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Review

Comparative analysis of antibiotic-administered vs. antibiotic-free farming in meat production: Implications for health, environment, and antibiotic resistance

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ABSTRACT

Antimicrobial resistance (AMR) is an escalating global health problem, endangering human, animal, and environmental health. In animal farming, the widespread use of antimicrobials is recognized one of the major drivers of AMR. Therefore, this review provides a meta-analysis of 37 studies published between 2014 and 2024, comparing the prevalence of antimicrobial resistance genes (ARGs) in antibiotic-free (ABF) versus conventional animal farming (CONV) systems. The statistical analysis revealed that CONV farms exhibited a higher likelihood of harboring ARGs, with a pooled odds ratio of 2.38 (95 % CI: 2.00–2.83) in the fixed-effects model and 3.21 (95 % CI: 1.68–6.13) in the random-effects model. Significant heterogeneity was observed ($I^2 = 82.8$ %, $p < 0.0001$), highlighting the variations across the study designs. However, ARGs were still detected in 97 % of ABF farms, suggesting that antibiotic reduction alone may not be enough to control AMR in animal farming. These findings underscore the complex nature of AMR, influenced by environmental contamination, microbial interactions, human practices, and ecological pressures such as climate change. Future strategies should adopt a holistic One Health approach to effectively mitigate AMR risks across sectors and safeguard public and planetary health.

1. Introduction

Antimicrobial resistance (AMR) is currently one of the pressing global health challenges. It limits the effective treatment of infections and increases the risk of disease spread, severe illness, and death. AMR arises when microorganisms, such as bacteria, viruses, and fungi, develop the ability to resist antimicrobial agents, making standard treatments ineffective (Van Boeckel et al., 2019; WHO, 2023). In 2019, bacterial AMR alone was responsible for an estimated 1.27 million deaths worldwide (Murray et al., 2022; WHO, 2023), and projections suggest that, if left unaddressed, AMR could surpass cancer as a leading cause of mortality (O'Neill, 2016).

In animal farming, antimicrobials have long been used not only to treat infections but also as growth promoters, to increase productivity. These practices are particularly common in conventional (CONV) intensive farming systems. However, the overuse and misuse of antibiotics in livestock contribute significantly to the emergence and spread of antibiotic-resistant bacteria (ARB) (Manyi-Loh et al., 2018; Szoke et al., 2025). These bacteria, along with their ARGs, can be transmitted to humans through direct contact, environmental contamination, or consumption of animal products, thus posing a public health risk (Manyi-Loh et al., 2018; Temple and Manteca, 2020).

To mitigate AMR risks in intense animal-based food production systems, alternative farming methods have been developed. The goal of alternative farming practices like organic (OR) and antibiotic-free (ABF) farming is to reduce the selective pressure that leads to resistance by using minimal or no antibiotics. However, current findings remain inconsistent. Some studies report significant differences in resistance levels among farming practices (Guo et al., 2018; Huizinga et al., 2019; Vieira et al., 2023; Buthasane et al., 2023), while others find no significant difference (De Cesare et al., 2022; Doster et al., 2018; Gerzova et al., 2015; Ishengoma et al., 2024). However, a few even indicate higher levels of AMR in ABF farms (Vikram et al., 2017; Li et al., 2020, 2022; Schmidt et al., 2021; Alvarado et al., 2022). These discrepancies

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underscore the need for a comprehensive analysis to clarify the relationship between farming practices and AMR development in food-producing animals.

This study presents a combined systematic review and meta-analysis to evaluate the prevalence of AMR in CONV versus ABF farming systems. By integrating both quantitative and qualitative evidence, we aim to assess the impact of antibiotic use in animal agriculture on resistance spread. In addition, we explore broader environmental reservoirs, community-level interactions, and farm management factors to offer a more comprehensive overview of AMR persistence. This study uniquely combines meta-analysis and systematic review approaches to address key knowledge gaps, linking statistical findings with a broader AMR context under the One Health framework.

2. Methodology

2.1. Literature search

A comprehensive literature search was conducted using Google Scholar, PubMed, and Scopus to identify peer-reviewed, original research articles published in English between 2014 and 2024. A wide range of keywords was employed, retrieving 299 studies. After thorough screening, 88 studies satisfied the selection criteria for inclusion in both the meta-analysis (37 studies) and the systematic review (51 studies). This review was conducted in accordance with PRISMA guidelines (Fig. 1), and the detailed search terms are provided in **(Supplementary_File_1)**.

The 37 studies selected for meta-analysis were categorized as follows: Conventional farming (CONV) refers to intensive animal production systems with unrestricted antimicrobial use. Antibiotic-free farming (ABF) describes systems that eliminate antimicrobial use, while organic systems (OR) are characterized by outdoor access for animals and prohibition of antimicrobials (QIMA/WQS, n.d.; Brasil, 2009; Vieira et al., 2023). For statistical analysis, ABF and OR were grouped together and compared against the CONV group.

2.2. Inclusion criteria (for meta-analysis)

1. Study Type & Timeframe: Original research articles, published in English between 2014 and 2024.
2. Analytical Methods: Studies employing molecular techniques such as PCR, qPCR, or sequencing-based approaches (e.g., amplicon sequencing, shotgun metagenomics) for microbiome or antibiotic resistance gene (ARG) analysis.
3. Comparative Focus: Comparative studies analysing CONV and ABF systems across different animal types and sample origins.
4. Data Scope: Articles reporting on the full microbiome, multiple serotypes, or resistome data (prevalence).

2.3. Exclusion criteria

- Reviews, meta-analyses, opinion articles, and grey literature (conference abstracts, thesis, reports, blog posts).
- Studies lacking direct comparative data between CONV and ABF.

2.4. Statistical analysis

All statistical analyses were performed in R (version 4.3.3) using the tidyverse and meta (v5.7-1) packages. First, descriptive statistics were used to explore the proportions of studies reporting ARG prevalence across farming methods (CONV vs ABF), host types (cattle, poultry, and swine), and sample origins (farm & environment, farm & retail product, and retail product only). After noticing high diversity in the targeted ARGs among studies, we tested data normality using the Shapiro–Wilk test. Based on these results, Wilcoxon rank-sum tests were used to compare ARG detections between groups.

For the meta-analysis, we estimated pooled odds ratios (ORs) with 95 % confidence intervals (CIs). Both fixed-effects models

