain gene by the number of literature reports on that farm. The proportion of the top 53 kinds of ARGs in each farm was calculated in accordance with the number of literature reports.

The ARGs data were processed using Microsoft Excel 2016. The website https://www.liuchengtu.com/home/myfile/ was used to make an article screening flow chart. A Sankey diagram was produced on the Pythonol website (https://www.genescloud.cn/chart/ChartOverview). A histogram was created on GraphPad Prism (version 8.0.2). Network analysis was conducted in Gephi platform (version 0.9). Venn diagrams were generated using EVenn [29]. The antibiotic species reported by different farms were visualized using python (version 3.11). The distribution of ARGs in different regions of China was presented using R (version 4.3.1) software.

3. Overall ARG Distribution in Farms

The literature search yielded 1955 nonduplicate publications, of which 103 eligible studies were reviewed in full text (**Figure 1**). A total of 1627 ARG subtypes extracted from the 103 studies were categorized into 16 ARG types and MGEs. Among them, 79 (77%) studies reported 84 tetracycline resistance gene subtypes, 67 (65%) studies reported 46 sulfonamide resistance gene subtypes, and 53 studies (51%) reported 126 macrolide-lincomycin-streptomycin B (MLSB) resistance gene subtypes, 40 (39%) studies reported 711 beta-lactamase resistance gene subtypes, 38 (37%) studies reported 211 aminoglycoside resistance gene subtypes, 36 (35%) studies reported 47 quinolone resistance gene subtypes, 34 (33%) studies reported 29 mobile genetic elements (MGEs), and 31 (30%) studies reported 146 multidrug resistance gene subtypes (**Figure 2**).

In accordance with the reported frequency of farm ARGs, the top 53 ARGs (detected in more than three articles) with the largest number of articles were selected, and their proportions in different farms were analyzed (**Figure 3**). They covered 10

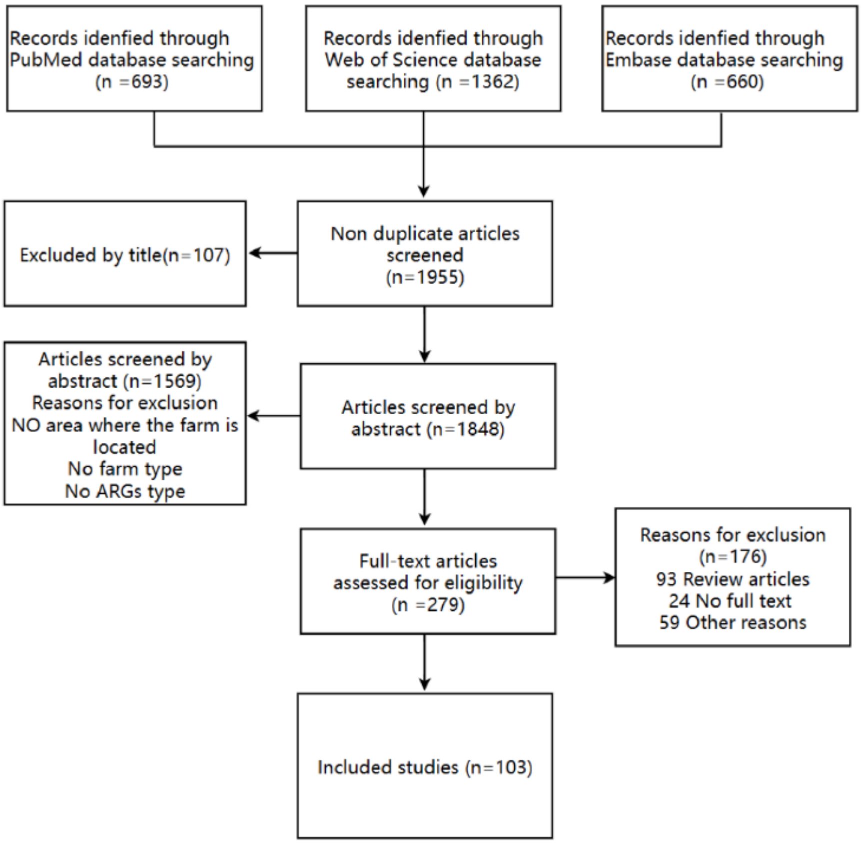

Figure 1. Articles and screening flow charts collected from *Pubmed*, *Web of science*, and *Embase*.

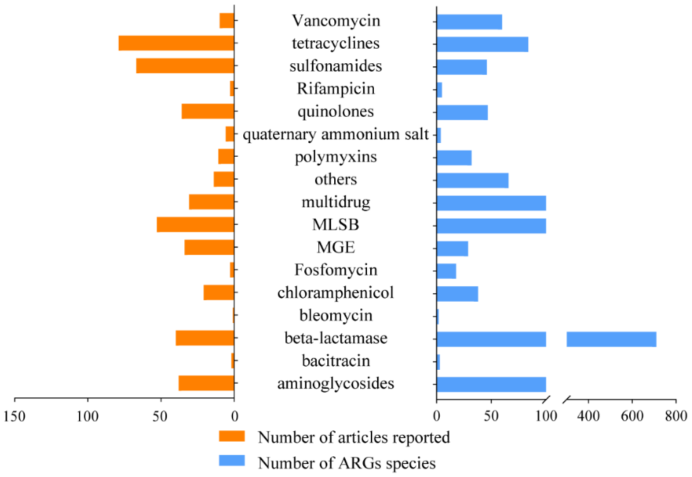

Figure 2. The number of ARGs species and literature reports collected in the 103 articles included in this study.

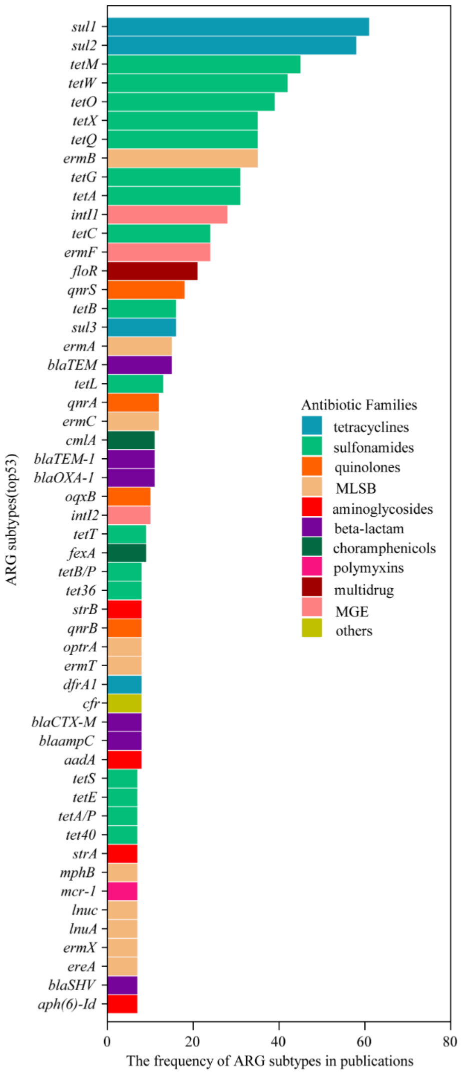

Figure 3. Reported frequencies of the top 53 ARG subtypes and their respective antibiotic families extracted from *Pubmed*, *Web of science*, *Embase* publications.

antibiotic families: tetracyclines (*tet*), sulfonamides (*sul*, and *dfr*), quinolones (*qnr*, and *oqx*), MLSBs (*erm*, *optr*, *ere*, *lnu*, and *mph*), aminoglycosides (*aad*, *str*, and *aph*), beta-lactamase (*bla*), chloramphenicols (*cml*, and *fex*), polymyxins (*mcr*), multi-resistant type (*flo*), unclassified (*cfr*) antibiotic types, and MGEs (*intI*). The sulfonamide ARG subtypes *sul1* and *sul2* were the highest rates reported in literature, followed by tetracyclines and MLSB.

4. Characteristics of the Regional Distribution of ARGs

China was divided into seven regions: South China, North China, Central China, East China, Southwest, Northwest, and Northeast. The ARG distribution in Southwest, Northwest and Northeast regions into other categories. Most publications were reported in South China, followed by East China, other categories, North China, and Central China. Among the 103 studies of ARGs/MGEs related in farms, 29% (30/103) of studies reported on farms in South China, with 472 ARG subtypes. They were categorized into 14 ARG types and MGEs, of which Guangdong Province reported the highest number of ARGs. In addition, the highest number of ARGs in East China, with 1382 subtypes, belonging to 15 ARG types and MGEs. Among them, the species of ARGs reported in farms in Shandong Province were the most abundant, followed by Fujian Province. The serious ARG pollution in farms in Central China was mainly concentrated in Henan Province (**Table 1**).

