Role of Escherichia coli, Staphylococcus, Salmonella and Brucella Species in Spread of Antimicrobial Resistance Across Species

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ABSTRACT

Antimicrobial Resistance (AMR) has emerged as a critical global concern in the 21st century, presenting a "Quiet Pandemic" with escalating infection occurrences and a dearth of novel antimicrobial drugs. This paper explores the causes, prevalence, and regional implications of AMR, focusing on the One Health Approach initiated by international organizations like OIE and FAO. In Pakistan, a national action plan has been implemented to address AMR. The causes of AMR include the unnecessary use and misuse of antimicrobials, inappropriate prescribing patterns, and the lack of new novel antibiotics. The global prevalence of AMR is particularly high in sub-Saharan Africa and low- to middle-income countries, with specific concerns about colistin resistance mediated by MCR-1 in China. Insufficient public understanding of antimicrobials is also identified as a significant factor contributing to AMR. A comparative study between the UK and India highlights variations in public awareness, potentially impacting the incidence of infectious diseases. Vigilant monitoring of AMR-related infections and mortality rates is crucial, with projections indicating a potential rise in global mortality by 2050. The roles of key bacteria, including Escherichia coli, Staphylococcus aureus, Salmonella, and Brucella, in the spread of AMR are discussed. E. coli, for example, harbors resistance genes from both human and animal sources, posing a threat to both populations. Similarly, the emergence of methicillin-resistant Staphylococcus aureus (MRSA) complicates treatment, while Salmonella contributes to global foodborne illnesses.

Keywords: Antimicrobial Resistance, One Health Approach, Global Prevalence, Public Awareness, Regional Perspectives

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1. INTRODUCTION

Antimicrobial Resistance (AMR) arises when microorganisms, including bacteria, fungi, parasites, and viruses, undergo evolutionary changes that lead to their reduced susceptibility to the antimicrobial drugs, such as antibiotics, that are commonly employed for their treatment (Nabil et al. 2022). In the 21st century, AMR has elevated to become a paramount global apprehension, primarily due to the swift escalation of AMR infection occurrences and the scarcity of novel antimicrobial drugs being introduced to address this global challenge (Prestinaci et al. 2015). AMR is commonly labeled the "Quiet Pandemic," demanding immediate and more efficient measures for management rather than being regarded as a concern that can be addressed in the future (Founou et al. 2021). In the absence of preventive actions, projections suggest that by 2050, Antimicrobial Resistance (AMR) might emerge as the leading global contributor to mortality (O'Neill 2016). In light of AMR, numerous international health organizations and governments have initiated measures to address this concern. The "One Health Approach" was established, necessitating a worldwide collaborative endeavor involving a diverse array of disciplines. This includes organizations like the World Organization of Animal Health (OIE) and the Food and Agriculture Organization of the United Nations (FAO), which make sure that each organization operates within its area of competence while working with others to lessen the potential effect of AMR. The Ministry of National Health Services announced the release of Pakistan's national action plan (NAP) for AMR in May 2017. Based on the NAP, strategies have been initiated on a national and provincial scale in Pakistan (Saleem et al. 2022).

2. CAUSES OF AMR

2.1. UNNECESSARY USE OR MISUSE OF ANTIMICROBIALS

When we make misuse of antimicrobials there will be chances of development of resistant bacteria and as a result there will be limited treatment options (Abushaheen et al. 2020).

2.2. INAPPROPRIATE PRESCRIBING PATTERNS

When we prescribe inappropriate prescriptions there will be chances of complications and mortalities as well as increased healthcare costs (Darkwah et al. 2021).

2.3. LACK OF NEW NOVEL ANTIBIOTICS

When we use excess antimicrobials, it reduces effectiveness of other treatments and produces global public health impact and as result lack of new novel antibiotics (Udaondo and Matilla 2020).

3. GLOBAL PREVALENCE OF AMR

As a recent study on the global burden of bacterial antimicrobial resistance in 2019 showed, the AMR burden in that year was highest in sub-Saharan Africa and higher in low- and middle-income countries (LMICs) than in East Asia, Australasia, and Western Europe, with species of One Health importance in their transmission accounting for the highest attributable mortality (Murray et al. 2022).

