

REVIEW ARTICLE

A Review on Usage of Agricultural Antibiotics and Evolution of Environmental Resistomes in Humans



Syed Ansar Ahmed^{*1}, Madhuri Vishwanath Swami², Shoaib Ali Khan³, Pawar Shubhangi Namdev⁴, Mahendra Subhash Patil⁵

¹ Associate Professor, Department of Pharmaceutical Chemistry, Indira College of Pharmacy, Vishnupuri, Nanded, Maharashtra, India

² Assistant Professor, Department of Quality Assurance, Indira College of Pharmacy, Vishnupuri, Nanded, Maharashtra, India

³ PG Scholar, Department of Pharmacology, Indira College of Pharmacy, Vishnupuri, Nanded, Maharashtra, India

⁴ Assistant Professor, Department of Pharmacy, Swargiya Lilawati Satish Awbad Pharmacy College, Mukhed, Nanded, Maharashtra, India

⁵ Associate Professor, Department of Pharmaceutics, Shri Sai Samarth Pharmacy College and Research Centre, Bhadgaon, Jalgaon, Maharashtra, India

Publication history: Received on 3rd July 2025; Revised on 10th Aug 2025; Accepted on 19th August 2025

Article DOI: 10.69613/8fahzb85

Abstract: Antimicrobial resistance (AMR) is a global health crisis characterized by the increasing inability of conventional antibiotics to combat pathogenic microorganisms. This study discusses about the AMR mechanisms, surveillance systems, and interventions across human health, agriculture, and environmental sectors. The inter-relationship of factors driving AMR, including inappropriate antibiotic usage, agricultural practices, environmental contamination, and healthcare-associated infections were also discussed in this review. The main findings highlight the effectiveness of integrated One Health approaches, combining improved surveillance, stewardship programs, and policy interventions. Economic analyses show substantial societal costs of AMR, while emerging technologies in genomic surveillance and rapid diagnostics offer promising solutions for resistance monitoring and containment. The regional variations in AMR patterns and intervention outcomes, particularly in low- and middle-income countries, where infrastructure and resource limitations pose significant challenges. The preventive measures should focus on strengthening global coordination, implementing evidence-based policies, and developing innovative techniques to preserve antimicrobial effectiveness while ensuring equitable access to these critical medicines.

Keywords: Antimicrobial resistance; Environmental resistome; Agricultural antibiotics; One Health; Horizontal gene transfer

1. Introduction

The global escalation of antibiotic use in agriculture represents a critical intersection of food security, environmental health, and public health concerns. Since their introduction in the 1940s, antibiotics have transformed agricultural practices, particularly in intensive livestock farming [1]. The scale of agricultural antibiotic consumption has reached unprecedented levels, with global usage exceeding 130,000 tons annually and projections indicating a 67% increase by 2030 [2]. This massive utilization stems from three primary applications: therapeutic treatment of bacterial infections, prophylactic disease prevention, and growth promotion in livestock [3].

The environmental consequences of such extensive antibiotic use extend far beyond their intended agricultural applications. These compounds, along with their metabolites, persist in environmental matrices, creating sustained selective pressures on microbial communities [4]. The resulting acceleration of evolutionary processes has led to the emergence and proliferation of antimicrobial resistance (AMR) genes within environmental bacteria [5]. Modern molecular techniques have revealed that these resistance determinants often pre-date human antibiotic use, but their abundance and diversity have increased dramatically in response to anthropogenic antibiotic pressure [6].

The environmental resistome, including all antibiotic resistance genes and their precursors in both pathogenic and non-pathogenic bacteria, has expanded significantly due to agricultural practices [7]. Recent metagenomic studies have uncovered vast arrays of resistance genes in agricultural soils, many of which were previously uncharacterized [8]. This expansion of the resistome presents a complex ecological challenge, as these genes can transfer between environmental bacteria and clinically relevant pathogens [9]. The movement of resistance determinants through environmental matrices creates multiple exposure routes for human populations. Horizontal gene transfer mechanisms, including conjugation, transformation, and transduction, facilitate the spread of resistance genes across bacterial species [10]. This genetic mobility, coupled with selective pressure from continuous antibiotic exposure, has accelerated the evolution of multi-drug-resistant pathogens [11]. The emergence of such resistant organisms in agricultural settings poses serious threats to both food security and clinical medicine [12].

* Corresponding author: Syed Ansar Ahmed

2. Environmental Impact of Agricultural Antibiotic Use

2.1. Alterations in Soil Microbiome

Agricultural soils function as complex ecosystems harboring diverse microbial communities that play crucial roles in nutrient cycling, organic matter decomposition, and plant health [13]. The introduction of antibiotics through animal waste and direct soil treatment has fundamentally altered these microbial ecosystems. Studies utilizing high-throughput sequencing technologies have revealed significant shifts in bacterial community structures, with resistant strains gaining competitive advantages over susceptible populations [14].

The persistence of antibiotics in soil environments varies significantly depending on compound properties, soil characteristics, and environmental conditions. Tetracyclines and fluoroquinolones, commonly used in agriculture, can persist for months to years due to their strong binding to soil particles [15]. This extended persistence creates prolonged selective pressure, leading to the establishment of stable resistant populations [16].

The impact on soil microbial communities extends beyond simple shifts in population dynamics. Research has shown alterations in essential ecosystem functions, including nitrogen cycling, carbon mineralization, and enzyme activities [17]. These changes can have cascading effects on soil fertility, plant growth, and overall ecosystem health [18].

Table 1. Major Classes of Antibiotics Used in Agriculture and Their Environmental Impact

Antibiotic Class	Common Usage in Agriculture	Environmental Persistence (Half-life)	Primary Environmental Concerns	Detection Methods
Tetracyclines	Growth promotion, Disease prevention	100-180 days in soil	High soil binding capacity, Vertical soil migration	HPLC-MS/MS, Biosensors
Fluoroquinolones	Treatment of respiratory infections	60-90 days in soil	Photostability, Water contamination	LC-MS/MS, Immunoassays
Beta-lactams	Treatment of mastitis	5-10 days in soil	Rapid hydrolysis, Metabolite formation	Bioassays, UPLC-MS
Sulfonamides	Broad spectrum treatment	30-90 days in soil	High water solubility, Groundwater contamination	LC-MS/MS, Electrochemical sensors
Macrolides	Growth promotion, Respiratory diseases	14-30 days in soil	Surface contamination, water Bioaccumulation	HPLC, Biosensors

2.1.1. Changes in Microbial Diversity

Long-term exposure to antibiotics has led to measurable reductions in soil microbial diversity. Molecular analyses have shown decreased species richness and evenness in antibiotic-impacted soils [19]. Particularly affected are slow-growing bacteria and specialists that perform unique ecosystem functions. For instance, studies have documented significant declines in nitrogen-fixing bacteria populations in soils containing high levels of veterinary antibiotics [20].

The loss of microbial diversity affects soil ecosystem resilience and functionality. The main bacterial groups involved in organic matter decomposition and nutrient cycling show reduced abundance and activity in antibiotic-contaminated soils [21]. These changes can persist long after antibiotic exposure ceases, indicating potential long-term impacts on soil health [22].

2.1.2. Resistance Gene Proliferation

Metagenomic analyses have revealed an extensive array of resistance genes in agricultural soils, representing multiple mechanisms of antibiotic resistance [23]. These include genes encoding efflux pumps, target modification enzymes, and antibiotic-inactivating proteins. The abundance and diversity of these genes show strong correlations with historical antibiotic usage patterns in specific agricultural regions [24].

Studies utilizing quantitative PCR techniques have showed exponential increases in resistance gene copy numbers following repeated antibiotic exposure [25]. Of particular concern is the co-occurrence of multiple resistance genes on mobile genetic elements, facilitating their simultaneous transfer between bacterial species [26]. Research has identified numerous novel resistance determinants in agricultural soils, including variants capable of conferring resistance to last-resort antibiotics [27].

Table 2. Distribution of Antibiotic Resistance Genes in Agricultural Environments

Environmental Matrix	Major Resistance Determinants	Findings	Research Implications
Agricultural Soil	tetA, tetB, sul1, sul2, qnrS	High prevalence in top soil layers; Seasonal variations observed; Correlation with manure application	Indicates long-term persistence and potential for horizontal gene transfer
Water Systems	blaCTX-M, ermB, mcr-1, floR	Higher concentrations in surface water near farms; Groundwater contamination in agricultural regions	Suggests widespread dissemination through water systems
Animal Housing	mecA, vanA, cfr, aadA	Abundant in ventilation systems and settled dust; Multiple resistance patterns observed	Demonstrates occupational exposure risks
Manure Storage	sul1, tetM, blaTEM, aac(6)-Ib	High diversity of resistance genes; Active horizontal gene transfer detected	Highlights need for improved waste management

2.2. Water System Contamination

The impact of agricultural antibiotics extends significantly into aquatic ecosystems, creating complex networks of contamination [28]. Various transport mechanisms, including surface runoff, leaching, and wind-blown particles, facilitate the movement of antibiotics and resistant bacteria from agricultural sources into water bodies [29].

2.2.1. Surface Water Impact

Surface waters near agricultural operations frequently contain measurable concentrations of multiple antibiotic compounds. Studies have documented concentrations ranging from ng/L to µg/L, with higher levels observed during rainfall events and seasonal agricultural activities [30]. The presence of these compounds creates selective pressure for resistance development in aquatic bacterial communities [31].

