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ASSESSMENT OF ANTIBIOTIC USE PRACTICES AND THEIR ASSOCIATION WITH ANTIMICROBIAL RESISTANCE IN DAIRY CATTLE

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Abstract

Antimicrobial resistance (AMR) constitutes one of the most pressing global health threats, with livestock production serving as a critical reservoir and amplifier of resistant bacteria and resistance genes. Dairy cattle production relies heavily on antimicrobial agents for the treatment, control, and prevention of infectious diseases—particularly mastitis, respiratory infections, and neonatal calf diarrhea—creating sustained selective pressure that drives the emergence and dissemination of AMR. This comprehensive review synthesizes current scientific evidence on antibiotic use practices in dairy cattle and their association with antimicrobial resistance, examining the quantitative relationship between antimicrobial consumption and resistance prevalence, the molecular mechanisms underlying resistance development, and the epidemiological patterns of resistant pathogens in dairy systems worldwide. The review documents that mastitis treatment accounts for the majority of antimicrobial use in dairy herds, with significant regional variation in consumption patterns and regulatory oversight. Critically, a positive association between antimicrobial exposure and the prevalence of resistance is consistently observed across multiple pathogens and production systems. Resistance rates exceeding 50% have been reported for penicillin and tetracycline in Staphylococcus aureus and Escherichia coli isolates from dairy cattle, with multidrug-resistant phenotypes increasingly documented globally. The transmission of resistant bacteria and resistance genes from dairy cattle to humans occurs through multiple pathways, including consumption of contaminated milk and dairy products, direct contact with animals, and environmental dissemination. Addressing this complex challenge requires integrated One Health approaches encompassing antimicrobial stewardship, enhanced surveillance systems, alternative therapeutic strategies, and improved farm management practices. This review concludes that prudent antimicrobial use, supported by robust diagnostic capabilities and farmer education, is essential for preserving antibiotic efficacy

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while maintaining animal health and welfare in dairy production systems.

1. Introduction

The discovery and clinical application of antibiotics revolutionized medical and veterinary practice, transforming the management of bacterial infections across human and animal populations (Laxminarayan, 2002). However, the therapeutic success of these agents has been progressively undermined by the emergence and global spread of antimicrobial resistance (AMR), a phenomenon now recognized as one of the most significant challenges to public health in the modern era (Van Boeckel et al., 2015). Between 2000 and 2015, global antibiotic consumption increased by 65%, reaching 34.8 billion tons, with approximately 73% of this total used in food-producing animals (Van Boeckel et al., 2015). The projected growth in global demand for animal protein, particularly in low- and middle-income countries, is expected to further intensify antimicrobial use in livestock production, exacerbating the selective pressure that drives resistance emergence (Laxminarayan, 2002; Pires et al., 2024). Dairy cattle production represents a significant component of global livestock systems and a substantial contributor to antimicrobial consumption in food animals (Oliver & Murinda, 2011; Oliver & Murinda, 2012). The primary drivers of antimicrobial use in dairy herds are infectious diseases that compromise animal health, welfare, and productivity—most notably mastitis, which remains the most common and economically significant disease affecting dairy cattle worldwide (Benić et al., 2018; Ghafar et al., 2020). Reproductive disorders, bovine respiratory disease, and neonatal calf diarrhea also contribute substantially to antimicrobial consumption in dairy operations (Zhang et al., 2024; Cole et al., 2024).

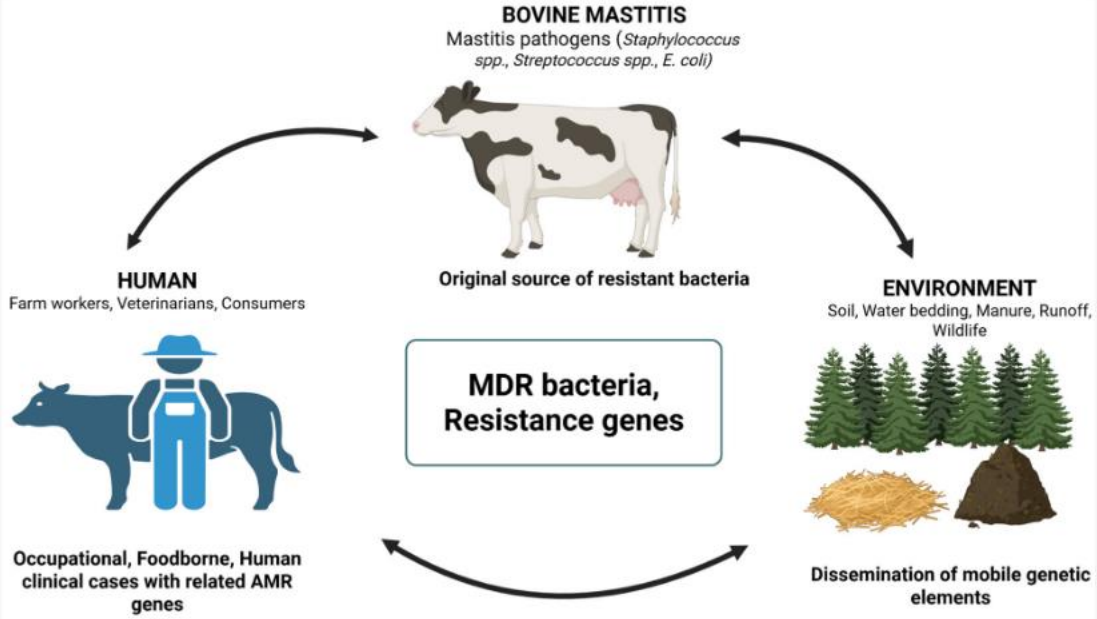
The association between antimicrobial use and resistance in dairy cattle is well-established, with numerous studies demonstrating positive correlations between treatment intensity and the prevalence of resistant bacteria in dairy herds (Pires et al., 2024; Tomanić et al., 2025). The mechanisms underlying this relationship are grounded in fundamental principles of microbial evolution: antimicrobial exposure creates selective pressure that favors the survival and proliferation of resistant bacterial strains, which may then spread within herds, between farms, and across species boundaries (Oliver & Murinda, 2011; Call et al., 2008). Understanding the patterns of antimicrobial use in dairy cattle and their consequences for AMR is essential for developing effective interventions to preserve antibiotic efficacy while maintaining animal health and ensuring food safety (Gruetzmacher et al., 2021; Zinsstag et al., 2012). This review aims to provide a comprehensive synthesis of current knowledge on antibiotic use practices in dairy cattle and their association with antimicrobial resistance. Specifically, this review examines: (i) the patterns and drivers of antimicrobial use in dairy production systems; (ii) the molecular mechanisms by which resistance emerges and disseminates; (iii) the epidemiological evidence linking antimicrobial use to resistance in major dairy pathogens; (iv) the transmission pathways through which resistant bacteria and resistance genes move from dairy cattle to humans and the environment; and (v) the strategies and interventions available to mitigate AMR in dairy production within a One Health framework (Ostrom, 2009; Gruetzmacher et al., 2021).