According to Chinese research, the establishment of colistin resistance mediated by MCR-1 poses a danger to antimicrobial resistance (AMR), especially because zoonosis might result in the spread of this resistance gene from animals to people (Ben et al. 2019). Based on this research, the presence of MCR-1 was identified in E. coli isolates obtained from both animals and commercially available meat sources. MCR-1 is suspected to have experienced extensive transmission among food-producing animals in southern China. Conversely, the detection rate of MCR-1 was notably lower in samples of human origin. This variance in the prevalence of MCR-1 between animal and human populations suggests a potential avenue for zoonotic transmission originating from animals and affecting humans (Hu et al. 2021).

Insufficient understanding of antimicrobials also plays a significant role in the emergence of AMR. In 2017, Public Health England conducted a survey in the UK to assess the public's awareness and comprehension of antibiotics (Parveen et al. 2022). A total of 83% of respondents acknowledged the appropriateness of antibiotics for bacterial infections, while 35% of participants held the belief that antibiotics could effectively combat viral infections. These results indicate improvement over the last poll from 2014, indicating that the general population in the UK has grown awareness and understanding about the appropriate use of antibiotics (Parveen et al. 2022). In comparison to an Indian poll, it was found that 49% of participants thought antibiotics might treat viral illnesses, whereas 45% of respondents used medicines to treat cold symptoms (Niyomyart et al. 2023). As a result, India's incidence of infectious diseases, including those attributed to multi-resistant pathogens, was noted to be among the highest (Torumkuney et al. 2022). These studies suggest a correlation between antimicrobial resistance (AMR) and the level of public awareness.

As the emergence of AMR accelerates, vigilant monitoring of infection and mortality rates associated with AMR remains a priority. The projected incidence of AMR-related illnesses in the United Kingdom increased from the 61,946 patients reported in 2018 to 65,162 diagnosed cases in 2019 (Moser et al. 2018). On the other hand, the European Centre for Disease Prevention and Control (ECDC) has reported that the yearly incidence of AMR-related illnesses has topped 670,000 cases in the European Union alone (Mestrovic et al. 2022). According to the results of a previous study's data analysis, 1.27 million of the estimated 4.95 million global fatalities in 2019 that were linked to bacterial antimicrobial resistance (AMR) were directly attributable to bacterial AMR (Murray et al. 2022). It was previously highlighted in a well-known estimate that the projected yearly mortality rate directly attributable to AMR is expected to reach 10 million by 2050. The regions most affected by this prediction are expected to be Asia and Africa, primarily due to their substantial populations and limited regulatory measures pertaining to the prevention of AMR (Tang et al. 2023). Based on earlier studies, the Sub-Saharan Africa region experiences the highest overall mortality rate across all age groups attributed to conditions directly associated with or connected to Antimicrobial Resistance (AMR). In contrast, Australasia exhibited the lowest rate of mortality linked to AMR-related factors in the year 2019 (Tang et al. 2023). In Pakistan a survey of 411 students, only 6.3% had undergone antimicrobial resistance (AMR) training. 16.1% of students believed that antibiotics are effective for viral ailments. More than half of the students agreed that AMR is a major healthcare problem in Pakistan (65.9%). Most students viewed poor infection control practices (66.9%), the use of too many broad-spectrum antibiotics (68.4%) for a longer duration (62.8%) with inadequate doses (67.9%) as the causes of AMR (Hayat et al. 2022).

Recent research examining antibiotic accessibility in low and middle-income nations revealed that Vietnam and Bangladesh exhibited the highest ratio of unlicensed establishments dispensing antibiotics. These essential medications were commonly present in conventional drug stores for minor ailments, making them easily accessible to the general population (Pulingam et al. 2022). Given the convenient availability of antibiotics within these communities, persisting with this approach could result in various challenges. These challenges encompass inappropriate antibiotic utilization due to a general lack of comprehension regarding antibiotics and limited awareness about antimicrobial resistance (AMR),

compounded by inadequate consideration of the antibiotics' quality. Such factors collectively have the potential to give rise to the development of AMR.