Table 1. Distribution characteristics of ARGs species in different regions.

Province	Total species of ARGs subtype
Beijing	44
Tianjin	60
Hebei	14
Shanxi	10
Inner Mongolia	5
Liaoning	28
Heilongjiang	46
Shanghai	7
Jiangsu	85
Zhejiang	71
Anhui	1
Fujian	618
Jiangxi	55
Shandong	1102
Henan	193
Hubei	66

Continued

Hunan	11
Guangdong	689
Guangxi	41
Hainan	11
Sichuan	1
Guizhou	42
Yunnan	23
Shaanxi	58
Ningxia	12

In South China, East China, and Central China, sulfonamide ARGs, such as *sul1* and *sul2*, were the type with a high rate of literature report. Moreover, the number of literature reports on *tetM* in East China was the largest, followed by *tetO* and *tetW*. In South China, *tetX* had the largest number of literature reports, followed by *tetM* and *tetA*. In North China, *tetW*, *tetM*, and *tetO* had the largest number of articles, followed by *intI1*, *tetQ*, *blaTEM-1*, *intI2*, *sul1*, *sul2*, and *tetC*. Similar trends were reported in publications from other regions, indicating widespread antibiotic use in farms throughout China. The distribution of the top 40 ARGs in different regions of China is shown in **Figure 4**, covering 9 antibiotic families: tetracyclines, sulfonamides, quinolones, aminoglycosides, beta-lactamases, MLSB, multidrugs, other resistant drugs, chloramphenicol, and MGEs. MLSBs (*ermB* and *ermF*) were found to be common in Chinese farms. Meanwhile, the sulfonamide ARG *dfrA1* was also abundant in South China. The quinolone gene *qnrS* had the greatest number of literature reports in East China.

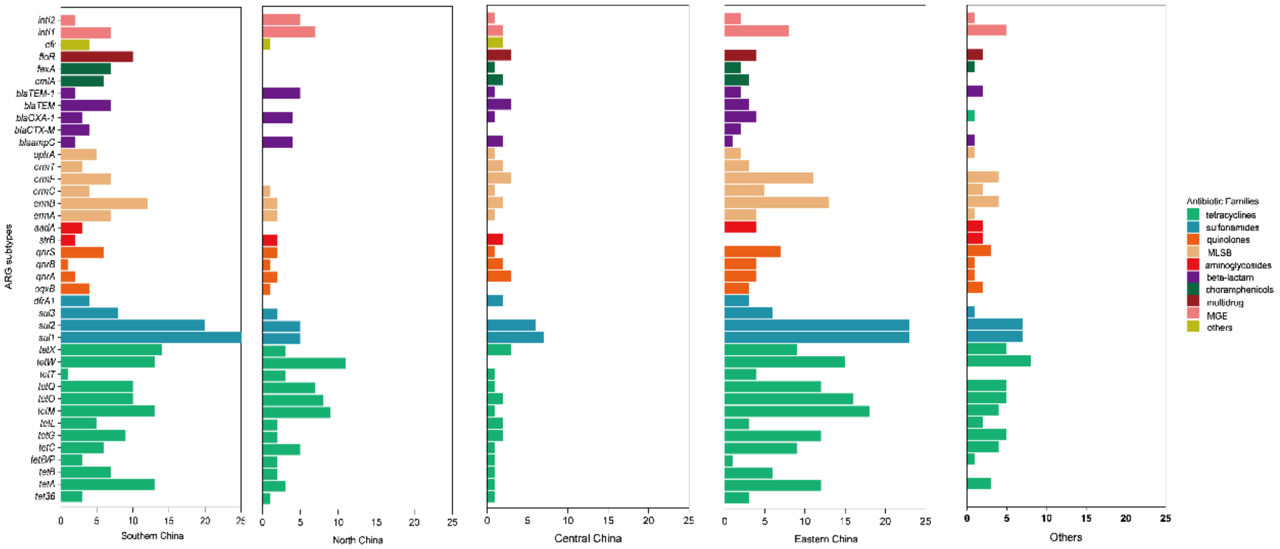

Figure 4. Reported frequency of the top 40 ARG subtypes extracted from Pubmed, Web of science, Embase publications grouped by region.

5. Distributional Characteristics of ARGs in Different Farms

5.1. Livestock Farms

5.1.1. Swine Farms

Among the 103 studies of ARGs related to farms, 54 (52%) articles on pig farms were screened, reporting 1427 ARG subtypes belonging to 16 ARG types and MGEs. The beta-lactamase subtype of ARGs had the highest number of reports, followed by aminoglycosides, multidrug resistance, and MLSB (**Table 2**; **Figure 6(a)**; **Figure 7**). Among the first 53 types of ARGs, the reporting rate of beta-lactamase ARGs (*blaTEM-1*, *blaSHV*, *blaOXA-1*, *blaCTX–M* and *blaampC*) was the highest. The aminoglycoside ARGs [*aph(6)–Id*] [and *aadA*] and some MLSB ARG subtypes were more abundant than in other farms (**Figure 5**). In addition, among the 54 studies on pig farms, the ARG subtypes with the highest number of literature reports were sulfonamide ARGs (*sul1* and *sul2*), followed by tetracycline ARGs (*tetM*, *tetW*, and *tetO*) and MLSB ARGs (*ermB*).

Livestock feces is an important reservoir and vehicle for the trans-environmental spread of ARGs [30]. In total, 1272 subtypes of ARGs and MGEs were reported in pig feces, and they were classified into 16 ARG types. Beta-lactamase was the most abundant ARG type, with a total of 533 subtypes, followed by aminoglycosides, multidrugs, and MLSB. A total of 433 subtypes of ARGs and MGEs were reported in wastewater, and they were classified into 15 ARG types. Among various mediators, the wastewater of pig farms, had the largest number of MGEs subtypes. In the soil of pig farms, 512 subtypes of ARGs/MGEs were reported. The amount of beta-lactamase ARGs in soil was higher than in wastewater and air. The aminoglycoside and tetracycline ARGs were more abundant in the air of pig farms (**Figure 6(b)**).

5.1.2. Cattle Farms

Among the 103 studies of ARGs related to farms, 18% (19/103) of articles on cattle farms were screened, reporting 186 ARG subtypes belonging to 11 ARG types and MGEs**.** The number of tetracycline ARGs was the highest, followed by beta-lactamase ARGs (**Table 2**; **Figure 6(a)**). Among the 19 studies related to cattle farms, the literature reports on sulfonamide ARGs (*sul1* and *sul2*) were the most numerous, followed by tetracycline ARGs (*tetW* and *tetQ*). Among the types of farms, cattle farms had the higher number of species with MGE subtypes. Among the first 53 types of ARGs, the literature on quinolone ARG *oqxB* had the highest proportion, followed by *tetT* and *ermC*. Moreover, the reporting rate of aminoglycoside ARG (*strB*) was higher than that in pig farms (**Figure 5**).

In feces from cattle farms, 170 ARG subtypes belonging to 11 ARG types and MGEs were reported. Tetracycline and beta-lactamase ARGs had multiple subtypes. The wastewater of cattle farm contained a high number of MLSB ARG subtypes. Similar to the distribution of ARGs in wastewater, the ARGs in cattle farm soil were classified into eight ARG types. Besides *intI1* and *intI2*, *intI3*, *tnpA-01*, *trb-C*, *tnpA-02* and *tnpA-05* were found in cattle farm soil. Some research data