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Figure 1. One Health perspective on the emergence and dissemination of bacteria with antimicrobial resistance (AMR) and resistance genes in bovine mastitis, illustrating the interconnected risks across animals, humans, and the environment. All arrows indicate potential routes of pathogen or resistance gene transmission.



2. Antimicrobial Use Practices in Dairy Cattle

2.1 Major Indications for Antimicrobial Use

The use of antimicrobial agents in dairy cattle is primarily driven by the need to manage infectious diseases that threaten animal health, milk production, and farm profitability (Oliver & Murinda, 2011; Benić et al., 2018). Mastitis, an inflammatory condition of the mammary gland, constitutes the predominant indication for antimicrobial therapy in dairy herds (Shafeeq et al., 2021; Sattar, 2020). Bovine mastitis manifests in two principal forms: clinical mastitis, characterized by visible abnormalities in milk and udder inflammation, and subclinical mastitis, which presents no overt signs but results in elevated somatic cell counts and reduced milk quality (Oliver & Murinda, 2012). Both forms impose substantial economic burdens on dairy operations through reduced milk yield, decreased milk quality, increased treatment costs, and premature culling (Ghafar et al., 2020; Benić et al., 2018). Antimicrobial therapy for mastitis is administered through several routes, including intramammary infusion for localized treatment of infected quarters and systemic parenteral administration for severe cases (Wagner, 2024; Antimicrobials in the management of bovine mastitis, n.d.). The dry period—the interval between lactation cycles when cows are not being milked—represents a critical period for mastitis management, with blanket dry cow therapy (BDCT) historically involving the administration of long-acting intramammary antibiotics to all cows at drying off (The future of udder health, 2025; Selective dry cow therapy, 2025). This practice has been widely adopted to eliminate existing intramammary infections and prevent new infections during the dry period. However, growing concerns about antimicrobial resistance have prompted the development and adoption of selective dry cow therapy (SDCT), which targets treatment only to cows at higher risk of intramammary infection based on diagnostic criteria such as somatic cell count or bacteriological culture (Selective dry cow therapy, 2025; Antimicrobial resistance and use on Chinese dairy farms, 2024). Beyond mastitis, antimicrobials are used in dairy cattle for the treatment of reproductive disorders, particularly metritis and

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retained placenta, which are common in the postpartum period (Pajoro et al., 2024). Bovine respiratory disease, especially in calves and young stock, also contributes to antimicrobial consumption, though to a lesser extent than mastitis (Zhang et al., 2024). Calf diarrhea, caused by a range of bacterial and viral pathogens, represents another important indication for antimicrobial therapy in dairy calves (Zhang et al., 2024; Cole et al., 2024).

Table 1: ***Common Indications for Antimicrobial Use in Dairy Cattle***

Indication	Importance/Economic Impact	Major Pathogens	Common Antimicrobial Classes	Refernces
Clinical mastitis	The most common infectious disease; major economic losses due to reduced milk yield, treatment costs, and culling	*Staphylococcus aureus*, *Streptococcus* spp., *Escherichia coli*, *Klebsiella* spp.	β-lactams, cephalosporins, tetracyclines, aminoglycosides, macrolides	Oliver & Murinda (2012); Benić et al. (2018); Ghafar et al. (2020); Wagner (2024)
Subclinical mastitis	Reduced milk quality and elevated somatic cell count; often undetected	*S. aureus*, *Streptococcus agalactiae*, coagulase-negative staphylococci	Intramammary β-lactams, tetracyclines	Oliver & Murinda (2011); Oliver & Murinda (2012); Boireau et al. (2018)
Dry cow therapy	Prevents new intramammary infections during the dry period	*S. aureus*, *Streptococcus* spp., environmental pathogens	Long-acting intramammary β-lactams (BDCT/SDCT)	Wagner (2024)
Calf diarrhea	The major cause of morbidity and mortality in pre-weaned calves	*E. coli*, *Salmonella* spp., *Clostridium perfringens*	β-lactams, tetracyclines, fluoroquinolones	Zhang et al. (2024); Cole et al. (2024)
Calf pneumonia	An important cause of respiratory disease and economic losses	*Mannheimia haemolytica*, *Pasteurella multocida*, *Mycoplasma* spp.	Macrolides, tetracyclines, fluoroquinolones	Zhang et al. (2024)
Reproductive disorders	Postpartum infections such as metritis and retained placenta	*Trueperella pyogenes*, *E. coli*, mixed anaerobes	Penicillins, ceftiofur, tetracyclines	Pajoro et al. (2024); Wagner (2024)