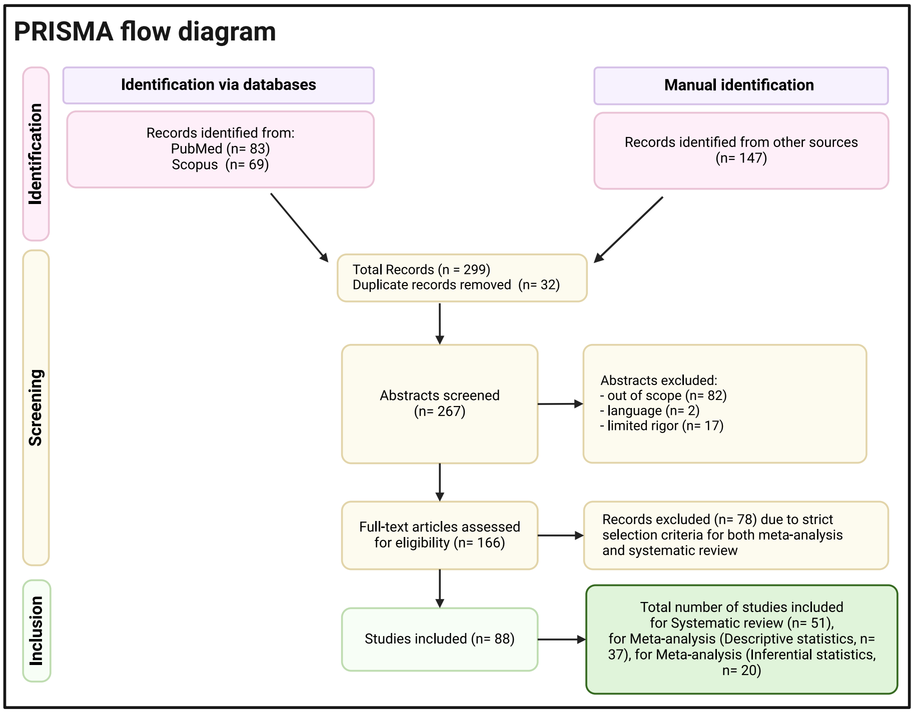

Fig. 1. This diagram outlines the systematic process used to identify and filter studies for the integrated meta-analysis and systematic review. A total of 299 records were initially identified from PubMed (n = 83) and Scopus (n = 69). An additional 147 records were identified through manual searches and other sources. With 32 duplicates removed, yielding 267 abstracts for screening. Of these, 166 full-text articles were assessed for eligibility. Based on strict inclusion criteria regarding timeframe, scope, language, and methodological rigor, 78 records were excluded. Ultimately, 37 studies were included in the meta-analysis and 51 studies were included in the systematic review, resulting in 88 studies overall. *Created in BioRender. RAHMAN, A. (2025)* https://BioRender.com/s43w442.

(Mantel–Haenszel method), assuming a common true effect across studies, and random-effects models (Inverse-Variance method), accounting for variation between studies, were applied. To evaluate inter-study heterogeneity, three approaches were used: Tau-squared (τ^2) was estimated using the Q-profile method. Restricted maximum likelihood was used for more accurate estimation of τ, τ^2, and their confidence intervals. Cochran's Q-test was applied to assess the overall heterogeneity among studies. A continuity correction of 0.5 was added to studies with zero events in one or both groups. To better understand potential variations, subgroup analyses were pre-specified by host type and sample origin. Differences between subgroups were tested using the Chi-squared (χ^2) test.

2.5. *Limitations*

A major limitation was the diversity in study designs and objectives across retrieved articles. Comparative analyses were complicated by variability in host species, sample locations, sampling periods, antimicrobial administration modalities, and focus (individual ARGs versus full resistomes). Similarly, additional factors like climate, farm size, and location were inconsistently reported. Such variability increases between-study variance (I^2) and may bias pooled estimates. We therefore interpret our findings as indicative of overall trends rather than precise quantitative differences and highlight the need for standardized studies. To address these concerns and to acquire a general overview, we focused on direct comparative results reporting variations in microbial species and ARG prevalence between farming systems, while broader environmental influences are discussed in (One Health Narrative) section as potential contributing factors to AMR persistence. This systematic approach allowed us to obtain significant insights into the complex interconnected factors influencing AMR within and beyond animal food systems.

3. Results and discussion

This study analyzed the impact of farming practices (CONV vs ABF) on the composition of microbial species and ARGs prevalence across 37 eligible studies. Among these, 15 studies focused on poultry, 9 on swine, and 13 on cattle. Regarding sample origins, 24 studies examined farm and environmental samples (including feces, cecum, ileum, litter, feed, and water), 5 included both farm and retail products (such as colon contents, feces, and carcasses, meat trimmings), and 8 focused on retail products alone (such as chicken breast, minced beef, or retail carcasses). Further details about the host types, sampling types and study designs are detailed in (Supplementary Table 1). The total number of samples investigated across all studies was 61315 (minimum = 20, mean = 1657, median = 128, maximum = 46937).

Out of the 37 studies, only 3 (8 %) reported differences in the prevalence of major microbial phyla, including Firmicutes, Proteobacteria, Actinobacteria, Bacteroidetes, Spirochaetes, and Tenericutes. Regarding microbial species abundance, 20 studies (54 %) found no significant difference between CONV and ABF systems, 12 studies (32 %) reported higher abundance in CONV, while 5 studies (13 %) reported higher abundance in ABF. These findings suggest that farming practices may not strongly influence overall microbial diversity. However, the abundance of specific microbial taxa could still vary depending on farming conditions. Similarly, different studies applied varied detection methods such as shotgun metagenomics, 16S rRNA amplicon sequencing, and qPCR, each measuring relative rather than absolute abundance. Thus, the patterns reported mainly reflect general trends rather than focusing on individual bacterial taxa among the studies.

Regarding ARG prevalence, the data were as follows: total ARGs detected = 2273; ARGs detected in CONV = 993; ARGs detected in ABF = 764. On average, CONV farms reported 27 ARG detections per study, compared to 21 in ABF systems, although CONV farms showed a slightly higher number of ARG detections. Nevertheless, the statistical difference in prevalence was not significant ($p > 0.05$), either across host types (Fig. 2A) or sample origins (Fig. 2B). This suggests that both CONV and ABF practices do not appear to contribute differently to ARG dissemination in animal farming. Despite reduced or eliminated antibiotic use in ABF systems, factors such as cross-contamination, farm management practices, and environmental reservoirs (like water, air, and feed) likely maintain the spread of ARGs. This pattern may also reflect the widespread use of similar antimicrobial treatments across conventional cattle, swine, and poultry operations. Indeed, all three often receive the same antibiotic classes (e.g., tetracyclines, β-lactams, macrolides).

Regarding the composition of ARG classes among the 37 studies included in our meta-analysis, ARGs conferring tetracycline resistance were detected in 96 % of studies, followed by ARGs associated with multiple antibiotic classes in 80 % of studies, aminoglycoside-resistance genes in 54 %, beta-lactams in 50 %, and macrolide-lincosamide-streptogramin (MLS) genes in 18 % of studies, respectively. All species showed tetracycline resistance as dominant, followed by multiple ARGs. Across host types, cattle and poultry showed high diversity in ARG classes as compared to swine, but with varied abundance (Fig. 3A). When stratified by sample origin, cattle showed high diversity as compared to poultry and swine in the farm and environmental samples. In farm samples and retail product samples, only multiple ARGs were detected; in contrast, poultry products from retail samples exhibited higher ARG diversity than beef products. These results also indicate, that while tetracycline resistance predominates all other classes across all farming systems, cattle farming may contribute more to ARG diversity compared to poultry and swine (Fig. 3B). However, in farm and retail product samples, poultry displayed a relatively balanced distribution between tetracycline, beta-lactams, and multiple ARGs. Although fewer studies investigated ARGs in retail meat, available evidence suggests that farming practices may have limited influence on resistomes at the retail stage. For example, De Cesare et al. (2022) reported no significant difference in ARG abundance between retail products coming from different farming systems, underscoring the need for further research (De Cesare et al., 2022). Furthermore, when examining ARG abundance, 15 studies reported higher ARG levels in CONV systems compared to 5 studies favouring ABF, while 17 studies found no significant differences.

To further examine the number of ARGs detected across farming systems, we performed a meta-analysis using the meta package in R. In the initial descriptive analysis, 17 studies showed no significant difference in ARG prevalence between CONV and ABF systems. Therefore, to reduce the influence of these null effects and to better estimate the true impact of antibiotic use on ARG prevalence, we excluded these 17 studies from the primary meta-analysis. This step helped minimize bias and allowed a clearer comparison between CONV and ABF farming practices. However, to ensure transparency and address any concerns about this study selection, forest plots including all 37 studies (including the 17 null-effect reports) covering both host types and sample origins are provided in the supplementary materials (Supplementary Figs. S1 and S2).

3.1. *Subgroup analysis by host type*

In total, 2570 observations from 20 studies were analyzed, with an equal number of samples from CONV ($n = 1285$) and ABF ($n = 1285$) farming systems. Across these, 1339 ARG detection events were recorded. The fixed-effects model showed that animals raised in CONV systems were significantly more likely to carry ARGs, with an odds ratio (OR) of 2.38 (95 % CI: 2.00–2.83; $p < 0.0001$). Using the random-effects model, the association was even stronger, with an OR of 3.21 (95 % CI: 1.68–6.13; $p = 0.0004$; Fig. 4). The random-effects model was chosen to account for differences between studies, like sample types, study designs, and animal host types.

