

Antimicrobial Resistance of *Staphylococcus Aureus* in The Dairy Industry: A One Health Concern

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ABSTRACT

The global dairy industry faces a persistent and escalating challenge from *Staphylococcus aureus*, a primary agent of bovine mastitis and a major public health pathogen. This review synthesizes evidence to examine the complex epidemiology of antimicrobial resistance (AMR) in dairy-associated *S. aureus*, a crisis propelled by antimicrobial misuse in livestock and facilitated by dynamic transmission at the human-animal-environment interface. Studies from Africa, Asia, Europe, and America reveal a high and geographically variable prevalence of multidrug-resistant (MDR) and methicillin-resistant *S. aureus* (MRSA) strains, with particularly concerning resistance to beta-lactams and tetracyclines. Molecular analyses highlight the adaptation of successful clonal complexes (e.g., CC97, ST-1) in dairy herds and the widespread carriage of enterotoxin genes, resulting in zoonotic and food safety risks independent of AMR status. The transmission of resistant strains is amplified by suboptimal farm hygiene, direct occupational contact, and environmental contamination, with raw milk serving as a key vehicle for human exposure. The convergence of MDR, methicillin resistance, and potent virulence determinants in these strains poses a severe One Health threat, leading to difficult-to-treat infections that increase morbidity and healthcare costs. Mitigating this crisis requires an integrated, multi-pronged strategy. This includes stringent antimicrobial stewardship such as culture-guided therapy and selective dry cow treatment coupled with improved biosecurity, milking hygiene, and comprehensive surveillance. The development and adoption of alternative interventions, including vaccines, bacteriophages, and probiotics, are promising avenues to reduce antibiotic dependence. Concerted, cross-sectoral action under a One Health framework is urgently needed to curb the spread of AMR, protect animal welfare, ensure dairy sector sustainability, and safeguard global public health security.

Key words: Antimicrobial resistance; *Staphylococcus aureus*; mastitis; One Health; zoonosis.

INTRODUCTION

The global dairy industry faces a persistent and significant threat from *Staphylococcus aureus*, a primary cause of bovine mastitis with substantial economic impacts. Beyond its effects on animal health and productivity, *S. aureus* is a pathogen of major public health concern due to its zoonotic potential and formidable capacity to develop and disseminate antimicrobial resistance (AMR). The epidemiology of AMR in dairy-associated *S. aureus* is a complex, interconnected issue involving animal and human health, characterized by considerable geographical variation that reflects differences in antimicrobial usage practices, farm management, and surveillance systems. This variation has created a global network of diverse and evolving resistance patterns. The emergence of multidrug-resistant (MDR) and methicillin-resistant *S. aureus* (MRSA) strains within the dairy production chain poses a direct threat to food safety and complicates the treatment of infections in both veterinary and human medicine. This review aims to comprehensively examine the global scope of this challenge, exploring the molecular drivers of resistance, the dynamics of transmission at the human-animal-environment interface, the consequent public health risks, and the integrated strategies necessary for mitigation and control.

Global Epidemiology of AMR in *Staphylococcus aureus* from Dairy Sources

Internationally, the dairy industry faces a persistent and significant threat from *Staphylococcus aureus*, which is a primary cause of bovine mastitis. *S. aureus* is also a pathogen of major concern of public health owing to its zoonotic potential and its ability to cause antimicrobial resistance (AMR). The epidemiology of AMR in dairy which is associated with *S. aureus* is a complex, interconnected issue involving animal and human health, which is also characterized by a considerable geographical variation that reflects in the differences in antimicrobial usage practices, farm management, and surveillance systems. Therefore, this variation has created a global network of resistance patterns.

Studies conducted in Africa show a concerning AMR prevalence. For example, a high resistance of about 85% and 75% to penicillin and ampicillin respectively to ampicillin in Ethiopia, while there is susceptibility to other drugs like ciprofloxacin (Gutama & Anberber, 2025). In Southern Mozambique a high frequency of *S. aureus* was detected in raw milk, with notable penicillin resistance (43%) and, critically, the presence of human-adapted strains (e.g., ST1/CC1) in cattle, suggesting anthroponotic transmission (Nhatsave et al., 2021). Across Asia, the situation is particularly severe and heterogeneous. A scoping review by Veloo et al. (2025) highlighted significant research and surveillance gaps outside China, confirming *S. aureus* as a key pathogen resistant to critically important antimicrobials. Country-specific studies from Pakistan document high resistance to amoxicillin (85%) and penicillin (71%) in raw milk (Batool et al., 2025), while research in northern Bangladesh presents an extreme case, with 100% resistance to penicillin, 64% of isolates classified as multidrug-resistant (MDR), and 21.4% carrying the *mecA* gene (MRSA) (Islam et al., 2025).