2.2 Patterns of Antimicrobial Consumption

Significant regional variation exists in antimicrobial consumption patterns in dairy cattle, reflecting differences in production systems, disease prevalence, regulatory frameworks, and cultural practices (Pajoro et al., 2024; Antimicrobial usage in animal production, 2018). In high-income countries with well-developed veterinary infrastructure and regulatory oversight, antimicrobial use is generally more constrained, with increasing emphasis on prudent use principles and stewardship programs (Cole et al., 2024). In contrast, low- and middle-income countries often face challenges including limited access to

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veterinary services, inadequate diagnostic capabilities, and weak regulatory enforcement, resulting in higher and often inappropriate antimicrobial use (Antimicrobial usage in animal production, 2018; Iraguha et al., 2024). The classes of antimicrobials most commonly used in dairy cattle include β-lactams (particularly penicillin and cephalosporins), tetracyclines, macrolides, aminoglycosides, and fluoroquinolones (Oliver & Murinda, 2011; Boireau et al., 2018). The selection of specific agents depends on the target pathogen, the site and severity of infection, pharmacokinetic properties, cost, and regulatory considerations (Wagner, 2024). Critically important antimicrobials for human medicine, including third-generation cephalosporins and fluoroquinolones, are also used in dairy cattle, raising particular concerns about the potential for cross-species resistance transmission (Pires et al., 2024; Carbapenem-resistant Enterobacteriaceae, 2024). Quantitative data on antimicrobial consumption in dairy cattle remain limited in many regions, hampering efforts to establish meaningful benchmarks and track trends over time (Zhang et al., 2024; Cole et al., 2024). A systematic review of antimicrobial use in dairy calves identified 19 studies reporting use data, revealing substantial variation in consumption patterns between herds and regions (Zhang et al., 2024). Most antimicrobial use was attributed to treatment of clinical disease, with a smaller proportion accounted for by prophylactic administration. Organic farming systems were found to use significantly fewer antimicrobials for calf disease treatment compared to conventional systems (Pajoro et al., 2024).

2.3 Factors Influencing Antimicrobial Use

Multiple factors influence antimicrobial use decisions on dairy farms, operating at the levels of the individual animal, the herd, the farm enterprise, and the broader production system (Cole et al., 2024; Iraguha et al., 2024). Clinical factors include the severity and duration of disease, the suspected or confirmed pathogen, and the response to previous therapy (Oliver & Murinda, 2012). Farm-level factors encompass herd size, production intensity, housing and management practices, biosecurity measures, and the availability of veterinary services (Pajoro et al., 2024; Antimicrobial resistance and use on Chinese dairy farms, 2024). Socioeconomic and behavioral factors also play important roles in shaping antimicrobial use practices (Iraguha et al., 2024; Ágredo-Campos et al., 2025). Farmer knowledge, attitudes, and perceptions regarding antimicrobials and AMR influence treatment decisions, with limited awareness of resistance risks often associated with higher and less judicious use (Cole et al., 2024). Economic considerations, including the cost of treatment, the value of affected animals, and the potential losses from reduced production, also influence decisions about antimicrobial use (Laxminarayan, 2002). In many low- and middle-income countries, the lack of access to veterinary diagnostic services leads to empirical treatment based on clinical signs alone, contributing to inappropriate antimicrobial selection and dosing (Iraguha et al., 2024; Antimicrobial usage in animal production, 2018).

