Opinion
Volume 11:05, 2025

Journal of Antimicrobial Agents

ISSN: 2472-1212

Open Access

One Health Approach to Combating Antimicrobial Resistance

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Introduction

Antimicrobial resistance (AMR) in zoonotic pathogens represents a critical and growing global health challenge, demanding immediate and comprehensive attention. These pathogens, capable of transmission between animal and human populations, present a dual-pronged issue: the effective treatment of infections in both veterinary and human medicine is complicated by their resistance capabilities. A primary driver behind the development and widespread dissemination of AMR is the extensive use of antimicrobials in livestock, often for purposes such as growth promotion and disease prevention. This practice contributes directly to the emergence of resistant bacterial strains that can then transfer to humans through various pathways, including direct contact, the consumption of inadequately processed food products, or environmental dissemination. Understanding and embracing the One Health approach, which fundamentally acknowledges the profound interconnectedness of human, animal, and environmental health, is therefore absolutely crucial for devising and implementing effective strategies to combat this escalating crisis. Current research efforts are increasingly focusing on the discovery and development of novel antimicrobial agents, alongside the exploration of alternative control measures and the enhancement of surveillance systems, all aimed at mitigating the significant impact of AMR in zoonotic diseases. [1]

The transmission of antimicrobial-resistant (AMR) zoonotic bacteria from animals to humans is an intricate process, significantly influenced by a multitude of factors. These include the specific agricultural practices employed, the methodologies used in food processing, and the varied behaviors of human populations. This article delves deeply into the molecular mechanisms by which resistance genes are acquired and subsequently spread among diverse bacterial populations, with a particular emphasis on the crucial role of horizontal gene transfer. It further highlights key zoonotic pathogens, such as Salmonella, Campylobacter, and E. coli, meticulously detailing their individual roles in the broader dissemination of AMR. The authors strongly advocate for the adoption of a multidisciplinary approach that necessitates robust collaboration among veterinarians, public health officials, and policymakers. Such collaboration is essential for the successful implementation of stricter regulations governing the use of antimicrobials in animal husbandry and for the promotion of enhanced hygiene practices throughout the entire food chain. [2]

The emergence of multidrug-resistant (MDR) zoonotic viruses and parasites poses a significant and increasingly recognized threat to global health security. Moving beyond the well-documented challenges associated with resistant bacteria, resistance to antiviral and antiparasitic drugs in pathogens that possess the ability to jump between species is becoming a subject of growing concern. This paper undertakes a comprehensive review of the current understanding concerning MDR zoonotic viruses, including prominent examples such as influenza and coronaviruses, as well as MDR zoonotic parasites, with Toxoplasma gondii serving as a key example. It meticulously discusses the various contributing factors, notably the off-label use of antimicrobials in companion animals and wildlife populations, and the potential for the development of cross-resistance. The authors underscore the urgent need for enhanced surveillance mechanisms and the accelerated development of both diagnostics and therapeutics capable of effectively countering these emerging and evolving threats. [3]

This particular study undertakes an in-depth investigation into the prevalence and the underlying genetic basis of colistin resistance within Enterobacteriaceae strains. These bacteria were specifically isolated from poultry farms situated in China. Colistin, being a last-resort antibiotic, makes the emergence of resistance to it a particularly serious concern, especially when mediated by mobile genetic elements like the mcr-1 gene. The research successfully identified the presence of the mcr-1 gene in multiple strains of E. coli and Klebsiella pneumoniae, thus demonstrating its widespread dissemination within the animal population. The findings from this study strongly underscore the critical necessity for the implementation of stringent regulations governing the use of colistin in livestock. Such measures are vital to prevent the further propagation of this resistance determinant, which has a significant potential for easy transfer to human pathogens. [4]

The One Health approach is unequivocally fundamental to the effective containment and combating of antimicrobial resistance (AMR) in zoonotic pathogens. This perspective piece powerfully argues that any successful strategy for AMR containment must necessarily involve integrated approaches that holistically consider human, animal, and environmental health as intrinsically interconnected components. The authors meticulously highlight the significant role that environmental contamination, arising from both resistant bacteria and residual antimicrobial compounds originating from agricultural and human waste, plays in the broader AMR landscape. They propose a model of enhanced collaboration between the public health, veterinary, and environmental sectors. This, coupled with robust and widespread public awareness campaigns, is deemed essential to effectively curb the rising tide of AMR. The critical importance of diligently monitoring resistance trends across these distinct yet interconnected domains is emphatically emphasized. [5]

Emerging zoonotic diseases that are characterized by antimicrobial resistance (AMR) represent a persistent and significant global threat. This comprehensive review meticulously examines the current global landscape of AMR within key zoonotic pathogens. These include notable examples such as methicillin-resistant Staphylococcus aureus (MRSA), vancomycin-resistant Enterococci (VRE), and drug-resistant Salmonella strains. It critically discusses the various evolutionary pressures, with the sub-therapeutic use of antibiotics in intensive farming practices being a primary example, that actively drive the development of resistance. The article further explores the complex genetic mechanisms underlying resistance development and their propagation through mobile genetic elements. Key recommendations put forth include the active promotion of judicious antimicrobial use, the improvement of biosecurity measures within livestock operations, and a substantial increase in investment in research dedicated to discovering new antimicrobial agents. [6]