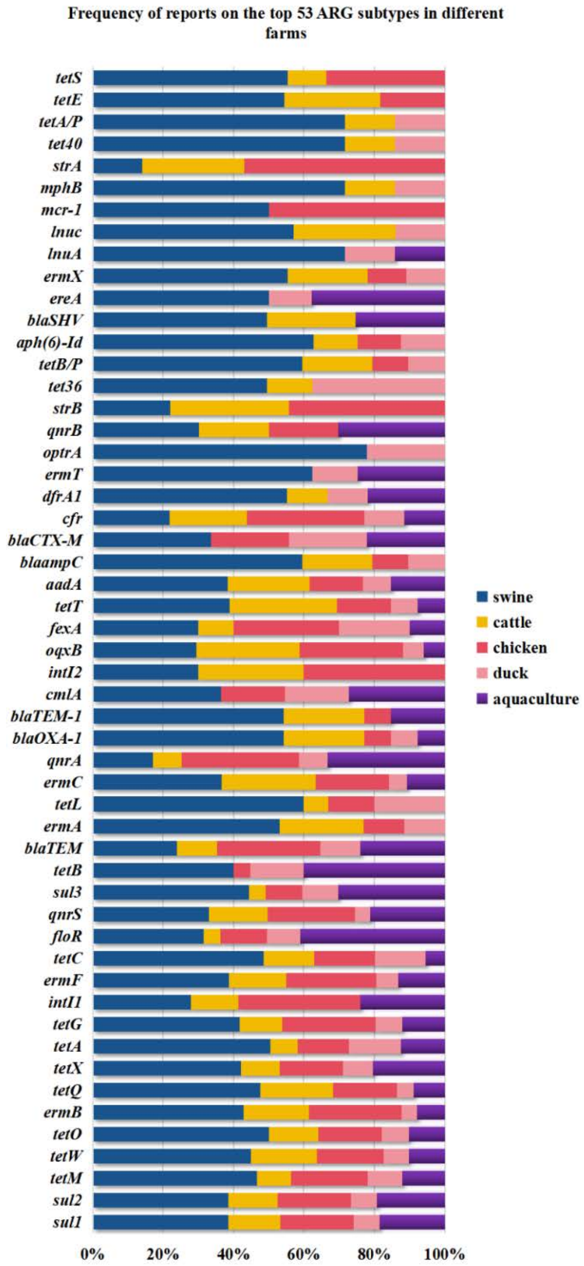

Figure 5. Distribution of the top 53 ARG subtypes in different farms.

Table 2. Article report on antibiotic resistance genes in different farms.

Farm types	Number of articles	Total number of articles	percentage	Number of ARG subtype species	Total species of ARG subtype	percentage
chicken	27	103	26%	134	1627	8%
cattle	19	103	18%	186	1627	11%
aquaculture	24	103	23%	165	1627	10%
duck	8	103	8%	347	1627	21%
swine	54	103	52%	1427	1627	88%

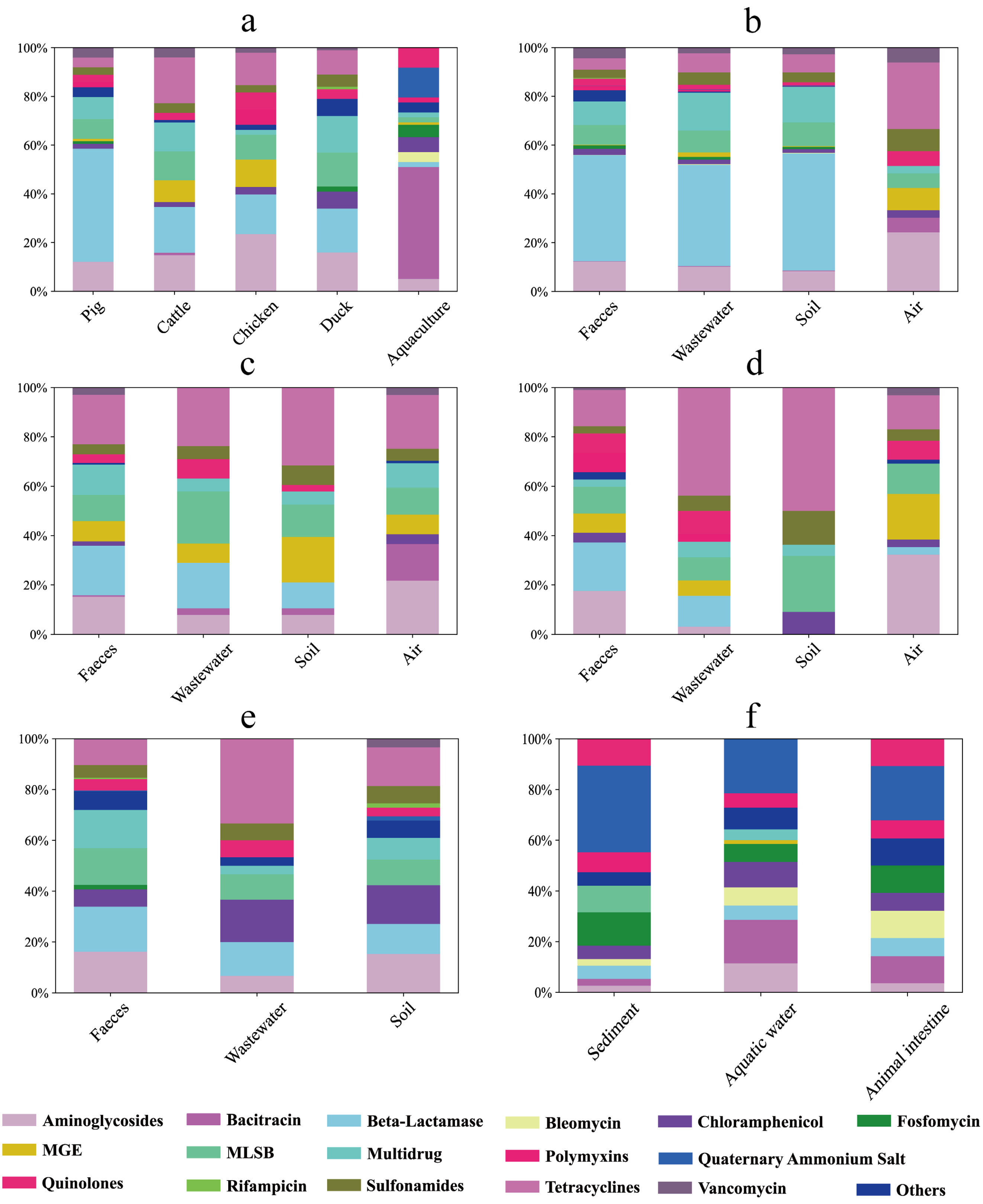

Figure 6. (a) Types of antibiotics in pig farms, cattle farms, chicken farms, duck farms, aquaculture farms. (b)-(e) Distribution of antibiotic species in feces, wastewater, soil and air from pig, cattle, chicken and duck farms, respectively. (f) Distribution of antibiotic species in aquaculture farms sediments, aquaculture water and animal intestines.

showed that the detection rate of *intI1* in all soil samples of dairy farms was 100% [31]. In the air of cattle farms, a total of 101 ARG subtypes were reported, with tetracycline and aminoglycoside ARG subtypes being the most abundant, followed by beta-lactamase and MLSB subtypes (**Figure 6(c)**).

5.2. Poultry Farms

5.2.1. Chicken Farms

Among the 103 studies of ARGs related to farms, 26% (27/103) of articles reported farm-associated ARGs in chicken farms, including 134 ARG subtypes belonging to 11 ARG types and MGEs (**Table 2**; **Figure 6(a)**). Except in pig farms, polymyxin had the largest number of subtypes reported in chicken farms. Among the first 53 subtypes of ARGs, the aminoglycoside ARG (*strA*) in chicken farms had the highest reporting rate among all farms (**Figure 5**). Of the 27 studies conducted in chicken farms, sulfonamide ARG subtypes (*sul1* and *sul2*) were reported in 17 and 16 articles, respectively, followed by MLSB ARG (*ermB*) and tetracycline ARGs *tetM* and *tetG*.

Previous studies have shown that the concentration of ARGs in poultry feces was higher than that in livestock [32]-[34]. In the feces of chicken farms, a total of 102 ARG subtypes, belonging to 11 ARG types and MGEs were reported, with beta-lactamase being the most abundant ARG type. In wastewater, with tetracycline was the most abundant ARG type. Twenty-two ARGs were reported in soils, and they were classified into five ARG types. Research has shown that the prevalence of ARGs in agricultural soils may be a source of groundwater pollution through vertical migration [35]. In the air of chicken farms, aminoglycosides had the largest number of subtypes. The high abundance of ARGs in chicken farms may be related to the prevalence of MGEs (**Figure 6(d)**).

5.2.2. Duckery

Among the 103 studies of ARGs related to farms, 8% (8/103) of articles reported farm-associated ARGs in duck farms, including 347 ARG subtypes, belonging to 12 ARG types and MGEs (**Table 2**; **Figure 6(a)**; **Figure 7**). Among them, beta-lactamase had the largest number of subtypes, with 62 species, followed by aminoglycosides, multidrugs and MLSB. Among the first 53 subtypes of ARGs, *tet36* had the highest reporting rate, followed by *tetL* and *tetC* (**Figure 5**). In addition, among the eight studies on duck farms, sulfonamide ARGs (*sul1* and *sul2*) still had the largest number of reports, followed by *tetA*, *tetM*, and *tetC*.