There was significant heterogeneity found across studies ($I^2 = 82.8$ %, $\tau^2 = 1.4809$, $\tau = 1.2169$). Further confirmed by Q test ($Q = 110.61$; $p < 0.0001$). We found very high between-study heterogeneity ($I^2 = 82.8$

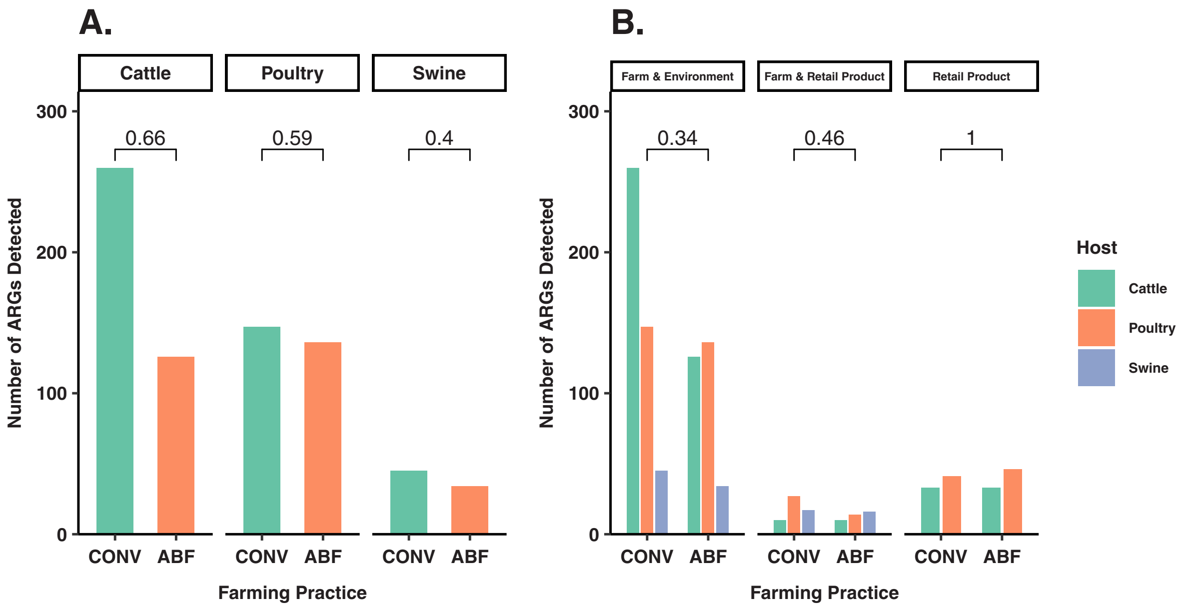

Fig. 2. **(A)** Number of detected ARGs across different host types. Cattle exhibited the highest number of ARG detections, followed by poultry and swine. However, Wilcoxon rank-sum tests showed no statistically significant differences between the groups. Values above the brackets are P-values from pairwise Wilcoxon rank-sum tests (all $p > 0.05$). **(B)** ARG counts further classified by both host type and sample origin. In farm and environmental samples, cattle had the highest number of detected ARGs, followed by poultry. In contrast, poultry showed higher ARG detection in retail product samples compared to cattle.

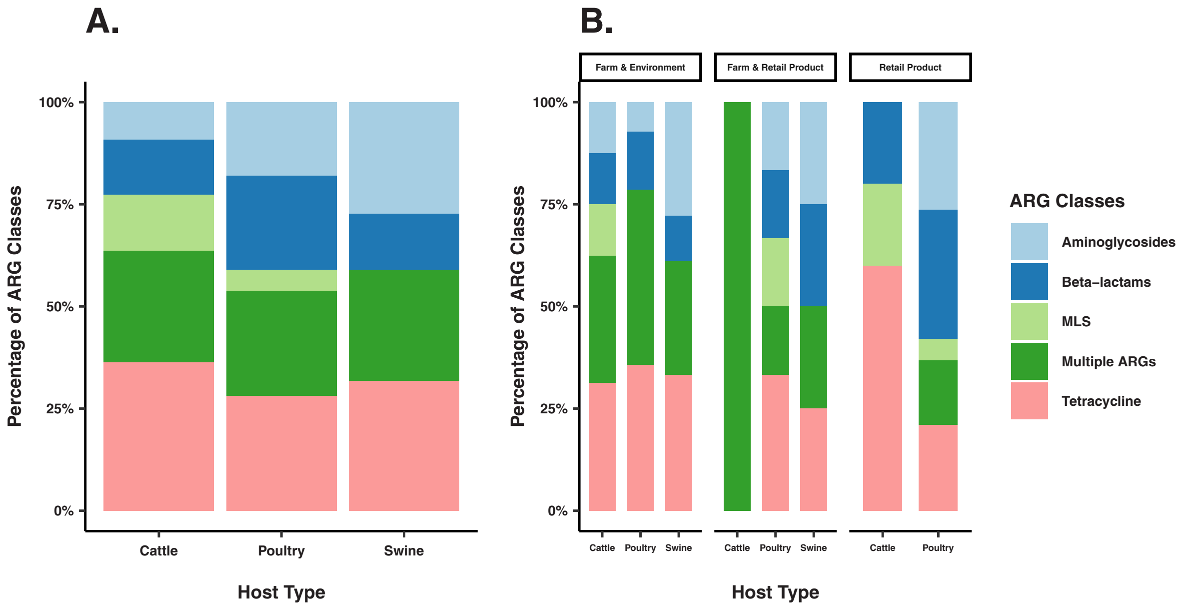

Fig. 3. **(A)** Distribution of ARG classes among host types. While cattle and poultry exhibited similar ARG class diversity, their relative prevalence varied. Swine samples showed lower ARG class diversity compared to both cattle and poultry. **(B)** ARG class distribution further stratified by host type and sample origin. In farm and environmental samples, cattle had the highest ARG class diversity, while poultry showed higher diversity in both farm and retail product samples, as well as retail-only samples.

%; $Q = 110.6$, $p < 0.0001$), indicating that our pooled ORs describe broad trends rather than exact magnitudes. This variability likely arises not only from study design differences (targeted ARGs vs. full resistomes) but also from unmeasured factors such as farm scale, regional climate, biosecurity practices, feed/water quality, and detection methods, that our meta-analysis cannot disentangle.

When grouped by host type under a fixed-effects model, swine exhibited the highest odds of ARG detection (OR = 3.49; 95 % CI: 1.96–6.20; $I^2 = 37.6$ %), followed by cattle (OR = 3.30; 95 % CI: 2.58–4.21; $I^2 = 73.7$ %) and poultry (OR = 1.38; 95 % CI: 1.04–1.84; $I^2 = 86.5$ %). The subgroup test showed significant differences among species ($Q = 22.63$; $p < 0.0001$) (Fig. 4). However, under the random-effects model, the differences between cattle, poultry, and swine were not significant ($Q = 0.17$; $p = 0.9199$). Again, the high I^2 values in some subgroups (e.g. 86.5 % for poultry) underscore that these species-level comparisons reflect overarching patterns more than definitive quantitative differences. This suggests that even though cattle and swine may have higher ARG levels in some studies, the overall trend is similar when study variability is taken into account.