Table 1: A brief overview of losses because of antimicrobial resistance (AMR)

Sr.	Source	Region	DATA of AMR	Reference
1.	ECDC Report	European Union	Over 670,000 cases of AMR infection annually	(Mestrovic et al. 2022)
2.	Data Analysis of 204 countries (1990-2019)	Global	4.95 million deaths worldwide linked to bacterial AMR in 2019 1.27 million deaths directly caused by bacterial AMR in 2019	(Murray et al. 2022)

ECDC; European Centre for Disease Prevention and Control.

Research on this matter presents contradictory results, with a recent study revealing that China, classified as a developing nation, emerged as the leading consumer of veterinary antimicrobials in 2017. This consumption constituted approximately 45% of the global total and is projected to maintain its position as the largest user by the year 2030. Furthermore, there is substantiating evidence indicating that developed nations have witnessed a decline in their overall antimicrobial sales. For instance, the United Kingdom experienced a notable reduction of 39.2% from 2015 to 2017 (Tiseo et al. 2020). These findings indicate that the risk factors observed in emerging countries are starting to converge with those seen in developed nations.

Children from Haiti, Kenya, Malawi, Namibia, Nepal, Senegal, Tanzania, and Uganda participated in the research study, which lasted from May 2006 to December 2016. It was found that antibiotics were prescribed to 80.5% of the children with respiratory illnesses, 50.1% of the children with diarrhea, and 28.3% of the children with malaria. For children between the ages of one and five, the average number of antibiotic prescriptions written was 24.5 (95% CI 22.6-26.7), with differences ranging from 7.1 (6.3-7.9) in Senegal to 59.1 (54.1-64.6) in Uganda (Fink et al. 2020).

In North Africa, the Middle East, and South Asia, there were notable surges in the utilization of fluoroquinolones and third-generation cephalosporin's (Mestrovic et al. 2022). In the high-income region, the utilization of carbapenems exhibited the highest levels, rising from 0.05 to 0.09 Defined Daily Doses (DDD) per 1,000 individuals per day between the years 2000 and 2018 (Tang et al. 2023).

As indicated by recent studies, there has been a notable 67% rise in the utilization of final-resort antibiotics like polymyxin among individuals within the European Union/European Economic Area (EU/EEA). Typically administered within hospital environments, these ultimate-line antibiotics serve as a final option for treating individuals grappling with severe infections, particularly in cases involving multidrug-resistant bacteria.

4. MECHANISM OF ACTION OF ANTIMICROBIAL RESISTANCE

Figure 1 shows the mechanism of antimicrobial resistance.

5. ROLE OF ESCHERICHIA COLI IN AMR SPREAD

E. coli holds a unique position in microbiology, causing serious infections in humans and animals while also being a substantial component of diverse host microbiomes (Riley 2020). "Colibacillosis" refers to an ailment resulting from the bacterium E. coli, typically present in the lower intestines of warm-blooded mammals. Intestinal pathogenic E. coli variants induce gut disorders, spanning mild diarrhea to colitis, while extra-intestinal pathogenic E. coli variants, initially residing in the gut, trigger diseases in distant body sites post-migration, like the urinary tract or bloodstream. Among animals, E. coli ranks among the