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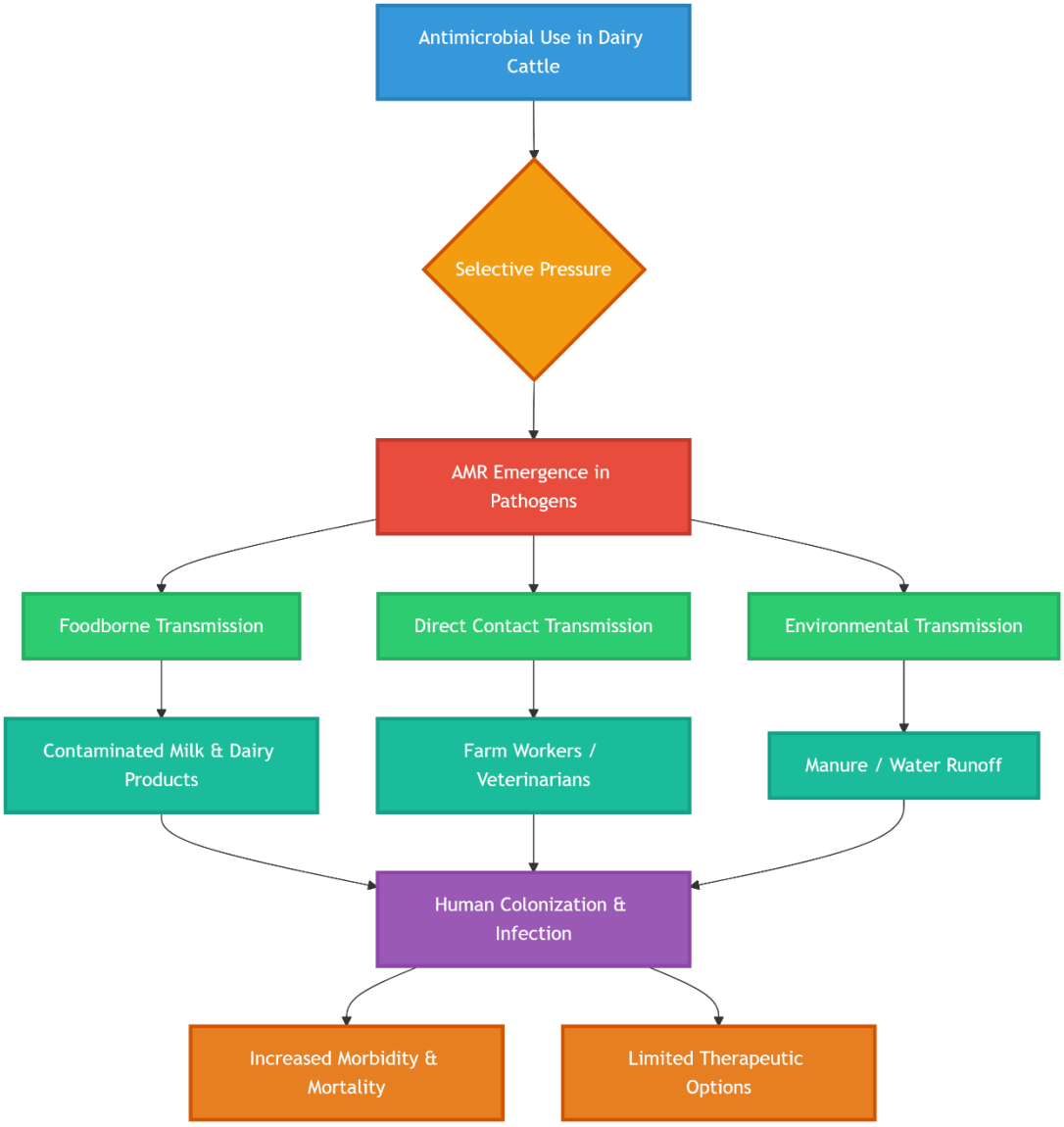


Figure 2: The major transmission pathways of antimicrobial-resistant bacteria from dairy cattle to humans and the environment.

3. Mechanisms of Antimicrobial Resistance in Dairy Cattle Pathogens

3.1 Intrinsic and Acquired Resistance Mechanisms

Bacteria employ diverse mechanisms to withstand the antimicrobial effects of antibiotics, which can be broadly categorized as intrinsic (inherent to the bacterial species) or acquired (resulting from genetic changes) (Oliver & Murinda, 2011; Call et al., 2008). Intrinsic resistance arises from structural or functional characteristics of the bacterium that limit antibiotic efficacy, such as the impermeability of the outer membrane in Gram-negative bacteria or the activity of efflux pumps that expel antibiotics from the cell (Pires et al., 2024). Acquired resistance results from genetic mutations or the acquisition of new genetic material encoding resistance determinants (Oliver & Murinda, 2012). Mutations can alter the target site of an antibiotic, reducing its binding affinity and thus its efficacy

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(Parmar & Kachchhi, 2026). For example, mutations in the gene encoding penicillin-binding proteins can confer resistance to β-lactam antibiotics, while mutations in the genes encoding DNA gyrase or topoisomerase IV can confer resistance to fluoroquinolones (Epidemiology, antimicrobial resistance, economic burden, 2025).

3.2 Horizontal Gene Transfer

The horizontal transfer of antimicrobial resistance genes (ARGs) between bacteria represents a particularly important mechanism for the dissemination of resistance in dairy cattle pathogens (Call et al., 2008; Oliver & Murinda, 2011). Horizontal gene transfer occurs through three principal mechanisms: conjugation, transformation, and transduction (Parmar & Kachchhi, 2026). Conjugation involves the transfer of genetic material via direct cell-to-cell contact, often mediated by plasmids or conjugative transposons (A newly identified IncY plasmid, 2024; Genomic characterization of plasmids, 2025). Plasmids carrying multiple resistance genes—conferring resistance to several antibiotic classes simultaneously—are commonly identified in dairy cattle isolates, facilitating the spread of multidrug resistance (Genetic comparison of virulence and resistance, 2025). Transformation involves the uptake of free DNA from the environment, which may include resistance genes released from lysed bacterial cells (Oliver & Murinda, 2012). Transduction is mediated by bacteriophages that transfer genetic material between bacterial cells (Call et al., 2008). Mobile genetic elements, including plasmids, transposons, and integrons, play crucial roles in the acquisition and dissemination of ARGs (Parmar & Kachchhi, 2026; Genomic insights into *Mammaliicoccus sciuri*, 2026).

3.3 Biofilm-Mediated Resistance

Biofilm formation represents an important survival strategy for many dairy cattle pathogens, particularly *Staphylococcus aureus*, and contributes significantly to treatment failure and resistance development (Bovine mastitis therapy at a crossroads, 2026; Antimicrobial resistance and residues from biofilms, 2025). Biofilms are structured communities of bacterial cells encased in a self-produced extracellular matrix that adheres to surfaces (Oliver & Murinda, 2012). Bacteria within biofilms exhibit enhanced resistance to antimicrobial agents compared to their planktonic counterparts, due to reduced penetration of antibiotics through the biofilm matrix, altered metabolic states of biofilm cells, and the presence of persister cells that survive antibiotic exposure (Antimicrobial resistance and residues from biofilms, 2025). The capacity of *S. aureus* to form biofilms in mammary tissue and on teat canal surfaces enables this pathogen to evade both antimicrobial therapy and host immune responses, contributing to its persistence in dairy herds and its role as a major mastitis pathogen (Epidemiology, antimicrobial resistance, economic burden, 2025). Biofilm-associated resistance complicates treatment and may promote the emergence of more resistant strains through prolonged antibiotic exposure (Bovine mastitis therapy at a crossroads, 2026).