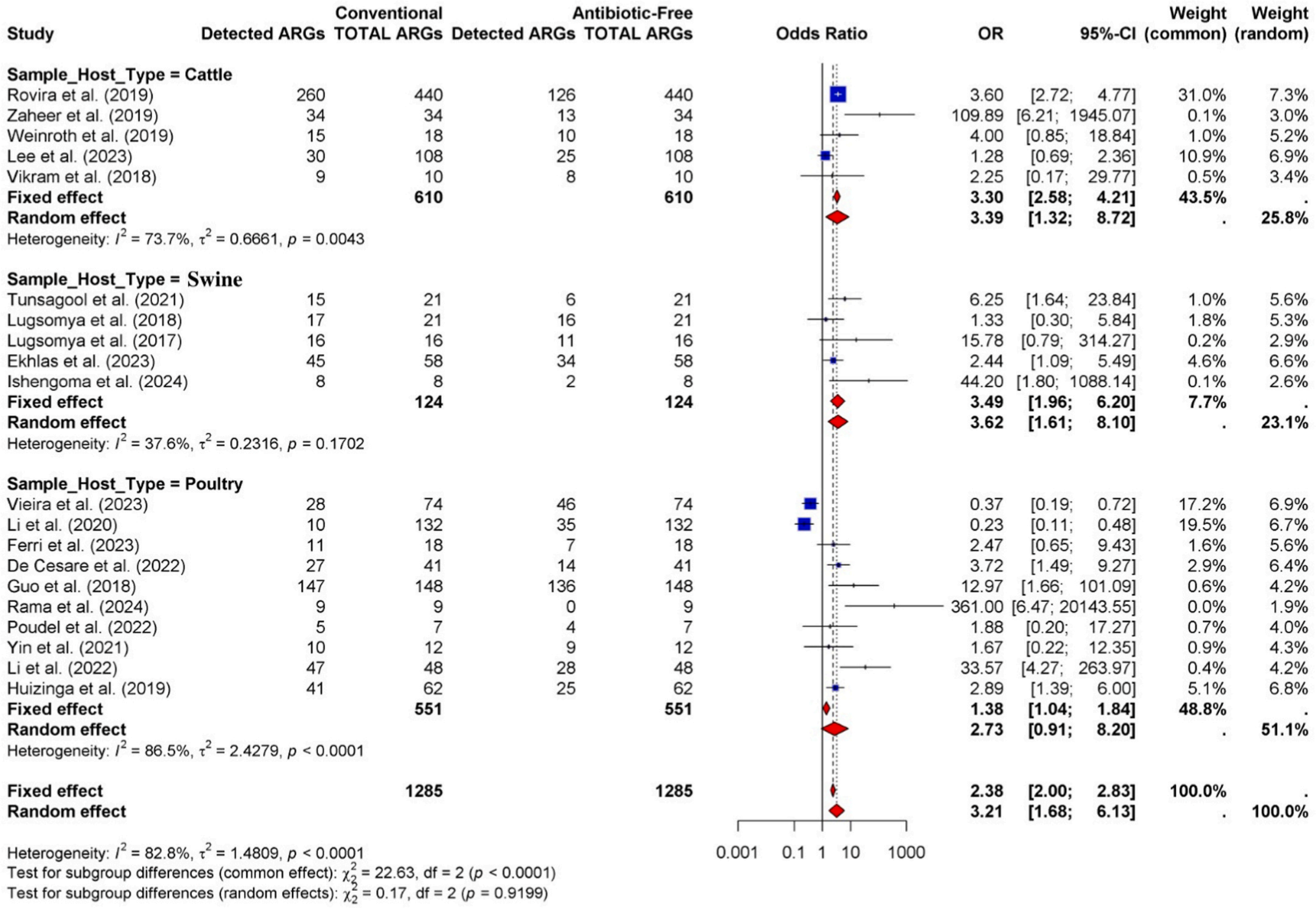

Fig. 4. Forest plot summarizing the odds ratios (OR) for the detection of ARGs in CONV versus ABF systems across cattle, poultry, and pigs. Using a fixed-effects model, the pooled OR is 2.38 (95 % CI: 2.00–2.83), and the random-effects model yields an OR of 3.21 (95 % CI: 1.68–6.13), indicating that conventional systems have a significantly higher prevalence of ARGs. Significant heterogeneity was observed ($I^2 = 82.8$ %, $\tau^2 = 1.4809$, $p < 0.0001$). Subgroup analysis under the fixed-effects model showed significant differences among host types ($\chi^2 = 22.63$, df = 2, $p < 0.0001$), whereas the random-effects model did not reveal significant subgroup differences ($\chi^2 = 0.17$, df = 2, p = 0.9199). In this plot, the blue squares represent the individual study effect estimates and their weights, while the red diamond shows the overall pooled estimate with its confidence interval. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

3.2. Subgroup analysis by sample origin

A similar pattern was seen when we divided the data by where samples were collected (sample location). Both fixed and random-effects models showed that CONV farms had a significantly higher risk of ARG detection compared to ABF farms. Samples collected from farm and environment showed the highest odds for ARG detection (Fixed-effect OR = 3.84; 95 % CI: 3.08–4.79; $I^2 = 68.8$ %). Farm and retail product samples had an OR of 2.62 (95 % CI: 1.39–4.97; $I^2 = 0.0$ %). However, retail product samples had even a lower OR of 0.65 (95 % CI: 0.45–0.94; $I^2 = 85.7$ %), suggesting a possible reduction in ARGs after processing.

The subgroup differences were significant (Q = 65.99; $p < 0.0001$), confirming that where the sample came from matters. In the random-effects model, the trend stayed the same: farm samples had the highest OR (7.31; 95 % CI: 3.12–17.13), followed by farm and retail samples (2.63; 95 % CI: 1.38–5.01). Retail products again showed a low OR (0.83; 95 % CI: 0.27–2.57), with significant subgroup differences (Q = 9.34; p = 0.0094) (Fig. 5).

These findings suggest that CONV farming practices are more strongly associated with the presence of ARGs compared to ABF systems, especially at the farm level. These findings are in line with previous meta-analyses, which observed reduced ARG levels in ABF systems compared to CONV ones (Nobrega et al., 2021; Ager et al., 2023). Notably, ARG levels in retail products appeared lower. This could partly be reflected due the smaller number of studies focused on retail samples. However, some studies reported inconsistent findings between products from CONV and ABF systems, while others reported no significant differences in ARG composition (Vikram et al., 2018; De Cesare et al., 2022). These inconsistencies highlight the need for more standardized, large-scale studies to better understand how farming practices influence ARG propagation.

However, targeted interventions such as on-farm biosecurity measures (e.g., enhanced sanitation, controlled animal flow), judicious feed and water management, and processing-stage decontamination (e.g., steam pasteurization, organic acid washes) are critical to reduce ARG levels before meat reaches consumers. The relationships between antibiotic use and resistance are still complex. They can vary widely depending on the specific antibiotic administration model, host, pathogen, detection methods used, sample source, study design, country-specific regulations, and all direct and indirect-environmental factors (Andersson et al., 2020; Larsson and Flach, 2022). This complexity was also reflected in our findings: studies targeting specific ARGs versus whole resistomes produced variable results.