In duck feces, a total of 339 ARG subtypes, belonging to 12 ARG types and MGEs were reported (**Figure 6(e)**). Among them, aminoglycosides, beta-lactamase, MLSB, multidrug, vancomycin, tetracycline had many ARG subtypes. All 34 tetracycline and 17 sulfonamide ARG subtypes in duck farms were present in feces. Thirty subtypes of ARGs were reported in duck farm wastewater, belonging to eight ARG types and MGEs, with tetracycline subtypes being the most abundant.

5.3. Distribution of ARGs in Aquaculture

Aquaculture is one of the fastest growing industries in the world [36]. However,

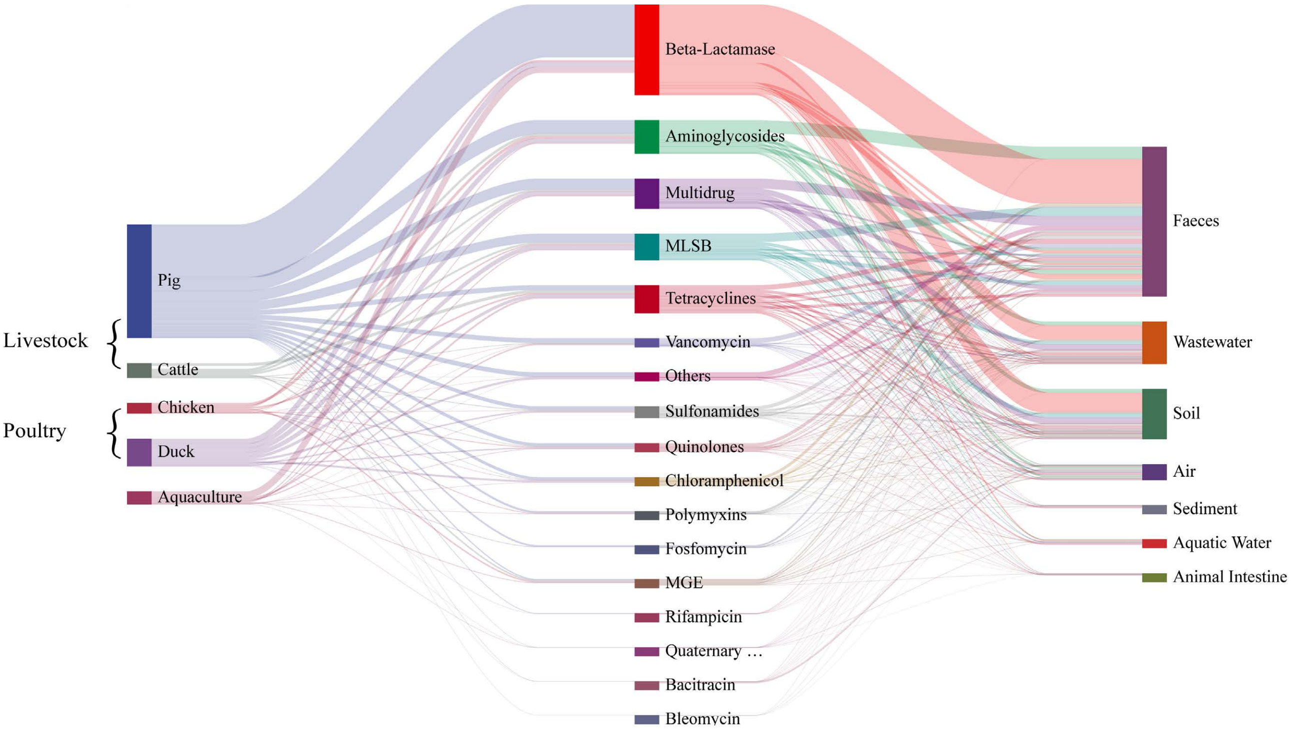

Figure 7. Sangki map of antibiotic species in different farms and environmental media.

high-density and mixed farming has led to a decline in water quality and outbreaks of aquatic animal diseases [37], and the consequent high use of antibiotics in feeds and aquaculture medicines has resulted in elevated drug resistance.

Among the 103 studies of ARGs related to farms, 23% (24/103) of articles reported farm-associated ARGs in aquaculture farms, including 165 ARG subtypes, belonging to 12 ARG types and MGEs (**Table 2**; **Figure 6(a)**). Among them, β-lactamase subtypes and quantities were the largest, followed by tetracycline and vancomycin. In the first 53 subtypes of ARGs/MGEs, tetracycline ARG subtypes, such as *tetB*, were the most dominant, followed by *tetX* (**Figure 5**). *Sul3* had a high reporting rate in aquaculture farms. In addition, among the 24 studies on aquaculture, *sul1* and *sul2* had the largest number of literature reports, followed by tetracycline ARGs (*tetX*, and *tetB*) *and* multidrug ARG *floR*.

ARGs are widely distributed in the intestines of aquaculture animals [38]. In total, 70 subtypes of ARGs/MGEs were reported in aquaculture water, and they were classified into 10 ARG types (**Figure 6(f)**). Tetracycline ARG subtypes were the most abundant, followed by beta-lactamase. A total of 34 ARG subtypes were reported in sediments, including 13 kinds of tetracycline ARGs, which were similar to those in aquaculture water. However, *qacED1*, *bacA*, *acrB* and *ompF* were mainly present in sediments. The sulfonamide ARGs in sediments mainly included *sul1*, *sul2* and *sul3*. In addition, the ARGs present in the intestines of cultured fish and shrimp did not considerably differ from the ARGs in cultured sediments. A total of 28 ARG subtypes in animal intestines were reported. Among them, the most diverse ARG types were tetracycline, sulfonamide, and quinolones.

6. Shared and Unique ARGs

ARGs are also likely to be shared among various environmental media in livestock, poultry, and aquaculture farms. Among these shared ARGs, the number of common genes reported in pig, cattle, chicken, duck, and aquaculture farms was 28, belonging to nine ARG types and MGEs. They included tetracycline ARGs (*tetA*, *tetC*, *tetG*, *tetM*, *tetO*, *tetQ*, *tetW*, *tetX*, and *tetT*), sulfonamide ARGs (*sul1*, *sul2*, and *sul3*), MLSB ARGs (*ermB*, *ermC*, *and ermF*), beta-lactamase ARGs (*blaOXA-1*, *and blaTEM*), multidrug ARGs (*acrA*, *acrB*, *and floR*), aminoglycoside ARGs (*aadA*, *aadA1*, *and aadE*), quinolone ARGs (*qnrA*, *qnrS*, *and oqxB*), chloramphenicol ARGs (*fexA*), and other classes of ARGs (*cfr*). Seven ARG subtypes belonging to four types were shared by aquaculture, pig, cattle, and chicken farms, including quinolone ARGs (*qnrB*, *and qnrD*), beta-lactamase ARGs (*blaTEM-1*, *blaGES*), vancomycin ARGs (*vanA*, *and vanB*) and MGE (*intI1*). In livestock and poultry farms, 15 ARG subtypes belonging to six types were shared by pig, cattle, and chicken farms, including tetracyclines ARGs (*tetS*, *tetT*, and *tetB/P*), quinolone ARG (*qepA*), aminoglycoside ARGs [*aadA*] [*aac*(*6*)*-Ib*(*akaaacA4*)] [*and strB*], beta-lactamase ARGs (*blaOXA-1*, *blaTEM-1*, and *blaampC*, *blaGES-1*), multidrug ARGs (*acrA*, and *acrB*), other unclassified ARG (*catB3*), and MGE (*intI1*). *ErmX*, *ermA*, *ermQ*, *tetB/P*, *tetL*, *tet32*, *blaampC*, *blaNDM*, *catB3*, *mefA*, and *aph*(*6*)*Id* also shared in swine, cattle, chicken, and duck farms (**Figure 8(a)**, **Figure 8(b)**).

