Antimicrobial Resistance (AMR) and Extended-Spectrum-Beta-Lactamases (ESBL) -Producing Bacteria Importance and Transmission in Animals

Muhammad Tahir Sarfraz Khan[1,*], Muhammad Tauseef Ahmad[2], Muhammad Kashif[1], Habtamu Endale[3], Arslan Mahmood[1], Muhammad Muneeb[1] and Zeeshan Afzal[1]

[1]Department of Pathology, University of Agriculture, Faisalabad, Pakistan
[2]Faculty of Veterinary Science, University of Veterinary and Animals Science, Lahore, Pakistan
[3]School of Veterinary Medicine, Wolaita Sodo University, Ethiopia
*Corresponding author: drtahirsarfraz94@gmail.com

Abstract

Antimicrobial resistance (AMR) is the ability of microorganisms to resist against various antimicrobial drugs. AMR in the livestock is currently a major especially bacterial resistance in *Escherichia coli* and *Salmonella species,* mainly caused by irrational use of antibiotics, prevention and as growth promotors. The genetic flexibility of these bacteria enhances the transmission of genes responsible for the resistance across species, surrounding ecosystem, which is exaggerated by the improper surveillance and livestock manure spread in the environment. Despite various efforts including "One Health" concept, sustainability and production balance, consumption of antibiotics remains area of concern. Strict control measures, tough surveillance, use of antibiotics alternatives such as probiotics & prebiotics and vaccination programs. Worldwide coordinated initiatives are vital for mitigating resistance effects, ensuring the sustainable livestock production, safeguarding the well-being of both humans and animals, keeping the ecosystem safe.

Keywords: *E. coli,* Phenotypic, Genotypic, Livestock, Sequence-Types

Cite this Article as: Khan MTS, Ahmad MT, Kashif M, Endale H, Mahmood A, Muneeb M and Afzal Z, 2025. Antimicrobial Resistance (AMR) and Extended-Spectrum-Beta-Lactamases (ESBL) -producing bacteria importance and transmission in animals. In: Zaman MA, Farooqi SH and Khan AMA (eds), Holistic Health and Antimicrobial Resistance: A Zoonotic Perspective. Unique Scientific Publishers, Faisalabad, Pakistan, pp: 92-102. https://doi.org/10.47278/book.HH/2025.42

A Publication of Unique Scientific Publishers

Chapter No: 25-294

Received: 01-Feb-2025
Revised: 15-March-2025
Accepted: 16-Apr-2025

Introduction

Antimicrobial resistance (AMR) has been identified thousands of centuries ago and is the natural evolution in microbial competitiveness in the surroundings (S' Costa et al 2011; Davies and Davies 2010; Marinez, 2009). Antimicrobial resistance (AMR) has existed for millions of years and is an inevitable evolutionary consequence of microbial competition in the environment (Davies & Davies, 2010; Martinez, 2009; Schwarz et al., 2005) While the increasing prevalence of AMR in clinically important and commensal bacteria in both humans and livestock can be attributed largely to selection using antimicrobials (Ibrahim et al., 2016; Karesh et al., 2012). AMR has also been reported in the commensal bacteria of wildlife (Arnold et al., 2016). Commensal bacteria have the potential to act as reservoirs of resistance genes, contributing to the development of AMR in pathogens by horizontal transmission (Arnold et al., 2016; Taylor et al., 2011; von Wintersdorff et al., 2016). AMR is a problem in human and veterinary medicine worldwide, inhibiting the treatment of bacterial infections and estimated to be responsible for 25,000 preventable human deaths in Europe annually (Marston et al., 2016) and an estimated global economic cost of 100 trillion USD by 2050 if not addressed (O'Neill, 2016). Antimicrobial resistance (AMR) is defined by several parameters, including genetic, biochemical, microbiological, and clinical. A bacterial strain is resistant if it keeps growing at higher drug dosages, identification is done by comparing two or more strains (Davies & Davies, 2010; Schwarz et al., 2005) .While multiple drug resistance (MDR) is the specific subset of the AMR where different microorganisms present resistance to more than three antibacterial or antimicrobial agents, thus reducing the options of treatment (Magiorakos et al., 2012).The bacterial resistance is more threating to public health (Davies & Davies, 2010) and it can be monitored through global collaboration (Laxminarayan et al., 2013).

The transfer of poultry diseases to people via food or the environment poses a significant public health risk (Apata, 2009; Davies & Davies, 2010). Infections with multidrug-resistant bacteria, such as ESBL-producing bacteria, are difficult to treat and result in severe mortality and morbidity in humans (Davies & Davies, 2010). Trivially, the responsible microorganisms are frequently referred to as "superbugs". *Escherichia coli*, *Salmonella enterica*, and *Klebsiella pneumoniae* are three prevalent bacteria found in poultry's gastrointestinal tracts (Apata, 2009; Davies & Davies, 2010; Rehman et al., 2007).

Antimicrobial resistance (AMR) poses a significant threat to livestock health and food security. One Health approach that considers the effects of antimicrobial resistance on animal health, human health, and environmental viability. The problem of rising antimicrobial resistance is even more alarming when considering the very small number of novel antimicrobial drugs that are in development (Boucher et al., 2009; ECDC, 2009).

The focus should be on legislative frameworks, alternative antimicrobial strategies, and the necessity of surveillance systems using effective procedures and regional cooperation. It is an invaluable resource for policymakers, academics, and stakeholders seeking to limit the impact of AMR and promote sustainable livestock management while protecting public health. The efforts to address antimicrobial resistance (AMR) in livestock in Pakistan (Figure 1 and 2) and other members states vary in different aspects (Ali, et al., 2024). This chapter addresses the emergence of high-risk microbial lineages with increased virulence, resistance, and capacity to spread across varied settings. It will look into the manmade variables that influence their evolution and spread, such as antibiotic abuse. Furthermore, the chapter will look at the mechanism of resistance, transmission, emphasising how it can be transmitted to humans and causes a threat to public health

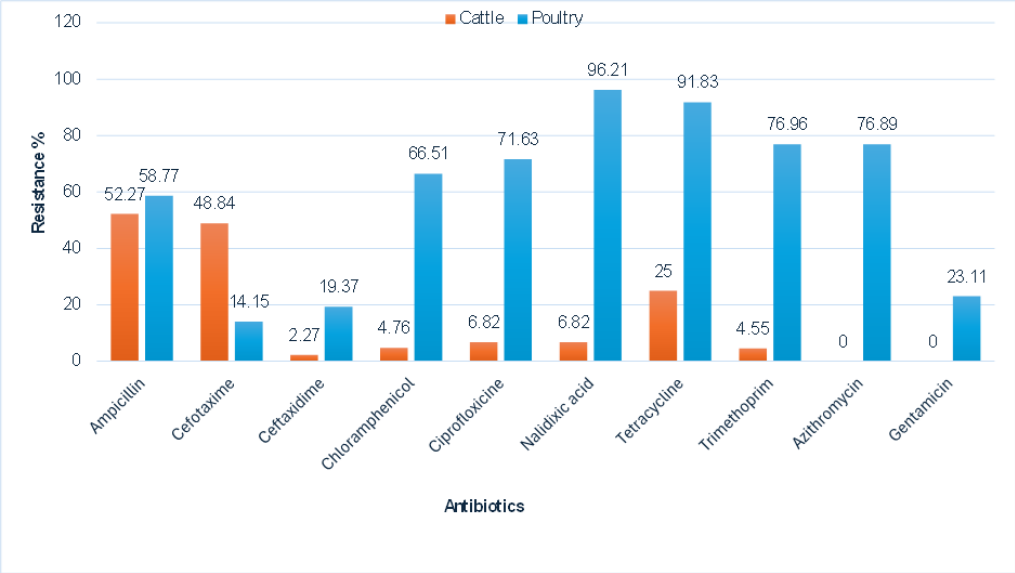

Fig. 1: *Salmonella spp.* Resistance percentages to different antibiotics in cattle and poultry