However, despite these differences, ARGs were detected in both farming systems. Notably, 97 % (n = 36) of studies reported ARG detection in ABF settings, suggesting that AMR is not solely driven by

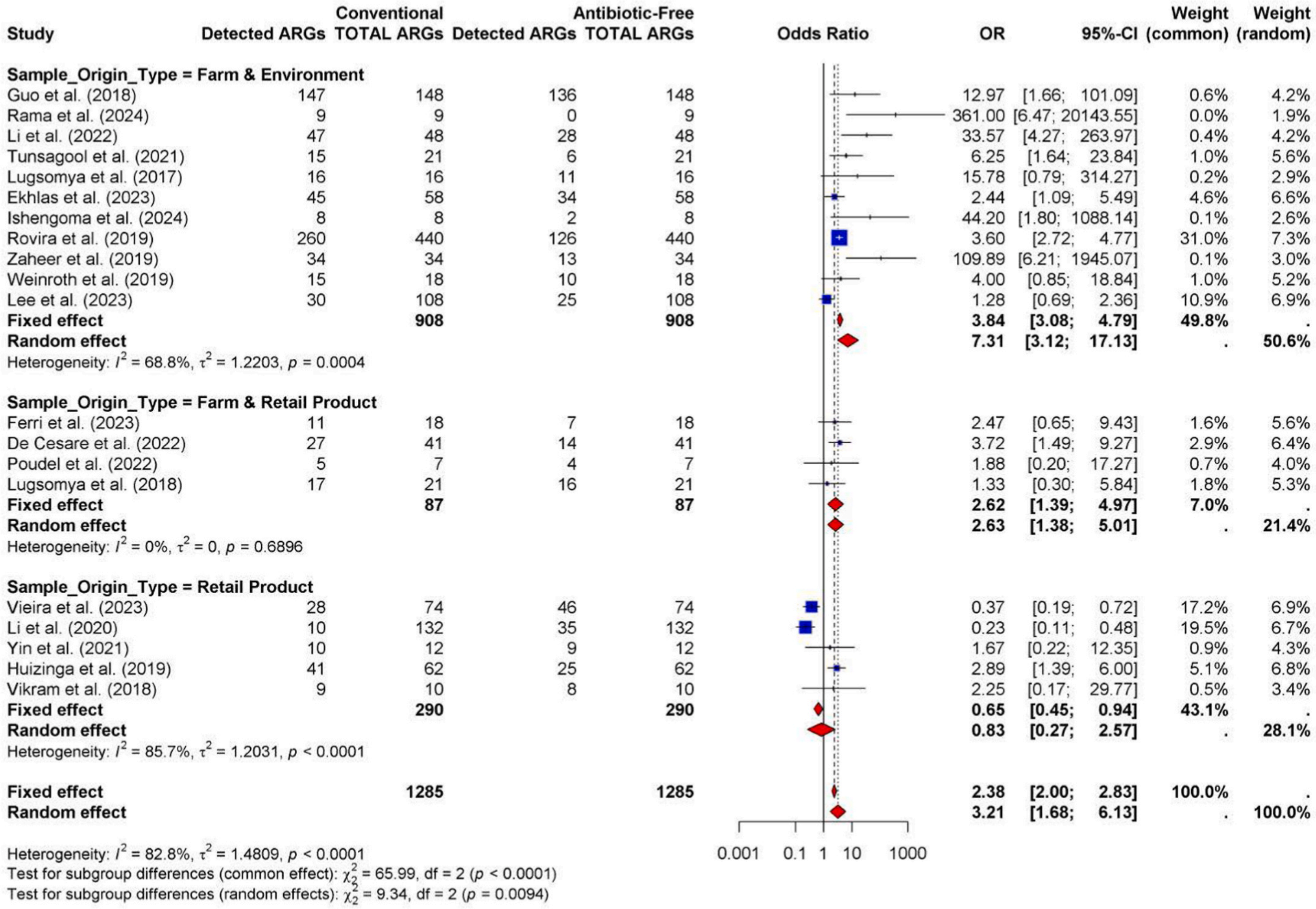

Fig. 5. Forest plot comparing ARG prevalence based on sample origin, categorized as farm & environment, combined farm and retail products, and retail products only in CONV versus ABF systems. The fixed-effects model yields a pooled OR of 2.38 (95 % CI: 2.00–2.83) and the random-effects model yielded an OR of 3.21 (95 % CI: 1.68–6.13), reinforcing that conventional systems tend to have higher ARGs prevalence. Heterogeneity was high ($I^2 = 82.8$ %, $\tau^2 = 1.4809$, $p < 0.0001$). Subgroup analyses indicated that sample origin significantly influences ARG detection, with the common effect model yielding $\chi^2 = 65.99$ (df = 2, $p < 0.0001$) and the random effects model yielding $\chi^2 = 9.34$ (df = 2, p = 0.0094). In this plot, the blue squares represent the individual study effect estimates and their weights, while the red diamond shows the overall pooled estimate with its confidence interval. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

direct antibiotic use. Other factors, including contaminated animal feed, environmental exposure (air, water, and waste), poor farm management, and human activity, likely contribute to AMR spread (Gemeda et al., 2021; Mak et al., 2022). Together, the reviewed studies show that environmental reservoirs, farming practices, and microbial evolution each contribute to ARG dissemination. Our results closely mirror those of (Nobrega et al., 2021; Ager et al., 2023), reinforcing that on-farm antibiotic bans alone do not eliminate the resistome burden. We acknowledge that ARG prevalence is modulated by farm size, climate, biosecurity protocols, feed/water quality, and laboratory methods, and recommend future multivariable meta-regression to untangle these effects. Since multiple meta-analyses are finding the same patterns, we need large, coordinated studies using the same methods to tell apart the effects of farming system from environmental factors on AMR. Addressing AMR effectively will require a broader One Health approach that considers not just antimicrobial use, but also environmental contamination and farm management strategies.

4. Importance of AMR in a One Health concept

4.1. AMR at farms

Beyond farming practices, environmental factors also play a critical role in shaping AMR patterns. For example, agricultural soil acts as a natural reservoir for a variety of microorganisms. Hence, the application of pesticides, herbicides, insecticides, and antimicrobials exerts selective pressure on microbes inhabiting feed crops and soil, promoting multidrug and cross-resistance traits (Qiu et al., 2022). Additionally, the combination of antimicrobials with toxic metals such as copper further enhances this resistance (Jun et al., 2019). Moreover, the use of contaminated water and manure application in agriculture may further introduce ARGs in soil, water, and air. Indeed, manure-amended soils were found to have higher levels of ARGs than soils treated with chemical fertilizers (Tiedje et al., 2019; He et al., 2020). Beyond soil, contaminated animal feed, resulting from poor storage hygiene or exposure to wildlife (e.g., rodents, birds), can further introduce and spread ARGs (Auffret et al., 2017). Similarly, drinking water, even from private wells, can also serve as a vector for ARB transmission (Hayward et al., 2020; Alawi et al., 2024). Additionally, farm dust (airborne particles), migrating birds, rodents, pets, and insects are other components that may contribute to the spread of ARGs between farms and the environment (Gwenzi et al., 2021; Bai et al., 2022; Guardia et al., 2024) (Fig. 6).

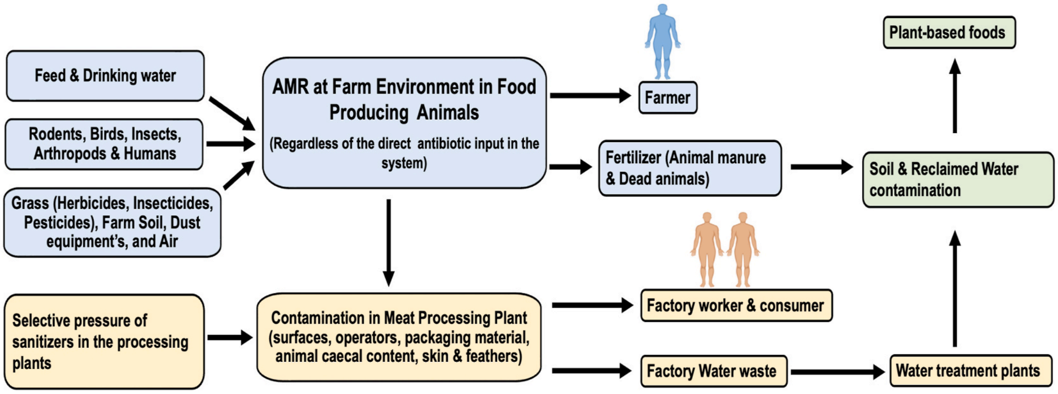

Fig. 6. A schematic representation that illustrates the flow of antimicrobial resistance (AMR) among livestock animals, humans, and their associated environments. The light-blue pathway shows AMR flow related to livestock animals, farms, and their associated environments at the farm level, showing how different factors like rodents, insects, drinking water, herbicides, pesticides, and farm soil play their role in AMR development and propagation in food-producing animals. The light-yellow pathway indicates AMR flow associated with the environment and equipment within the processing plants, their retail products, and their effluents (e.g., water and solid waste). The light-green boxes represent AMR flow linked to environmental sources such as field soil, plant-based foods, underground and freshwater sources. This whole workflow demonstrates how AMR circulates among different contributors, irrespective of the direct introduction of antimicrobials into livestock farming. It also highlights the importance of the co-evolution of antimicrobial resistance genes (ARGs) in response to other selective pressures. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