Monitoring programs have revealed complex patterns of antibiotic distribution in surface waters:

- Seasonal variations correlating with agricultural application schedules
- Spatial gradients extending downstream from agricultural sources
- Accumulation in sediments, creating long-term reservoirs
- Interactions with other agricultural pollutants, including pesticides and fertilizers [32, 33]

The impact on aquatic ecosystems includes:

- Alterations in natural bacterial community structures
- Development of resistant bacterial populations
- Effects on algal communities and aquatic food webs
- Potential impacts on fish and other aquatic organisms [34, 35]

2.2.2. Groundwater Concerns

The vertical migration of antibiotics through soil profiles presents significant challenges for groundwater quality [36]. Factors influencing this transport include:

- Soil composition and structure
- Hydrological conditions
- Chemical properties of specific antibiotics
- Presence of preferential flow paths
- Interaction with soil organic matter [37]

Studies utilizing multilevel sampling wells have showed the presence of both antibiotic compounds and resistant bacteria at various depths in aquifers [38]. This contamination poses particular challenges for rural communities relying on groundwater for drinking water supplies [39]. Research has shown that conventional water treatment methods may not effectively remove all antibiotic compounds or resistant bacteria, raising concerns about exposure through drinking water [40].

3. Transmission Routes and Human Exposure

3.1. Food Chain

The movement of antibiotic-resistant bacteria through the food supply chain represents a primary route of human exposure [41]. This transmission pathway involves multiple stages and complex interactions between various agricultural and food processing environments.

3.1.1. Primary Production Phase

During livestock production, resistant bacteria can colonize animals receiving antibiotics, creating reservoirs of resistance [42]. These bacteria may include both animal pathogens and commensal organisms carrying resistance genes. Studies have shown that resistant bacteria can persist throughout the production cycle, even after antibiotic withdrawal [43].

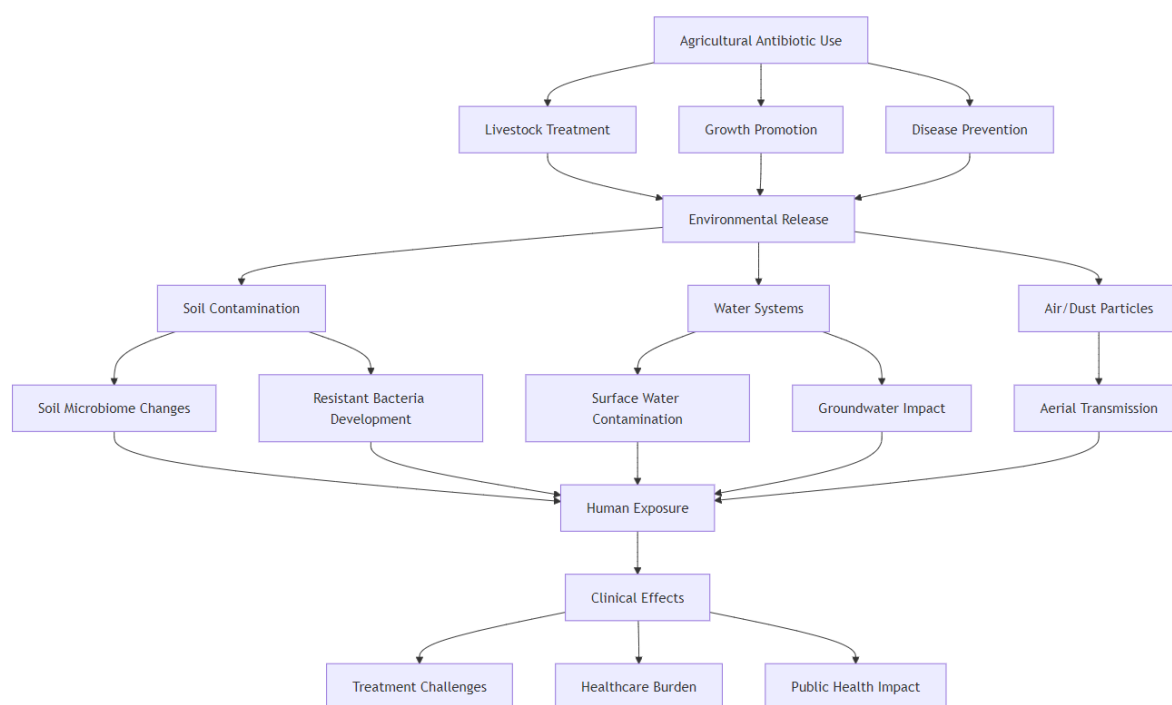


Figure 1. Transmission Routes of Agricultural Antibiotics and Resistance

The farm environment itself becomes a reservoir for resistant organisms, with contamination extending throughout various agricultural settings [44]. Animal housing facilities harbor significant populations of resistant bacteria, particularly in areas with high animal density and limited ventilation. Feed storage areas frequently show contamination with resistant organisms, potentially serving as a source of continuous exposure to livestock. Waste management systems, particularly in intensive farming operations, concentrate both antibiotic residues and resistant bacteria, creating optimal conditions for resistance gene transfer [45].

Table 3. Transmission Pathways and Associated Health Risks

Transmission Route	Primary Mechanisms	Risk Factors	Public Health Impact
Food Chain	Direct bacterial transfer; Residue consumption	Processing methods; Storage conditions	Foodborne infections; Chronic exposure effects
Environmental Exposure	Dust inhalation; Water contact; Soil exposure	Proximity to farms; Occupational exposure	Respiratory infections; Skin colonization
Direct Contact	Animal handling; Surface contamination	Farm workers; Veterinarians	Occupational health issues; Resistant infections
Vector-mediated	Insect carriers; Wildlife transmission	Ecological factors; Season variation	Community spread of resistance

Farm equipment and materials regularly contact both animals and their waste, facilitating the spread of resistant organisms throughout the production facility. Air handling systems in confined animal feeding operations (CAFOs) can distribute resistant bacteria via bioaerosols, affecting both indoor and outdoor air quality. The persistence of these organisms in farm environments creates continuous exposure risks for both animals and workers [46].

3.1.2. Processing and Distribution

The slaughter and processing phases present critical control points for bacterial transmission [47]. Despite hygiene protocols, resistant bacteria can survive processing procedures and contaminate final products. Research has documented the presence of resistant organisms at various stages of meat processing, including cutting, packaging, and storage [48].

Cross-contamination during food processing represents a significant concern. Equipment surfaces, processing water, and handling procedures can transfer resistant bacteria between products. Studies utilizing molecular tracking methods have shown the persistence of specific resistant strains throughout processing facilities [49]. Temperature abuse or inadequate processing parameters may allow resistant bacteria to survive and potentially multiply during distribution [50].

3.1.3. Retail and Consumer Exposure

At the retail level, multiple factors influence the survival and transmission of resistant bacteria. Storage conditions, handling practices, and cross-contamination between products affect the final bacterial load reaching consumers [51]. Surveillance studies have consistently detected resistant organisms in retail meat products, with some samples harboring bacteria resistant to multiple antibiotic classes [52].

The consumer phase presents additional opportunities for bacterial transmission. Improper food handling, inadequate cooking temperatures, and cross-contamination in home kitchens can lead to exposure to resistant organisms. Research has shown that resistant bacteria can transfer from contaminated meat products to kitchen surfaces and other foods during meal preparation [53].

3.2. Environmental Exposure

Environmental routes of exposure to antibiotic-resistant bacteria extend beyond the food chain, creating a complex web of transmission possibilities [54]. These pathways operate through multiple environmental matrices and involve various exposure scenarios affecting different population groups.

3.2.1. Occupational Exposure

Agricultural workers face heightened exposure risks through direct contact with livestock, contaminated environments, and agricultural materials [55]. Farmers, veterinarians, and farm workers show higher colonization rates with resistant organisms compared to the general population. Long-term exposure studies have shown that these occupational groups often carry similar resistance patterns to those found in farm animals under their care [56].

Exposure intensity varies with specific agricultural activities. Workers involved in animal handling, waste management, and feed preparation experience different levels and types of exposure. Research has documented increased prevalence of resistant organisms in nasal swabs and hand samples from workers performing high-risk tasks [57]. The duration of occupational exposure correlates positively with colonization rates, suggesting cumulative risk effects over time [58].

3.2.2. Environmental Media

The movement of resistant bacteria through environmental media creates diverse exposure pathways [59]. Soil serves as both a reservoir and transport medium for resistant organisms. Agricultural activities, including tilling, irrigation, and fertilizer application, can aerosolize soil particles containing resistant bacteria. Wind erosion of contaminated soils contributes to the atmospheric transport of resistance genes across significant distances [60].

Water systems facilitate the widespread distribution of resistant organisms throughout the environment. Surface runoff from agricultural lands carries both antibiotic residues and resistant bacteria into water bodies. Irrigation with contaminated water spreads resistant organisms to crops and agricultural soils. Groundwater contamination through leaching processes creates potential exposure through drinking water sources, particularly in rural areas relying on private wells [61].

3.2.3. Community Exposure

Communities located near agricultural operations experience increased exposure risk through multiple pathways [62]. Atmospheric transport of contaminated dust particles affects air quality in surrounding areas. Studies utilizing air sampling techniques have detected resistant organisms at considerable distances from source farms, with concentration gradients correlating to wind patterns and agricultural activity levels [63].

Recreational activities in contaminated environments present additional exposure routes. Water-based recreation in affected water bodies increases contact with resistant organisms. Soil-based activities in agricultural areas or regions receiving agricultural waste application similarly enhance exposure potential. Children may face higher risks due to their behavioral patterns and developing immune systems [64].