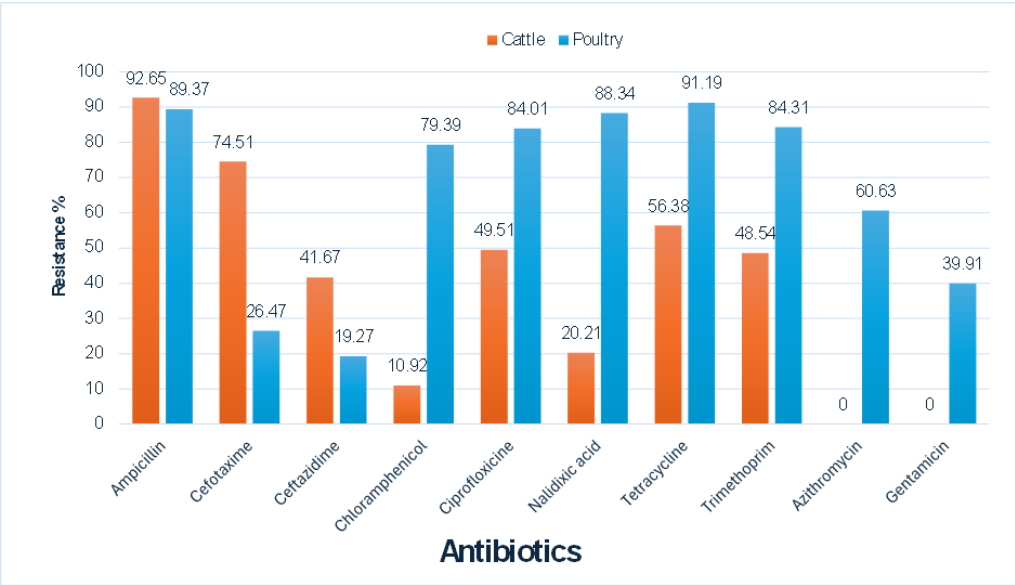

Fig. 2: *E. coli*. Resistance percentages to different antibiotics in cattle and poultry

2. Antimicrobial Resistance (AMR): Mechanisms and Drivers

2.1 Mechanisms of Antibiotic Resistance

Intrinsic vs Acquired Resistance

Since the first antibiotic, penicillin was discovered antibiotic, many antibiotic-resistant bugs have gradually developed (Mohr, 2016) Starting an armed race between germs and creatures. Many synthetic and natural antibiotics have been introduced in therapeutics, but bacteria will always find ways to counteract their effectiveness (Badr et al., 2022).

There are two main types of resistance: acquired and natural. Normal resistance is classified into two types: mediated (genes which are naturally existing in bacteria but are activated only to resistance levels after antibiotic treatment) and innate (genes which are naturally expressed in organisms) (Reygaert, 2018). Bacterial accession of genetic information by translation, conjugation, or translocation (Lerminiaux & Cameron, 2019) or modifications in its DNA sequence (Culyba et al., 2015) can result in acquired resistance. Extrinsic antimicrobial resistance, or AMR, processes are distributed into four categories: (1) drug efflux, (2) change in drug target of Drug, (3) inactivation of drug, and (4) drug uptake limitation (Munita & Arias, 2016) as demonstrated by the Figure 3.

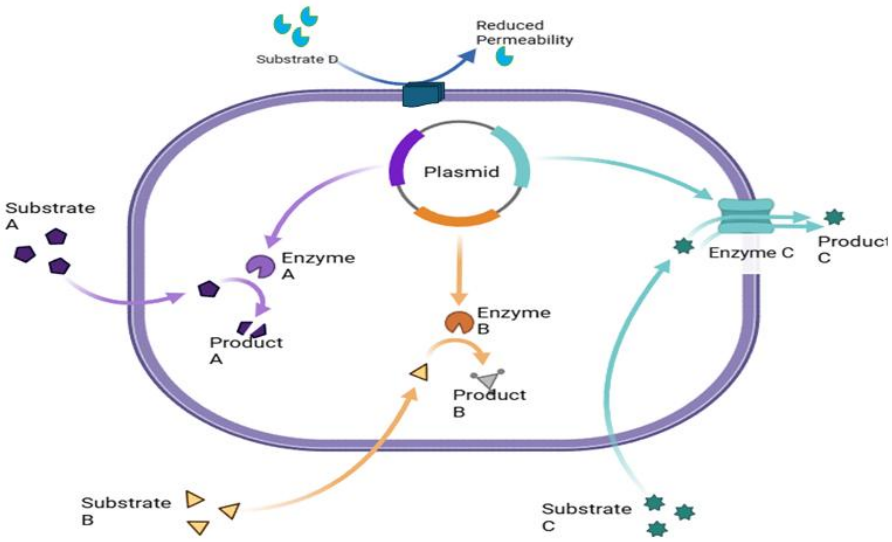

Fig. 3: illustrates the mechanism by which the bacteria can become resistant to various antimicrobial agents as mentioned as substrates A, B, C and D.

A-Intrinsic Causes

AMR can happen in many ways and is mostly brought on by changes in the bacteria (Ventola, 2015).

1) Mutations in the Genome

Changes in a genomic base pair that happen during bacterial replication and create new resistant strains lead to the substitution of one or small number amino acids in a crucial target at enzyme, cell wall, or cell structure level and modification in the regulatory genes or chromosomal structure might result from point mutations. Antibiotics, that were designed to be capable to combat the organism for years, may become useless due to the recently established protection (von Wintersdorff et al., 2016).

2) Horizontal Gene Transfer (HGT)

An initially sensitive strain may develop resistance from several species or genera. Having plasmids and other mobile genetic components, most antibacterial resistance genes can ensure the movement to bacteria belonging to different species and genera. Bacteria that are resistant to drugs can transfer a copy of their genes to bacteria that are not. As a result of collecting extra DNA, the non-resistant bacteria become resistant to drugs (von Wintersdorff et al., 2016).

B-Extrinsic Mechanisms

1) Restricting Drug Intake

Gram-negative bacteria have a lipopolysaccharide (LPS) layer present on outer membrane, which acts as a permeability shield, making them inherently not susceptible to some antibiotics than Gram-positive bacteria. This natural barrier's effectiveness is best demonstrated by the fact that glycopeptide antibiotics, such as vancomycin, are not effective against Gram-negative bacteria because of their lack of ability to pass via their outer membrane. Because of the changes in the outer membrane's permeability, hydrophilic compounds such as certain fluoroquinolones, tetracyclines, β-lactams are greatly impacted (Blair et al., 2015).

Because of the downregulation of porin channels or perhaps their replacement with non-selective channels, which provide an innate tolerance to aminoglycosides, polar molecules have trouble penetrating the cell membrane of enterococci. (Iredell et al., 2016). The production of biofilms is another mechanism that aids in bacterial colonization. (Pang et al., 2019)The biofilm matrix, which is composed of proteins, DNA, and polysaccharides, make resistance by restricting antibacterial substances from entering the bacterium. (Hall & Mah, 2017).

2) Efflux Pumps

Efflux pumps of bacteria actively transport several antibiotics out of the cell, which is a major factor in the inherent resistance of Gram-negative bacteria. Most bacteria have different types of efflux pumps. The efflux pump is classified into five main families based on its structure and energy source: the (ABC) ATP-binding cassette family, (SMR) small multidrug resistance, family, (MATE) multidrug and toxic compound extrusion family, (RND) resistance-nodulation-cell division family and (MFS) large facilitator superfamily (Reygaert, 2018). Remaining efflux pump families are single pumps that distribute contents via cytoplasmic membrane, except for the RND family, which are multi-part pumps that efflux substrates over the cell envelope (Munita & Arias, 2016).

3) Inactivation of Drug

Bacteria can inactivate antimicrobials in two ways: either by making chemical changes in the structure of an antibiotic or by destroying its structure completely (Blair et al., 2015).Enzymes that bacteria produce can bind different chemical groups of drugs and change their chemical structure which is critical to act on specific targets. As a result, the antibiotic is unable to attach to the bacteria. The most successful method for the inactivation of drug by chemical group transfer is the transfer of acetyl, phosphoryl and adenyl groups to the molecule (Lin et al., 2015).

