Antimicrobial Resistance and Zoonotic Pathogens Evolution: Global Trends, Challenges and Solution

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Abstract

Antimicrobial resistance (AMR) in zoonotic pathogens is an emerging global health challenge spread in both animal and human populations. The spread of resistant zoonotic infections is increasingly linked to antimicrobial use in agriculture, wildlife and healthcare as well as to environmental pollution. Misuse or overuse of antibiotics in human medicine and veterinary practices coupled with the close interaction between animals, humans and the ecosystem accelerate the development and spread of resistant pathogens. These factors accelerate complex transmission pathways and AMR. The chapter examined the evolution of AMR in zoonotic pathogens mainly focusing on global trends, challenges and potential solutions for controlling AMR and zoonosis. One Health in collaboration with WHO and the World Organization for Animal Health (OIE) have been contributing to gathering data on AMR global trends. A key focus of the chapter is the role of surveillance systems in monitoring AMR spread. The chapter also highlights the possible mechanisms lying behind resistance development and solutions to combat AMR in zoonotic pathogens. It is crucial to address AMR and must have universal access to high-quality diagnosis and appropriate treatment of infections, innovations like surveillance of AMR and research on medications in control of AMR in human health.

Keywords: Antimicrobial, Public Health, Antibiotic Resistance, One Health Approach

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Introduction

Antimicrobial resistance (AMR) has emerged as a significant global health threat causing 1.27 million deaths worldwide in 2019 (Salam et al., 2023). AMR is driven by various factors particularly the excessive use of antimicrobials in clinical, agricultural and veterinary contexts. In livestock, the overuse of antibiotics for growth promotion and disease prevention accelerates the development of resistance which can be transmitted to humans through the food chain, animal products and direct contact (Uddin et al., 2021).

Historically, resistance existed even before the finding of antibiotics. Research has shown that bacteria from glacier waters over 2,000 years ago displayed ampicillin resistance, while microbes from permafrost over 30,000 years ago exhibited resistance to vancomycin (Morrison & Zembower, 2020). However, AMR has become a more crucial issue today with prognoses signifying that the number of deaths could rise to 20 million by 2050 due to the overuse of antibiotics in human and veterinary medicine (Doma et al., 2020).

The One Health (OH) approach works for the interdependence of humans and animals and their shared environment as well as identifying AMR development and zoonotic pathogens. The OH approach collaborates across sectors at the local community, national and international levels to combat the proliferation of zoonotic diseases that cause over 60% of human pathogens (Organization, 2022). In addition, environmental changes such as climate change contribute to the emergence and re-emergence of zoonotic diseases making the OH concept an important strategy for combating AMR and its effect on human and food safety.

AMR bacteria are global in the gut of livestock because antimicrobials are used on a routine basis in animal husbandry. The gut acquiesces as a habitat for these resistant bacteria that are spread to humans through horizontal gene transfer and zoonotic pathogens (Prevention et al., 2017). Understanding the pathways of transfer of AMR genes between animals and humans is crucial for limiting the spread of AMR. Early detection, enhanced management strategies and strict regulations on the use of antimicrobials in food-producing animals are key to preventing the development of resistance in animals and humans (Dafale et al., 2020). This chapter highlights the emergence of antimicrobial resistance in zoonotic pathogens, Global trends in the spread of resistance, solutions to combat AMR and emphasize OH approach to address global threats.

Pathways of Zoonotic Pathogen Transmission (Direct and Indirect)

Direct and indirect routes can transmit zoonotic pathogens. Direct transmission occurs through direct physical contact with infectious animals, such as handling livestock, bites and contact with animal open wounds. People in close contact with animals such as farmers and

vets are at increased risk. Direct contact with pigs carrying methicillin-resistant Staphylococcus aureus for example has been responsible for human cases of MRSA infections. Indirect or environmental transmission happens when people are exposed to contaminated food, water, or soil even through vectors. Such resistant bacteria can make their way into the human food supply via undercooked meats and pasteurized milk or crops contaminated with animal feces and antibiotic residues in animal waste (Rahman et al., 2020) are diagrammatically presented as Fig. 1.