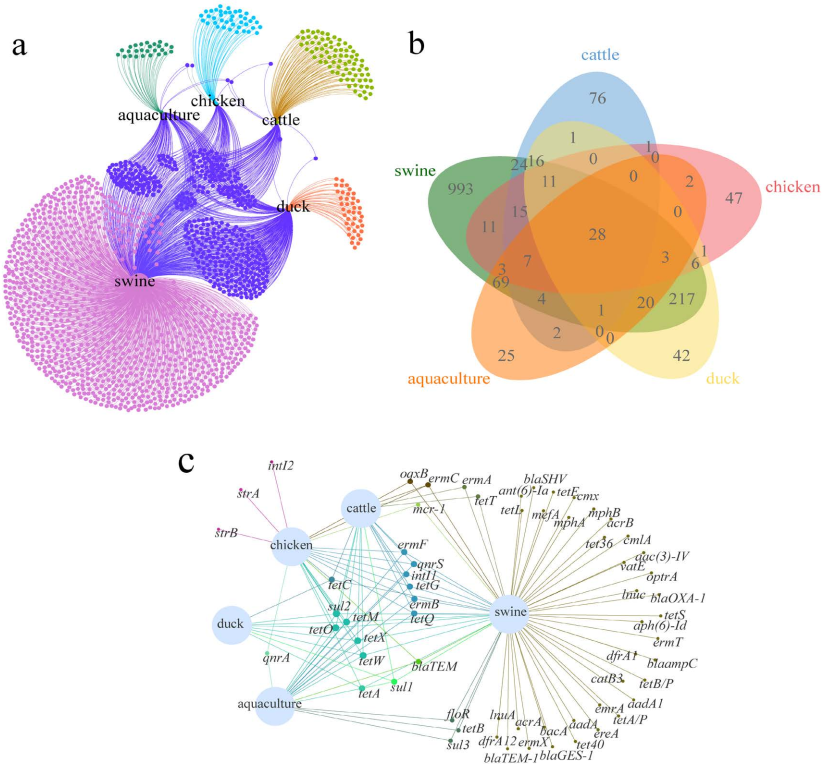

Figure 8. (a)-(b) Co-occurrence and number of ARG subtypes in pig farms, cattle farms, chicken farms, duck farms and aquaculture farms. (c) The frequency of literature reports on different farms is greater than or equal to 5.

For the majorly shared ARGs with more than or equal to five articles reports in different farms (**Figure 8(c)**). The largest number of shared genes was in pig, cattle, chicken, and aquaculture farms, including genes (*ermB*, *tetQ*, *tetG*, *ermF*, *intI1*, and *qnrS*), followed by *sul2*, *tetM*, *tetW*, *tetO*, and *tetX*. The results also showed a large number of shared ARGs between pig farms and other farms. The number of ARG subtypes shared by pig and duck farms was the largest, with 217 ARG subtypes, followed by pig and aquaculture farms, with 69 ARG subtypes shared on them. A total of 993 unique ARG subtypes were found in pig farms (**Figure 8(a)**, **Figure 8(b)**), indicating that the research on ARGs in China was mostly biased towards pig farms.

In this study, a large number of ARG subtypes were shared in the environmental media of different farms (**Figure 9**). In livestock farms, the most abundant

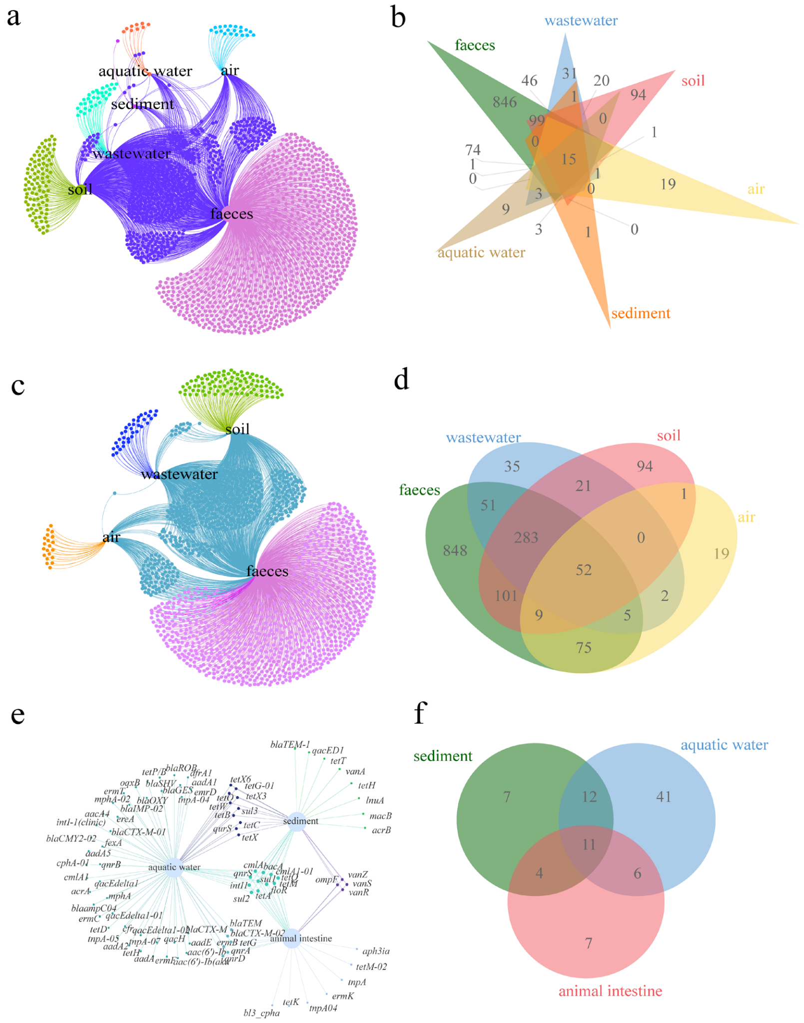

Figure 9. Venn diagram of ARGs and quantity shared by different farms and different environmental media. (a) Venn network diagram of ARG subtypes shared in livestock farms and aquafarms. (b) Venn diagram of the number of ARG subtypes shared in livestock farms and aquafarms. (c) Venn network diagram of shared ARG subtypes in livestock farms. (d) Venn diagram of the number of ARG subtypes shared in livestock farms. (e) Venn network diagram of ARG subtypes shared in aquafarms. (f) Venn diagram of the number of ARG subtypes shared in aquafarms.

ARG subtypes were shared in feces, wastewater, and soil, with 283 ARG subtypes, followed by 101 ARG subtypes, shared between feces and soil. From all media in livestock and aquaculture farms, the largest number of genes was shared in feces and soil, with 99 ARG subtypes. In addition, 848 ARG subtypes were specifically present in feces. A total of 52 ARG subtypes were shared among feces, wastewater, soil, and air. Of these 52 ARG subtypes, 15 were shared with sediments, aquatic water, and animal intestines.

7. Discussion

In this systematic review, the distribution characteristics of ARGs in different farms in China from 103 studies were analyzed. The findings indicated that the number and types of ARG reports were the highest in East China, with Shandong Province and Fujian Province being the most polluted. The pig farms in China had the largest number of ARG subtypes and species, followed by duck farms, cattle farms, aquaculture farms, and chicken farms. Antibiotics, ARBs, and ARGs have been reported to be widely distributed in various environmental substrates [39]. Here, the distribution law of ARGs in the feces, soil, wastewater, and air of animal husbandry and poultry farms, and in the aquatic water, sediments, and animal intestines from aquaculture were summarized.

Among the 103 studies on the Chinese farm industry, different degrees of ARG and MGE contamination of tetracycline, sulfonamide, quinolone, aminoglycoside, beta-lactamase, MLSB, multidrug, and chloramphenicol were found in farms from different regions of China. Previous studies have shown that sulfonamides, tetracyclines, quinolones, and macrolides are widely used in modern livestock farm industries [33] [40]. The findings of the present study are consistent with those of previous studies [41]. Furthermore, more research on aquaculture due to the coastal characteristics of South China, so it can be increased in the use of antibiotics in aquaculture in South China of management, especially in Guangdong Province and Guangxi Province. The results also suggested that among the types of ARGs, the number of beta-lactamase ARG subtypes was the highest in pig, duck and aquaculture farms. To date, beta-lactamase antibiotics have been widely applied in livestock husbandry to treat bacterial infections, and resistance to beta-lactamase antibiotics is categorized as high-risk multidrug resistance, which is closely associated with the human health [42]. The results of a study on the distribution of ARGs in the gut of Chinese crayfish, demonstrated that the beta-lactamase class had the highest absolute abundance of the nine resistance genes tested [43], may be due to the high sales of beta-lactamases in aquaculture [44].