4) Enzymatic Degradation

β-lactam antibiotics, such as cephalosporins and penicillin, are the most widely used. All members of this pharmacological class have a four-sided β-lactam loop as their basic structure. β-lactam resistance is primarily caused by β-lactamases breaking down the β-lactam loop. β-lactamases hydrolyse β-lactam ring formation, preventing it from binding to penicillin-binding proteins (PBP)(Bush & Bradford, 2016).

5) Target Modification

One common process by which bacteria develop antibiotic resistance is the alteration of the drug's target (Reygaert, 2018). Alterations in the quantity and/or arrangement of PBPs is one of the mechanisms of β-lactam antibiotics. The number of PBPs influences the amount of medication that can bind to the target (Bush & Bradford, 2016). A structural alteration, like the introduction of the mecA gene in S. aureus, will reduce or abolish drug binding(Foster, 2017). The erythromycin ribosomal methylase (erm) gene family provides another example; it methylates the 16S rRNA and changes the drug-binding site, blocking the binding of lincosamides, streptogramins, and macrolides (Nainu et al., 2021).

2.2. Drivers of AMR in Animals: Overuse of Antimicrobials in Veterinary Practice

Global demand for meat and dairy products has been steadily rising since the 1950s, which has increased the use of antimicrobial antibiotics in the agricultural sector. These compounds are utilized not only as treatments but also as growth boosters, prophylactics, and metaphylactics. Antibiotic-resistant-bacteria and the AMR-genes carry have the potential to proliferate and be transferred to humans via the food chain because of this overuse. In 2017, around 85,330 tons of veterinary antibiotics were used globally. By 2030, there will likely be an 11.5% increase in the usage of antibiotics in animals raised for food (Tiseo et al., 2020).

5. Use of Antimicrobials as Growth Promoters in Livestock

Using sub-therapeutic antibiotics in feed of various animal has been shown to greatly boost the output of livestock and poultry (Rathnayaka et al., 2021). Sub-therapeutic antibiotics are good growth promoters because they reduce the incidence of subclinical diseases, lower morbidity and mortality, enhanced daily growth rate, lower feeding costs (less than 10–15% of feed is needed to reach the desired level of growth), maximize feed conversion to animal products, and improve quality of meat and reproduction (less fat and more protein) (Tiseo et al., 2020). While some families of antibiotics, including tetracyclines, penicillin, and aminoglycosides, are frequently used to treat bacterial infections in humans, others, like ionophores, are only employed within animal husbandry. These antibiotics are utilized as growth promoters in poultry and animals.

6. Poor Regulatory Frameworks and Antibiotic Misuse

Using a new alternative as an antibiotic growth promoter must be evaluated for efficacy, acceptability, practicality, and security for the environment, consumer, user, and animal. Ultimately, several factors decide whether a certain option is effectively commercialized. Important criteria include, for instance, target species, regulatory permission, and overall costs and benefits (von Rosenvinge et al., 2013). The analysis procedure is largely the same, however, regulatory approval differs from nation to nation. The options presented in this publication require careful consideration because they are based on novel technologies with modes of action that regulators have not yet examined. Innovation is accelerating and includes a broad range of products that don't always fit neatly into any of the categories of current product or meet the old definition of a veterinary medical product (Motta et al., 2021). As a result, it's important to clarify the regulatory framework and criteria that should be applied to these products.

6. Environmental Contamination

The ecosystem acts as a link between different animal compartments, soil, water, sand, and sewage. Mobile genetic components that interact and propagate to other areas or human and animal hosts are mixed in the environment

The ecosystem connects distinct animal compartments, soil, water, sand, and sewage. According to (Puvača et al., 2022), the environment contains mobile genetic components that can spread to other locations or between humans and animals. Researchers and stakeholders are increasingly worried that the environment acts as a reservoir for antimicrobial resistance genes (AMR) and contributes to their dissemination. Some factors that contribute to the emergence of bacteria that are resistant to antibiotics and related gene mutations include the use of antimicrobial drugs in the medical, agricultural, veterinary, and environmental fields as well as the spread of antibiotic residues from various living environments. (Samreen et al., 2021).

7.1 Extended-Spectrum-Beta-Lactamase Resistance

ESBLs are those bacteria which can hydrolyze penicillin, cephalosporins (1st, 2nd and 3rd generations) and aztreonam. They can disassociate carbapenems and cephamycin (Castanheira et al., 2021). ESBLs producing bacteria are prevalent in various parts of the globe in various animals. The most common source of Extended-spectrum BLs is Escherichia coli and *Klebsiella* pneumonia (Tseng et al., 2023). There are nine different structural and evolutionary families of ESBLs classified based on amino acids sequence which includes TEM, GES, SHV, VEB, BES, CTX-M, OXA, TLA and TLA as described by (Paterson & Bonomo, 2005) and TEM, CTX-M, SHV and OXA are the major groups which are identified as ESBL resistant genes (Ur Rahman et al., 2018) (Tängdén et al., 2010). In poultry and human the most widely spread ESBL gene is CTX-M and the variants of this ESBL gene vary in both species (Gundran et al., 2019); (Platell et al., 2011).

There are several family groups of ESBL encoding genes including *bla*$_{CTX-M}$ *bla*$_{TEM,}$ *bla*$_{SHV}$ etc. In ancient times, SHV and TEM-type extended-spectrum beta-lactamases were the prominent ESBLs. Although, Nowadays CTX-M type enzymes are dominantly identified in the ESBL type latest research (Castanheira et al., 2021). *Bla*$_{SHV,}$ *bla*$_{CTX-M}$ and *bla*$_{TEM}$ are the most prevalent ESBLs resistant genes in different countries (Tseng

et al., 2023). The dominant ESBL gene in Asia is CTX-M-14 While Europe is facing the problem of CTX-M-1 in the poultry industry (Ewers et al., 2012). Several plasmids carrying genes are linked with health fitness value for the bacterium host. Antibiotics range for the treatment of infections caused by the ESBL bacteria has limited due to the presence of carbapenemase-carrying gram negative families. Recent research suggests that the in empirical therapy antibiotics β-lactam/ β-lactamase inhibitor combined usage is an alternative of the carbapenem antibiotics. However, high prevalence of gram-negative *E. coli* strains which is resistant to β-lactamases inhibitors /β-lactams has been great hindrance in this treatment approach (Wilson & Török, 2018).

A comprehensive table (Table.1) has been formulated for understanding the clonal genetics lineages (Multi-locus Sequence Typing- MLST) in food producing animals where sequence and Multiple drug resistance (MDR) lineages of *E. coli* in different regions worldwide is analyzed.

Table 1: demonstrates the linage, Multi-Locus-Sequence-types (MLST), Multi-drug resistance phenotype, genotypes of *E. coli* samples throughout the globe targeting various animal species.