Fig. 1: Transmission Routes of Zoonotic Pathogens from Animals to Humans

Development Sites of Antimicrobial Resistance

AMR is a global threat to the economic status of a nation. Factors contributing to the spread of AMR are lack of public knowledge, insufficient infrastructure for healthcare, poor infection control practices and restricted access to clean water (Table 1) (Graham et al., 2019).

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Location of Resistance	Example (Bacteria/Pathogen with	
Development	Antibiotic resistance)	
Digestive System High diversity of bacterial species, promoting resistance.		Escherichia coli (E. coli) - Resistance
	Antibiotics enter through oral intake or bile, affecting gut flora.	to Ampicillin
Other Potential Sites	Direct contact between bacteria and antibiotics in places like abscesses and	Staphylococcus aureus (MRSA) -
	urine.	Resistance to Methicillin
Environmental	Antibiotics in the environment (e.g., water, soil, animal waste, hospital	Pseudomonas aeruginosa – Resistance
Locations	surfaces). to Ciprofloxacin in healthcare setting	
Co-selection & Multi-	Multiple antibiotics in environments lead to resistance to various drugs	<i>Klebsiella pneumoniae</i> – Resistance to
drug Resistance	ultaneously. Carbapenems and Ceftriaxone	
	Resistant bacteria accumulate additional resistance genes.	

Table 1: Developmental Sites, Possible Contributing Factors and Pathogen Resistance to Antibiotics (Urban-Chmiel et al., 2022)

Evolution of Antimicrobial Resistance in Zoonotic Pathogens

I. Mechanisms of Antimicrobial Resistance

Based on the mechanism of action AMR agents are categorized into subgroups such as disruption of cell wall, inhibition of protein and nucleic acid synthesis, depolarization of cell membrane in bacteria represented as Figure 2 (Reygaert, 2018). Resistance to multiple antibiotics arises from changes in porins or the action of efflux pumps leading to resistance across various drug classes. HGT plays a significant role in the spread of resistance against microbes. The booster of these mechanisms of resistance is overuse of antimicrobial drugs and antibiotics, broad-spectrum drugs, improper or mis-prescribed microbial therapy and toxicity all factors that lead to the emergence of resistance mentioned as Figure 3 (Cloeckaert et al., 2017).

II. The Role of Genetic Mutations and Horizontal Gene Transfer in AMR Evolution

Resistance genes typically emerge from random mutations during DNA replication with mutation rates ranging from 1 in 10^{6} to 1 in 10^{9} cell divisions. Although mutation rates are low the rapid replication of bacteria leads to the frequent emergence of resistant strains. Resistance genes are spread via conjugation, transduction, or transformation with conjugation being the most common method, especially in Gramnegative bacteria. Introns and transposons work together to accumulate and express multiple resistance genes promoting multidrug resistance presented as Figure 3 (Michaelis & Grohmann, 2023).

III. Impact of Human-Animal-Environment Interactions on AMR Evolution

In animal farming, antibiotics are often misused due to complications in accurate diagnosis. Antibiotics are used prophylactically to promote growth mostly in low and middle-income countries (LMICs). The misuse of critical antibiotics like vancomycin in veterinary medicine threatens their effectiveness for human health. Antibiotic residues from animal farms pollute soil and water increase the spread of resistant bacteria. Manure used as fertilizer and wastewater from farms act as reservoirs for resistant pathogens spreading them through the food supply chain. International trade in animal products and human travel further disseminate antimicrobial-resistant bacteria across borders accelerating the spread of resistance genes globally (Meier et al., 2022).



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IV. Increasing Resistance in Small Companion Animals

Resistance to pathogens such as E. coli and Staphylococcus species is increasing in small companion animals diminishing the effectiveness of newer therapies. In Canada, between 1984 and 1998 resistance to Cephalothin and Enrofloxacin increased while decreased resistance to Penicillin G and Ampicillin. In the U.S. there was an increase in resistance to ciprofloxacin and Enrofloxacin in E. coli isolated from dog urinary tracts (Pomba et al., 2017).