4.2. AMR in meat processing plants

Meat processing facilities serve as crucial hotspots for the emergence and dissemination of AMR. For instance, mixing animals from different farms during transportation and at lairage sites increases the risk of cross-contamination (Hazards et al., 2022). Additionally, procedures such as evisceration, defeathering, and de-hiding elevate initial microbial loads, resulting in further ARB and ARG contamination. Indeed, ARG abundance in a new meat processing plant increased significantly over 1.5 years, due to the transfer of ARB from animal carcasses to surfaces, tools, and drains, highlighting their role as reservoirs of ARGs (Cobo-Díaz et al., 2021). Despite sanitation measures, biofilms on processing surfaces may retain ARB, facilitating their spread throughout the entire food production chains, as demonstrated for several types of foods (De Filippis et al., 2021, 2024; Valentino et al., 2022, 2023; Sequino et al., 2024; Barcenilla et al., 2024). Moreover, cleaning agents used for disinfection in processing environments apply a selective pressure on foodborne bacteria, potentially resulting in adaptive changes in their genomes, transcriptomes, and proteomes, further enhancing their resistance to disinfectants and antibiotics (Marmion et al., 2022; Xiao et al., 2024). Therefore, the wastewater generated in food processing facilities has high levels of ARB and ARG, leading to the environmental contamination of other water bodies (Stošić et al., 2016) (Fig. 6). Beyond the food production sector, the spread of AMR in the environment is influenced by a multitude of factors, including clinical settings, domestic practices, climate change, and various ecological and human-related activities. Indeed, AMR spread is a "One Health" issue, that summarizes well that the health of humans, animals, and the environment is strictly interconnected and should be addressed with a more comprehensive approach, tackling all the aspects involved.

4.3. AMR in health settings

The relationship between antibiotic administration in animal farming and the dissemination of AMR remains a subject of current debate. Nevertheless, various investigations suggest that the misuse of antibiotics in humans, along with environmental influences, could play a more crucial role (Mather et al., 2013). For instance, approximately 60.1 % of cases involving extended-spectrum beta-lactamase-producing *E. coli* (relevant ARGs are *CTX-M, TEM,* and *SHV* families) and plasmid-mediated AmpC-producing (cephalosporinases) *E. coli* were associated with human-to-human transmission, especially in household and healthcare settings. In contrast, minimal contributions came from food (18.9 %), companion animals (7.9 %), farm animals (3.6 %), and various environmental sources (2.6 %) (Mughini-Gras et al., 2019). Furthermore, 63.5 % of the estimated 671,689 AMR infections in EU and EEA countries were associated with transmission linked with healthcare settings (Cassini et al., 2019). This emphasizes the impact of clinical antibiotic use and human interactions in AMR onset and transmission, which frequently outweigh the impact of animal farming (Fig. 7).

4.4. AMR in household settings

Similarly, practices regarding household cleaning and the extensive use of personal care products are gaining acknowledgment as vital contributors to global AMR persistence. For instance, typical formulations in personal care products, such as those containing platinum-based compounds, exhibit antimicrobial capabilities by denaturing enzymes, destroying DNA, lysing cells, and generating reactive oxygen species (Stokes et al., 2024; Tahir et al., 2017). These chemical residues are washed away in greywater systems, where they interact with environmental bacteria and micropollutants, promoting ARB emergence (Pruden et al., 2018; Mim et al., 2024). Finally, also household animals may serve as reservoirs and vectors for the spread of antimicrobial resistance to humans (Bhat, 2021) (Fig. 7).

4.5. AMR at global level

In addition to the previously discussed factors, AMR is also influenced by a wide range of ecological and climate factors that extend beyond agricultural, hospital, and household contexts (Fig. 8). For example, elevated temperatures, increased humidity, and higher pollution levels promote the proliferation of microbes and facilitate gene transfer. A 1 °C rise in average ambient temperature is associated with a 1.14-fold and a 1.06-fold increase, respectively, in the **population-level prevalence of carbapenem-resistant** *Klebsiella pneumoniae* **and** *Pseudomonas aeruginosa* **clinical isolates** (Li et al., 2023). This elevated global temperature also mediates the release of ARB from the thawing permafrost. A comprehensive review encompassing 574 studies revealed that 39 % identified detrimental synergies between climate change and AMR, with 19 % establishing a direct connection between climate change and the emergence of AMR, while 12 % observed beneficial interactions between climate interventions and AMR control (Bavel et al., 2024). Human activities such as deforestation also increase the