Animals	location	Samples	Sampling Data	MLST	MDR	AMR Phenotypes	Genotypes	References
Pigs	Brazil	Meat	2016-2019	ST117, ST410	ND	B-Lactams, Trimethoprm, tetracyclines, Phenols, lacosamide, Sulfonamides, Fosfomycin, quinolones, Macrolides, Aminoglycosides	$bla_{CTX-M-55}$, blaCTX-M-15, $bla_{CTX-M-2}$, bla_{CTY-2} StrA, strB, dfrA17, aadA1, tet (A), dfrA1, tet(A), tet(B), Sul1, Sul2	(Soncini et al., 2022)
	United Kingdom	Faecal	2017-2018	ST10, ST44, ST88, ST58, ST48, ST117, ST744, ST2721	7	B-lactams, tetracyclines, Sulfonamides, Fluoroquinolones, Aminoglycosides	bla_{TEM-1b}, sul, sul2, dfrA5, tetB, tetAB, mphA, strBaph(6) -1b AadA5, strA	(Storey et al., 2022)
	Italy	Faecal	2010-2018	ST10, ST88, ST100, ST410, ST641, ST206, ST20, ST871, ST575, ST3744, ST7093		Streptomycin, Trimethoprim, tetracyclines, chloramphenicol, lacosamide, Sulfisoxazole, Nilidixic Oxides, quinolones, Colistin Enrofloxacin	bla_{TEM-1b}, strA, strB, sul1, tetB, dfrA1, aadA1	(Massella et al., 2021)
	Nigeria	Faecal	2015-2106	ST131, ST2348	42.1	Penicillin, Clindamycin, Tobramycin, Ceftazidime, Cefazoline, Enrofloxacin, Sulfamethoxazole/trimethoprom, Cefuroxime, kanamycine, Tazobactum/pipercillin, Cefalexin, ampicillin, doxycyclin, streptomycin, spectinomycin, neomycin, clavulanate/amoxicillin, sulabactam/ampicillin, sulfamethoxazole, ticarcillin, cefotaxime, ciprofloxacin, trimethoprim, tetracycline	$bla_{CTX-M-1}$, $bla_{CTX-M-2}$, $bla_{CTX-M-9}$, $bla_{CTX-M-15}$	(Adefioye et al., 2021)
	Switzerland	Rectal	ND	ST10, ST34, ST744		Sulfonamides, tetracycline, tobramycin, gentamycin, kanamycin	$bla_{CTX-M-1}$	(Fournier et al., 2021)
	South Africa and Cameron	Nasal and Rectal	2016	ST10, ST44, ST88, ST69, ST2144, ST4455, ST226, ST944	18.18	Cefuroxime, ampicillin, cefotaxime, cefuroxime acetyl, sulfamethoxazole-trimethoprim, cefepime	$bla_{CTX-M-15}$, bla_{TEM-1b}, $bla_{TEM-142}$, $bla_{TEM-206}$, aph (3'')-1b, aadA1, aaA5, qnrS1, aph(6)-1d, aac(6')-1b-cr, oqxAB, gyrA, sul1, sul2,dfrA14, dfrA17	(Founou et al., 2022)
	Austria	Gut associated	ND	ST10, ST131, ST354, ST100, ST6405, STST107, ST636, ST1112, ST760, ST744, ST641, ST101, ST23, ST56, ST42, ST12009, ST12008, ST12010	36.2 7	Tobramycin, Piperacillin, ceftazidime, Chloramphenicol, Gentamycin, Colistin, Fosfomycin, Aztreonam, Sulfamethoxazole/trimethoprim, streptomycin, ampicillin, cefotaxime,	$bla_{CTX-M-1}$, bla_{TEM-1}, bla_{CTX}, bla_{CTY-2}, mcr-1.1, parC, gyrA	(Bernreiter-Hofer et al., 2021)
	Brazil	Meat	2016-2019	ST38, ST117, ST131ST1196, ST354	ND	β-lactam, Aminoglycosides, Sulfonamides, trimethoprim tetracycline, quinolones,	StrA, strB, dfrA, Sul1, Sul2, aadA1, Teta(A), dfrA17, Teta(B),	(Soncini et al., 2022)

						Lincosamides, Fosfomycin, Macrolides, Phenicols	
	Hungary	Cecum faecal and Bone Marrow	2016-2018	ST162, ST10, ST93, ST117, ST155, ST8702, ST1008	ND	B-lactam, Aminoglycosides, sulphonamides, trimethoprim tetracycline, fluoroquinolones	bla_{TEM-1}, aaaA1, Aph(6')-1d, aph(3'')-1b, tet(A), Sul2	(Szmolka et al., 2021)
Poultry	Italy	Food	2010-2018	ST23, ST131, ST101, ST359, ST117, ST48, ST744, ST57, ST162, ST2614, ST10, ST155, ST297, ST1286, ST93, ST69	64	Gentamicin, Streptomycin, Trimethoprim/Sulfamethoxazole, Sulfisoxazole, Chloramphenicol, Enrofloxacin, Nalidixic acid, tetracycline	bla_{TEM-1b}, aadA1, dfrA1, strA, strB, sul1, tetA, tetB	(Massella et al., 2021)
	Korea	Chicken Meat and Environment	2019	ST93, ST131, ST362, ST457, ST117, ST48, ST57, ST162, ST2614, ST297, ST93, ST69, ST115, ST770, ST919, ST1011, ST143, ST1485, ST163, ST165, ST2179, ST2334, ST278, ST2792, ST328, ST3941, ST455, ST6779	ND	Ciprofloxacin, Tetracycline, Nalidixic acid, Gentamicin, Cotrimoxazole, Chloramphenicol	Bla, str, aad, aac, mph, aph, Qnr, sul, tet, cat, fos, dfr, aac(6')lb-cr, AAR-3, Inu, CTX-M-1, CTX-M-15, CTX-M-14, CTX-M-65, CTX-M-61, CTX-M-27	(Kim et al., 2021)
	Nigeria	Feacal	2015-2016	ST131, ST167, ST156, ST410, ST1056	38.9	Penicillin, Clindamycin, Tobramycin, Ceftazidime, Cefazoline, Enrofloxacin, Sulfamethoxazole/trimethoprom, Cefuroxime, kanamycine, Tazobactum/pipercillin, Cefalexin, ampicillin, doxycyclin, streptomycin, spectinomycin, neomycin, clavulanate/amoxicillin, sulabactam/ampicillin, sulfamethoxazole, ticarcillin, cefotaxime, ciprofloxacin, trimethoprim, tetracycline	*bla*$_{CTX-M-15}$ *bla*$_{CTX-M-1}$, *bla*$_{CTX-2}$, *bla*$_{CTX-M-9}$	(Adefioye et al., 2021)
Cattle	Nigeria	Faecal	2015-2016	ST131, ST405	33.3	Penicillin, Clindamycin, Tobramycin, Ceftazidime, Cefazoline, Enrofloxacin, Sulfamethoxazole/trimethoprom, Cefuroxime, kanamycine, Tazobactum/pipercillin, Cefalexin, ampicillin, doxycyclin, streptomycin, spectinomycin, neomycin, clavulanate/amoxicillin, sulabactam/ampicillin, sulfamethoxazole, ticarcillin, cefotaxime, ciprofloxacin, trimethoprim, tetracycline	*bla*$_{CTX-M-15}$ *bla*$_{CTX-M-1}$, *bla*$_{CTX-2}$, *bla*$_{CTX-M-9}$	(Adefioye et al., 2021)
	Nigeria	Beef	2015-20016	ST405, ST58, ST131	22.6	Same	Same	(Adefioye et al., 2021)
	China	Cloacal/ Beef Cattle	2016	ST48, ST202, ST297, ST398, ST4977, ST7130	ND	β-lactam, derivative of penicillin and third generation cephalosporins	*Bla*CTX-M, *bla*TEM, *bla*SHV	(Zhao et al., 2018)
Dairy Farms	Canada	Faecal	ND	ST744, ST10, ST4981, ST88, ST48, ST2500, ST11813, ST540, ST34,	ND	Ampicillin, Ceftriaxone, Ceftiofur, Sulfisoxazole, ciprofloxacin, enronrofloxacin,	Sul2, tet(A), strA/strB, aph(3')-1°, ampC, gyrA, parE,	(Massé et al., 2023)