primary contributors to diarrhea, often accompanied by pathogens like Rotavirus, Coronavirus (Tchatchouang 2017). Cryptosporidium parvum, or a synergistic blend of these agents. ETEC (Enterotoxigenic E. coli) impacts a range of animal species, primarily affecting young animals including food-producing ones (such as piglets, newborn calves, and chickens) as well as companion animals like dogs. Diarrhea is a significant livestock ailment capable of spreading among animals, potentially resulting in substantial consequences for the entire herd or flock. E. coli harbors numerous genes from both human and animal sources that provide resistance to β-lactams, including blaTEM-1, which is prevalent in animal origin E. coli but encodes for narrow-spectrum β-lactamases targeting penicillin and aminopenicillins. Clinically significant in veterinary medicine, ESBL (Extended-Spectrum β Lactamase) producing E. coli strains confer resistance to a range of antibiotics, including penicillin, aminopenicillins, and various cephalosporin, approved for veterinary use (Christopher 2023).
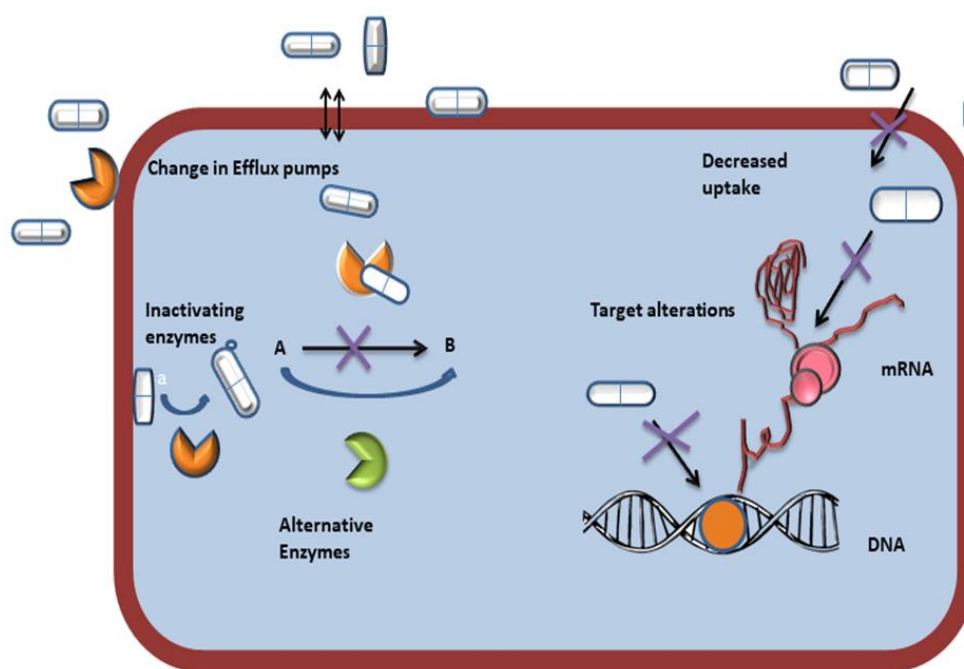

Fig. 1: Antimicrobial Resistance mechanism.

While class A ESBL enzymes are frequently responsible for acquired resistance to broad-spectrum cephalosporins in E. coli, AmpC-type enzymes, classified as class C β-lactamases, also contribute to substantial resistance against these antimicrobial agents. Quinolones and fluoroquinolones, vital for treating infections in humans and animals, exhibit broad bactericidal activity; resistance typically results from mutations in DNA gyrase and topoisomerase IV, the drug targets. Fosfomycin targets the MurA enzyme, crucial for peptidoglycan synthesis, and is employed in veterinary medicine to combat infections from various Gram-positive and Gram-negative pathogens, including E. coli. Sulfonamide resistance in E. coli from animals results from sul genes, namely sul1, sul2, or sul3 (Singh et al. 2023).

6. ROLE OF S. AUREUS IN AMR SPREAD

Methicillin-resistant Staphylococcus aureus (MRSA) is a common nosocomial and community-associated pathogen that can colonize or cause infections in both human and animals. S. aureus is a Gram-positive

bacterium and causative agent of wide range of infectious diseases such as skin infections, bacteremia, endocarditis, pneumonia, and food poisoning (Yildiz 2022). The organism was originally a leading nosocomial pathogen and afterwards epidemiologically distinct clones emerged in community settings. S. aureus expresses number of virulence factors which help to establish infection by facilitating tissue attachment, tissue invasion and evading from host immune response. The ability to acquire resistance to multiple antibiotics classes makes S. aureus, a challenging pathogen to treat. Emergence and spread of S. aureus strains which are resistant to methicillin, referred to as methicillin-resistant S. aureus (MRSA) resulted in high morbidity, high mortality, and increased treatment costs (Willis et al. 2022).