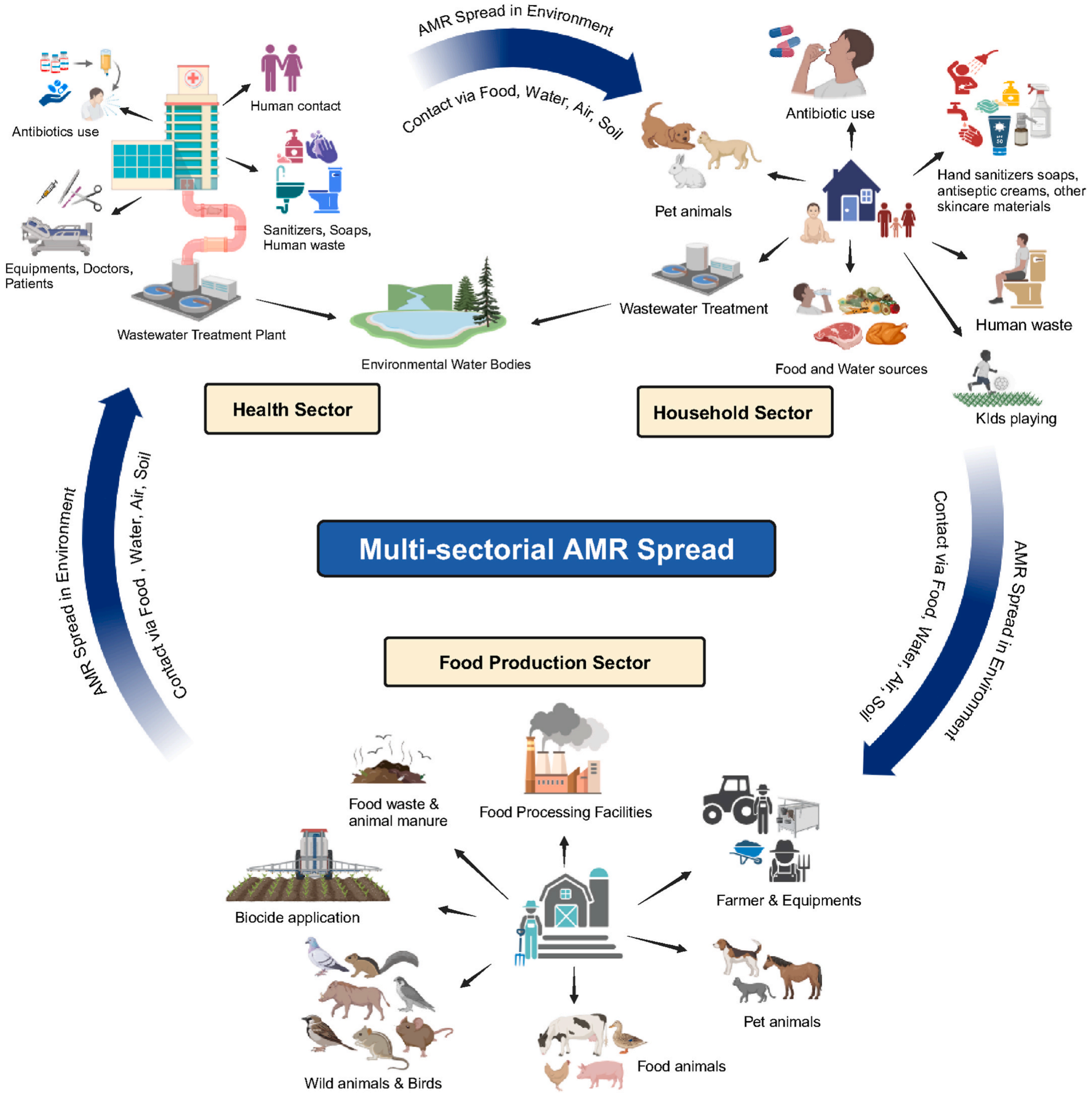

Fig. 7. Overview of AMR flow across clinical, domestic, and agricultural systems. This scheme outlines a particular subset of the broad AMR landscape, illustrating the role of clinical treatments, household cleaning, and agricultural practices in the development of AMR. Created in BioRender. RAHMAN, A. (2025) https://BioRender.com/m51i802.

prevalence of ARGs in soils by exerting environmental selective pressures on un-exposed soil microbial communities (Lemos et al., 2021). Similarly, the combination of these activities with microplastic and chemical pollution further accelerates the evolution of ARGs (Rzymski et al., 2024). For instance, a 1 % rise in airborne particulate matter (PM2.5) is related to a 0.7 % increase in AMR (Natali, 2025). Likewise, global travel and trade play a substantial role in the transboundary spread of resistant strains (Fig. 8) (Mendelsohn et al., 2023).

In addition to the environmental drivers, microbial evolution itself plays a key role in AMR persistence. Resistance can arise naturally through spontaneous mutations and spread through vertical and horizontal gene transfer, aided by mobile genetic elements like plasmids and transposons (Djordjevic et al., 2013). Moreover, co-selection mechanisms such as cross-resistance, co-resistance, and co-regulation allow bacteria to acquire multiple resistance traits even without direct antibiotic exposure (Murray et al., 2024). Together, these biological and environmental factors underscore the need for coordinated interventions, which are discussed in the following recommendations (Fig. 9).

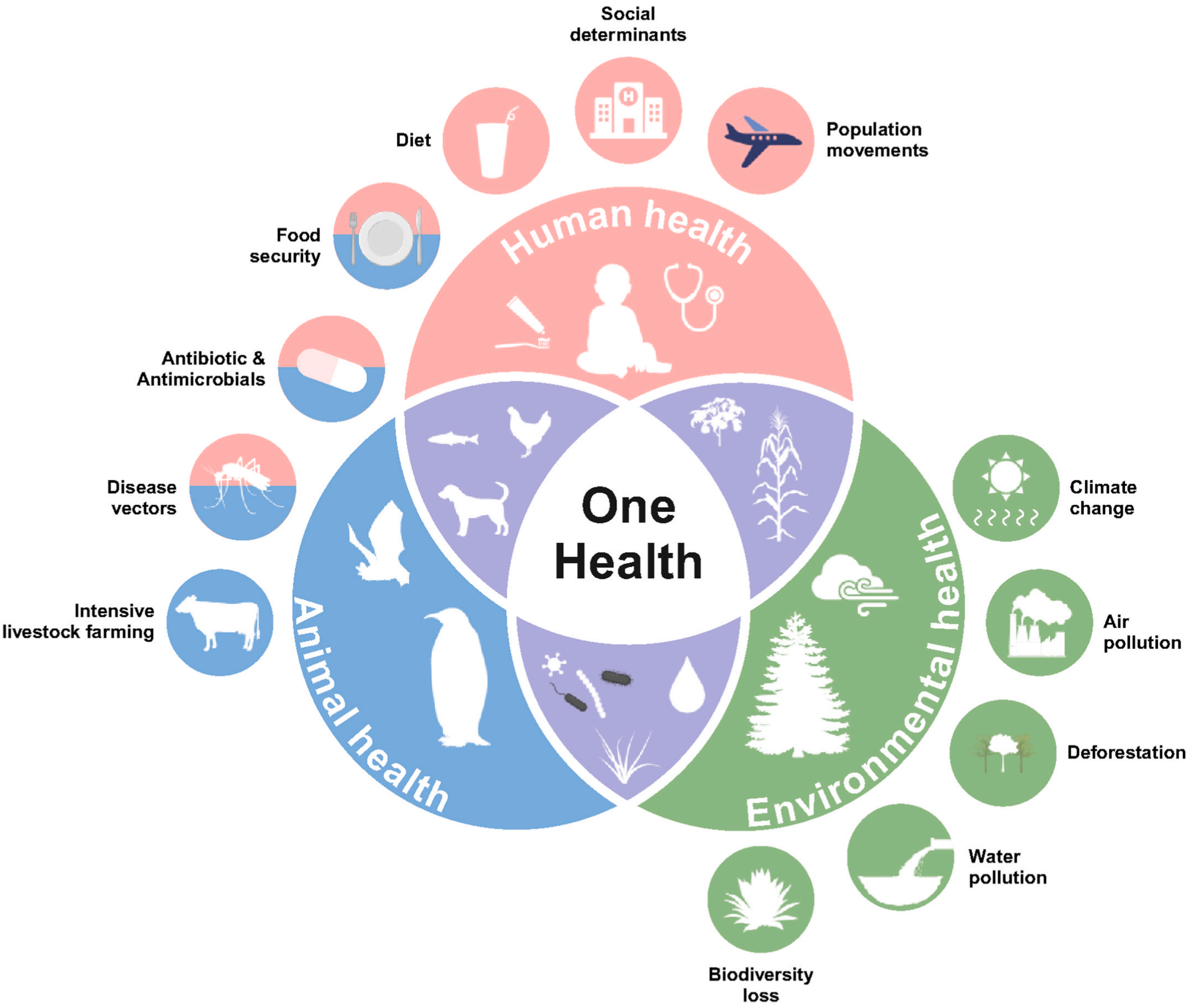

Fig. 8. The One Health concept scheme showing how the health of people, animals, and the environment are all connected within the One Health framework. *Created in BioRender. RAHMAN, A. (2025)* https://BioRender.com/e08j265.

5. Future research recommendations

5.1. *Advancing surveillance and diagnostics*

Comprehensive and real-time monitoring of AMR is crucial in various ecosystems to detect resistance trends in animals, humans, and the environment. Conventional monitoring is based on a restricted set of pathogens, often missing the emerging resistance threats. However, innovations in metagenomics, AI-enhanced predictive models, and machine learning can provide a proactive approach to detect emerging AMR hotspots prior to the onset of outbreaks (de la Lastra et al., 2024). Furthermore, misdiagnosis within both human and veterinary medicine plays a substantial role in the rise of AMR (Chan et al., 2020). The development of affordable, user-friendly, rapid, and reliable diagnostic tests is essential for decreasing dependence on broad-spectrum antibiotics and encouraging targeted antimicrobial treatments.

5.2. *Mitigation strategies at the farm and processing levels*

Prompt surveillance and instant isolation of infected animals can mitigate the AMR spread at the farm level. Additionally, decreasing stock density, increasing rearing space, and increasing farm biosecurity and herd management can further mitigate the spread of AMR (Dhaka et al., 2023). Post-slaughter washing of beef, pork, and lamb carcasses can effectively reduce contamination loads and improve meat hygiene at the initial stages of processing. Furthermore, the implementation of advanced on-site wastewater treatment, air filtration, and ventilation systems are essential to prevent the discharge of ARB and ARG into the environment. Similarly, the final meat products frequently contain spoilage microorganisms, pathogens, ARGs, and even antibiotic residues; however, studies on their effects on the human oral and gut microbiome following ingestion remain limited and insufficiently investigated. Although comprehensive cooking diminishes bacterial populations, the fate of ARGs or antibiotic residues during digestion, as well as the possible transmission of ARGs to the gut microbiome are still unclear.