				ST408, ST57008, ST219, ST38, ST1204, ST2449, ST3018, ST69, ST1163, ST967, ST657, ST21, ST117, ST783, ST4559, ST172, ST162, ST2522, ST345, ST683, ST155, ST297		tetracycline, danofloxacin, gentamycin, azithromycin, nalidixic acid	parC, *bla*CTX-M, *bla*CTX-M-15, *bla*CTX-M-1, qnrS1, *bla*C-2	
Goats	Italy	Faecal	2019	ST675	ND	Tetracycline, colistin	*acrD, KpnF, KpnE, baeS, baeR, tolC, soxS, cpxA, SoxR, ampC, ampC1, marA, acrB, acrF, acrE ,acrS, acrR, gadW, gadX, evgA, emrE, CRP, evgE, evgS*	(Smoglica et al., 2023)
	Nigeria	Faecal	2015-2016	ST155, ST131, ST167, ST406, ST1771	50	Penicillin, Clindamycin, Tobramycin, Ceftazidime, Cefazoline, Enrofloxacin, Sulfamethoxazole/trimethoprom , Cefuroxime, kanamycine, Tazobactum/pipercillin, Cefalexin, ampicillin, doxycyclin, streptomycin, spectinomycin, neomycin, clavulanate/amoxicillin, sulabactam/ampicillin, sulfamethoxazole, ticarcillin, cefotaxime, ciprofloxacin, trimethoprim, tetracycline	*bla*$_{CTX-M-15}$ *bla*$_{CTX-M-1}$, *bla*$_{CTX-2}$, *bla*$_{CTX-M-9}$, *bla*$_{CTX-M-11}$	(Adefioye et al., 2021)
Sheep	China	Cloacal Swabing	2019-2020	ST10, ST58, ST23, ST162, ST361, ST167, ST1137, ST602	6.7	Ceftiofur, cefixime, ceftazidime, ceftriaxone, cefpime, florfenicol, sulfisoxazole, mequindox, tetracyclines, ampicillin, enrofloxacin, spectinomycin, colistin, gentamicin	*bla*$_{CTX-M}$, *bla*$_{TEM}$, *bla*KPC, *blaSHV*, *bla*$_{CMY}$, *bla*$_{OXA}$	(Zhao et al., 2022)
	Nigeria	Faecal	2015-2016	ST2348, ST1056, ST405, ST156, ST131, ST58, ST155, ST167, ST406, ST1771	5.5	Penicillin, Clindamycin, Tobramycin, Ceftazidime, Cefazoline, Enrofloxacin, Sulfamethoxazole/trimethoprom , Cefuroxime, kanamycine, Tazobactum/pipercillin, Cefalexin, ampicillin, doxycyclin, streptomycin, spectinomycin, neomycin, clavulanate/amoxicillin, sulabactam/ampicillin, sulfamethoxazole, ticarcillin, cefotaxime, ciprofloxacin, trimethoprim, tetracycline	*ND*	(Adefioye et al., 2021)

7.2 Plasmids Involved in ESBL-Bacteria

The plasmids involved in the ESBL production, have the potential to cause resistance to the other antibiotic classes including fluoroquinolones, trimethoprim and aminoglycosides, because they carry resistant genes for them too (Paterson & Bonomo, 2005). As a result, the treatment of diseases becomes an issue due to ESBL resistance and the presence of ESBL plasmids exacerbates the issue of antimicrobial resistance and reduces the treatment options. Finally, the uncontrol use of antimicrobial drugs is proving the favourable environment for the prevalence of ESBL plasmids, hence the antimicrobial resistance keeps on increasing. The worldwide use of antibiotics is a major factor in increasing antimicrobial resistance, especially in bacteria involved in ESBL production. Recent investigations have identified that application of different antibiotics within the recent 3 months and one-time therapy with specific antibiotic classes (tetracycline, cotrimoxazole,

cephalosporins and macrolides) are linked with the prevalence of gram-negative bacteria (Tacconelli et al., 2020; Zhu et al., 2019). One of the first detection of extended-spectrum beta-lactamases was done in Spain between year 2000 and 2001 by (Briñas et al., 2003) the ESBL resistant genes have been separated throughout the world including Europe (Aworh et al., 2020; Blaak et al., 2015; Briñas et al., 2003; Brower et al., 2017; Maamar et al., 2016; Overdevest et al., 2011).

The prevalence of ESBL resistance genes in poultry is problematic as it causes serious concern for one health issue due to the zoonotic potential of some of the bacteria especially *Salmonella* through food consumption, which can increase the risk of prolonged hospitalization and poor prognosis of an infection (Olsen et al., 2014; Ramos et al., 2020). The spread of pathogen bacteria between poultry and humans was suggested as beta-lactamase CTXM-15 and its closely related ESBL genes were identified in *E. coli* isolates of poultry and humans (Dierikx et al., 2013; Falgenhauer et al., 2019). Different ESBL-resistant genes were extracted from different animals including poultry from *Escherichia coli* isolated and separated from different regions of Pakistan (Shafiq et al., 2022). The CTX-M genes were identified in the UK in *Salmonella* isolates of animals and humans together and in human isolates in Germany, respectively (Pfeifer et al., 2009; Randall, 2004).

Conclusion

Antimicrobial resistance (AMR) in livestock is an increasing global issue, caused by the overuse of antibiotics for treatment, prevention, and growth promotion. The rise in Escherichia coli cases that cause BLSE (*E. coli*) is a serious zoonotic issue that affects both human and animal health. Despite global attempts like the One Health strategy, many challenges still exist, particularly in low- or middle-income countries. This includes inadequate surveillance systems, insufficient regulatory frameworks, and a general lack of awareness. The increased demand for proteins has accelerated the elution process, which has led to an accumulation of antibiotic dependence and accelerated the emergence of *E. coli* along with other bacteria that are resistant to various antimicrobials. Furthermore, improper handling of animal waste increases environmental contamination, and the risks associated with antibiotic resistance. The limited treatment options also make it more difficult to effectively control animal infections. It is also critical to educate farmers and veterinarians on how to use antibiotics wisely. The livestock sector may play a vital role in reducing antimicrobial resistance by encouraging environmentally friendly practices and encouraging international cooperation. Such initiatives and projects will improve animal health, protect public health, and ecosystems, resulting in a highly sustainable and secure future.

References

Adefioye, O. J., Weinreich, J., Rödiger, S., Schierack, P., & Olowe, O. A. (2021). Phylogenetic Characterization and Multilocus Sequence Typing of Extended-Spectrum Beta Lactamase-Producing Escherichia coli from Food-Producing Animals, Beef, and Humans in Southwest Nigeria. *Microbial Drug Resistance*, *27*(1), 111–120. https://doi.org/10.1089/mdr.2019.0397

Ali, Md. Y., Samanta, A. K., & Rashid, Md. H. (2024). *Preparedness of Member Countries for Addressing Antimicrobial Resistance (AMR) in Livestock*. SAARC Agriculture Centre.

Apata, D. F. (2009). Antibiotic resistance in poultry. *International Journal of Poultry Science*, *8*(4), 404–408.

Arnold, K. E., Williams, N. J., & Bennett, M. (2016). 'Disperse abroad in the land': The role of wildlife in the dissemination of antimicrobial resistance. *Biology Letters*, *12*(8), 20160137. https://doi.org/10.1098/rsbl.2016.0137

Aworh, M. K., Kwaga, J., Okolocha, E., Harden, L., Hull, D., Hendriksen, R. S., & Thakur, S. (2020). Extended-spectrum ß-lactamase-producing Escherichia coli among humans, chickens and poultry environments in Abuja, Nigeria. *One Health Outlook*, *2*(1), 8. https://doi.org/10.1186/s42522-020-00014-7

Badr, H., Reda, R. M., Hagag, N. M., Kamel, E., Elnomrosy, S. M., Mansour, A. I., Shahein, M. A., Ali, S. F., & Ali, H. R. (2022). Multidrug-Resistant and Genetic Characterization of Extended-Spectrum Beta-Lactamase-Producing E. coli Recovered from Chickens and Humans in Egypt. *Animals*, *12*(3), 346. https://doi.org/10.3390/ani12030346

Bernreiter-Hofer, T., Schwarz, L., Müller, E., Cabal-Rosel, A., Korus, M., Misic, D., Frankenfeld, K., Abraham, K., Grünzweil, O., Weiss, A., Feßler, A. T., Allerberger, F., Schwarz, S., Szostak, M. P., Ruppitsch, W., Ladinig, A., Spergser, J., Braun, S. D., Monecke, S., & Loncaric, I. (2021). The Pheno- and Genotypic Characterization of Porcine Escherichia coli Isolates. *Microorganisms*, *9*(8), 1676. https://doi.org/10.3390/microorganisms9081676