Table 2: ***Major Antimicrobial Resistance Mechanisms in Dairy Cattle Pathogens***

Resistance Mechanism	Molecular Basis	Representative Organisms	Clinical Significance	Key References
Enzymatic degradation	Production of β-lactamases and ESBL enzymes	*E. coli*, *Klebsiella pneumoniae*, *S. aureus*	Resistance to β-lactam antibiotics	Oliver & Murinda (2012); Pires et al. (2024)
Target-site modification	Mutation in PBPs, DNA gyrase, ribosomal proteins	MRSA, Fluoroquinolone-resistant *E. coli*	Reduced drug efficacy	Call et al. (2008); Parmar & Kachchhi (2026)
Efflux pumps	Active transport of antibiotics outside bacterial cells	*E. coli*, *S. aureus*	Multidrug resistance	Oliver & Murinda (2011); Pires et al. (2024)
Reduced membrane	Altered porins decrease antibiotic	Gram-negative bacteria	Reduced intracellular	Call et al. (2008)

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permeability	uptake		antibiotic concentration	
Horizontal gene transfer	Plasmids, integrons, transposons, bacteriophages	Most dairy pathogens	Rapid dissemination of AMR genes	Call et al. (2008); Oliver & Murinda (2011);
Biofilm formation	Extracellular polymeric matrix protects bacteria	*S. aureus*, CNS	Chronic infection and treatment failure	Oliver & Murinda (2012); Bovine Mastitis

4. Antimicrobial Resistance in Major Dairy Cattle Pathogens

4.1 Mastitis Pathogens

4.1.1 *Staphylococcus aureus*

Staphylococcus aureus is one of the most prevalent and persistent pathogens associated with bovine mastitis worldwide (Oliver & Murinda, 2011; Benić et al., 2018). The pathogen's capacity to evade antimicrobial therapy through multiple mechanisms, including intracellular survival, biofilm formation, and the acquisition of resistance genes, makes it a particularly challenging target for treatment (Epidemiology, antimicrobial resistance, economic burden, 2025; Bovine mastitis and antimicrobial resistance in Pakistan, 2026). Resistance to penicillin in *S. aureus* from dairy cattle is widespread, with many isolates producing penicillinase (β-lactamase) that inactivates the antibiotic (Oliver & Murinda, 2012; Boireau et al., 2018). Methicillin-resistant *S. aureus* (MRSA) has been increasingly documented in dairy cattle populations globally, representing a significant public health concern due to the limited therapeutic options available for MRSA infections (Pires et al., 2024; One Health perspective on antimicrobial resistance, 2026). Multidrug-resistant (MDR) *S. aureus* isolates, resistant to three or more antimicrobial classes, are commonly reported in dairy herds, particularly in regions with high antimicrobial use (Bovine mastitis and antimicrobial resistance in Pakistan, 2026; Pajoro et al., 2024).

4.1.2 *Escherichia coli* and *Klebsiella* spp.

Gram-negative pathogens, particularly *Escherichia coli* and *Klebsiella* spp., are increasingly recognized as important causes of clinical mastitis, especially in well-managed herds where contagious pathogens are well-controlled. The global prevalence of *E. coli* in milk and dairy products has been estimated at 25%, with resistance to multiple antimicrobial classes commonly documented (Network meta-analysis of *E. coli*, 2025). Extended-spectrum β-lactamase (ESBL)-producing *E. coli* has been identified in dairy cattle isolates, conferring resistance to extended-spectrum cephalosporins and posing significant public health concerns (Extended-spectrum beta-lactamase-producing *E. coli*, 2026; Carbapenem-resistant Enterobacteriaceae, 2024). The prevalence of ESBL-producing Enterobacteriaceae in dairy cattle varies widely between regions and production systems, but the detection of these organisms in milk and dairy products underscores the potential for foodborne transmission of resistant bacteria (One Health perspective on antimicrobial resistance, 2026; Application of the One Health approach, 2025).

4.1.3 Other Mastitis Pathogens

Streptococcus agalactiae and *Streptococcus uberis* remain important mastitis pathogens in many dairy herds, with resistance to penicillin and tetracycline commonly reported (Oliver & Murinda, 2012; Boireau et al., 2018). Coagulase-negative staphylococci, historically considered minor pathogens, are increasingly recognized as emerging mastitis agents with significant antimicrobial resistance profiles (Pajoro et al., 2024).

4.2 Calf Diarrhea and Pneumonia Pathogens

Antimicrobial resistance in pathogens associated with calf diarrhea and pneumonia is a growing concern, with resistance rates often higher than those observed in mastitis pathogens (Zhang et al., 2024; Cole et al., 2024). A systematic review of AMR in dairy calf pathogens documented high resistance rates in *E. coli*, *Salmonella* spp., and respiratory pathogens, including *Mannheimia*

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haemolytica and *Pasteurella multocida* (Zhang et al., 2024).