V. Methicillin Resistance and Emerging Concerns

In France, over 60% of Staphylococcus intermedius strains were found to produce beta-lactamase making them resistant to penicillin G. Methicillin resistance in small animal isolates continues to rise particularly in postoperative and wound infections in dogs in the U.S., U.K. and Ireland. Resistance to macrolides, lincosamides and fluoroquinolones in MRSA strains limits available treatment options (Stefani & Varaldo, 2003).

VI. Resistance in Gram-Negative Bacteria

Some bacterial strains acquire resistance to most of antibiotics. In 2017, WHO published a report on antibiotic-resistant bacteria. The majority of the list included were Gram-Negative bacterial pathogens. Gram-Negative Bacteria are more resistant than gram-positive due to distinctive structure cause mortality and morbidity. For example: Resistance in E. coli to antibiotics like tetracycline, sulfamethoxazoletrimethoprim and enrofloxacin is rising in areas such as Italy and Trinidad. In Trinidad, more than one-third of Salmonella species from dogs

showed resistance to Cephalothin. The strategies to control these resistant bacteria includes, existing antibiotics structural modification, study of mechanisms and sensitivity of chemical structures, and antimicrobial auxiliary agent's development. Research studies have been made by deactivating the resistance mechanisms to treat resistant Gram-Negative Bacteria (Breijyeh et al., 2020).

VII. Introduction of New Antibacterial Agents

New antibacterial agents such as methicillin and linezolid were developed to combat resistance. However, as multidrug-resistant bacteria emerge drugs like vancomycin and teicoplanin are now used as last-resort treatments. (Dafale et al., 2020). The approval rate of new antibacterial drugs by the U.S. FDA has dropped by over 50% in the past two decades. Economic incentives often favor drugs for chronic conditions over new antibiotics discouraging the development of new drugs to reduce antimicrobial resistance.

VIII. Need for Concerted Efforts

To extend the effectiveness of current antibiotics it is crucial to discover new bacterial target mechanisms and modify existing drugs to overcome resistance. Limiting the development of resistance through responsible antibiotic use is essential in sustaining the effectiveness of antibiotics and preventing future public health crises (Cloeckaert et al., 2017).

Case Studies of AMR Zoonotic Pathogens

1. Resistance to Methicillin MRSA: A specific case of zoonotic antimicrobial resistance (AMR) is *Staphylococcus aureus* (MRSA). The ST398 strain of livestock-associated MRSA (LA-MRSA) is more prevalent in pigs, cattle, and poultry. Individuals who interact with these animals are more likely to get infected. Humans are susceptible to these strains through contact with polluted environments or animals. LA-MRSA spread in animal farms as demonstrated by its identification in healthcare settings (Lee et al., 2018).

2. β -Lactamase (ESBL)

E. coli and *K. pneumoniae* are common bacteria in cattle that produce β -lactamase extended-spectrum. These bacteria can infect humans through contaminated food, dairy products and the environment. These resistant bacteria have become more prevalent as a result of the widespread use of antibiotics particularly cephalosporins in animal husbandry. Research demonstrating that some human infections are caused by ESBL-producing strains that are identical to those in animals has brought attention to the direct transmission of resistance (Adelowo et al., 2018).

3. Identification of the blaVEB-1 Gene and Strain

A Chinese study revealed a distinct strain of *Wohlfahrtiimonas chitiniclastica* (BM-Y) in a deceased zebra. The blaVEB-1 gene was found on a plasmid for the first time in this strain which detailed spreading resistance genes between species. The inclusion of the blaVEB-1 gene which is associated makes treating infections caused by the strain difficult. New insertion sequences that contribute to the increase of resistance gene expression due to strains were discovered during genome sequencing. (Yuan et al., 2024).