Enrichment was most pronounced in animal feces, followed by soil and wastewater. In aquaculture farms, the types and quantities of ARGs in the aquatic water, sediment, and animal intestines were relatively similar (**Figure 5**). Previous studies have shown that feces samples had the highest abundance and diversity of ARGs, and that they were one of the potential contributors to the surrounding environment and workers [45]. However, studies have shown that, many swine bacterial species cannot survive in the human gut. Moreover, farm workers are more mobile and have a [46] more diverse diet, hence more opportunities to acquire resistance to bacteria [47]. Therefore, the spread of ARGs in farm workers may be influenced by more than the farm environment. ARGs are also abundant in soils around livestock farms and fertilized farmland, the abundance of ARGs in fertilized soil was 2.1 - 138.0 times that in unfertilized soil [48]. The concentrations of ARGs in soil were lower than those in feces, possibly due to the dilution effect of the soil matrix during fertilization. The application of wastewater in farmland is a major route of dissemination of ARGs to the environment, increasing the ARG level in soils and in runoffs [49] [50]. The presence of multiple antibiotics in wastewater fertilization soils has been observed in several studies [51] [52]. Therefore, wastewater, as one of the wastes of animal production, is considered to be a hot environment for antibiotic resistance [53]. Some studies have shown that the relative abundance of ARGs in aquaculture environmental sediments was higher than that in aquaculture water [54]. However, the results of the present study indicated a greater variety and quantity of ARGs in aquaculture water. The reason may be related to different farming practices and environments. Other studies have shown that integrated culture ponds (duck and fish ponds) exhibited the lowest absolute abundance of ARGs in culture waters, and the highest absolute abundance of ARGs was found in sediments [55]. The possible reason is that ARGs spread over time, leading to their long-term accumulation in sediments and enhancing antibiotic resistance [15]. In summary, the difference in the distribution of ARGs in different types of farms may be attributed to the sample types, animal types, and sampling time affecting the detection rate and distribution rule of genes [56].

ARGs may be transferred between bacteria via genetic factors, for instance, MGEs, plasmids, transposons, and integrons, act as resistance genes transmitting agents in different environmental media [57]. The present study found that proportion of MGEs was the highest in the wastewater of cattle and pig farms. In chicken farms, the MGE subtypes mainly existed in soil. A comprehensive study examining ARGs in livestock farms in East China, found 10 *tet* resistance genes and two *sul* genes, as well as a genetic element, *intl1*, associated with mobile ARGs [13] [32]. In broiler farms, *tnpA* and *intl1* were significantly and positively correlated with seven and five ARG subtypes, respectively [58]. The presence of abundant MGE subtypes, including *intI1*, *tnpA*, *tnpA04*, and *tnpA-05*, in aquatic water, sediments, and animal intestine, may be the reason for the water environment's ARG contamination levels being similar.

To sum up, the spread of ARGs on farms is a more serious problem in China. Corresponding measures must be taken to rectify the phenomenon of excessive use of veterinary drugs and exceeding residue limits in breeding. First, drug sensitivity tests must be carried out, and correct and efficient antibiotics for large-scale farms to choose from and refer to must be selected. Second, the technical guidance on the use of veterinary antibiotics must be strengthened, and their awareness and level of standardized drug use must be improved. When using antibiotics, the principle of correct usage must be strictly followed, excessive or insufficient use should be avoided, and the combined use of antibiotics should generally not exceed three types. In addition, strengthening the disinfection of the breeding environment and strictly implementing the disinfection and quarantine system are necessary. With the advancement of isotope labeling and fluorescent labeling technologies, the visualization of the ARG propagation process by labeling bacteria, plasmids or other genetic elements to design bonding conditions [59] is an effective means to control ARG propagation and diffusion on the basis of process resistance, and it is the focus of future research.

The limitations of this study must be acknowledged. First, the extraction of ARG diversity and the distribution information of different types of farms had limitations and information biases. One study that contained ARG information on multiple types of farms and media was included in the present study. In the subsequent studies, some scientifically rigorous methods should be used to extract information, and more than two people should be involved in the verification and entry of data.

8. Conclusion

This study showed that the pollution of various types of ARGs is serious in Chinese farms. Nine ARG types were shared in pig, cattle, chicken, duck, and aquaculture farms. ARGs were mainly present in animal feces, followed by soil and wastewater. In aquaculture farms, aquacultural water was the main source and repository of ARGs. Various ARG subtypes in livestock and aquaculture farms have demonstrated certain differences, which may be caused by animal types, breeding conditions, and sample types. The reporting rate of ARGs in farms in South China was the highest, and the number of ARG species in East China was the highest. Overall, the findings provide a scientific basis for corresponding measures to reduce the production and transmission of ARGs in livestock farms.

Acknowledgements

This work was financially supported by the National Science and Technology Specific Projects (grant number2018ZX10301407).

Data Availability

Data generated analyzed during this study are provided in full within the published article.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

References

[1] Laxminarayan, R., Duse, A., Wattal, C., Zaidi, A.K.M., Wertheim, H.F.L., Sumpradit,

N., *et al.* (2013) Antibiotic Resistance—The Need for Global Solutions. *The Lancet Infectious Diseases*, **13**, 1057-1098. https://doi.org/10.1016/s1473-3099(13)70318-9

[2] Laxminarayan, R., Matsoso, P., Pant, S., *et al.* (2016) Access to Effective Antimicrobials: A Worldwide Challenge. *The Lancet*, **387**, 168-175.

[3] Lim, C., Takahashi, E., Hongsuwan, M., Wuthiekanun, V., Thamlikitkul, V., Hinjoy, S., *et al.* (2016) Epidemiology and Burden of Multidrug-Resistant Bacterial Infection in a Developing Country. *eLife*, **5**, e18082. https://doi.org/10.7554/elife.18082

[4] Shankar, P. (2016) Book Review: Tackling Drug-Resistant Infections Globally. *Archives of Pharmacy Practice*, **7**, 110-111. https://doi.org/10.4103/2045-080x.186181

[5] Kümmerer, K. (2009) Antibiotics in the Aquatic Environment—A Review—Part I. *Chemosphere*, **75**, 417-434. https://doi.org/10.1016/j.chemosphere.2008.11.086

[6] Ben, W., Qiang, Z., Adams, C., Zhang, H. and Chen, L. (2008) Simultaneous Determination of Sulfonamides, Tetracyclines and Tiamulin in Swine Wastewater by Solid-Phase Extraction and Liquid Chromatography-Mass Spectrometry. *Journal of Chromatography A*, **1202**, 173-180. https://doi.org/10.1016/j.chroma.2008.07.014

[7] Zhao, L., Dong, Y.H. and Wang, H. (2010) Residues of Veterinary Antibiotics in Manures from Feedlot Livestock in Eight Provinces of China. *Science of the Total Environment*, **408**, 1069-1075. https://doi.org/10.1016/j.scitotenv.2009.11.014

[8] Zhou, Q., Wang, M. and Liang, J. (2008) Ecological Detoxification of Methamidophos by Earth-Worms in Phaiozem Co-Contaminated with Acetochlor and Copper. *Applied Soil Ecology*, **40**, 138-145.

[9] Pokharel, S., Shrestha, P. and Adhikari, B. (2020) Antimicrobial Use in Food Animals and Human Health: Time to Implement "One Health" Approach. *Antimicrobial Resistance & Infection Control*, **9**, Article No. 181. https://doi.org/10.1186/s13756-020-00847-x

[10] Pan, X., Qiang, Z., Ben, W. and Chen, M. (2011) Residual Veterinary Antibiotics in Swine Manure from Concentrated Animal Feeding Operations in Shandong Province, China. *Chemosphere*, **84**, 695-700. https://doi.org/10.1016/j.chemosphere.2011.03.022

[11] Wei, R., Ge, F., Huang, S., Chen, M. and Wang, R. (2011) Occurrence of Veterinary Antibiotics in Animal Wastewater and Surface Water around Farms in Jiangsu Province, China. *Chemosphere*, **82**, 1408-1414. https://doi.org/10.1016/j.chemosphere.2010.11.067

[12] Janusch, F., Scherz, G., Mohring, S.A.I. and Hamscher, G. (2014) Determination of Fluoroquinolones in Chicken Feces—A New Liquid-liquid Extraction Method Combined with LC-MS/MS. *Environmental Toxicology and Pharmacology*, **38**, 792-799. https://doi.org/10.1016/j.etap.2014.09.011