Table 2: Antimicrobial resistance in *E. coli* represented against various classes of antibiotics

Antibiotic Class	Specific Antibiotic	Resistance in *E. coli*	Reference
Beta-lactams	Ampicillin	Commonly resistant due to beta-lactamase production	(Peng et al. 2022)
	Amoxicillin	Often resistant due to beta-lactamase	(Góchez et al.
	Ceftriaxone	Increasing resistance, especially in some strains	2019)
	Carbapenems	Increasing resistance, especially in healthcare settings	(Davies and
Fluoroquinolones	Ciprofloxacin	Increasing resistance, especially in urinary tract infections	Wright 1997)
	Levofloxacin	Similar resistance pattern to ciprofloxacin	(Kenyon 2021)
Aminoglycosides	Gentamicin	Varies, some strains may exhibit resistance	
	Amikacin	Generally less resistance compared to other classes	
Tetracyclines	Tetracycline	Varies, some strains may be resistant	
Sulfonamides	Trimethoprim/ sulfamethoxazole	Varies, resistance can be common	
Nitrofurans	Nitrofurantoin	Generally still effective for uncomplicated UTIs	

Table 3: Host Spectrum of *E. coli*:

E. coli Species	Host Spectrum	Reference
E. coli K-12	Primarily found in humans and mammals	
	Used as a model organism for research	
E. coli O157:H7	Mostly associated with cattle and other ruminants	
	Causes foodborne illnesses in humans	
E. coli B	Isolated from humans and mammals	(Cao et al. 2015)
	Used in various laboratory applications	
E. coli C	Found in humans and some mammals	(Rangel et al. 2005)
	May cause urinary tract infections	
E. coli Nissle 1917	Isolated from human intestines	
	Used as a probiotic for gastrointestinal health	
E. coli DH5α	Commonly used in molecular biology and genetics	
	Easily manipulated for cloning experiments	
E. coli BL21	Widely used in protein expression and biotechnology	
	Not typically associated with a specific host	

Vancomycin remained gold standard drug to tackle these strains for years but the emergence of resistance restricted its clinical utility. Newer anti-MRSA antibiotics which were approved by U.S FDA came as respite for clinicians (Phillips-Jones and Harding 2018). The bacterium typically colonizes the anterior nares, mucous membrane, and skin, and can be carried asymptomatically. However, it can penetrate into deep tissues and other normally sterile sites in the body when cutaneous and mucosal barriers are disrupted (e.g., due to wounds, invasive medical devices, or chronic skin conditions). It is well recognized that S. aureus is a multispecies pathogen, able to cause disease in humans and livestock. The diseases in livestock include mastitis in cows, goats, sheep and rabbits, skin infections in pigs and rabbits and invasive infections in chickens.

Table 4: Medicine Resistance to *Staphylococcus aureus*:

Antibiotic Class	Specific Antibiotic	Resistance in *Staph aureus*	Reference
Beta-lactams	Methicillin	Methicillin-resistant *S. aureus* (MRSA)	
	Oxacillin	MRSA	
	Penicillin	High resistance due to beta-lactamase	
Glycopeptides	Vancomycin	Rare resistance, but emerging cases of vancomycin-resistant MRSA	
	Teicoplanin	Generally effective against MRSA	
Macrolides	Erythromycin	Variable resistance, especially in community-acquired MRSA	(Mwangi
	Clarithromycin	Similar resistance pattern to erythromycin	et al.
Fluoroquinolones	Ciprofloxacin	Increasing resistance, especially in healthcare settings	2013)
	Levofloxacin	Similar resistance pattern to ciprofloxacin	
Aminoglycosides	Gentamicin	Variable resistance, depending on strain and location	(Yao et al.
	Amikacin	Generally less resistance compared to other classes	2019)
Tetracyclines	Tetracycline	Varies, some strains may exhibit resistance	
Sulfonamides	Trimethoprim/ sulfamethoxazole	Varies, resistance can be common	