Resistance to critically important antimicrobials, including third-generation cephalosporins and fluoroquinolones, has been documented in calf pathogens, raising concerns about the therapeutic options available for treating these infections (Carbapenem-resistant Enterobacteriaceae, 2024; Antimicrobial resistance in dairy systems, 2026). The positive association between antimicrobial exposure and resistance prevalence observed in calf pathogens mirrors the patterns documented in adult dairy cattle (Zhang et al., 2024; Cole et al., 2024).

5. Epidemiological Evidence Linking Antimicrobial Use to Resistance

5.1 Quantitative Associations

Numerous studies have demonstrated positive associations between antimicrobial use intensity and the prevalence of resistance in dairy cattle populations (Pires et al., 2024; Tomanić et al., 2025). A systematic review of AMU and AMR in dairy calves found that "there seems to be a positive association between exposure to antimicrobials and occurrence of resistance" (Zhang et al., 2024, p. 1). This association is consistent across multiple pathogens and production systems, supporting the fundamental principle that antimicrobial use drives resistance selection (Oliver & Murinda, 2011; Call et al., 2008). Comparative studies of different production systems have provided further evidence for the antimicrobial use-resistance link (Pajoro et al., 2024). Organic farming systems, which restrict antimicrobial use, have been found to have significantly lower antimicrobial consumption compared to conventional systems (Pajoro et al., 2024). However, the relationship between farming system and resistance prevalence is more complex. While AMR was generally more prevalent on conventional dairy farms compared to organic ones, the prevalence of specific pathogens and resistance types was frequently associated with risk factors not strictly related to the farming system (Pajoro et al., 2024).

5.2 Regional and Temporal Trends

The global distribution of AMR in dairy cattle shows substantial regional variation, reflecting differences in antimicrobial use patterns, production systems, and surveillance capacity (Carbapenem-resistant Enterobacteriaceae, 2024; Network meta-analysis of *E. coli*, 2025). A meta-analysis of carbapenem-resistant Enterobacteriaceae in dairy cattle milk estimated a global prevalence of 0.73% (95% CI: 0.37-1.41), with no significant differences among continents (Carbapenem-resistant Enterobacteriaceae, 2024). However, this finding should be interpreted cautiously given the limited data available from many regions. Temporal trends in AMR prevalence suggest increasing resistance in some pathogen-antimicrobial combinations, particularly in regions with high and increasing antimicrobial use. A meta-analysis of *Klebsiella* spp. in mastitis cases found a marked increase in prevalence from 3.85% during 2007-2012 to 12.16% during 2013-2020, potentially reflecting both improved detection and true increases in infection rates.

5.3 Risk Factors for Resistance

Beyond antimicrobial use, several other risk factors have been associated with increased AMR prevalence in dairy cattle (Cole et al., 2024; Pajoro et al., 2024). Farm-level factors including herd size, housing conditions, biosecurity practices, and management intensity have been identified as important determinants of resistance prevalence (Pajoro et al., 2024; A scoping review of antimicrobial resistance in the Australian dairy cattle industry, n.d.). The feeding of waste milk or pasteurized milk to calves has been associated with a higher risk of AMR in pathogens, potentially due to the presence of antimicrobial residues in waste milk (Zhang et al., 2024).

6. Transmission Pathways to Humans and the Environment

6.1 Foodborne Transmission

The consumption of milk and dairy products represents a primary pathway for the transmission of antimicrobial-resistant bacteria from dairy cattle to humans (Oliver & Murinda, 2011; Network meta-analysis of *E. coli*, 2025). Raw milk, in particular, can be contaminated with opportunistic pathogens carrying ARGs, and the consumption of unpasteurized dairy products has been associated with foodborne infections caused by resistant bacteria (Oliver & Murinda, 2011). While

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pasteurization effectively eliminates viable bacteria, the presence of ARGs in dairy products—even following pasteurization—remains a concern for the potential horizontal transfer of resistance genes to human-associated bacteria (Antibiotic residues in milk, 2025).

6.2 Direct Contact Transmission

Direct contact with dairy cattle provides another pathway for the transmission of resistant bacteria from animals to humans (Call et al., 2008; One Health perspective on antimicrobial resistance, 2026). Farm workers, veterinarians, and other individuals with occupational exposure to dairy cattle are at increased risk of colonization or infection with livestock-associated bacteria, including MRSA and ESBL-producing Enterobacteriaceae (Extended-spectrum beta-lactamase-producing *E. coli*, 2026). The potential for subsequent transmission from these individuals to the broader community represents a public health concern (Pires et al., 2024).

6.3 Environmental Transmission

The environmental dissemination of antimicrobial-resistant bacteria and ARGs from dairy operations occurs through multiple routes (Antimicrobial resistance and residues from biofilms, 2025; Climate change as a driver of bovine mastitis, 2026). The application of manure from treated cattle to agricultural land can introduce resistant bacteria and resistance genes into soil and water systems (Antimicrobial resistance and residues from biofilms, 2025). Antimicrobial residues excreted in urine and feces further contribute to environmental contamination, facilitating the spread of resistance (Antibiotic residues in milk, 2025). Runoff from manure-applied fields can transport resistant bacteria and ARGs to surface waters, potentially affecting downstream communities (Call et al., 2008).