This specific research initiative concentrates on the detection and detailed characterization of extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae. These bacteria were identified in companion animals, specifically dogs and cats. These domestic animals can potentially serve as crucial reservoirs and, consequently, as important sources for the transmission of AMR to human populations. The study successfully identified a variety of ESBL genes, including the well-known blaCTX-M and blaTEM genes, within E. coli and K. pneumoniae strains isolated from these animals. The findings derived from this research strongly highlight the critical importance of incorporating companion animals within the broader One Health framework for the effective surveillance and control of AMR. Furthermore, it emphasizes the paramount need for responsible antimicrobial stewardship within the practice of veterinary medicine. [7]

The impact of ongoing climate change on the emergence and subsequent spread of antimicrobial-resistant (AMR) zoonotic pathogens is a matter of growing and significant concern. This particular article undertakes an exploration of how shifting environmental conditions, such as elevated temperatures and altered precipitation patterns, can profoundly influence the survival rates, transmission dynamics, and evolutionary trajectories of resistant microbes. This influence is observed across both animal and human populations. The authors discuss the plausible scenario of an enhanced movement of resistant bacteria and the associated resistance genes through contaminated water and food sources, particularly under the projected impacts of a changing climate. They issue a strong call for the development of integrated research efforts and comprehensive policy frameworks that meticulously account for these complex and interconnected interactions. [8]

This systematic review offers a comprehensive overview of the current body of knowledge pertaining to the genetic diversity and the evolutionary patterns of antimicrobial resistance (AMR) observed in zoonotic bacteria. A central focus of this review is the critical role played by mobile genetic elements, such as plasmids and transposons, in the acquisition and subsequent dissemination of resistance genes. This process occurs across a wide array of different bacterial species and diverse host organisms. The review pointedly highlights the remarkably rapid pace at which resistance develops and spreads, thereby posing a continuous and significant challenge to global public health initiatives. The authors emphatically emphasize the indispensable need for the development and utilization of advanced genomic surveillance tools. Such tools are essential for accurately tracking resistance trends and for effectively informing the development of timely and relevant intervention strategies. [9]

The development and subsequent implementation of highly effective vaccines specifically targeting zoonotic pathogens are recognized as absolutely critical components in the broader strategy to combat antimicrobial resistance (AMR). This article critically discusses the mechanisms by which vaccines can effectively reduce the overall need for antimicrobial treatment within animal populations. By diminishing the reliance on antimicrobials, vaccines can consequently lessen the selective pressure that drives the development of resistance. It systematically reviews existing vaccines that are available for various zoonotic diseases and further explores the significant potential for developing novel vaccines. These new vaccines would ideally target key zoonotic pathogens such as Salmonella and Campylobacter. The authors strongly advocate for a substantial increase in investment directed towards vaccine research and development, viewing it as a sustainable and highly effective strategy for mitigating AMR within the crucial One Health framework. [10]

Description

Antimicrobial resistance (AMR) in zoonotic pathogens constitutes a significant and escalating global health threat, demanding a comprehensive and integrated approach. These pathogens, characterized by their transmissibility between animals and humans, present a complex challenge that impacts both veterinary and public health sectors. The widespread utilization of antimicrobials in livestock for growth promotion and disease prevention stands as a primary driver in the development and dissemination of AMR. This practice fosters the emergence of resistant strains that can then spread to human populations through direct contact, consumption of contaminated food, or environmental pathways. Recognizing the interconnectedness of human, animal, and environmental health through the One Health approach is paramount for formulating effective strategies to combat this crisis. Ongoing research is actively exploring novel antimicrobials, alternative control measures, and improved surveillance systems to mitigate the impact of AMR in zoonotic diseases. [1]

The complex process of transmitting antimicrobial-resistant (AMR) zoonotic bacteria from animals to humans is influenced by numerous factors, including agricultural practices, food processing, and human behavior. This section scrutinizes the molecular mechanisms responsible for the acquisition and spread of resistance genes among bacterial populations, with a particular focus on horizontal gene transfer. It emphasizes key zoonotic pathogens such as Salmonella, Campylobacter, and E. coli, detailing their specific roles in AMR dissemination. The authors advocate for a multidisciplinary approach involving veterinarians, public health officials, and policymakers to implement stricter regulations on antimicrobial use in animal husbandry and promote enhanced hygiene practices throughout the food chain. [2]

The emergence of multidrug-resistant (MDR) zoonotic viruses and parasites represents a significant challenge to global health security, extending beyond bacterial resistance. Resistance to antiviral and antiparasitic drugs in pathogens that can transmit between species is an area of increasing recognition. This review examines the current understanding of MDR zoonotic viruses, such as influenza and coronaviruses, and MDR zoonotic parasites like Toxoplasma gondii. It discusses contributing factors, including the off-label use of antimicrobials in companion animals and wildlife, and the potential for cross-resistance. The authors highlight the imperative for enhanced surveillance and the development of diagnostics and therapeutics to counter these emerging threats. [3]