7. ROLE OF SALMONELLA IN AMR SPREAD

Salmonella, a genus-wide species with global health significance, is a primary contributor to foodborne illnesses, resulting in numerous fatalities worldwide (Shang et al. 2023). Salmonella, a Gram-negative, rod-shaped bacterium found within the Enterobacteriaceae family, encompasses two species: Salmonella enterica and Salmonella bongori. This diverse group includes over 2600 S. enterica serovars, many of which have the potential to cause diseases in both humans and animals (Zahra et al. 2023) while certain Salmonella variants like Salmonella gallinarum (SG) and Salmonella pullorum (SP) lack flagella and motility, most Salmonella strains exhibit motility through peritrichous flagella. The presence of SG and SP in poultry is associated with clinical illness and substantial economic impacts on poultry farming, particularly in less developed nations (Syed Abu Thahir et al. 2023). Based on recent data from the United States, Europe, and Low- and Middle-Income Countries (LMICs), Salmonella is a prevalent global source of foodborne illnesses, contributing to widespread food contamination across various natural settings (Shakeel et al. 2023). Salmonella enterica, frequently located in the gastrointestinal tract of food animals, displays persistence through chronic carriers who eliminate the bacteria via their fecal waste. Consequently, these carriers serve as a source for subsequent bacterial contamination, enabling the transmission of Salmonella through contaminated dairy, meat, eggs, and other agricultural products cultivated using manure contaminated with the bacterium (Manyi-Loh and Lues 2023).

Table 5: Host Spectrum of *S. aureus*:

Staphylococcus aureus Species	Host Spectrum	Reference
S.aureus in Humans	Commonly colonizes human skin and mucous membranes	
	Can cause a wide range of infections, including skin, respiratory, and bloodstream infections	
Methicillin-resistant *S.aureus* (MRSA)	Often found in healthcare settings, including hospitals and long-term care facilities	(Olaru et
	Community-acquired MRSA strains can affect otherwise healthy individuals	al. 2023)
S.aureus in Animals	Found in various animal species, including livestock and pets	
	May lead to skin and soft tissue infections in animals	
MRSA in Animals	Increasing concern in animal populations, including companion animals and livestock	
	Can lead to infections in animals and potential transmission to humans	
Methicillin-sensitive *S.aureus* (MSSA)	Common in humans and animals alike	
	May lead to various infections in both hosts	

Table 6: Host Spectrum of Salmonella:

Type of Hosts	Host Examples	Reference
Humans	Causes foodborne illnesses in humans	
	Can lead to gastroenteritis and typhoid fever	
	Infections often linked to contaminated food	
Domestic Animals	Found in a variety of domestic animals	
	Poultry, cattle, swine, and more	
	Can cause enteric infections	
Wild Animals	Present in wild animal populations	(Aung et al. 2019)
	Birds, rodents, reptiles, etc.	
	May serve as reservoirs for transmission	
Livestock	Found in livestock species, such as cattle, poultry, and pigs	
	Contamination of meat products possible	
Pets and Companion Animals	*Salmonella* can infect dogs, cats, and more	
	Contaminated pet food can lead to infections	
Reptiles and Amphibians	Salmonella carriage common in these animals	
	May pose a risk of transmission to humans	
Aquatic Animals	Can be present in aquatic environments	
	May affect fish and shellfish	
Invertebrates	Can be isolated from certain invertebrates	
	Potential role in transmission	

Table 7: Medicine resistance to *Salmonella*:

Antibiotic Class	Specific Antibiotic	Resistance in Salmonella	Reference
Beta-lactams	Ampicillin	Some Salmonella strains are resistant	(Burke et al. 2014)
	Amoxicillin	Varies among different serotypes	
Fluoroquinolones	Ciprofloxacin	Emerging resistance, especially in certain serotypes	(Carey et al. 2021)
	Levofloxacin	Similar resistance pattern to ciprofloxacin	
Aminoglycosides	Gentamicin	Some strains may exhibit resistance	(McArthur et al. 2013)
	Amikacin	Generally less resistance compared to other classes	
Tetracyclines	Tetracycline	Varies, some strains may be resistant	
Sulfonamides	Trimethoprim/ sulfamethoxazole (Co-trimoxazole)	Some Salmonella strains are resistant	
Nitrofurans	Nitrofurantoin	Generally still effective for uncomplicated infections	