4. Clinical Effects on Human Health

4.1. Impact on Human Microbiota

The exposure to agricultural-origin resistant bacteria significantly influences human microbiome composition [65]. The human gut microbiota, comprising thousands of bacterial species, plays crucial roles in health maintenance and disease prevention. Agricultural antibiotic exposure can disrupt this delicate microbial balance through multiple mechanisms [66].

4.1.1. Mechanisms of Microbiome Disruption

Exposure to sub-therapeutic levels of antibiotics through food and environmental sources can select for resistant strains within the human microbiota. Studies utilizing metagenomic sequencing have revealed shifts in microbial community structure following chronic low-level antibiotic exposure [67]. These alterations affect metabolic functions, immune system development, and colonization resistance against pathogens [68].

The transfer of resistance genes from agricultural-origin bacteria to human commensal organisms occurs through horizontal gene transfer within the gut environment. Research has shown that such transfers can occur rapidly and persist long after the initial exposure event [69]. The acquisition of resistance genes by commensal bacteria creates reservoirs of resistance within the human microbiome, potentially affecting future therapeutic outcomes [70].

4.1.2. Chronic Effects

Chronic disruption of the gut microbiota due to agricultural antibiotic exposure has been linked to various health conditions [71]. Longitudinal studies have revealed associations between altered microbiome compositions and metabolic disorders, immune system dysregulation, and increased susceptibility to infections [72].

The developmental impact on pediatric populations raises particular concerns. Early-life exposure to agricultural antibiotics through food and environmental sources may affect immune system maturation and metabolic programming. Research has documented correlations between early antibiotic exposure and increased risks of allergic conditions, obesity, and autoimmune disorders in later life [73].

4.2. Treatment Challenges

4.2.1. Treatment Failures

The emergence of resistant infections linked to agricultural sources has complicated clinical treatment decisions [74]. Healthcare providers increasingly encounter pathogens displaying resistance patterns similar to those observed in agricultural settings. Treatment failures occur when empirical antibiotic choices prove ineffective against resistant organisms, leading to prolonged infections and increased morbidity [75].

The timeline from infection onset to effective treatment lengthens when resistant organisms are involved. Traditional culture-based diagnostic methods may require additional time to identify resistance patterns, delaying appropriate therapeutic intervention. Studies in clinical settings have documented increased hospital stays and higher mortality rates associated with resistant infections of agricultural origin [76].

4.2.2. Limitation of Therapeutic Options

The reduced effectiveness of first-line antibiotics necessitates the use of broader-spectrum agents [77]. This escalation in antibiotic class often involves medications with:

- Higher toxicity profiles
- Increased risk of adverse effects
- Greater potential for collateral damage to beneficial bacteria
- Higher treatment costs

The limitation of therapeutic options particularly affects vulnerable populations, including immunocompromised patients and those with chronic conditions [78].

4.3. Impact on Healthcare Systems

4.3.1. Resource Utilization

The management of resistant infections strains healthcare resources through multiple mechanisms [79]. Extended hospital stays increase bed occupancy rates and staffing requirements. Additional diagnostic testing and consultation services add to the complexity of patient care. Infection control measures become more intensive and resource-demanding when dealing with resistant organisms [80].

4.3.2. Economic Burden

The financial impact of agricultural-origin resistant infections extends throughout the healthcare system [81]. Direct costs include:

- Extended hospitalization expenses
- Advanced diagnostic procedures
- Higher-cost antimicrobial agents
- Additional infection control measures
- Indirect costs include productivity losses, long-term disability expenses, and reduced quality of life impacts [82].

4.3.3. Public Health Infrastructure

The surveillance and management of resistant infections require substantial public health resources [83]. Health departments must maintain sophisticated monitoring systems to track resistance patterns and outbreak occurrences. The need for rapid response capabilities and coordinated intervention strategies places additional demands on public health infrastructure [84].

5. Mitigation Measures

5.1. Agricultural Practice Modifications

5.1.1. Alternative Disease Prevention Approaches

The implementation of enhanced biosecurity measures offers effective alternatives to routine antibiotic use [85]. Comprehensive biosecurity programs include multiple control points throughout the production system. Advanced ventilation systems, improved animal housing designs, and strategic animal flow management reduce disease transmission risks [86].

Table 4. Comparison of Alternative Disease Prevention Techniques in Agriculture

Prevention Strategy	Efficacy Level	Implementation Complexity	Cost-Effectiveness	Environmental Impact	Regulatory Acceptance
Bacteriophage Therapy	High	Moderate	Moderate	Minimal	High
Immunomodulators	Moderate to High	Low	High	Low	Very High
Competitive Exclusion	Moderate	Low	Very High	Minimal	High
Plant-Based Antimicrobials	Moderate	Low	Moderate	Low	Very High
Synthetic Peptides	High	High	Low	Low	Moderate

5.1.2. Nutritional Interventions

Advanced nutritional strategies have emerged as crucial components in reducing antibiotic dependence [87]. Optimized feed formulations enhance animal immune function and gut health through targeted nutrient supplementation. Research has showed that specific dietary components, including organic acids, essential oils, and specialized fiber sources, can improve gut barrier function and reduce pathogen colonization [88].

Probiotic supplementation is a promising approach for maintaining animal health. Selected bacterial strains, when administered through feed or water, establish beneficial gut populations that compete with potential pathogens. Studies have shown that well-designed probiotic protocols can achieve health outcomes comparable to traditional antibiotic prophylaxis [89].

5.1.3. Housing and Management

Environmental stress reduction plays a fundamental role in disease prevention [90]. Modern housing designs incorporating improved ventilation systems, optimal stocking densities, and enhanced waste management protocols significantly reduce disease pressure. Research has established clear correlations between environmental quality parameters and animal health outcomes [91].

The implementation of livestock farming enables early disease detection and targeted interventions [92]. Automated monitoring systems track behavioral patterns, feeding activities, and physiological parameters, allowing rapid identification of health issues before they require antibiotic treatment. These technologies support more precise and judicious use of therapeutic interventions [93].

5.2. Regulatory Guidelines

5.2.1. Policy Framework

Comprehensive regulatory frameworks addressing agricultural antibiotic use require careful balance between animal welfare, economic viability, and public health protection [94]. Successful policies incorporate:

Phase-out programs for growth promotion applications have shown effectiveness in reducing overall antibiotic consumption. Countries implementing such programs have documented significant decreases in resistant organism prevalence without compromising agricultural productivity [95].

Prescription requirements for therapeutic use ensure veterinary oversight of antibiotic administration. These systems improve treatment targeting and reduce unnecessary usage. Documentation requirements enable better tracking of consumption patterns and resistance development [96].

5.2.2. Implementation and Enforcement

Effective regulatory implementation requires robust monitoring and enforcement mechanisms [97]. Infrastructure development for compliance verification includes:

Regular inspection programs verify adherence to antibiotic use regulations. Training programs for agricultural workers and veterinarians ensure proper implementation of new requirements. Documentation systems track antibiotic usage patterns and facilitate regulatory oversight [98].

Enforcement protocols must address both routine compliance issues and serious violations. Graduated response systems balance educational approaches with punitive measures where necessary. Success requires coordination between agricultural, veterinary, and public health authorities [99].

5.3. Monitoring and Surveillance

5.3.1. Surveillance Systems

Modern surveillance programs integrate data from multiple sources to provide comprehensive resistance monitoring [100]. Environmental sampling programs track resistance patterns in soil, water, and air around agricultural operations. Animal health monitoring systems document resistance trends in livestock populations. Human health surveillance captures emerging resistance patterns in clinical settings [101].

Advanced molecular techniques enhance surveillance capabilities through:

- Rapid identification of resistance genes
- Tracking of resistance transmission patterns
- Early detection of emerging resistance mechanisms
- Assessment of intervention effectiveness [102]

Molecular surveillance techniques have revolutionized resistance monitoring capabilities. Rapid identification of resistance genes through real-time PCR and next-generation sequencing enables early detection of emerging threats. These methods allow researchers to track resistance transmission patterns across different environmental compartments and host populations [103]. The assessment of intervention effectiveness relies on sophisticated data analysis systems. Machine learning algorithms process complex surveillance data to identify trends and predict resistance emergence. Temporal and spatial analysis of resistance patterns provides insights into transmission dynamics and helps optimize control strategies [104].

Table 5. Measures for Resistance Monitoring and Control

Technology Type	Application Area	Advantages	Implementation Challenges
Next-Generation Sequencing	Resistome mapping; Transmission tracking	Comprehensive genetic analysis; Early detection capability	Cost; Technical expertise requirements
Real-time PCR Systems	Rapid resistance detection; Quantitative analysis	Quick results; High sensitivity	Limited resistance spectrum coverage
Biosensors	Environmental monitoring; Residue detection	Continuous monitoring; Field application	Calibration needs; Environmental interference
Machine Learning Models	Prediction systems; Risk assessment	Pattern recognition; Preventive action	Data quality; Model validation

5.3.2. Data Management

Data management systems form the backbone of effective surveillance programs [105]. Standardized reporting protocols ensure data compatibility across different monitoring networks. Integration of agricultural, environmental, and clinical data sources creates a more complete picture of resistance dynamics [106].

Advanced analytical tools transform raw surveillance data into actionable intelligence. Statistical modeling approaches identify risk factors and predict resistance emergence patterns. Geographic information systems map resistance spread and help target intervention efforts. Network analysis techniques reveal transmission pathways and potential control points [107].

6. Technological Innovations and Interventions

6.1. Advanced Detection Methods

Novel diagnostic platforms have transformed the landscape of resistance monitoring [108]. Real-time detection systems provide rapid identification of resistant organisms in agricultural settings. These technologies enable more timely and targeted interventions, reducing unnecessary antibiotic use [109].