4. Investigation on Non-Typhoidal Salmonella in Migratory Birds

In Bangladesh on migratory birds, a study was conducted on the frequency of multidrug-resistant (MDR) non-typhoidal *Salmonella*. The study identified *six Salmonella* servers with an overall incidence of 13%. Due to their multiple medication resistance, these strains posed a threat to human health. Genes from *Salmonella* Genomic were linked to the resistance with changes in the gyrB and parC genes were resistant to ciprofloxacin antibiotic. The strain S. Kentucky which is found in both humans and animals is becoming a bigger public health concern due to its widespread transmission (Card et al., 2023).

5. Antibiotic Resistant P. aeruginosa Bacteria

The study concentrated on resistant *Pseudomonas aeruginosa* carbapenem namely from ICU wards and sputum samples. The isolates exhibited a notable number of resistance genes including those for aminoglycosides, cephalosporins, and biofilm-related genes. Furthermore, the CRPA strains have genes associated with hypervirulence rendering them exceedingly risky to patients and complicating existing therapies (Huang et al., 2023).

6. Study on Dietary Antibiotics in Weaned Pigs

To prevent diarrhea caused by enterotoxigenic *E. coli* F18 (ETEC) during weaning stress antibiotics were frequently added to feed in weaned pigs. However, bacteria in the gut can become resistant to antibiotics and be expelled in urine or feces which can subsequently cause infection to humans if transmitted. In-feed growth-promoting antibiotics are banned. Therefore acidifiers, pharmaceutical doses of minerals probiotics, and phytochemicals are frequent alternatives (Jinno et al., 2023).

7. L-leucine Drug Resistant Sensitivity

The efficacy of antibiotics is directly related to the metaloic capacity of bacteria exogeneout L- leucine stimulates and elevates the level of metabolism state of bacteria like TCA cycle, ATP, ROS, and ETC metabolic pathways. This leucine administration also increases the killing of sparfloxacin in *Salmonella* SAR-R and against the drug fluoroquinolone as an antibiotic (Yang et al., 2023).

Global Trends in the Spread of AMR Zoonotic Pathogens

1. AMR Surveillance and Global Epidemiology in Pathogens

AMR is a progressively serious global threat with multidrug-resistant bacteria spreading rapidly. According to a WHO report in 2019, six of microbes were considered advanced in development (at phase 3 or beyond) from total 32 antimicrobials. Overuse of antimicrobials, lack of

sanitation, a lack of infection control in hospitals and insufficient access to medicines are the main drivers of AMR. Zoonotic diseases are inherently associated to AMR as the resistant bacteria are moved from animal to human. In agriculture and aquaculture antibiotics are commonly applied to promote growth and prevent disease leading to environmental contamination and dissemination of resistance (Sharan et al., 2023).

WHO Global Antimicrobial Resistance Surveillance System (GLASS)

WHO GLASS is significant in collecting and evaluating AMR data worldwide even from developing nations. With specific assistance for nations like Nigeria, Kenya, Uganda and South Africa to reinforce their response systems against zoonotic illnesses it helps countries upgrade their AMR surveillance, laboratory capability and national action plans.

The Interagency Coordination Group (IACG)

To promote awareness WHO, OIE and FAO has created organizations for governance such as the Global AMR Leaders Group and started the World Antimicrobial Awareness Week. By enhancing public health systems, hygiene and the safe use of antibiotics in agriculture the Global Action Plan on AMR intends to mitigate the emergence and spread of AMR.

One Health Approach to AMR and Zoonotic Pathogens

The One Health approach addresses antimicrobial resistance in humans, veterinary animals and the environment in zoonotic pathogens. Public training on antimicrobial overuse and misuse risks is crucial for reducing unnecessary prescriptions and preventing resistance. Strengthening hygiene measures in healthcare and communities can lower infection rates and reduce the demand for antimicrobials. Limiting antibiotic use in agriculture particularly for growth promotion and prophylaxis is essential to prevent resistance. Comprehensive surveillance of antimicrobial use in humans, animals and the environment help track resistance trends and predict future risks. Investment in vaccines and alternative therapies, such as phage therapy and probiotics can reduce reliance on antibiotics. Education and training of microbiologists, veterinarians and other health professionals are essential to combating AMR.