7. Public Health Implications

7.1 Impact on Human Health

The emergence and spread of AMR in dairy cattle have direct and indirect implications for human health (Oliver & Murinda, 2011; Pires et al., 2024). The transmission of resistant bacteria from dairy cattle to humans, whether through foodborne, direct contact, or environmental pathways, can result in infections that are more difficult or impossible to treat with available antibiotics (One Health perspective on antimicrobial resistance, 2026). When infections caused by resistant bacteria occur in humans, treatment options may be limited to more expensive, more toxic, or less effective antibiotics, resulting in increased morbidity, mortality, and healthcare costs (Laxminarayan, 2002). The presence of ARGs in dairy cattle and dairy products poses an additional concern through the potential for horizontal gene transfer to human-associated bacteria (Parmar & Kachchhi, 2026; Genetic comparison of virulence and resistance, 2025). Even when viable resistant bacteria are not transmitted directly, the transfer of resistance genes from dairy-associated bacteria to human pathogens could compromise the effectiveness of antibiotics used in human medicine (Call et al., 2008).

7.2 Antimicrobial Residues in Milk

The presence of antimicrobial residues in milk, resulting from the treatment of dairy cattle, has implications for both public health and food safety (Tomanić et al., 2025; Antibiotic residues in milk, 2025). Residue prevalence varies widely between regions, ranging from less than 1% in some European countries to over 80% in parts of Africa (Tomanić et al., 2025). Common residues include β-lactams, tetracyclines, and quinolones, which can disrupt human intestinal microbiota, promote resistant bacterial strains, trigger immunological reactions, and interfere with dairy processing (Antibiotic residues in milk, 2025). Compliance with withdrawal periods—the time required after antimicrobial administration before milk can be sold for human consumption—is critical for preventing residue contamination (Tomanić et al., 2025). However, inadequate adherence to withdrawal periods, often driven by economic pressures or lack of awareness, contributes to the presence of residues in marketed milk (Ágredo-Campos et al., 2025; Iraguha et al., 2024).

8. Strategies for Mitigating Antimicrobial Resistance in Dairy Cattle

8.1 Antimicrobial Stewardship

Antimicrobial stewardship programs in dairy production aim to optimize antimicrobial use while

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minimizing the selection pressure for resistance (Wagner, 2024; Selective dry cow therapy, 2025). Key components of stewardship include: (i) accurate diagnosis to ensure that antimicrobials are used only when indicated; (ii) selection of the appropriate antimicrobial agent based on susceptibility testing; (iii) use of the correct dose and duration of therapy; and (iv) regular monitoring and evaluation of antimicrobial use practices (Cole et al., 2024; From herd health to public health, 2024). The transition from blanket to selective dry cow therapy represents a significant stewardship intervention, reducing overall antimicrobial use while maintaining udder health (Selective dry cow therapy, 2025; The future of udder health, 2025). Selective therapy, guided by diagnostic criteria such as somatic cell count or bacteriological culture, targets treatment to cows at highest risk of intramammary infection, thereby reducing unnecessary antimicrobial exposure (Antimicrobial resistance and use on Chinese dairy farms, 2024).

8.2 Improved Farm Management and Biosecurity

Enhanced farm management and biosecurity practices can reduce the incidence of infectious diseases and the associated need for antimicrobial therapy (Pajoro et al., 2024; A scoping review of antimicrobial resistance in the Australian dairy cattle industry, n.d.). Key measures include: (i) maintaining clean and hygienic housing conditions; (ii) implementing effective milking hygiene practices; (iii) ensuring adequate nutrition and management to support immune function; (iv) isolating and promptly treating diseased animals; and (v) implementing biosecurity measures to prevent the introduction and spread of pathogens (Cole et al., 2024; Climate change as a driver of bovine mastitis, 2026).

8.3 Surveillance and Monitoring

Robust surveillance systems for antimicrobial use and resistance in dairy cattle are essential for tracking trends, identifying emerging problems, and evaluating the effectiveness of interventions (Carbapenem-resistant Enterobacteriaceae, 2024; Network meta-analysis of *E. coli*, 2025). Surveillance should encompass both clinical pathogens and commensal bacteria, providing a comprehensive picture of the AMR landscape in dairy production (One Health perspective on antimicrobial resistance, 2026). The integration of surveillance data across human, animal, and environmental sectors is critical for understanding the full scope of the AMR problem and developing coordinated responses (Gruetzmacher et al., 2021; Zinsstag et al., 2012).

8.4 One Health Approach

Addressing AMR in dairy cattle requires a coordinated One Health approach that recognizes the interconnectedness of human, animal, and environmental health as shown in figure 2 (Gruetzmacher et al., 2021; Ostrom, 2009). One Health strategies for AMR in dairy production encompass: (i) integrated surveillance across sectors; (ii) coordinated antimicrobial stewardship policies; (iii) research on transmission dynamics and resistance mechanisms; (iv) education and awareness programs for farmers, veterinarians, and the public; and (v) regulatory frameworks that promote prudent antimicrobial use (Zinsstag et al., 2012).