Blaak, H., Van Hoek, A. H. A. M., Hamidjaja, R. A., Van Der Plaats, R. Q. J., Kerkhof-de Heer, L., De Roda Husman, A. M., & Schets, F. M. (2015). Distribution, Numbers, and Diversity of ESBL-Producing E. coli in the Poultry Farm Environment. *PLOS ONE*, *10*(8), e0135402. https://doi.org/10.1371/journal.pone.0135402

Blair, J. M. A., Webber, M. A., Baylay, A. J., Ogbolu, D. O., & Piddock, L. J. V. (2015). Molecular mechanisms of antibiotic resistance. *Nature Reviews Microbiology*, *13*(1), 42–51. https://doi.org/10.1038/nrmicro3380

Boucher, H. W., Talbot, G. H., Bradley, J. S., Edwards, J. E., Gilbert, D., Rice, L. B., Scheld, M., Spellberg, B., & Bartlett, J. (2009). Bad Bugs, No Drugs: No ESKAPE! An Update from the Infectious Diseases Society of America. *Clinical Infectious Diseases*, *48*(1), 1–12. https://doi.org/10.1086/595011

Briñas, L., Moreno, M. A., Zarazaga, M., Porrero, C., Sáenz, Y., García, M., Dominguez, L., & Torres, C. (2003). Detection of CMY-2, CTX-M-14, and SHV-12 β-Lactamases in *Escherichia coli* Fecal-Sample Isolates from Healthy Chickens. *Antimicrobial Agents and Chemotherapy*, *47*(6), 2056–2058. https://doi.org/10.1128/AAC.47.6.2056-2058.2003

Brower, C. H., Mandal, S., Hayer, S., Sran, M., Zehra, A., Patel, S. J., Kaur, R., Chatterjee, L., Mishra, S., Das, B. R., Singh, P., Singh, R., Gill, J. P. S., & Laxminarayan, R. (2017). The Prevalence of Extended-Spectrum Beta-Lactamase-Producing Multidrug-Resistant *Escherichia Coli* in Poultry Chickens and Variation According to Farming Practices in Punjab, India. *Environmental Health Perspectives*, *125*(7), 077015. https://doi.org/10.1289/EHP292

Bush, K., & Bradford, P. A. (2016). β-Lactams and β-Lactamase Inhibitors: An Overview. *Cold Spring Harbor Perspectives in Medicine*, *6*(8),

a025247. https://doi.org/10.1101/cshperspect.a025247
Castanheira, M., Simner, P. J., & Bradford, P. A. (2021). Extended-spectrum β -lactamases: An update on their characteristics, epidemiology and detection. *JAC-Antimicrobial Resistance*, *3*(3), dlab092. https://doi.org/10.1093/jacamr/dlab092
Culyba, M. J., Mo, C. Y., & Kohli, R. M. (2015). Targets for Combating the Evolution of Acquired Antibiotic Resistance. *Biochemistry*, *54*(23), 3573–3582. https://doi.org/10.1021/acs.biochem.5b00109
Davies, J., & Davies, D. (2010). Origins and Evolution of Antibiotic Resistance. *Microbiology and Molecular Biology Reviews*, *74*(3), 417–433. https://doi.org/10.1128/mmbr.00016-10
Dierikx, C. M., Van Der Goot, J. A., Smith, H. E., Kant, A., & Mevius, D. J. (2013). Presence of ESBL/AmpC -Producing Escherichia coli in the Broiler Production Pyramid: A Descriptive Study. *PLoS ONE*, *8*(11), e79005. https://doi.org/10.1371/journal.pone.0079005
ECDC, E. (2009). *The bacterial challenge: Time to react European Centre for Disease Prevention and Control European Medicines Agency*.
Ewers, C., Bethe, A., Semmler, T., Guenther, S., & Wieler, L. H. (2012). Extended-spectrum β-lactamase-producing and AmpC-producing Escherichia coli from livestock and companion animals, and their putative impact on public health: A global perspective. *Clinical Microbiology and Infection*, *18*(7), 646–655. https://doi.org/10.1111/j.1469-0691.2012.03850.x
Falgenhauer, L., Imirzalioglu, C., Oppong, K., Akenten, C. W., Hogan, B., Krumkamp, R., Poppert, S., Levermann, V., Schwengers, O., Sarpong, N., Owusu-Dabo, E., May, J., & Eibach, D. (2019). Detection and Characterization of ESBL-Producing Escherichia coli from Humans and Poultry in Ghana. *Frontiers in Microbiology*, *9*. https://www.frontiersin.org/articles/10.3389/fmicb.2018.03358
Foster, T. J. (2017). Antibiotic resistance in Staphylococcus aureus. Current status and future prospects. *FEMS Microbiology Reviews*, *41*(3), 430–449. https://doi.org/10.1093/femsre/fux007
Founou, L. L., Founou, R. C., Allam, M., Ismail, A., & Essack, S. Y. (2022). Genome Analysis of ESBL-Producing Escherichia coli Isolated from Pigs. *Pathogens*, *11*(7), Article 7. https://doi.org/10.3390/pathogens11070776
Fournier, C., Nordmann, P., Pittet, O., & Poirel, L. (2021). Does an Antibiotic Stewardship Applied in a Pig Farm Lead to Low ESBL Prevalence? *Antibiotics*, *10*(5), Article 5. https://doi.org/10.3390/antibiotics10050574
Gundran, R. S., Cardenio, P. A., Villanueva, M. A., Sison, F. B., Benigno, C. C., Kreausukon, K., Pichpol, D., & Punyapornwithaya, V. (2019). Prevalence and distribution of blaCTX-M, blaSHV, blaTEM genes in extended- spectrum β- lactamase- producing E. coli isolates from broiler farms in the Philippines. *BMC Veterinary Research*, *15*(1), 227. https://doi.org/10.1186/s12917-019-1975-9
Hall, C. W., & Mah, T.-F. (2017). Molecular mechanisms of biofilm-based antibiotic resistance and tolerance in pathogenic bacteria. *FEMS Microbiology Reviews*, *41*(3), 276–301. https://doi.org/10.1093/femsre/fux010
Ibrahim, D. R., Dodd, C. E. R., Stekel, D. J., Ramsden, S. J., & Hobman, J. L. (2016). Multidrug resistant, extended spectrum β-lactamase (ESBL)-producing Escherichia coli isolated from a dairy farm. *FEMS Microbiology Ecology*, *92*(4), fiw013. https://doi.org/10.1093/femsec/fiw013
Iredell, J., Brown, J., & Tagg, K. (2016). Antibiotic resistance in Enterobacteriaceae: Mechanisms and clinical implications. *BMJ*, *352*, h6420. https://doi.org/10.1136/bmj.h6420
Karesh, W. B., Dobson, A., Lloyd-Smith, J. O., Lubroth, J., Dixon, M. A., Bennett, M., Aldrich, S., Harrington, T., Formenty, P., Loh, E. H., Machalaba, C. C., Thomas, M. J., & Heymann, D. L. (2012). Ecology of zoonoses: Natural and unnatural histories. *The Lancet*, *380*(9857), 1936–1945. https://doi.org/10.1016/S0140-6736 (12)61678-X
Kim, H., Kim, Y. A., Seo, Y. H., Lee, H., & Lee, K. (2021). Prevalence and Molecular Epidemiology of Extended-Spectrum-β-Lactamase (ESBL)-Producing Escherichia coli from Multiple Sectors of Poultry Industry in Korea. *Antibiotics*, *10*(9), Article 9. https://doi.org/10.3390/antibiotics10091050
Laxminarayan, R., Duse, A., Wattal, C., Zaidi, A. K. M., Wertheim, H. F. L., Sumpradit, N., Vlieghe, E., Hara, G. L., Gould, I. M., Goossens, H., Greko, C., So, A. D., Bigdeli, M., Tomson, G., Woodhouse, W., Ombaka, E., Peralta, A. Q., Qamar, F. N., Mir, F., Cars, O. (2013). Antibiotic resistance—the need for global solutions. *The Lancet Infectious Diseases*, *13*(12), 1057–1098. https://doi.org/10.1016/S1473-3099 (13)70318-9
Lerminiaux, N. A., & Cameron, A. D. S. (2019). Horizontal transfer of antibiotic resistance genes in clinical environments. *Canadian Journal of Microbiology*, *65*(1), 34–44. https://doi.org/10.1139/cjm-2018-0275
Lin, J., Nishino, K., Roberts, M. C., Tolmasky, M., Aminov, R. I., & Zhang, L. (2015). Mechanisms of antibiotic resistance. *Frontiers in Microbiology*, *6*. https://doi.org/10.3389/fmicb.2015.00034
Maamar, E., Hammami, S., Alonso, C. A., Dakhli, N., Abbassi, M. S., Ferjani, S., Hamzaoui, Z., Saidani, M., Torres, C., & Boutiba-Ben Boubaker, I. (2016). High prevalence of extended-spectrum and plasmidic AmpC beta-lactamase-producing Escherichia coli from poultry in Tunisia. *International Journal of Food Microbiology*, *231*, 69–75. https://doi.org/10.1016/j.ijfoodmicro.2016.05.001
Magiorakos, A.-P., Srinivasan, A., Carey, R. B., Carmeli, Y., Falagas, M. E., Giske, C. G., Harbarth, S., Hindler, J. F., Kahlmeter, G., Olsson-Liljequist, B., Paterson, D. L., Rice, L. B., Stelling, J., Struelens, M. J., Vatopoulos, A., Weber, J. T., & Monnet, D. L. (2012). Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: An international expert proposal for interim standard definitions for acquired resistance. *Clinical Microbiology and Infection*, *18*(3), 268–281. https://doi.org/10.1111/j.1469-0691.2011.03570.x
Marston, H. D., Dixon, D. M., Knisely, J. M., Palmore, T. N., & Fauci, A. S. (2016). Antimicrobial Resistance. *JAMA*, *316*(11), 1193–1204. https://doi.org/10.1001/jama.2016.11764
Martinez, J. L. (2009). The role of natural environments in the evolution of resistance traits in pathogenic bacteria. *Proceedings of the Royal Society B: Biological Sciences*, *276*(1667), 2521–2530. https://doi.org/10.1098/rspb.2009.0320
Massé, J., Vanier, G., Fairbrother, J. M., de Lagarde, M., Arsenault, J., Francoz, D., Dufour, S., & Archambault, M. (2023). Description of Antimicrobial-Resistant Escherichia coli and Their Dissemination Mechanisms on Dairy Farms. *Veterinary Sciences*, *10*(4), 242. https://doi.org/10.3390/vetsci10040242
Massella, E., Giacometti, F., Bonilauri, P., Reid, C. J., Djordjevic, S. P., Merialdi, G., Bacci, C., Fiorentini, L., Massi, P., Bardasi, L., Rubini, S.,