[13] Yuan, X., Lv, Z., Zhang, Z., Han, Y., Liu, Z. and Zhang, H. (2023) A Review of Antibiotics, Antibiotic Resistant Bacteria, and Resistance Genes in Aquaculture: Occurrence, Contamination, and Transmission. *Toxics*, **11**, Article No. 420. https://doi.org/10.3390/toxics11050420

[14] Liao, H., Zhao, Q., Cui, P., Chen, Z., Yu, Z., Geisen, S., *et al.* (2019) Efficient Reduction of Antibiotic Residues and Associated Resistance Genes in Tylosin Antibiotic Fermentation Waste Using Hyperthermophilic Composting. *Environment International*, **133**, Article ID: 105203. https://doi.org/10.1016/j.envint.2019.105203

[15] Pruden, A., Pei, R., Storteboom, H. and Carlson, K.H. (2006) Antibiotic Resistance Genes as Emerging Contaminants: Studies in Northern Colorado. *Environmental Science & Technology*, **40**, 7445-7450. https://doi.org/10.1021/es060413l

[16] Azuma, T., Uchiyama, T., Zhang, D., Usui, M. and Hayashi, T. (2022) Distribution and Characteristics of Carbapenem-Resistant and Extended-Spectrum *β*-Lactamase (ESBL) Producing *Escherichia coli* in Hospital Effluents, Sewage Treatment Plants, and River Water in an Urban Area of Japan. *Science of the Total Environment*, **839**, Article ID: 156232. https://doi.org/10.1016/j.scitotenv.2022.156232

[17] Delgado-Baquerizo, M., Hu, H., Maestre, F.T., Guerra, C.A., Eisenhauer, N., Eldridge, D.J., *et al.* (2022) The Global Distribution and Environmental Drivers of the Soil Antibiotic Resistome. *Microbiome*, **10**, Article No. 219. https://doi.org/10.1186/s40168-022-01405-w

[18] Guo, H., Wang, C., Ju, L., Pan, L., Su, Z. and Sui, Z. (2022) Antibiotic Resistance Genes and Bacterial Community Distribution Patterns in Pig Farms. *Folia Microbiologica*, **67**, 913-921. https://doi.org/10.1007/s12223-022-00988-z

[19] Li, Y., Zhang, C., Mou, X., Zhang, P., Liang, J. and Wang, Z. (2022) Distribution Characteristics of Antibiotic Resistance Bacteria and Related Genes in Urban Recreational Lakes Replenished by Different Supplementary Water Source. *Water Science and Technology*, **85**, 1176-1190. https://doi.org/10.2166/wst.2022.018

[20] Xu, L., Ouyang, W., Qian, Y., Su, C., Su, J. and Chen, H. (2016) High-Throughput Profiling of Antibiotic Resistance Genes in Drinking Water Treatment Plants and Distribution Systems. *Environmental Pollution*, **213**, 119-126. https://doi.org/10.1016/j.envpol.2016.02.013

[21] Xu, Y., Guo, C., Luo, Y., Lv, J., Zhang, Y., Lin, H., *et al.* (2016) Occurrence and Distribution of Antibiotics, Antibiotic Resistance Genes in the Urban Rivers in Beijing, China. *Environmental Pollution*, **213**, 833-840. https://doi.org/10.1016/j.envpol.2016.03.054

[22] Xu, Y., Hou, M., Li, Y., Huang, L., Ruan, J., Zheng, L., *et al.* (2017) Distribution of Tetracycline Resistance Genes and AmpC *β*-Lactamase Genes in Representative Non-Urban Sewage Plants and Correlations with Treatment Processes and Heavy Metals. *Chemosphere*, **170**, 274-281. https://doi.org/10.1016/j.chemosphere.2016.12.027

[23] Zhang, Y., Zheng, Y., Zhu, Z., Chen, Y. and Dong, H. (2021) Dispersion of Antibiotic Resistance Genes (ARGs) from Stored Swine Manure Biogas Digestate to the Atmosphere. *Science of the Total Environment*, **761**, Article ID: 144108. https://doi.org/10.1016/j.scitotenv.2020.144108

[24] He, Y., Yuan, Q., Mathieu, J., Stadler, L., Senehi, N., Sun, R., *et al.* (2020) Antibiotic Resistance Genes from Livestock Waste: Occurrence, Dissemination, and Treatment. *NPJ Clean Water*, **3**, Article No. 4. https://doi.org/10.1038/s41545-020-0051-0

[25] Huijbers, P.M.C., Flach, C. and Larsson, D.G.J. (2019) A Conceptual Framework for the Environmental Surveillance of Antibiotics and Antibiotic Resistance. *Environment International*, **130**, Article ID: 104880. https://doi.org/10.1016/j.envint.2019.05.074

[26] Woolhouse, M., Ward, M., van Bunnik, B. and Farrar, J. (2015) Antimicrobial Resistance in Humans, Livestock and the Wider Environment. *Philosophical Transactions of the Royal Society B*: *Biological Sciences*, **370**, Article ID: 20140083. https://doi.org/10.1098/rstb.2014.0083

[27] Zhang, Y., Xu, S., Yang, Y., Chou, S. and He, J. (2021) A "Time Bomb" in the Human Intestine—The Multiple Emergence and Spread of Antibiotic-Resistant Bacteria. *Environmental Microbiology*, **24**, 1231-1246. https://doi.org/10.1111/1462-2920.15795

[28] van Herten, J., Bovenkerk, B. and Verweij, M. (2018) One Health as a Moral Dilemma: Towards a Socially Responsible Zoonotic Disease Control. *Zoonoses and Public Health*, **66**, 26-34. https://doi.org/10.1111/zph.12536

[29] Chen, T., Zhang, H., Liu, Y., Liu, Y. and Huang, L. (2021) Evenn: Easy to Create Repeatable and Editable Venn Diagrams and Venn Networks Online. *Journal of Genetics and Genomics*, **48**, 863-866. https://doi.org/10.1016/j.jgg.2021.07.007

[30] Peng, S., Zhang, H., Song, D., Chen, H., Lin, X., Wang, Y., *et al.* (2022) Distribution of Antibiotic, Heavy Metals and Antibiotic Resistance Genes in Livestock and Poultry Feces from Different Scale of Farms in Ningxia, China. *Journal of Hazardous Materials*, **440**, Article ID: 129719. https://doi.org/10.1016/j.jhazmat.2022.129719

[31] Sun, M., Ye, M., Wu, J., Feng, Y., Wan, J., Tian, D., *et al.* (2015) Positive Relationship Detected between Soil Bioaccessible Organic Pollutants and Antibiotic Resistance Genes at Dairy Farms in Nanjing, Eastern China. *Environmental Pollution*, **206**, 421-428. https://doi.org/10.1016/j.envpol.2015.07.022

[32] Cheng, W., Chen, H., Su, C. and Yan, S. (2013) Abundance and Persistence of Antibiotic Resistance Genes in Livestock Farms: A Comprehensive Investigation in Eastern China. *Environment International*, **61**, 1-7. https://doi.org/10.1016/j.envint.2013.08.023

[33] Mu, Q., Li, J., Sun, Y., Mao, D., Wang, Q. and Luo, Y. (2014) Occurrence of Sulfonamide-, Tetracycline-, Plasmid-Mediated Quinolone- and Macrolide-Resistance Genes in Livestock Feedlots in Northern China. *Environmental Science and Pollution Research*, **22**, 6932-6940. https://doi.org/10.1007/s11356-014-3905-5

[34] Qian, X., Gu, J., Sun, W., Wang, X., Su, J. and Stedfeld, R. (2018) Diversity, Abundance, and Persistence of Antibiotic Resistance Genes in Various Types of Animal Manure Following Industrial Composting. *Journal of Hazardous Materials*, **344**, 716-722. https://doi.org/10.1016/j.jhazmat.2017.11.020

[35] Koike, S., Krapac, I.G., Oliver, H.D., Yannarell, A.C., Chee-Sanford, J.C., Aminov, R.I., *et al.* (2007) Monitoring and Source Tracking of Tetracycline Resistance Genes in Lagoons and Groundwater Adjacent to Swine Production Facilities over a 3-Year Period. *Applied and Environmental Microbiology*, **73**, 4813-4823. https://doi.org/10.1128/aem.00665-07

[36] Wenning, R. (2020) The State of World Fisheries and Aquaculture (SO-FIA) 2020 Report. *Integrated Environmental Assessment and Management*, **16**, 800-801.