6.1.1. Advances in Molecular Diagnostic

High-throughput screening methods have enhanced the capability to detect and characterize resistance genes. Next-generation sequencing platforms enable comprehensive analysis of resistome composition in complex environmental samples. Metagenomic approaches reveal previously unidentified resistance mechanisms and their distribution patterns [110].

The development of portable diagnostic devices brings sophisticated testing capabilities to field settings. These tools enable on-site detection of resistant organisms and antibiotic residues. Real-time monitoring capabilities support more informed decision-making in agricultural operations [111].

6.1.2. Biosensor Technologies

Advanced biosensor platforms provide continuous monitoring of antibiotic concentrations and resistant organisms [112]. These systems utilize various detection principles, including electrochemical, optical, and biological recognition elements. Integration of multiple sensor types enables comprehensive monitoring of both antibiotics and resistance markers [113].

The miniaturization of biosensor systems has improved their practical applicability. Field-deployable devices provide rapid results without requiring sophisticated laboratory infrastructure. Wireless connectivity enables real-time data transmission and integration with central monitoring systems [114].

6.2. Alternative Agricultural Solutions

6.2.1. Bacteriophages

The development of bacteriophage therapy represents a promising alternative to conventional antibiotics [115]. Natural bacteriophages show high specificity for target pathogens, minimizing disruption of beneficial bacterial populations. Research has shown successful applications in treating bacterial infections in livestock, particularly in poultry and aquaculture settings [116].

Advanced phage technology has evolved beyond simple bacterial control. Engineered bacteriophages carry enhanced capabilities for pathogen detection and elimination. Synergistic approaches combining multiple phage types provide broader spectrum activity while maintaining specificity. Recent studies have shown the effectiveness of phage cocktails in reducing pathogen loads in animal production environments [117].

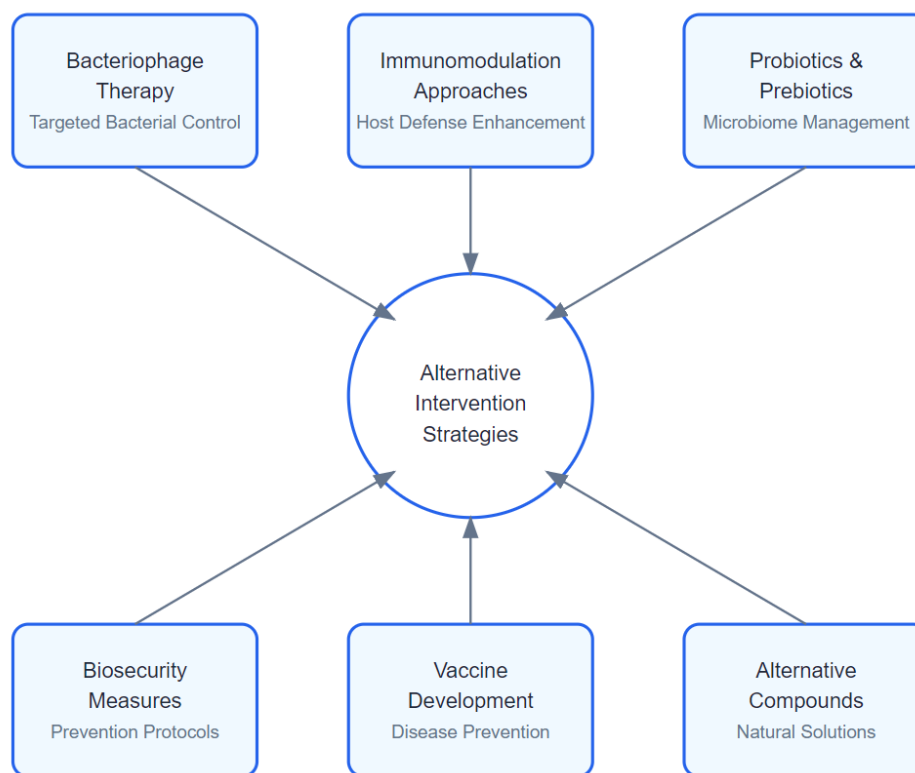


Figure 2. Alternative Intervention Techniques

Table 6. Impact of Different Agricultural Practices on Environmental Resistome

Agricultural Practice	Environmental Effect	Resistance Gene Profile	Mitigation Potential
Intensive Livestock Farming	High antibiotic residues in soil; Altered soil microbiome	Multiple drug resistance patterns; Enhanced gene transfer rates	Implementation of alternative health management strategies
Organic Farming	Reduced antibiotic pressure; Diverse soil microbiota	Lower resistance gene abundance; Different resistance patterns	Model for reduced antibiotic dependency
Aquaculture	Water system contamination; Sediment accumulation	Waterborne resistance spread; Novel resistance mechanisms	Development of closed systems and water treatment
Mixed Farming	Variable contamination patterns; Complex interaction networks	Diverse resistance profiles; Multiple transfer pathways	Integration of multiple control strategies

6.2.2. Immunomodulation

The enhancement of host immune function through targeted interventions offers sustainable disease prevention approaches [118]. Novel immunomodulatory compounds stimulate natural defense mechanisms, reducing susceptibility to bacterial infections. Research has identified specific molecular pathways for immune enhancement that can be targeted through feed additives or therapeutic interventions [119].

Vaccine development continues to advance, providing alternatives to prophylactic antibiotic use. New generation vaccines utilize advanced delivery systems and enhanced antigenic designs. Multiple-agent vaccines reduce administration complexity while providing broader protection. Studies have documented significant reductions in antibiotic usage following implementation of comprehensive vaccination programs [120].

6.2.3. Management of Microbiome

Strategic manipulation of animal microbiomes presents opportunities for improved health management [121]. Designer probiotics carry specific functional capabilities for pathogen exclusion and immune modulation. Metabolomic analysis has revealed key microbial interactions that can be enhanced to promote animal health [122].

Prebiotics and synbiotics support beneficial microbial populations through selective nutrient provision. Advanced formulations target specific bacterial groups crucial for maintaining gut health. Research has showed that optimized prebiotic-probiotic combinations can significantly reduce disease susceptibility [123].

6.3. Recent Agriculture Technologies

6.3.1. Smart Monitoring Systems

Integration of sensor networks throughout agricultural operations enables precise health monitoring [124]. Automated systems track multiple parameters including:

Temperature patterns, respiratory rates, feeding behaviors, and movement patterns provide early indication of health issues. Advanced algorithms process this data to identify subtle changes indicating potential disease onset [125].

6.3.2. Data-Driven Decision Support

Artificial intelligence systems analyze complex data streams to optimize health management decisions [126]. Machine learning algorithms identify patterns predictive of disease outbreaks. These systems enable proactive intervention before clinical symptoms appear, reducing the need for therapeutic antibiotic use [127].

Real-time analysis capabilities support dynamic adjustment of management practices. Environmental parameters can be modified based on early warning signals. Feed formulations and health interventions can be tailored to specific animal groups or individuals based on monitored parameters [128].

6.3.3. Automated Intervention Systems

Precision delivery systems enable targeted administration of health management compounds [129]. Automated systems adjust treatment protocols based on real-time monitoring data. This approach optimizes intervention timing and dosing, improving efficacy while reducing overall antimicrobial use [130].

7. One Health Policy

7.1. Collaborative Policy

The One Health approach recognizes the intricate connections between agricultural practices, environmental health, and human well-being [131]. Implementation requires coordinated efforts across multiple sectors and disciplines. Successful programs establish formal mechanisms for information sharing and joint decision-making among veterinary, medical, and environmental professionals [132].

Integrated surveillance networks form the foundation of effective One Health programs. These systems combine data from agricultural monitoring, environmental sampling, and human health surveillance. Advanced data integration platforms enable real-time synthesis of information from diverse sources, facilitating rapid response to emerging threats [133].

7.1.1. Cross-Sectoral Coordination

Professional collaboration across disciplines requires structured communication channels [134]. Regular joint meetings and workshops facilitate knowledge exchange between agricultural specialists, environmental scientists, and healthcare providers. Case-based learning approaches help participants understand complex interactions between different sectors [135].

Training programs develop cross-disciplinary expertise among professionals. Curriculum development incorporates perspectives from multiple fields, creating a new generation of practitioners equipped to address complex resistance challenges. Continuing education programs keep professionals updated on emerging issues and intervention strategies [136].

7.2. Knowledge Translation

7.2.1. Evidence-Based Practice Integration

The translation of research findings into practical applications requires systematic approaches [137]. Implementation science frameworks guide the adoption of new practices across agricultural and healthcare settings. Evaluation protocols assess the effectiveness of interventions under real-world conditions [138]. Demonstration projects showcase successful implementation strategies. These initiatives provide practical examples of One Health principles in action. Documentation of outcomes helps build evidence for broader adoption of integrated approaches [139].