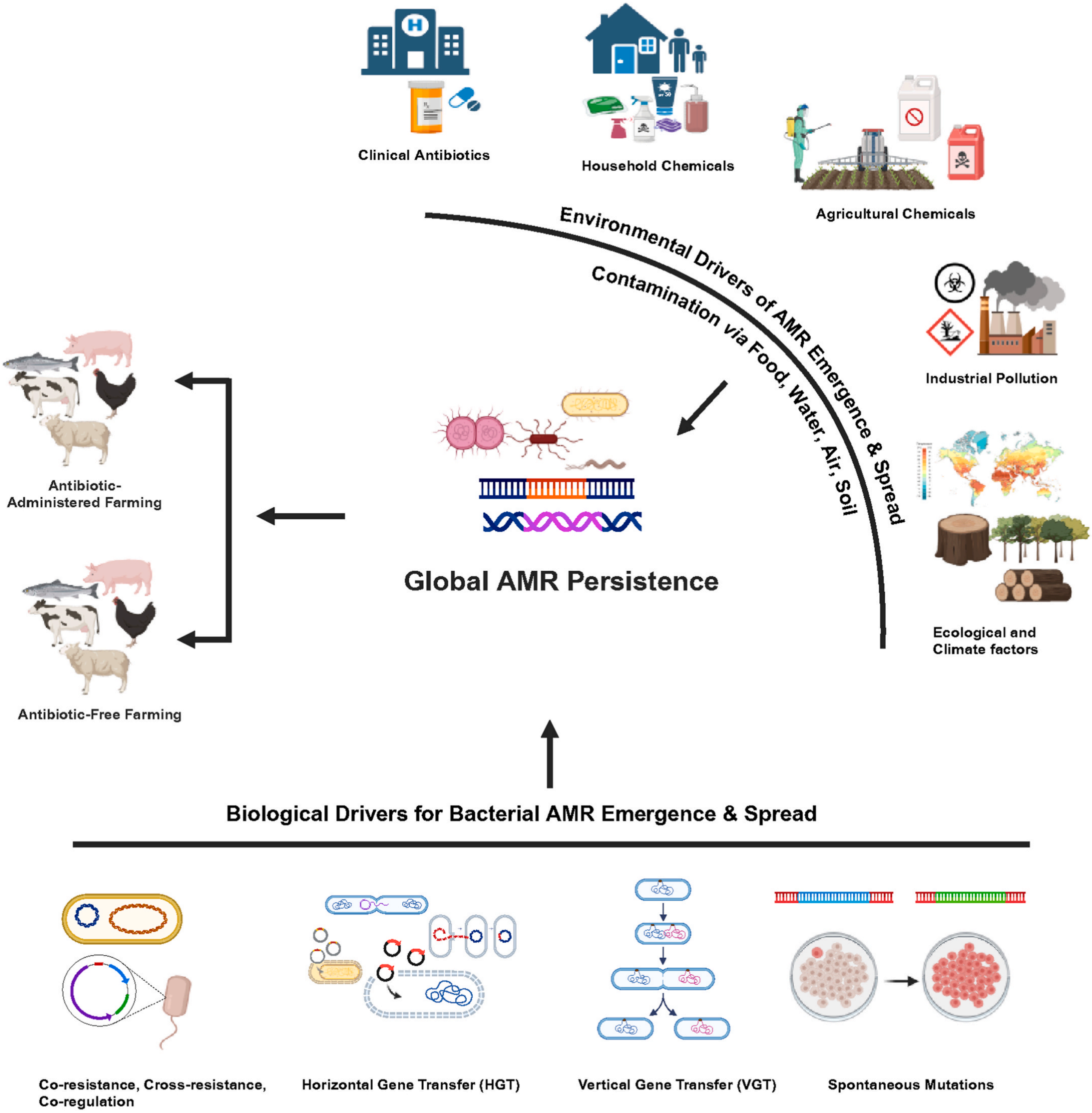

Fig. 9. Visual summary of the environmental and biological drivers of persistent AMR in animal food systems. The figure illustrates how various sources including environmental contamination, microbial evolution, and cross-sectoral influences contribute to the persistence and spread of AMR. Created in BioRender by Rahman, A. (2025). https://BioRender.com/r26z013.

5.3. *Reducing antibiotic dependence, exploring alternatives and public awareness*

Alternative treatments to traditional antibiotics, such as probiotics, prebiotics, bacteriophage therapy, and vaccinations, show promise in lowering infection rates and reducing antibiotic use. Furthermore, innovative conjugated antibiotic formulations may also enhance therapeutic efficacy against resistant microbes (Padilla and Nowick, 2025). Public involvement is also critical, yet it is frequently overlooked in AMR mitigation. Public education campaigns, using the most popular social media platforms should educate the public about how their everyday lifestyle choices influence the global AMR spread.

5.4. *Global collaboration and policy integration*

Considering the transboundary characteristics of AMR, public health agencies, environmental organizations, policymakers, and industry stakeholders need to collaborate on a global scale. Regulatory frameworks need to encompass a broader range of substances, including.

- Biocides, pesticides, heavy metals, and household chemicals.
- Enhanced wastewater management strategies aimed at minimizing ARG contamination in natural water systems.
- Strengthened data-sharing initiatives to facilitate coordinated global efforts in AMR control.

While ongoing surveillance and improved diagnostic capacity are essential for early detection of AMR trends, we recommend rebalancing funding priorities. Core surveillance should be maintained at a baseline level, enough to monitor emerging threats, while the bulk of financial resources should be redirected from this intensive surveillance and quantification of AMR toward solution-driven research. AMR is a well-documented problem; nevertheless, funding should now be focused on discovering novel solutions rather than sustaining the documentation.

6. Conclusions

This study systematically reviewed and meta-analyzed the presence of ARGs in CONV and ABF animal farming systems. ARGs were detected in both systems, with higher average counts in CONV farms. However, statistical differences in ARG prevalence across farming systems, host types, and sample origins were not significant. Subgroup analysis showed higher ARG presence in cattle and environmental samples, suggesting farm-level conditions may play a more critical role in ARG transmission than retail product exposure. However, this analysis is limited by the predominance of poultry studies, variability in study designs and ARG detection methods, and the lack of geographic metadata across the included research.

Notably, 97 % of studies on ABF farms still reported the presence of ARGs, suggesting that reducing antibiotic use alone may not be sufficient to control AMR. Broader factors such as poor farm hygiene, environmental contamination, inadequate waste management, and microbial evolution likely contribute to its persistence. While minimizing antibiotic use in animal farming has been a longstanding goal, the spread of AMR along the meat production chain involves many other drivers. Therefore, it is important to recognize that AMR is not solely caused by the overuse or misuse of antimicrobials in animals. Rather, AMR is a global issue that demands shared responsibility across agriculture, healthcare, households, and environmental sectors, particularly in the context of climate change.

These findings support the One Health narrative, where effective AMR control requires coordinated action across sectors. Targeted interventions at the farm and processing level, combined with policies addressing environmental and societal drivers, are urgently needed to reduce the risk of ARG transmission and protect public health.

CRediT authorship contribution statement

Asim Ur Rahman: Writing – original draft, Visualization, Formal analysis, Data curation. **Vincenzo Valentino:** Writing – review & editing, Formal analysis. **Giuseppina Sequino:** Writing – review & editing, Data curation. **Danilo Ercolini:** Writing – review & editing, Resources. **Francesca De Filippis:** Writing – original draft, Supervision, Resources, Conceptualization.

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Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.fm.2025.104877.

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