This study investigates the prevalence and genetic underpinnings of colistin resistance in Enterobacteriaceae isolated from poultry farms in China. Colistin, a last-resort antibiotic, makes the emergence of resistance, particularly mediated by the mobile gene mcr-1, a serious global concern. The research successfully identified mcr-1 in multiple strains of E. coli and Klebsiella pneumoniae, confirming its widespread dissemination within the animal population. These findings underscore the critical need for stringent regulations on colistin use in livestock to prevent the further spread of this resistance determinant, which poses a significant risk of transfer to human pathogens. [4]

The One Health approach is fundamental to effectively addressing antimicrobial resistance (AMR) in zoonotic pathogens. This perspective asserts that successful AMR containment necessitates integrated strategies that consider human, animal, and environmental health as interconnected. The authors emphasize the role of environmental contamination with resistant bacteria and antimicrobial residues from agricultural and human waste. They propose enhanced collaboration between public health, veterinary, and environmental sectors, coupled with robust public awareness campaigns, to curb the rising tide of AMR. The importance of continuous monitoring of resistance trends across these diverse domains is critically emphasized. [5]

Emerging zoonotic diseases associated with antimicrobial resistance (AMR) pose a constant global threat. This review examines the current worldwide situation of AMR in key zoonotic pathogens, including methicillin-resistant Staphylococcus aureus (MRSA), vancomycin-resistant Enterococci (VRE), and drug-resistant Salmonella. It discusses the evolutionary pressures, such as the sub-therapeutic use of antibiotics in intensive farming, that drive resistance development. The article explores the genetic mechanisms of resistance and their spread via mobile genetic elements. Recommendations include promoting judicious antimicrobial use, improving biosecurity in livestock, and investing in research for new antimicrobial agents. [6]

This research focuses on detecting and characterizing extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae in companion animals like dogs and cats. These animals can act as reservoirs and potential sources for AMR transmission to humans. The study identified various ESBL genes, including blaCTX-M and blaTEM, in E. coli and K. pneumoniae strains. The findings underscore the importance of including companion animals within the One Health framework for AMR surveillance and control, emphasizing responsible antimicrobial stewardship in veterinary medicine. [7]

The impact of climate change on the emergence and spread of antimicrobial-resistant (AMR) zoonotic pathogens is a growing concern. This article explores how changing environmental conditions, such as increased temperatures and altered precipitation patterns, can influence the survival, transmission, and evolution of resistant microbes in both animal and human populations. The authors discuss the potential for enhanced movement of resistant bacteria and resistance genes through contaminated water and food sources under a changing climate. They advocate for integrated research and policy development that accounts for these complex interactions. [8]

This systematic review provides an overview of current knowledge regarding the genetic diversity and evolution of antimicrobial resistance (AMR) in zoonotic bacteria. It highlights the role of mobile genetic elements, such as plasmids and transposons, in the acquisition and dissemination of resistance genes across different bacterial species and hosts. The review emphasizes the rapid pace of resistance development and spread, posing a continuous challenge to public health. The authors stress the need for advanced genomic surveillance tools to track resistance trends and inform intervention strategies. [9]

The development and implementation of effective vaccines against zoonotic pathogens are critical for combating antimicrobial resistance (AMR). This article discusses how vaccines can reduce the need for antimicrobial treatment in animal populations, thereby decreasing the selective pressure for resistance development. It reviews existing vaccines for zoonotic diseases and explores the potential for developing new vaccines targeting key pathogens like Salmonella and Campylobacter. The authors advocate for increased investment in vaccine research and development as a sustainable strategy to mitigate AMR within the One Health context. [10]

Conclusion

Antimicrobial resistance (AMR) in zoonotic pathogens is a major global health threat driven by antimicrobial use in livestock. Understanding the One Health approach, which integrates human, animal, and environmental health, is crucial for combating AMR. Resistance spreads through complex mechanisms like horizontal gene transfer, affecting bacteria, viruses, and parasites. Specific concerns include colistin resistance in poultry and ESBL-producing Enterobacteriaceae in companion animals. Environmental contamination and climate change further exacerbate AMR spread. Advanced genomic surveillance and effective vaccines are essential strategies. Addressing AMR requires multidisciplinary collaboration and stringent regulations to curb the rising tide of resistance.

Acknowledgement

None.

Conflict of Interest

None.

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How to cite this article: Zhang, Wei. "One Health Approach to Combating Antimicrobial Resistance." *J Antimicrob Agents* 11 (2025):425.

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Received: 01-Oct-2025, Manuscript No. antimicro-26-183050; **Editor assigned:** 03-Oct-2025, PreQC No. P-183050; **Reviewed:** 17-Oct-2025, QC No. Q-183050; **Revised:** 22-Oct-2025, Manuscript No. R-183050; **Published:** 29-Oct-2025, DOI: 10.37421/2472-1212.2025.11.425