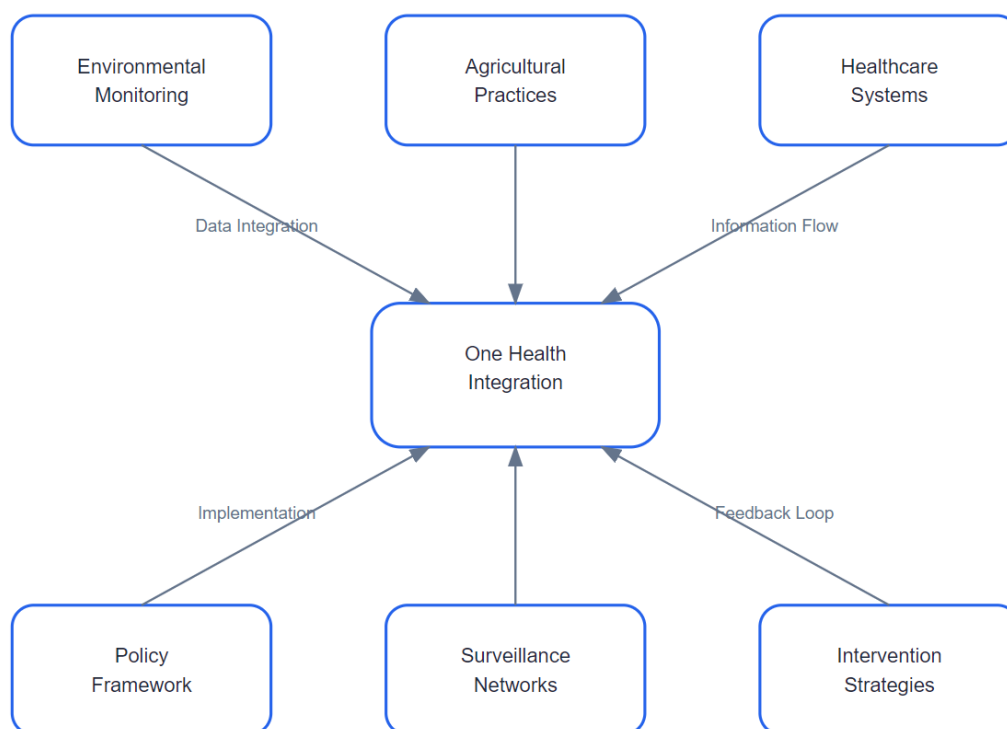


Figure 3. One Health Integration for the Management of Antibiotic Resistance

7.2.2. Stakeholders

Effective implementation depends on active participation from all stakeholder groups. Farmers, veterinarians, healthcare providers, and environmental managers must understand their roles in resistance management. Engagement programs address specific needs and concerns of different stakeholder groups.

Community participation strengthens implementation efforts. Local knowledge contributes to program design and adaptation. Feedback mechanisms ensure interventions remain relevant and effective for specific contexts [140].

8. Economic Factors

8.1. Agricultural Industry Impact

8.1.1. Production Cost

The transition to reduced antibiotic use affects multiple aspects of agricultural production. Initial implementation costs include infrastructure modifications, training programs, and new health management systems. Operating costs may shift as alternative disease prevention strategies are adopted.

Productivity implications vary across different agricultural sectors. Some operations experience temporary production decreases during transition periods. Others maintain or improve productivity through enhanced management practices. Long-term economic analyses show the viability of reduced antibiotic production systems [141].

8.1.2. Market Adaptations

Consumer demand for antibiotic-free products influences market dynamics. Premium pricing for certified low-antibiotic products can offset increased production costs. Market segmentation creates opportunities for producers adopting advanced health management practices [142].

8.1.3. Investment Requirements

Transitioning to reduced antibiotic systems necessitates significant capital investment. Infrastructure modifications may include improved ventilation systems, enhanced waste management facilities, and automated monitoring equipment. Technology adoption

requires investment in both hardware and training programs. Financial analysis indicates variable payback periods depending on operation size and market conditions [143].

8.2. Healthcare Economics

8.2.1. Direct Medical Costs

The treatment of resistant infections significantly impacts healthcare economics. Extended hospitalizations increase facility utilization costs and staffing requirements. Advanced diagnostic procedures add to patient care expenses. The use of alternative antimicrobial agents often involves higher medication costs. Hospital systems face increased operational costs related to infection control measures. Enhanced cleaning protocols, protective equipment requirements, and isolation procedures contribute to elevated expenses. Additional staff training and monitoring programs further impact institutional budgets [141].

8.2.2. Indirect Economic Effects

Societal costs extend beyond direct medical expenses. Lost productivity due to extended illness affects both individual and national economies. Disability costs may persist long after initial infection resolution. The burden on family caregivers creates additional economic ripples throughout communities [144].

Insurance systems experience increased claims related to resistant infections. Coverage policies must adapt to changing treatment requirements. Premium adjustments reflect higher treatment costs and extended care requirements [144].

8.3. Public Health Economics

Maintaining comprehensive resistance monitoring programs requires substantial investment. Laboratory infrastructure, personnel training, and data management systems represent ongoing expenses. The integration of advanced molecular testing capabilities adds significant cost components. Public health response capabilities require dedicated funding streams. Emergency response systems must maintain readiness for resistance-related outbreaks. Prevention programs need sustained support to remain effective [145].

9. Conclusion

The environmental impact of agricultural antibiotic use extends far beyond immediate agricultural environment. Soil microbiome alterations and water system contamination create persistent reservoirs of resistance genes, while multiple transmission routes facilitate their spread to human populations. The clinical implications of this spread manifest in treatment challenges, altered human microbiota, and increased healthcare burdens. Technological innovations offer promising solutions, from advanced detection methods to alternative disease prevention measures. The integration of precision agriculture technologies, coupled with novel interventions such as bacteriophage therapy and immunomodulation, provides pathways for reducing antibiotic dependence while maintaining agricultural productivity. However, successful implementation requires careful consideration of economic implications and regional variations in agricultural practices. The One Health approach can address these challenges, emphasizing the interconnected nature of agricultural, environmental, and human health systems. Success in managing agricultural antibiotic use and its consequences requires continued advancement in multiple areas: technological innovation, policy development, surveillance systems, and stakeholder engagement. The evolution of resistance in agricultural fields serves as a reminder of the dynamic nature of bacterial adaptation and the need for continued vigilance in antimicrobial stewardship. Policies should be developed to implement effective solutions that protect both agricultural productivity and public health.

References

- [1] Zhao Y, Liu D, Huang R, Zhang Y, Yang M, Xiao L, et al. Exposure to antibiotics in early life alters gut microbiota and decreases brain dopamine levels in male mice. *Neuropharmacology*. 2021;184:108411.
- [2] Wang Y, Lu J, Mao L, Li J, Yuan Z, Bond PL, et al. Antiepileptic drug carbamazepine promotes horizontal transfer of multiple antibiotic resistance genes in bacterial community. *ISME J*. 2019;13(2):509-522.
- [3] Van Boeckel TP, Brower C, Gilbert M, Grenfell BT, Levin SA, Robinson TP, et al. Global trends in antimicrobial use in food animals. *Proc Natl Acad Sci USA*. 2015;112(18):5649-5654.
- [4] Graham DW, Knapp CW, Christensen BT, McCluskey S, Dolfing J. Appearance of β -lactam resistance genes in agricultural soils and clinical isolates over the 20th century. *Sci Rep*. 2016;6:21550.
- [5] Zhu YG, Johnson TA, Su JQ, Qiao M, Guo GX, Stedtfeld RD, et al. Diverse and abundant antibiotic resistance genes in Chinese swine farms. *Proc Natl Acad Sci USA*. 2013;110(9):3435-3440.