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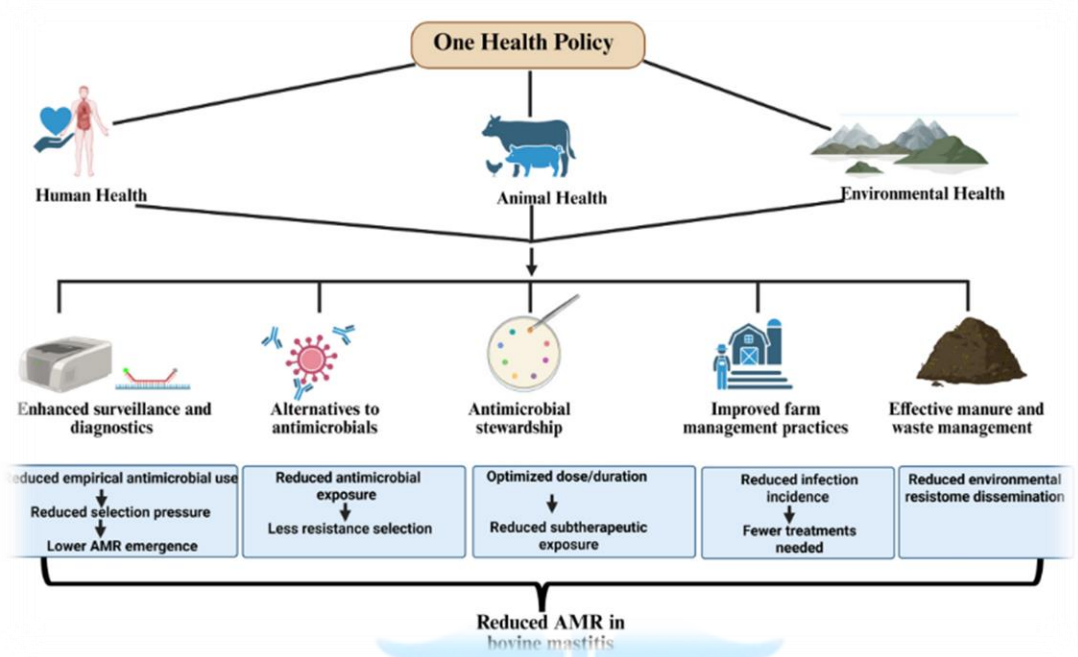


***Figure 2:** Integration of One Health strategies to mitigate antimicrobial resistance (AMR) in bovine mastitis, along with their biological or epidemiological mechanisms.*

Table 3. ***Strategies for Mitigating Antimicrobial Resistance in Dairy Cattle***

Strategy	Key Components	Expected Outcomes	Key References
Antimicrobial stewardship	Culture-based therapy, susceptibility testing, prudent antibiotic use	Reduced unnecessary antimicrobial exposure	Wagner (2024); Cole et al. (2024)
Selective dry cow therapy	Treat only infected/high-risk cows	Reduced antibiotic consumption without compromising udder health	Selective Dry Cow Therapy (2025); The Future of Udder Health (2025)
Improved farm management	Hygiene, nutrition, vaccination, and milking management	Lower disease incidence	Pajoro et al. (2024); Cole et al. (2024)
Biosecurity	Isolation, sanitation, controlled animal movement	Reduced pathogen transmission	Cole et al. (2024); Gruetzmacher et al. (2021)
Surveillance	Monitoring AMU and AMR trends	Early detection of resistance	Zinsstag et al. (2012); Gruetzmacher et al. (2021)
Farmer education	Training on prudent antibiotic use and withdrawal periods	Improved stewardship compliance	Iraguha et al. (2024); Ágredo-Campos et al. (2025)
One Health approach	Integrated animal, human, and environmental health strategies	Sustainable AMR control	Gruetzmacher et al. (2021); Zinsstag et al. (2012); Pires et al. (2024)

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9. Conclusion

The intricate relationship between antibiotic use practices and the emergence of antimicrobial resistance in dairy cattle represents one of the most critical challenges at the intersection of veterinary medicine, food safety, and public health. This comprehensive review has established that mastitis management remains the dominant driver of antimicrobial consumption in dairy herds, with dry cow therapy and clinical mastitis treatments accounting for the majority of antibiotic exposures. The substantial regional disparities in consumption patterns—influenced by regulatory frameworks, economic constraints, and diagnostic capacities—highlight the urgent need for globally harmonized stewardship guidelines that are adaptable to local contexts. Critically, the epidemiological evidence overwhelmingly confirms a positive, dose-dependent association between antimicrobial exposure and the prevalence of resistant pathogens. The widespread detection of multidrug-resistant *Staphylococcus aureus*, extended-spectrum beta-lactamase-producing *Escherichia coli*, and emerging resistance in *Klebsiella* species within dairy operations underscores the evolutionary adaptability of bacterial populations under sustained selective pressure. The molecular mechanisms driving this crisis—particularly horizontal gene transfer via plasmids and biofilm-mediated persistence—ensure that resistance determinants do not remain confined to individual farms but disseminate across bacterial communities, production systems, and ultimately, species barriers. The transmission pathways identified in this review—spanning foodborne contamination of dairy products, occupational direct contact, and environmental dissemination through manure and water runoff—confirm that dairy cattle serve as a significant reservoir for resistance genes that can reach human populations. This interconnectedness necessitates a departure from siloed approaches to disease management. The public health implications are profound: the diminishing efficacy of critically important antibiotics for human medicine, driven in part by agricultural use, threatens to reverse decades of medical progress. Addressing this multifaceted problem demands a paradigm shift toward integrated One Health frameworks. The transition from blanket to selective dry cow therapy exemplifies a successful stewardship intervention, but it must be complemented by robust investments in rapid diagnostic technologies, the development and validation of alternative therapies—including vaccines, probiotics, and phage-based treatments—and enhanced biosecurity measures that reduce disease incidence at its source. Furthermore, the establishment of continuous, transparent surveillance systems that monitor both antimicrobial consumption and resistance trends across the human-animal-environment interface is non-negotiable for evaluating intervention efficacy and detecting emerging threats. Ultimately, the preservation of antibiotic efficacy in dairy production is not an impediment to productivity but a prerequisite for its long-term sustainability. Empowering farmers through education, ensuring access to veterinary diagnostic support, and enforcing prudent use regulations are essential pillars of this transition. As global demand for dairy products continues to rise, the collective commitment of veterinarians, farmers, researchers, and policymakers to responsible antimicrobial stewardship will determine whether these vital medicines remain effective for future generations of both animals and humans.

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