8. ROLE OF BRUCELLA IN AMR

Brucellosis is a worldwide, chronic infectious disease caused by small aerobic, non-motile, Gram-negative coccobacilli of the genus Brucella. There are 12 established species within the genus that are recognized based on preferential host specificity (Celik et al. 2023). B. melitensis infection causes abortion, stillbirths and the birth of weak offspring, and occasionally epididymo-orchitis in goats and sheep and is the most virulent Brucella species for humans (zoonotic), responsible for a severely debilitating and disabling illness that results in high morbidity with low mortality. B. melitensis has been controlled in most industrialized countries; however, it remains endemic and associated with an extensive negative impact on the productivity of flocks in low and middle-income nations, where goats and sheep are the major livestock species and the main economical livelihood, such as the Mediterranean region, the Middle East, Central Asia, Sub-Saharan Africa, and parts of Latin America (Rossetti et al. 2022). On the contrary, B. ovis seems to be non-pathogenic for humans and the main clinical sign of infection is epididymitis in rams, with occasional abortions in ewes and increased perinatal death. In small ruminants, there are reports of B. ovis specific antibodies in goats from Brazil (Pereira et al. 2023) and Bulgaria (Arnaudov, 2012). Today, the

disease likely exists in numerous global sheep-farming areas, including Australia, New Zealand, Russia, France, Spain, Portugal, South Africa, the United States, Mexico, Argentina, and Brazil.

Table 8: Host Spectrum of *Brucella*:

Brucella Host Spectrum	Host Examples	Reference
Humans	Causes human brucellosis	
	Acquired through contact with infected animals	
	Can lead to flu-like symptoms	
Domestic Livestock	Affects various livestock species	
	Cattle, goats, sheep, and more	
	Leads to reproductive issues in animals	
Wild Animals	Found in a variety of wild animals	
	Bison, elk, deer, and more	
	Can be transmitted to humans through exposure	(Abdel-Glil et al. 2022)
Pets and Companion Animals	Can infect dogs and other pets	
	Exposure through contact with infected animals	
Wildlife	Carried by various wildlife species	
	Elk, bison, and other mammals	
	Transmission to livestock and humans possible	
Marine Mammals	Isolated from marine mammals	
	Dolphins, seals, and more	
	Potential for transmission to humans	

Table 9: Medicine Resistance to *Brucella*:

Antibiotic Class	Specific Antibiotic	Resistance in *Brucella*	Reference
Aminoglycosides	Streptomycin	Variable resistance	
	Gentamicin	Varies among strains	
Tetracyclines	Tetracycline	Varies among species and strains	
Sulfonamides	Trimethoprim/sulfamethoxazole	Varies among strains	
Rifamycins	Rifampin	Resistance uncommon	(Shahrabi et al. 2023)
Quinolones	Ciprofloxacin	Varies among species and strains	
Macrolides	Azithromycin	Variable resistance	
Aminopenicillins	Ampicillin	Resistance observed	
	Amoxicillin	Resistance reported in some strains	

9. CONCLUSION

Antimicrobial resistance remains a critical global public health challenge in the 21st century, garnering significant political attention from G7 countries and persisting on the agendas of various political conferences. While efforts to implement mitigation strategies are yielding positive outcomes, failure to address AMR could lead to a return to the pre-antibiotic era, where common infections posed life-threatening risks. AMR embodies a complex interplay of factors, encompassing social dynamics, conflicts, healthcare, economics, behavior, climate events, and pharmaceutical innovation. Crafting a comprehensive solution for AMR requires collaborative actions by individuals, communities, and nations to ensure the continued availability of effective antimicrobials for sustaining human and animal health.

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