- [6] Ghosh S, LaPara TM. The effects of subtherapeutic antibiotic use in farm animals on the proliferation and persistence of antibiotic resistance among soil bacteria. *ISME J.* 2007;1(3):191-203.
- [7] McEwen SA, Collignon PJ. Antimicrobial Resistance: a One Health Perspective. *Microbiol Spectr.* 2018;6(2):521-547.
- [8] Manyi-Loh C, Mamphweli S, Meyer E, Okoh A. Antibiotic use in agriculture and its consequential resistance in environmental sources: potential public health implications. *Molecules.* 2018;23(4):795.
- [9] Landers TF, Cohen B, Wittum TE, Larson EL. A review of antibiotic use in food animals: perspective, policy, and potential. *Public Health Rep.* 2012;127(1):4-22.
- [10] Pruden A, Larsson DGJ, Amézquita A, Collignon P, Brandt KK, Graham DW, et al. Management options for reducing the release of antibiotics and antibiotic resistance genes to the environment. *Environ Health Perspect.* 2013;121(8):878-885.
- [11] Forsberg KJ, Reyes A, Wang B, Selleck EM, Sommer MO, Dantas G. The shared antibiotic resistome of soil bacteria and human pathogens. *Science.* 2012;337(6098):1107-1111.
- [12] Wang M, Sun Y, Liu P, Sun J, Zhou Q, Xiong W, et al. The longitudinal pattern of antibiotic resistance genes and bacterial communities in river sediments under tetracycline selection. *Environ Pollut.* 2020;261:114152.
- [13] Martínez JL, Coque TM, Baquero F. What is a resistance gene? Ranking risk in resistomes. *Nat Rev Microbiol.* 2015;13(2):116-123.
- [14] Kumar K, Gupta SC, Baidoo SK, Chander Y, Rosen CJ. Antibiotic uptake by plants from soil fertilized with animal manure. *J Environ Qual.* 2005;34(6):2082-2085.
- [15] Huijbers PMC, Blaak H, de Jong MCM, Graat EAM, Vandenbroucke-Grauls CMJE, de Roda Husman AM. Role of the environment in the transmission of antimicrobial resistance to humans: a review. *Environ Sci Technol.* 2015;49(20):11993-12004.
- [16] Gillings MR, Gaze WH, Pruden A, Smalla K, Tiedje JM, Zhu YG. Using the class 1 integron-integrase gene as a proxy for anthropogenic pollution. *ISME J.* 2015;9(6):1269-1279.
- [17] Bengtsson-Palme J, Kristiansson E, Larsson DGJ. Environmental factors influencing the development and spread of antibiotic resistance. *FEMS Microbiol Rev.* 2018;42(1):fux053.
- [18] Von Wintersdorff CJH, Penders J, Van Niekerk JM, Mills ND, Majumder S, Van Alphen LB, et al. Dissemination of antimicrobial resistance in microbial ecosystems through horizontal gene transfer. *Front Microbiol.* 2016;7:173.
- [19] Zhao Y, Su JQ, An XL, Huang FY, Rensing C, Brandt KK, et al. Feed additives shift gut microbiota and enrich antibiotic resistance in swine gut. *Sci Total Environ.* 2018;621:1224-1232.
- [20] Wang Y, Yang J, Wang J, Qiao F, Chen H, Zhang J, et al. Spatial-temporal evolution of gut microbiota and antibiotic resistome in pigs from farm to slaughter. *Environ Int.* 2021;148:106363.
- [21] Cai L, Ju F, Zhang T. Tracking human sewage microbiome in a municipal wastewater treatment plant. *Appl Microbiol Biotechnol.* 2014;98(7):3317-3326.
- [22] Allen HK, Donato J, Wang HH, Cloud-Hansen KA, Davies J, Handelsman J. Call of the wild: antibiotic resistance genes in natural environments. *Nat Rev Microbiol.* 2010;8(4):251-259.
- [23] Wright GD. Environmental and clinical antibiotic resistomes, same only different. *Curr Opin Microbiol.* 2019;51:57-63.
- [24] Andersson DI, Hughes D. Microbiological effects of sublethal levels of antibiotics. *Nat Rev Microbiol.* 2014;12(7):465-478.
- [25] Berendonk TU, Manaia CM, Merlin C, Fatta-Kassinos D, Cytryn E, Walsh F, et al. Tackling antibiotic resistance: the environmental framework. *Nat Rev Microbiol.* 2015;13(5):310-317.
- [26] Robinson TP, Bu DP, Carrique-Mas J, Fèvre EM, Gilbert M, Grace D, et al. Antibiotic resistance is the quintessential One Health issue. *Trans R Soc Trop Med Hyg.* 2016;110(7):377-380.
- [27] Guardabassi L, Apley M, Olsen JE, Toutain PL, Weese S. Optimization of antimicrobial treatment to minimize resistance selection. *Microbiol Spectr.* 2018;6(3):ARBA-0018-2017.
- [28] Tang KL, Caffrey NP, Nóbrega DB, Cork SC, Ronksley PE, Barkema HW, et al. Restricting the use of antibiotics in food-producing animals and its associations with antibiotic resistance in food-producing animals and human beings: a systematic review and meta-analysis. *Lancet Planet Health.* 2017;1(8):e316-e327.
- [29] Wernli D, Jørgensen PS, Harbarth S, Carroll SP, Laxminarayan R, Levrat N, et al. Antimicrobial resistance: The complex challenge of measurement to inform policy and the public. *PLoS Med.* 2017;14(8):e1002378.
- [30] O'Neill J. Tackling drug-resistant infections globally: final report and recommendations. *Review on Antimicrobial Resistance.* 2016:1-84.

- [31] Wall BA, Mateus A, Marshall L, Pfeiffer DU, Lubroth J, Ormel HJ, et al. Drivers, dynamics and epidemiology of antimicrobial resistance in animal production. Food and Agriculture Organization of the United Nations. 2016.
- [32] Hoelzer K, Wong N, Thomas J, Talkington K, Jungman E, Coukell A. Antimicrobial drug use in food-producing animals and associated human health risks: what, and how strong, is the evidence? BMC Vet Res. 2017;13(1):211.
- [33] Koch BJ, Hungate BA, Price LB. Food-animal production and the spread of antibiotic resistance: the role of ecology. Front Ecol Environ. 2017;15(6):309-318.
- [34] Singer AC, Shaw H, Rhodes V, Hart A. Review of antimicrobial resistance in the environment and its relevance to environmental regulators. Front Microbiol. 2016;7:1728.
- [35] Luepke KH, Suda KJ, Boucher H, Russo RL, Bonney MW, Hunt TD, et al. Past, present, and future of antibacterial economics: increasing bacterial resistance, limited antibiotic pipeline, and societal implications. Pharmacotherapy. 2017;37(1):71-84.
- [36] Cuong NV, Padungtod P, Thwaites G, Carrique-Mas JJ. Antimicrobial usage in animal production: a review of the literature with a focus on low- and middle-income countries. Antibiotics. 2018;7(3):75.
- [37] Van Boeckel TP, Glennon EE, Chen D, Gilbert M, Robinson TP, Grenfell BT, et al. Reducing antimicrobial use in food animals. Science. 2017;357(6358):1350-1352.
- [38] Postma M, Speksnijder DC, Jaarsma AD, Verheij TJ, Wagenaar JA, Dewulf J. Opinions of veterinarians on antimicrobial use in farm animals in Flanders and the Netherlands. Vet Rec. 2016;179(3):68.
- [39] Founou LL, Founou RC, Essack SY. Antibiotic resistance in the food chain: a developing country-perspective. Front Microbiol. 2016;7:1881.
- [40] Lhermie G, Gröhn YT, Raboisson D. Addressing antimicrobial resistance: an overview of priority actions to prevent suboptimal antimicrobial use in food-animal production. Front Microbiol. 2017;7:2114.
- [41] Tacconelli E, Sifakis F, Harbarth S, Schrijver R, van Mourik M, Voss A, et al. Surveillance for control of antimicrobial resistance. Lancet Infect Dis. 2018;18(3):e99-e106.
- [42] Carraro N, Rivard N, Burrus V, Ceccarelli D. Mobilizable genomic islands, different strategies for the dissemination of multidrug resistance and other adaptive traits. Mob Genet Elements. 2017;7(2):23-36.
- [43] World Health Organization. Global antimicrobial resistance surveillance system (GLASS) report: early implementation 2020. Geneva: WHO; 2020.
- [44] Woolhouse M, Ward M, van Bunnik B, Farrar J. Antimicrobial resistance in humans, livestock and the wider environment. Philos Trans R Soc Lond B Biol Sci. 2015;370(1670):20140083.
- [45] Mendelson M, Rottingen JA, Gopinathan U, Hamer DH, Wertheim H, Basnyat B, et al. Maximising access to achieve appropriate human antimicrobial use in low-income and middle-income countries. Lancet. 2016;387(10014):188-198.
- [46] Collineau L, Rojo-Gimeno C, Léger A, Backhans A, Loesken S, Nielsen EO, et al. Herd-specific interventions to reduce antimicrobial usage in pig production without jeopardising technical and economic performance. Prev Vet Med. 2017;144:167-178.
- [47] Coyne LA, Latham SM, Williams NJ, Dawson S, Donald IJ, Pearson RB, et al. Understanding the culture of antimicrobial prescribing in agriculture: a qualitative study of UK pig veterinary surgeons. J Antimicrob Chemother. 2016;71(11):3300-3312.
- [48] Suresh G, Das RK, Kaur Brar S, Rouissi T, Avalos Ramirez A, Chorfi Y, et al. Alternatives to antibiotics in poultry feed: molecular perspectives. Crit Rev Microbiol. 2018;44(3):318-335.
- [49] Angevine PD, Berven S. Health economic studies: an introduction to cost-benefit, cost-effectiveness, and cost-utility analyses. Spine. 2014;39(22S):S9-S15.
- [50] Raasch S, Postma M, Dewulf J, Stärk KDC, Grosse Beilage E. Association between antimicrobial usage, biosecurity measures as well as farm performance in German farrow-to-finish farms. Porcine Health Manag. 2018;4:30.
- [51] Speksnijder DC, Mevius DJ, Bruschke CJ, Wagenaar JA. Reduction of veterinary antimicrobial use in the Netherlands. The Dutch success model. Zoonoses Public Health. 2015;62(s1):79-87.
- [52] Rushton J, Pinto Ferreira J, Stärk KD. Antimicrobial resistance: the use of antimicrobials in the livestock sector. OECD Food, Agriculture and Fisheries Papers. 2014;68:1-37.
- [53] Hernando-Amado S, Coque TM, Baquero F, Martínez JL. Defining and combating antibiotic resistance from One Health and Global Health perspectives. Nat Microbiol. 2019;4(9):1432-1442.