[37] Abdel-Latif, H.M.R., Dawood, M.A.O., Alagawany, M., Faggio, C., Nowosad, J. and Kucharczyk, D. (2022) Health Benefits and Potential Applications of Fucoidan (FCD) Extracted from Brown Seaweeds in Aquaculture: An Updated Review. *Fish & Shellfish Immunology*, **122**, 115-130. https://doi.org/10.1016/j.fsi.2022.01.039

[38] Zhao, Y., Zhang, X., Zhao, Z., Duan, C., Chen, H., Wang, M., *et al.* (2018) Metagenomic Analysis Revealed the Prevalence of Antibiotic Resistance Genes in the Gut and Living Environment of Freshwater Shrimp. *Journal of Hazardous Materials*, **350**, 10-18. https://doi.org/10.1016/j.jhazmat.2018.02.004

[39] Wang, N., Guo, X., Yan, Z., Wang, W., Chen, B., Ge, F., *et al.* (2016) A Comprehensive Analysis on Spread and Distribution Characteristic of Antibiotic Resistance Genes in Livestock Farms of Southeastern China. *PLOS ONE*, **11**, e0156889. https://doi.org/10.1371/journal.pone.0156889

[40] Chen, B., Hao, L., Guo, X., Wang, N. and Ye, B. (2015) Prevalence of Antibiotic Resistance Genes of Wastewater and Surface Water in Livestock Farms of Jiangsu Province, China. *Environmental Science and Pollution Research*, **22**, 13950-13959. https://doi.org/10.1007/s11356-015-4636-y

[41] Yang, F., Gao, Y., Zhao, H., Li, J., Cheng, X., Meng, L., *et al.* (2021) Revealing the Distribution Characteristics of Antibiotic Resistance Genes and Bacterial Communities in Animal-Aerosol-Human in a Chicken Farm: From One-Health Perspective.

Ecotoxicology and Environmental Safety, **224**, Article ID: 112687. https://doi.org/10.1016/j.ecoenv.2021.112687

[42] Rood, I.G.H. and Li, Q. (2017) Review: Molecular Detection of Extended Spectrum-*β*-Lactamase- and Carbapenemase-Producing Enterobacteriaceae in a Clinical Setting. *Diagnostic Microbiology and Infectious Disease*, **89**, 245-250. https://doi.org/10.1016/j.diagmicrobio.2017.07.013

[43] Wanyan, R., Pan, M., Mai, Z., Xiong, X., Su, W., Yang, J., *et al.* (2023) Distribution and Influencing Factors of Antibiotic Resistance Genes of Crayfish (*Procambarus clarkii*) Intestine in Main Crayfish Breeding Provinces in China. *Science of the Total Environment*, **857**, Article ID: 159611. https://doi.org/10.1016/j.scitotenv.2022.159611

[44] Jang, H.M., Kim, Y.B., Choi, S., Lee, Y., Shin, S.G., Unno, T., *et al.* (2018) Prevalence of Antibiotic Resistance Genes from Effluent of Coastal Aquaculture, South Korea. *Environmental Pollution*, **233**, 1049-1057. https://doi.org/10.1016/j.envpol.2017.10.006

[45] Xiong, W., Yang, J., Zeng, J., Xiao, D., Tong, C. and Zeng, Z. (2023) Metagenomic Analysis of Antimicrobial Resistance in Ducks, Workers, and the Environment in Duck Farms, Southern China. *Ecotoxicology and Environmental Safety*, **262**, Article ID: 115191. https://doi.org/10.1016/j.ecoenv.2023.115191

[46] Zhang, X., Gong, Z., Allinson, G., Xiao, M., Li, X., Jia, C., *et al.* (2022) Environmental Risks Caused by Livestock and Poultry Farms to the Soils: Comparison of Swine, Chicken, and Cattle Farms. *Journal of Environmental Management*, **317**, Article ID: 115320. https://doi.org/10.1016/j.jenvman.2022.115320

[47] Sun, J., Huang, T., Chen, C., Cao, T., Cheng, K., Liao, X., *et al.* (2017) Comparison of Fecal Microbial Composition and Antibiotic Resistance Genes from Swine, Farm Workers and the Surrounding Villagers. *Scientific Reports*, **7**, Article No. 4965. https://doi.org/10.1038/s41598-017-04672-y

[48] Tang, X., Lou, C., Wang, S., Lu, Y., Liu, M., Hashmi, M.Z., *et al.* (2015) Effects of Long-Term Manure Applications on the Occurrence of Antibiotics and Antibiotic Resistance Genes (ARGs) in Paddy Soils: Evidence from Four Field Experiments in South of China. *Soil Biology and Biochemistry*, **90**, 179-187. https://doi.org/10.1016/j.soilbio.2015.07.027

[49] Ghosh, S. and LaPara, T.M. (2007) The Effects of Subtherapeutic Antibiotic Use in Farm Animals on the Proliferation and Persistence of Antibiotic Resistance among Soil Bacteria. *The ISME Journal*, **1**, 191-203. https://doi.org/10.1038/ismej.2007.31

[50] Joy, S.R., Bartelt-Hunt, S.L., Snow, D.D., Gilley, J.E., Woodbury, B.L., Parker, D.B., *et al.* (2013) Fate and Transport of Antimicrobials and Antimicrobial Resistance Genes in Soil and Runoff Following Land Application of Swine Manure Slurry. *Environmental Science & Technology*, **47**, 12081-12088. https://doi.org/10.1021/es4026358

[51] Chen, F., Ying, G., Kong, L., Wang, L., Zhao, J., Zhou, L., *et al.* (2011) Distribution and Accumulation of Endocrine-Disrupting Chemicals and Pharmaceuticals in Wastewater Irrigated Soils in Hebei, China. *Environmental Pollution*, **159**, 1490-1498. https://doi.org/10.1016/j.envpol.2011.03.016

[52] Shi, Y., Gao, L., Li, W., Liu, J. and Cai, Y. (2012) Investigation of Fluoroquinolones, Sulfonamides and Macrolides in Long-Term Wastewater Irrigation Soil in Tianjin, China. *Bulletin of Environmental Contamination and Toxicology*, **89**, 857-861. https://doi.org/10.1007/s00128-012-0761-1

[53] Zhu, Y., Johnson, T.A., Su, J., Qiao, M., Guo, G., Stedtfeld, R.D., *et al.* (2013) Diverse and Abundant Antibiotic Resistance Genes in Chinese Swine Farms. *Proceedings of*

the National Academy of Sciences, **110**, 3435-3440.
https://doi.org/10.1073/pnas.1222743110

[54] Yuan, J., Ni, M., Liu, M., Zheng, Y. and Gu, Z. (2019) Occurrence of Antibiotics and Antibiotic Resistance Genes in a Typical Estuary Aquaculture Region of Hangzhou Bay, China. *Marine Pollution Bulletin*, **138**, 376-384.
https://doi.org/10.1016/j.marpolbul.2018.11.037

[55] Huang, L., Xu, Y., Xu, J., Ling, J., Chen, J., Zhou, J., *et al.* (2017) Antibiotic Resistance Genes (ARGs) in Duck and Fish Production Ponds with Integrated or Non-Integrated Mode. *Chemosphere*, **168**, 1107-1114.
https://doi.org/10.1016/j.chemosphere.2016.10.096

[56] Wang, N., Yang, X., Jiao, S., Zhang, J., Ye, B. and Gao, S. (2014) Sulfonamide-Resistant Bacteria and Their Resistance Genes in Soils Fertilized with Manures from Jiangsu Province, Southeastern China. *PLOS ONE*, **9**, e112626.
https://doi.org/10.1371/journal.pone.0112626

[57] Xu, H., Broersma, K., Miao, V. and Davies, J. (2011) Class 1 and Class 2 Integrons in Multidrug-Resistant Gram-Negative Bacteria Isolated from the Salmon River, British Columbia. *Canadian Journal of Microbiology*, **57**, 460-467.
https://doi.org/10.1139/w11-029

[58] Chen, T., Zhang, S., Zhu, R., Zhao, M., Zhang, Y., Wang, Y., *et al.* (2022) Distribution and Driving Factors of Antibiotic Resistance Genes in Treated Wastewater from Different Types of Livestock Farms. *Science of the Total Environment*, **849**, Article ID: 157837. https://doi.org/10.1016/j.scitotenv.2022.157837

[59] Yu, Z., Wang, Y., Lu, J., Bond, P.L. and Guo, J. (2021) Nonnutritive Sweeteners Can Promote the Dissemination of Antibiotic Resistance through Conjugative Gene Transfer. *The ISME Journal*, **15**, 2117-2130.
https://doi.org/10.1038/s41396-021-00909-x