In AMR treatments increased funding is needed for early-stage research, especially in developing areas. Policies are necessary to address AMR risks and the emergence of new antibiotics against resistant pathogens. One health work for international collaboration which is critical for tackling AMR effectively. It also ensures global health. All these aspects are aimed under OH approach, as illustrated in Figure 4 (Van Boeckel et al., 2019).



Fig. 4: One Health (OH) approach collaboration and strategies

2. Role of Wildlife, Livestock and Humans in AMR Dissemination

Antibiotics are frequently used to treat, prevent and even encourage the growth in livestock. AMR ecology is complicated by genes encoding HGT pattern among species and genera of bacteria or mobile genetics factor such as plasmid and chemical stressors exposed in the environment. Thus through these global patterns resistant microbes are transmitted from wildlife to humans. For example; resistance patterns in *E. coli* are transmitted from feces of livestock, rats, wild migratory birds and wild mammals are ultimately prevalent to humans. This resistance is influenced by overuse of antibiotics and poor sanitary conditions. The spread of AMR to humans is lined by direct or indirect contact to food

producing farm animals or pet. The increased human population and habitat fragmentation encourage the contact of wildlife to human and their livestock and increase AMR transmission to long distances globally (Arnold et al., 2016).

3. Antimicrobial use in Food Animals and its Impact

The productivity and health enhancement antimicrobials are used in livestock. This practices leads to spread of drug resistant pathogens among species and increased health risks. In food animals these microbes are excessively used to inhibit or promote growth. In UK about 80% of the antimicrobial consumption in food animals was estimated annually. The most fractions of antimicrobials included in the survey were the microbes used in human treatments and in medical procedures. In developing and low income countries to fulfill the demands of growth and proteins demand antimicrobials are used globally as growth and nutritional purposes. This act increased resistance in pathogens and increase health effects on population. Therefore, nutritional transition to balanced protein based diet challenge and rising resistance microbes are closely linked to each other (Ma et al., 2021).

4. Environmental Impact and Spread of Resistance Genes

Bacteriophage transmission in antibiotic resistance genes are gaining momentum. And the drivers of transduction are antibiotic residues, humans and most important is environment home of these bacteriophage. Thus the increased of antibiotic resistant genes increase resistant bacteria in environment and lead to antibiotic resistance. Antibiotic residues from polluted soil can be absorbed by plants thereby introducing AMR bacteria up the food chain. As environmental resistance is disseminated through crops that humans eats. This problem intensifies the spread of resistance and highlights the growing concern for human health (Van Boeckel et al., 2019).

5. Public Health Risks Posed by Zoonotic Pathogens

Antimicrobial resistance genes are primarily found in zoonotic diseases such as *Campylobacter* and *E. coli* which can spread from animals to humans or through contaminated food. When AMR infections are spread from animals to humans, they can cause serious health issues. AMR is a major issue in modern healthcare because these organisms become more challenging to treat as they develop resistance to treatment, such as in household inter-species transmission among humans and chickens of *E. coli* bacteria. There is a need to reduce the AMR burden by biocontainment and hygiene with interspecies limitations (Antilles et al., 2021).

Approaches to Monitor AMR

I. Culture-Based Approaches

Culture-based methods are widely used in the WHO Global Action Plan for Antimicrobial Resistance, especially for monitoring pathogens like ESBL-producing *E. coli*. They can be used for both High and Low-Income Countries. They allow for comparisons of bacterial prevalence in different regions, facilitating surveillance of both environmental and clinical samples. However, a major limitation is that nonpathogenic, environmental bacteria, which could serve as resistance reservoirs, are often not easily cultured, leaving some resistance mechanisms undetected.

II. Molecular Approaches

Molecular methods such as DNA sequencing and metagenomics, are effective for tracking antimicrobial resistance genes (ARGs) in environmental samples. While these methods can provide detailed insights into the spread of AMR they come with challenges due to the need for centralized facilities and expensive equipment these methods are not suitable for widespread use, particularly in LMICs. The vast amount of genomic data generated poses challenges in analyzing and interpreting results. Machine learning techniques are being developed to better parse these data and identify risks associated with different resistomes.