- [54] Guardabassi L, Larsen J, Weese JS, Butaye P, Battisti A, Kluytmans J, et al. One Health and antimicrobial resistance: a united front. *Lancet Infect Dis*. 2018;18(7):681-683.
- [55] Collignon P, Beggs JJ, Walsh TR, Gandra S, Laxminarayan R. Anthropological and socioeconomic factors contributing to global antimicrobial resistance: a univariate and multivariable analysis. *Lancet Planet Health*. 2018;2(9):e398-e405.
- [56] Reid CJ, DeMaere MZ, Djordjevic SP. Australian porcine clonal complex 10 (CC10) *Escherichia coli* belong to multiple sublineages of a highly diverse global CC10 phylogeny. *Microb Genom*. 2019;5(3):e000225.
- [57] Thanner S, Drissner D, Walsh F. Antimicrobial resistance in agriculture. *mBio*. 2016;7(2):e02227-15.
- [58] Munk P, Knudsen BE, Lukjancenko O, Duarte ASR, Van Gompel L, Luiken REC, et al. Abundance and diversity of the faecal resistome in slaughter pigs and broilers in nine European countries. *Nat Microbiol*. 2018;3(8):898-908.
- [59] Wang Y, Xu C, Zhang R, Chen Y, Shen Y, Hu F, et al. Changes in colistin resistance and *mcr-1* abundance in *Escherichia coli* of animal and human origins following the ban of colistin-positive additives in China: an epidemiological comparative study. *Lancet Infect Dis*. 2020;20(10):1161-1171.
- [60] Tiedje JM, Wang F, Manaia CM, Virta M, Sheng H, Ma L, et al. Antibiotic resistance genes in the human-impacted environment: a One Health perspective. *Pedosphere*. 2019;29(3):273-282.
- [61] Cheng G, Ning J, Ahmed S, Huang J, Ullah R, An B, et al. Selection and dissemination of antimicrobial resistance in Agri-food production. *Antimicrob Resist Infect Control*. 2019;8:158.
- [62] Heinemann JA, Ankenbauer RG, Amabile-Cuevas CF. Do antibiotics maintain antibiotic resistance? *Drug Discov Today*. 2000;5(5):195-204.
- [63] McEachran AD, Blackwell BR, Hanson JD, Wooten KJ, Mayer GD, Cox SB, et al. Antibiotics, bacteria, and antibiotic resistance genes: aerial transport from cattle feed yards via particulate matter. *Environ Health Perspect*. 2015;123(4):337-343.
- [64] Kraemer SA, Ramachandran A, Perron GG. Antibiotic pollution in the environment: from microbial ecology to public policy. *Microorganisms*. 2019;7(6):180.
- [65] Aarestrup FM, Woolhouse MEJ. Using sewage for surveillance of antimicrobial resistance. *Science*. 2020;367(6478):630-632.
- [66] Larsson DGJ, Andremon A, Bengtsson-Palme J, Brandt KK, de Roda Husman AM, Fagerstedt P, et al. Critical knowledge gaps and research needs related to the environmental dimensions of antibiotic resistance. *Environ Int*. 2018;117:132-138.
- [67] Robinson TP, Wertheim HFL, Kakkar M, Kariuki S, Bu D, Price LB. Animal production and antimicrobial resistance in the clinic. *Lancet*. 2016;387(10014):e1-e3.
- [68] Hendriksen RS, Munk P, Njage P, van Bunnik B, McNally L, Lukjancenko O, et al. Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. *Nat Commun*. 2019;10(1):1124.
- [69] Lin J, Nishino K, Roberts MC, Tolmasky M, Aminov RI, Zhang L. Mechanisms of antibiotic resistance. *Front Microbiol*. 2015;6:34.
- [70] Cassini A, Högberg LD, Plachouras D, Quattrocchi A, Hoxha A, Simonsen GS, et al. Attributable deaths and disability-adjusted life-years caused by infections with antibiotic-resistant bacteria in the EU and the European Economic Area in 2015: a population-level modelling analysis. *Lancet Infect Dis*. 2019;19(1):56-66.
- [71] Dadgostar P. Antimicrobial resistance: implications and costs. *Infect Drug Resist*. 2019;12:3903-3910.
- [72] Lima T, Domingues S, Da Silva GJ. Plasmid-mediated colistin resistance in *Salmonella enterica*: a review. *Microorganisms*. 2019;7(2):55.
- [73] MacFadden DR, McGough SF, Fisman D, Santillana M, Brownstein JS. Antibiotic resistance increases with local temperature. *Nat Clim Chang*. 2018;8(6):510-514.
- [74] Karkman A, Pärnänen K, Larsson DGJ. Fecal pollution can explain antibiotic resistance gene abundances in anthropogenically impacted environments. *Nat Commun*. 2019;10:80.
- [75] Van Puyvelde S, Deborggraeve S, Jacobs J. Why the antibiotic resistance crisis requires a One Health approach. *Lancet Infect Dis*. 2018;18(2):132-134.
- [76] Reverter M, Sarter S, Caruso D, Avarre JC, Combe M, Pepey E, et al. Aquaculture at the crossroads of global warming and antimicrobial resistance. *Nat Commun*. 2020;11:1870.
- [77] Holmes AH, Moore LS, Sundsfjord A, Steinbakk M, Regmi S, Karkey A, et al. Understanding the mechanisms and drivers of antimicrobial resistance. *Lancet*. 2016;387(10014):176-187.
- [78] Zhao X, Yu Z, Ding T. Quorum-sensing regulation of antimicrobial resistance in bacteria. *Microorganisms*. 2020;8(3):425.

- [79] Muloi D, Ward MJ, Pedersen AB, Fèvre EM, Woolhouse MEJ, van Bunnik BAD. Are food animals responsible for transfer of antimicrobial-resistant *Escherichia coli* or their resistance determinants to human populations? A systematic review. *Foodborne Pathog Dis.* 2018;15(8):467-474.
- [80] Wu J, Huang Y, Rao D, Zhang Y, Yang K. Evidence for environmental dissemination of antibiotic resistance mediated by wild birds. *Front Microbiol.* 2018;9:745.
- [81] European Medicines Agency. Sales of veterinary antimicrobial agents in 31 European countries in 2018. Trends from 2010 to 2018. Tenth ESVAC report. 2020.
- [82] Crofts TS, Gasparrini AJ, Dantas G. Next-generation approaches to understand and combat the antibiotic resistome. *Nat Rev Microbiol.* 2017;15(7):422-434.
- [83] Nadimpalli M, Delarocque-Astagneau E, Love DC, Price LB, Huynh BT, Collard JM, et al. Combating global antibiotic resistance: emerging One Health concerns in lower- and middle-income countries. *Clin Infect Dis.* 2018;66(6):963-969.
- [84] Fernandes MR, Sellera FP, Esposito F, Sabino CP, Cerdeira L, Lincopan N. Colistin-resistant mcr-1-positive *Escherichia coli* in public beaches, an infectious threat emerging in recreational waters. *Antimicrob Agents Chemother.* 2017;61(7):e00234-17.
- [85] Laxminarayan R, Van Boeckel T, Frost I, Kariuki S, Khan EA, Limmathurotsakul D, et al. The Lancet Infectious Diseases Commission on antimicrobial resistance: 6 years later. *Lancet Infect Dis.* 2020;20(4):e51-e60.
- [86] Pokharel S, Raut S, Adhikari B. Tackling antimicrobial resistance in low-income and middle-income countries. *BMJ Glob Health.* 2019;4(6):e002104.
- [87] Peacock SJ, Newton PN. Public health impact of establishing the cause of bacterial infections in rural Asia. *Nature.* 2019;571(7764):S31-S33.
- [88] Klein EY, Van Boeckel TP, Martinez EM, Pant S, Gandra S, Levin SA, et al. Global increase and geographic convergence in antibiotic consumption between 2000 and 2015. *Proc Natl Acad Sci USA.* 2018;115(15):E3463-E3470.
- [89] Mellor KC, Petrovska L, Thomson NR, Harris K, Reid SWJ, Mather AE. The vector-borne zoonotic potential of antimicrobial resistant bacteria. *Nat Commun.* 2019;10:2643.
- [90] Interagency Coordination Group on Antimicrobial Resistance. No time to wait: securing the future from drug-resistant infections. Report to the Secretary-General of the United Nations. 2019.
- [91] Knight GM, Costelloe C, Murray KA, Robotham JV, Atun R, Holmes AH. Addressing the unknowns of antimicrobial resistance: quantifying and mapping the drivers of burden. *Clin Infect Dis.* 2018;66(4):612-616.
- [92] Sharland M, Pulcini C, Harbarth S, Zeng M, Gandra S, Mathur S, et al. Classifying antibiotics in the WHO Essential Medicines List for optimal use—be AWARe. *Lancet Infect Dis.* 2018;18(1):18-20.
- [93] Wang R, van Dorp L, Shaw LP, Bradley P, Wang Q, Wang X, et al. The global distribution and spread of the mobilized colistin resistance gene mcr-1. *Nat Commun.* 2018;9:1179.
- [94] Laxminarayan R, Matsoso P, Pant S, Brower C, Røttingen JA, Klugman K, et al. Access to effective antimicrobials: a worldwide challenge. *Lancet.* 2016;387(10014):168-175.
- [95] Dik JWH, Poelman R, Friedrich AW, Panday PN, Lo-Ten-Foe JR, van Assen S, et al. An integrated stewardship model: antimicrobial, infection prevention and diagnostic (AID). *Future Microbiol.* 2016;11(1):93-102.
- [96] Lammie SL, Hughes JM. Antimicrobial resistance, food safety, and One Health: the need for convergence. *Annu Rev Food Sci Technol.* 2016;7:287-312.
- [97] Smith TC. Livestock-associated *Staphylococcus aureus*: the United States experience. *PLoS Pathog.* 2015;11(2):e1004564.
- [98] Dyar OJ, Huttner B, Schouten J, Pulcini C. What is antimicrobial stewardship? *Clin Microbiol Infect.* 2017;23(11):793-798.
- [99] Kirchhelle C, Atkinson P, Broom A, Chuengsatiansup K, Ferreira JP, Fortane N, et al. Setting the standard: multidisciplinary hallmarks for structural, equitable and tracked antibiotic policy. *BMJ Glob Health.* 2020;5(9):e003091.
- [100] Hernando-Amado S, Coque TM, Baquero F, Martínez JL. Antibiotic resistance: moving from individual health norms to social norms in One Health and Global Health. *Front Microbiol.* 2020;11:1914.
- [101] Lugsomya K, Chatsuwat T, Niyomtham W, Tummaruk P, Hampson DJ, Prapasarakul N. Complex bacterial community patterns related to antibiotic use and biosecurity level in pig farms. *Sci Rep.* 2018;8(1):14832.
- [102] Magouras I, Carmo LP, Stärk KD, Schüpbach-Regula G. Antimicrobial usage and resistance in livestock: where should we focus? *Front Vet Sci.* 2017;4:148.