Savini, F., Serraino, A., & Piva, S. (2021). Antimicrobial Resistance Profile and ExPEC Virulence Potential in Commensal Escherichia coli of Multiple Sources. *Antibiotics*, *10*(4), 351. https://doi.org/10.3390/antibiotics10040351

Mohr, K. I. (2016). History of Antibiotics Research. In M. Stadler & P. Dersch (Eds.), *How to Overcome the Antibiotic Crisis: Facts, Challenges, Technologies and Future Perspectives* (pp. 237–272). Springer International Publishing. https://doi.org/10.1007/82_2016_499

Motta, J.-P., Wallace, J. L., Buret, A. G., Deraison, C., & Vergnolle, N. (2021). Gastrointestinal biofilms in health and disease. *Nature Reviews Gastroenterology & Hepatology*, *18*(5), 314–334. https://doi.org/10.1038/s41575-020-00397-y

Munita, J. M., & Arias, C. A. (2016). Mechanisms of Antibiotic Resistance. *Microbiology Spectrum*, 4(2), 481-511. https://doi.org/10.1128/microbiolspec.vmbf-0016-2015

Nainu, F., Masyita, A., Bahar, M. A., Raihan, M., Prova, S. R., Mitra, S., Emran, T. B., & Simal-Gandara, J. (2021). Pharmaceutical Prospects of Bee Products: Special Focus on Anticancer, Antibacterial, Antiviral, and Antiparasitic Properties. *Antibiotics*, *10*(7), 822. https://doi.org/10.3390/antibiotics10070822

Olsen, R. H., Bisgaard, M., Löhren, U., Robineau, B., & Christensen, H. (2014). Extended-spectrum β-lactamase-producing *Escherichia coli* isolated from poultry: A review of current problems, illustrated with some laboratory findings. *Avian Pathology*, *43*(3), 199–208. https://doi.org/10.1080/03079457.2014.907866

O'Neill, J. (2016). *Tackling drug-resistant infections globally: Final report and recommendations*. https://www.cabidigitallibrary.org/doi/full/10.5555/20173071720

Overdevest, I., Willemsen, I., Rijnsburger, M., Eustace, A., Xu, L., Hawkey, P., Heck, M., Savelkoul, P., Vandenbroucke-Grauls, C., van der Zwaluw, K., Huijsdens, X., & Kluytmans, J. (2011). Extended-Spectrum β-Lactamase Genes of Escherichia coli in Chicken Meat and Humans, the Netherlands. *Emerging Infectious Diseases*, *17*(7), 1216–1222. https://doi.org/10.3201/eid1707.110209

Pang, Z., Raudonis, R., Glick, B. R., Lin, T.-J., & Cheng, Z. (2019). Antibiotic resistance in *Pseudomonas aeruginosa*: Mechanisms and alternative therapeutic strategies. *Biotechnology Advances*, *37*(1), 177–192. https://doi.org/10.1016/j.biotechadv.2018.11.013

Paterson, D. L., & Bonomo, R. A. (2005). *Extended-Spectrum β-Lactamases: A Clinical Update | Clinical Microbiology Reviews*. *18*(4), 657-686. https://doi.org/10.1128/cmr.18.4.657-686.2005

Pfeifer, Y., Matten, J., & Rabsch, W. (2009). Salmonella enterica Serovar Typhi with CTX-M β-Lactamase, Germany. *Emerging Infectious Diseases*, *15*(9), 1533–1535. https://doi.org/10.3201/eid1509.090567

Platell, J. L., Johnson, J. R., Cobbold, R. N., & Trott, D. J. (2011). Multidrug-resistant extraintestinal pathogenic Escherichia coli of sequence type ST131 in animals and foods. *Veterinary Microbiology*, *153*(1–2), 99–108. https://doi.org/10.1016/j.vetmic.2011.05.007

Puvača, N., Vapa-Tankosić, J., Ignjatijević, S., Carić, M., & Prodanovic, R. (2022). Antimicrobial Resistance in the Environment: Review of the Selected Resistance Drivers and Public Health Concerns. *Journal of Agronomy, Technology and Engineering Management*, *5*, 793–802. https://doi.org/10.55817/CSCQ3326

Ramos, S., Silva, V., Dapkevicius, M. de L. E., Caniça, M., Tejedor-Junco, M. T., Igrejas, G., & Poeta, P. (2020). Escherichia coli as commensal and pathogenic bacteria among food-producing animals: Health implications of extended spectrum β-lactamase (ESBL) production. *Animals*, *10*(12), 2239.