III. Nanotechnology Approaches

Nanotechnology is emerging as a potential tool for rapid and cost-effective detection of ARGs. For instance, gold nanoparticles (AuNPs) have been used to detect genes like mecA, which is responsible for methicillin resistance in *Staphylococcus aureus*. Detection limits of approximately 70 pM, which can be further improved with pre concentration techniques. These biosensors are being developed for on-site, low-cost detection of ARGs, such as mecA, with even lower detection limits (as low as 23 pM). As the field of nanotechnology advances it is expected that more ARGs will be targeted leading to improved detection methods and more rapid identification of resistant pathogens in the environment (Table 2) (Yamin et al., 2023).

Challenges in Controlling AMR in Zoonotic Pathogens

A. Data Gaps and Surveillance Challenges

Differences in resources and infrastructure between regions complicate the establishment of consistent surveillance systems. Many areas, predominantly in low-middle income countries (LMICs) lack the foundational infrastructure needed for systematic monitoring resulting in gaps in data collection and analysis.

Effective coordination and standardization of data collection are difficult due to the diversity of animal species and geographical variations. Ensuring that data is representative at the national level remains a significant challenge impeding the development of cohesive surveillance strategies. It is the major reason of insufficiency of laboratory resources for the accurate detection of resistant pathogens in low income countries and middle income countries. It also lemmatizes the data accuracy and validation. Data gap hinders the accurate detection and prevalence of disease causing agents.

Table 2: Modern Approaches to Monitor AMR (Gajic et al., 2	2022)
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Approach	Methods Included	Examples
Cultural	Bacterial Isolation	Culture clinical samples (blood, urine, sputum)
Approaches	Antibiotic Susceptibility Testing (AST)	Disk diffusion (Kirby-Bauer), Broth dilution methods
	Epidemiological Surveillance	Surveillance cultures from hospitals/animals
	Outbreak Tracking	Isolation of resistant bacteria
Molecular	Polymerase Chain Reaction (PCR)	Target resistance genes (e.g., bla genes), Real-time PCR for quantification
Approaches	Next-Generation Sequencing (NGS)	Whole Genome Sequencing (WGS), Metagenomics for gene detection
	Microarrays	Detect multiple resistance genes
	CRISPR-based Detection	Use CRISPR-Cas to track AMR genes
Nanotechnolog	Nanomaterial Sensors	Nano-sensors for rapid AMR detection,
y Approaches		Surface-Enhanced Raman Spectroscopy (SERS) for low-concentration detection
	Nanoparticle-Based Antibiotics	Nanoparticles to disrupt bacterial cell walls, Target antibiotics directly to bacterial cells
	Nanodiagnostics	Lab-on-a-chip devices for multiplex detection
	Nano-Antibiotics	Nanoparticle coatings for faster infection diagnosis

B. Therapeutic Challenges in Small Animal AMR

Increased multi-drug resistant microbes and AMR is the most important threat to public health. To control these resistant bacteria one health and surveillance control campaigns are in working since 2014. Companion animals are the major reservoir of transmission of AMR and antibiotic resistant pathogens to humans and food producing animals. As world major focus is on food producing farm animals. Antimicrobial resistance transmission through these reservoirs is life threatening to food animals and food chain. Due to lake of sufficient data collection and national programs on close contact between Companion animals, humans and surroundings leads to ineffective therapeutic treatments against antibiotic resistant and zoonotic pathogens especially reported in LMICs.

C. Introduction of New Antibacterial Agents

Historically, rising resistance was addressed by the conception of novel antibacterial drugs with mechanisms of action. For example, methicillin and cloxacillin were developed to combat penicillin resistance mediated by β -lactamase spectrum. Vancomycin and other medications were used as a last resort when multidrug-resistant bacteria appeared. But as vancomycin resistance grew substitute medications like linezolid and teicoplanin were discovered. The increasing demand for ongoing development of new medicinal treatments is highlighted by this cycle of resistance.