- [103] Mendelson M, Matsoso MP. The World Health Organization global action plan for antimicrobial resistance. *S Afr Med J*. 2015;105(5):325.
- [104] Schurch AC, van Schaik W. Challenges and opportunities for whole-genome sequencing-based surveillance of antibiotic resistance. *Ann N Y Acad Sci*. 2017;1388(1):108-120.
- [105] Schar D, Sommanustweechai A, Laxminarayan R, Tangcharoensathien V. Surveillance of antimicrobial consumption in animal production sectors of low- and middle-income countries: optimizing use and addressing antimicrobial resistance. *PLoS Med*. 2018;15(3):e1002521.
- [106] Robertson J, Iwamoto K, Hoxha I, Ghazaryan L, Abilova V, Cvijanovic A, et al. Antimicrobial medicines consumption in Eastern Europe and Central Asia: an updated cross-national study and assessment of quantitative metrics for policy action. *Front Pharmacol*. 2019;9:1156.
- [107] Collignon P, Athukorala PC, Senanayake S, Khan F. Antimicrobial resistance: the major contribution of poor governance and corruption to this growing problem. *PLoS One*. 2015;10(3):e0116746.
- [108] Góchez D, Raicek M, Pinto Ferreira J, Jeannin M, Moulin G, Erlacher-Vindel E. OIE annual report on antimicrobial agents intended for use in animals: methods used. *Front Vet Sci*. 2019;6:317.
- [109] Simpkin VL, Renwick MJ, Kelly R, Mossialos E. Incentivising innovation in antibiotic drug discovery and development: progress, challenges and next steps. *J Antibiot (Tokyo)*. 2017;70(12):1087-1096.
- [110] Hassell JM, Ward MJ, Muloi D, Bettridge JM, Robinson TP, Kariuki S, et al. Deterministic processes structure bacterial genetic communities across an urban landscape. *Nat Commun*. 2019;10:2643.
- [111] Van Boeckel TP, Pires J, Silvester R, Zhao C, Song J, Criscuolo NG, et al. Global trends in antimicrobial resistance in animals in low- and middle-income countries. *Science*. 2019;365(6459):eaaw1944.
- [112] Chaudhary AS. A review of global initiatives to fight antibiotic resistance and recent antibiotics discovery. *Acta Pharm Sin B*. 2016;6(6):552-556.
- [113] Pesesky MW, Hussain T, Wallace M, Wang B, Andleeb S, Burnham CD, et al. KPC and NDM-1 genes in related Enterobacteriaceae strains and plasmids from Pakistan and the United States. *Emerg Infect Dis*. 2015;21(6):1034-1037.
- [114] De Oliveira DMP, Forde BM, Kidd TJ, Harris PNA, Schembri MA, Beatson SA, et al. Antimicrobial resistance in ESKAPE pathogens. *Clin Microbiol Rev*. 2020;33(3):e00181-19.
- [115] Zhu YG, Zhao Y, Zhu D, Gillings M, Penuelas J, Ok YS, et al. Soil biota, antimicrobial resistance and planetary health. *Environ Int*. 2019;131:105059.
- [116] McEwen SA, Collignon PJ. Antimicrobial resistance: a One Health perspective. *Microbiol Spectr*. 2018;6(2):ARBA-0009-2017.
- [117] Aslam B, Wang W, Arshad MI, Khurshid M, Muzammil S, Rasool MH, et al. Antibiotic resistance: a rundown of a global crisis. *Infect Drug Resist*. 2018;11:1645-1658.
- [118] Cox JA, Vlieghe E, Mendelson M, Wertheim H, Ndegwa L, Villegas MV, et al. Antibiotic stewardship in low- and middle-income countries: the same but different? *Clin Microbiol Infect*. 2017;23(11):812-818.
- [119] Zellweger RM, Carrique-Mas J, Limmathurotsakul D, Day NPJ, Thwaites GE, Baker S, et al. A current perspective on antimicrobial resistance in Southeast Asia. *J Antimicrob Chemother*. 2017;72(11):2963-2972.
- [120] McCarthy M. Breaking the cycle of antibiotic resistance. *BMJ*. 2019;367:l6471.
- [121] Baker S, Thomson N, Weill FX, Holt KE. Genomic insights into the emergence and spread of antimicrobial-resistant bacterial pathogens. *Science*. 2018;360(6390):733-738.
- [122] Bloom G, Merrett GB, Wilkinson A, Lin V, Paulin S. Antimicrobial resistance and universal health coverage. *BMJ Glob Health*. 2017;2(4):e000518.
- [123] Caudell MA, Dorado-Garcia A, Eckford S, Creese C, Byarugaba DK, Afakye K, et al. Towards a bottom-up understanding of antimicrobial use and resistance on the farm: a knowledge, attitudes, and practices survey across livestock systems in five African countries. *PLoS One*. 2020;15(1):e0220274.
- [124] Wellcome Trust. Reframing Resistance: How to communicate about antimicrobial resistance effectively. London: Wellcome Trust; 2019.
- [125] White A, Hughes JM. Critical importance of a One Health approach to antimicrobial resistance. *EcoHealth*. 2019;16(3):404-409.

- [126] Rogers Van Katwyk S, Grimshaw JM, Nkangu M, Nagi R, Mendelson M, Taljaard M, et al. Government policy interventions to reduce human antimicrobial use: a systematic review and evidence map. *PLoS Med.* 2019;16(6):e1002819.
- [127] Köck R, Cuny C. The rise of methicillin-resistant *Staphylococcus aureus* in companion animals: a One Health perspective. *Microorganisms.* 2020;8(12):2007.
- [128] Rodriguez-Mozaz S, Chamorro S, Marti E, Huerta B, Gros M, Sànchez-Melsió A, et al. Occurrence of antibiotics and antibiotic resistance genes in hospital and urban wastewaters and their impact on the receiving river. *Water Res.* 2015;69:234-242.
- [129] Núñez-Núñez M, Navarro MD, Palomo V, Rajendran NB, Del Toro MD, Voss A, et al. The methodology of surveillance for antimicrobial resistance and healthcare-associated infections in Europe (SUSPIRE): a systematic review of publicly available information. *Clin Microbiol Infect.* 2018;24(2):105-109.
- [130] Guo W, Shan K, Xu B, Li J. Determining source-specific heavy metals and persistent organic pollutants in polar seawater. *Nat Commun.* 2019;10(1):3452.
- [131] Woolhouse M, Farrar J. Policy: An intergovernmental panel on antimicrobial resistance. *Nature.* 2014;509(7502):555-557.
- [132] Singer AC, Shaw H, Rhodes V, Hart A. Review of antimicrobial resistance in the environment and its relevance to environmental regulators. *Front Microbiol.* 2016;7:1728.
- [133] Limmathurotsakul D, Sandoe JAT, Barrett DC, Corley M, Hsu LY, Mendelson M, et al. 'Antibiotic footprint' as a communication tool to aid reduction of antibiotic consumption. *J Antimicrob Chemother.* 2019;74(8):2122-2127.
- [134] Ghafur A, Mathai D, Muruganathan A, Jayalal JA, Kant R, Chaudhary D, et al. The Chennai Declaration: a roadmap to tackle the challenge of antimicrobial resistance. *Indian J Cancer.* 2013;50(1):71-73.
- [135] Larsson DGJ, Flach CF. Antibiotic resistance in the environment. *Nat Rev Microbiol.* 2022;20(5):257-269.
- [136] Graham DW, Giesen MJ, Bunce JT. Strategic approaches for combating antimicrobial resistance: policy interventions and opportunities. *Curr Opin Environ Sci Health.* 2019;7:24-31.
- [137] Huijbers PMC, Blaak H, de Jong MCM, Graat EAM, Vandenbroucke-Grauls CMJE, de Roda Husman AM. Role of the environment in the transmission of antimicrobial resistance to humans: a review. *Environ Sci Technol.* 2015;49(20):11993-12004.
- [138] Brolund A, Lagerqvist N, Byfors S, Struelens MJ, Monnet DL, Albiger B, et al. Worsening epidemiological situation of carbapenemase-producing Enterobacteriaceae in Europe, assessment by national experts from 37 countries, July 2018. *Euro Surveill.* 2019;24(9):1900123.
- [139] Prestinaci F, Pezzotti P, Pantosti A. Antimicrobial resistance: a global multifaceted phenomenon. *Pathog Glob Health.* 2015;109(7):309-318.
- [140] Laxminarayan R, Duse A, Wattal C, Zaidi AK, Wertheim HF, Sumpradit N, et al. Antibiotic resistance-the need for global solutions. *Lancet Infect Dis.* 2013;13(12):1057-1098.
- [141] Tacconelli E, Carrara E, Savoldi A, Harbarth S, Mendelson M, Monnet DL, et al. Discovery, research, and development of new antibiotics: the WHO priority list of antibiotic-resistant bacteria and tuberculosis. *Lancet Infect Dis.* 2018;18(3):318-327.
- [142] O'Neill J. Tackling drug-resistant infections globally: final report and recommendations. Review on Antimicrobial Resistance. London: HM Government and Wellcome Trust; 2016.
- [143] Hendriksen RS, Bortolaia V, Tate H, Tyson GH, Aarestrup FM, McDermott PF. Using genomics to track global antimicrobial resistance. *Front Public Health.* 2019;7:242.
- [144] Walsh TR, Wu Y. China bans colistin as a feed additive for animals. *Lancet Infect Dis.* 2016;16(10):1102-1103.
- [145] Poirel L, Jayol A, Nordmann P. Polymyxins: antibacterial activity, susceptibility testing, and resistance mechanisms encoded by plasmids or chromosomes. *Clin Microbiol Rev.* 2017;30(2):557-596.