Randall, L. P. (2004). Antibiotic resistance genes, integrons and multiple antibiotic resistance in thirty-five serotypes of Salmonella enterica isolated from humans and animals in the UK. *Journal of Antimicrobial Chemotherapy*, *53*(2), 208–216. https://doi.org/10.1093/jac/dkh070

Rathnayaka, S. D., Selvanathan, S., & Selvanathan, E. A. (2021). Demand for animal-derived food in selected Asian countries: A system-wide analysis. *Agricultural Economics*, *52*(1), 97–122. https://doi.org/10.1111/agec.12609

Rehman, H. U., Vahjen, W., Awad, W. A., & Zentek, J. (2007). Indigenous bacteria and bacterial metabolic products in the gastrointestinal tract of broiler chickens. *Archives of Animal Nutrition*, *61*(5), 319–335. https://doi.org/10.1080/17450390701556817

Reygaert, W. C. (2018). An overview of the antimicrobial resistance mechanisms of bacteria. *AIMS Microbiology*, *4*(3), 482. https://doi.org/10.3934/microbiol.2018.3.482

Samreen, Ahmad, I., Malak, H. A., & Abulreesh, H. H. (2021). Environmental antimicrobial resistance and its drivers: A potential threat to public health. *Journal of Global Antimicrobial Resistance*, *27*, 101–111. https://doi.org/10.1016/j.jgar.2021.08.001

Schwarz, S., Cloeckaert, A., & Roberts, M. C. (2005). Mechanisms and Spread of Bacterial Resistance to Antimicrobial Agents. In *Antimicrobial Resistance in Bacteria of Animal Origin* (pp. 73–98). John Wiley & Sons, Ltd. https://doi.org/10.1128/9781555817534.ch6

Shafiq, M., Rahman, S. U., Bilal, H., Ullah, A., Noman, S. M., Zeng, M., Yuan, Y., Xie, Q., Li, X., & Jiao, X. (2022). Incidence and molecular characterization of ESBL-producing and colistin-resistant *Escherichia coli* isolates recovered from healthy food-producing animals in Pakistan. *Journal of Applied Microbiology*, *133*(3), 1169–1182. https://doi.org/10.1111/jam.15469

Smoglica, C., Barco, L., Angelucci, S., Orsini, M., Marsilio, F., Antonucci, A., & Di Francesco, C. E. (2023). Whole Genome Sequencing of *Escherichia coli* and *Enterococcus* spp. in wildlife-livestock interface: A pilot study. *Journal of Global Antimicrobial Resistance*, *32*, 118–121. https://doi.org/10.1016/j.jgar.2023.01.012

Soncini, J. G. M., Cerdeira, L., Sano, E., Koga, V. L., Tizura, A. T., Tano, Z. N., Nakazato, G., Kobayashi, R. K. T., Aires, C. A. M., Lincopan, N., & Vespero, E. C. (2022). Genomic insights of high-risk clones of ESBL-producing Escherichia coli isolated from community infections and commercial meat in southern Brazil. *Scientific Reports*, *12*(1), 9354. https://doi.org/10.1038/s41598-022-13197-y

Storey, N., Cawthraw, S., Turner, O., Rambaldi, M., Lemma, F., Horton, R., Randall, L., Duggett, N. A., AbuOun, M., Martelli, F., & Anjum, M. F. (2022). Use of genomics to explore AMR persistence in an outdoor pig farm with low antimicrobial usage. *Microbial Genomics*, *8*(3), 000782. https://doi.org/10.1099/mgen.0.000782

Szmolka, A., Wami, H., & Dobrindt, U. (2021). Comparative Genomics of Emerging Lineages and Mobile Resistomes of Contemporary Broiler Strains of Salmonella Infantis and E. coli. *Frontiers in Microbiology*, *12*. https://doi.org/10.3389/fmicb.2021.642125

Tacconelli, E., Górska, A., De Angelis, G., Lammens, C., Restuccia, G., Schrenzel, J., Huson, D. H., Carević, B., Preoţescu, L., Carmeli, Y., Kazma,

M., Spanu, T., Carrara, E., Malhotra-Kumar, S., & Gladstone, B. P. (2020). Estimating the association between antibiotic exposure and colonization with extended-spectrum β-lactamase-producing Gram-negative bacteria using machine learning methods: A multicentre, prospective cohort study. *Clinical Microbiology and Infection*, *26*(1), 87–94. https://doi.org/10.1016/j.cmi.2019.05.013

Tängdén, T., Cars, O., Melhus, Å., & Löwdin, E. (2010). Foreign Travel Is a Major Risk Factor for Colonization with *Escherichia coli* Producing CTX-M-Type Extended-Spectrum β-Lactamases: A Prospective Study with Swedish Volunteers. *Antimicrobial Agents and Chemotherapy*, *54*(9), 3564–3568. https://doi.org/10.1128/AAC.00220-10

Taylor, N. G. H., Verner-Jeffreys, D. W., & Baker-Austin, C. (2011). Aquatic systems: Maintaining, mixing and mobilising antimicrobial resistance? *Trends in Ecology & Evolution*, *26*(6), 278–284. https://doi.org/10.1016/j.tree.2011.03.004

Tiseo, K., Huber, L., Gilbert, M., Robinson, T. P., & Van Boeckel, T. P. (2020). Global Trends in Antimicrobial Use in Food Animals from 2017 to 2030. *Antibiotics*, *9*(12), 918. https://doi.org/10.3390/antibiotics9120918

Tseng, C.-H., Liu, C.-W., & Liu, P.-Y. (2023). Extended-Spectrum β-Lactamases (ESBL) Producing Bacteria in Animals. *Antibiotics*, *12*(4), 661. https://doi.org/10.3390/antibiotics12040661

Ur Rahman, S., Ali, T., Ali, I., Khan, N. A., Han, B., & Gao, J. (2018). The Growing Genetic and Functional Diversity of Extended Spectrum Beta-Lactamases. *BioMed Research International*, *2018*, 1–14. https://doi.org/10.1155/2018/9519718

Ventola, C. L. (2015). The Antibiotic Resistance Crisis. *Pharmacy and Therapeutics*, *40*(4), 277–283.

von Rosenvinge, E. C., O'May, G. A., Macfarlane, S., Macfarlane, G. T., & Shirtliff, M. E. (2013). Microbial biofilms and gastrointestinal diseases. *Pathogens and Disease*, *67*(1), 25–38. https://doi.org/10.1111/2049-632X.12020

von Wintersdorff, C. J. H., Penders, J., van Niekerk, J. M., Mills, N. D., Majumder, S., van Alphen, L. B., Savelkoul, P. H. M., & Wolffs, P. F. G. (2016). Dissemination of Antimicrobial Resistance in Microbial Ecosystems through Horizontal Gene Transfer. *Frontiers in Microbiology*, *7*. https://doi.org/10.3389/fmicb.2016.00173

Wilson, H., & Török, M. E. (2018). Extended-spectrum β-lactamase-producing and carbapenemase-producing Enterobacteriaceae. *Microbial Genomics*, *4*(7). https://doi.org/10.1099/mgen.0.000197

Zhao, X., Yang, J., Ju, Z., Chang, W., & Sun, S. (2018). Molecular Characterization of Antimicrobial Resistance in Escherichia coli from Rabbit Farms in Tai'an, China. *BioMed Research International*, *2018*(1), 8607647. https://doi.org/10.1155/2018/8607647

Zhao, X., Zhao, H., Zhou, Z., Miao, Y., Li, R., Yang, B., Cao, C., Xiao, S., Wang, X., Liu, H., Wang, J., & Yang, Z. (2022). Characterization of Extended-Spectrum β-Lactamase-Producing *Escherichia coli* Isolates That Cause Diarrhea in Sheep in Northwest China. *Microbiology Spectrum*, *10*(4), e01595-22. https://doi.org/10.1128/spectrum.01595-22

Zhu, F. H., Rodado, M. P., Asmar, B. I., Salimnia, H., Thomas, R., & Abdel-Haq, N. (2019). Risk factors for community acquired urinary tract infections caused by extended spectrum β-lactamase (ESBL) producing *Escherichia coli* in children: A case control study. *Infectious Diseases*, *51*(11–12), 802–809. https://doi.org/10.1080/23744235.2019.1654127