D. Declining Rate of New Antibiotic Development: A Global Concern

By last 20 years, given the rising incidence of AMR the rate of new antibiotics approved by the US FDA has decreased markedly slowing the development of new antibacterial medications. This trend is concerning, given the increasing prevalence of AMR. Economic factors often favor the development of drugs for chronic conditions like hypertension and arthritis, rather than antibacterial agents. This creates disincentives to invest in developing new antibiotics to target resistant microorganisms for pharmaceutical companies. Between 1998 and 2002, only two out of nine new antibacterial drugs introduced were based on novel mechanisms (linezolid and daptomycin). As of 2004, only five new antibacterial agents were under development, compared to a much higher number of drugs being developed for other conditions such as erectile dysfunction, bladder hyperactivity, and anxiety. This demonstrates the limited focus on new antibacterial drug development, despite the growing threat of AMR (Bhatia, 2021) briefly mentioned as Figure 5.

Solutions in Controlling AMR in Zoonotic Pathogens

a) Effective One Health Approaches to Reduce Zoonotic Diseases

To detect zoonotic diseases early, coordinated surveillance systems should be established across relevant sectors. These systems would enable the identification of disease events and foster timely responses, prevention, and mitigation efforts. Strengthening laboratory capacity is essential for detecting zoonotic pathogens. It will be convenient to detect common infections if laboratories from different sectors were integrated, shared training and laboratory techniques. Developing data-sharing platforms between organizations will allow for a more integrated understanding of the current disease burden. Timely access to data is vital for informed decision-making in response to zoonotic diseases (Paul & Varghese, 2020).

b) One Health and Zoonosis Assessment System

1. Interest Development

One Health and Engaging Stakeholders: In system development, relevant stakeholders from multiple sectors, such as the public, wildlife, agriculture, livestock, human, and environmental health, need to be identified and engaged must be identified. After stakeholder identification and engagement programs should be extended and organized to control zoonotic pathogens. In the next step there should be government support during zoonotic disease outbreaks. Campaigns should be conducted on low cost and through social media.

2. Assessment

Under one health there should proper infrastructure mapping to conduct realistic development of zoonotic pathogens or disease related programs. In network mapping there should proper collaboration, communication and coordination among sectors. Assessment must include mapping, establishing baseline, conducting gap analysis, economic assessment etc.



Fig. 5: Global Challenges to Control AMR and Zoonotic Pathogens

3. Planning

If gaps and weakness identified during assessment step, strategies should shaped collaboratively to developing multisector-one health strategy plan. There should proper strategic planning against zoonotic disease.

4. Implementation

For implementation of zoonotic pathogens related plans and programs, one health plan should budged and financed. After convenient and innovative implementation mechanisms the goal should to evaluate desired outcome related to disease control.

5. Monitoring and Evaluation

It is the last step to combat zoonotic pathogen prevalence to monitor and evaluate outputs. There should proper monitoring and standardization to demonstrate frameworks of one health approach. To complete these all steps there should aligned specific laboratory facilities, resources, techniques to diagnose zoonotic disease and treatment (Akinsuyi et al., 2021).

Future Research Directions and the Need for Enhanced Monitoring

It is essential to identifying the developing methods that effectively manage the spread of AMR and recognize mechanisms of action at molecular advanced level. To safeguard public health improved monitoring systems and tactics to track AMR are needed. There should sustainable practices, integrated approaches in addressing and control of zoonotic disease.

Conclusion

Antimicrobial resistance represents significant challenges to public health and modern medicine is a global problem mainly develops in bacteria. The spread of antimicrobial resistance in zoonotic pathogens is through contaminated areas through vectors, humans, animals and environment. Over use of antibiotics, horizontal gene transfer, cell wall eruption are the basic mechanisms of AMR evolution. Besides this, natural selection, genetic drift and mobile resistant genes are the key factor to resistance development. AMR spreads mostly through zoonotic illnesses which cause a large percentage of human infections. Effective synchronized surveillance, technology advancement, access equity, innovative funding and conservation policies under OH approach are needed to address the significant issue posed by the evolution of AMR in zoonotic diseases. With this effective, accurate and advanced study we can curb resistance transmission and preserve antimicrobial efficacy.

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