National insights further detail this complex landscape. In Egypt, Badawy et al. (2022) provided critical insights into the ecological distribution of virulent, MDR *S. aureus*, finding a high prevalence of MRSA (19.4% *mecA*-positive) and enterotoxigenic strains across milk, environmental samples, and dairy products, with 86.6% of isolates resistant to three or more antimicrobial classes. This underscores small-scale farms as critical reservoirs. Conversely, European data from Sicily, Italy, offers a contrasting yet concerning profile. The study by Russo et al. (2025) reported lower MRSA prevalence (1.98%) but high resistance to gentamicin (47.5%) and erythromycin (29.7%), with 33.7% MDR. Notably, it detected vancomycin-resistant and intermediate phenotypes without the corresponding *van* genes, pointing to complex, non-genotypic resistance mechanisms, and molecular typing revealed evidence of human-to-animal host jumps of clones like CC5 and CC97.

The emergence and spread of this resistance are driven by multifaceted factors. The routine and often unregulated use of antibiotics in livestock for treatment, prophylaxis, and growth promotion exerts a powerful selective pressure, evident in the consistently high global resistance to first-line beta-lactams (Pekana & Green, 2018; Batool et al., 2025; Islam et al., 2025). This is compounded by extrinsic factors on farms, such as inadequate milking hygiene, poor barn management, and infrequent equipment cleaning, which are significantly correlated with higher contamination rates (Gutama & Anberber, 2025; Batool et al., 2025). Critically, the dynamic interplay between human and animal reservoirs acts as a key driver of AMR epidemiology. Compelling evidence shows the bidirectional transmission of strains, with human-adapted lineages like CC1, CC5, CC8, and CC152 repeatedly isolated from bovine mastitis across continents (Nhatsave et al., 2021; Islam et al., 2025), and the global emergence of livestock-associated MRSA (LA-MRSA) clones. This dynamic facilitates the flow of resistance and virulence genes through mobile genetic elements within the farm environment (Nhatsave et al., 2021; Islam et al., 2025). Adding to the challenge is the genetic complexity of resistance, where instances of phenotypic resistance without known genetic determinants—such as oxacillin resistance without the *mecA* gene (Islam et al., 2025) or vancomycin resistance without *van* genes (Russo et al., 2025)—point to alternative or emerging mechanisms that complicate diagnosis and control.

The public health implications are severe. The convergence of MDR, MRSA, and a suite of potent virulence genes (e.g., PVL, enterotoxins, biofilm genes) in dairy-derived *S. aureus* strains creates a significant One Health threat (Nhatsave et al., 2021; Islam et al., 2025). These resistant and virulent pathogens can transfer to humans through direct contact with animals, environmental contamination of water, soil, and manure, or the consumption of unpasteurized dairy products like raw milk cheese, potentially leading to difficult-to-treat infections. In conclusion, the global challenge of AMR in dairy-related *S. aureus* is marked by the widespread distribution of resistant strains, with regional variations shaped by local practices. Addressing this escalating crisis requires an

integrated, One Health approach. Coordinated actions across veterinary, agricultural, and public health sectors are essential to promote prudent antimicrobial use, enhance and harmonize surveillance, improve farm hygiene standards, and support molecular research to track resistance gene flow. Without such coordinated efforts, the continued spread of multidrug-resistant *S. aureus* will persistently jeopardize animal health, dairy industry sustainability, and public health security worldwide.

Molecular Ecology and AMR in Dairy: Insights from *Staphylococcus aureus*

The molecular ecology of *Staphylococcus aureus* in dairy systems is a complex interplay between bacterial population genetics, virulence determinants, and antimicrobial resistance (AMR) profiles, shaped by host adaptation, management practices, and geographic factors. Recent genomic studies from diverse dairy-producing regions—including the United States, China, and New Zealand—highlight both conserved and divergent patterns in the population structure, resistance gene carriage, and virulence potential of mastitis-associated *S. aureus*.

In the United States, a large-scale study of bulk tank milk (BTM) samples revealed a high herd-level prevalence (62.4%) of *S. aureus*, with isolates exhibiting limited AMR gene carriage aside from the nearly ubiquitous efflux pump gene *norA* (Patel et al., 2021). Methicillin resistance was rare, with only one isolate (0.8%) carrying the *mecA* gene, belonging to ST72-CC8. The population was dominated by clonal complex CC97 (47.6%), particularly ST2187, suggesting the circulation of a successful bovine-adapted lineage. Notably, virulence gene carriage was high, with enterotoxin genes such as *sen*, *sem*, *sei*, and *seg* detected in over 30% of isolates, indicating a latent risk for staphylococcal food poisoning despite low AMR prevalence (Patel et al., 2021).

In contrast, Chinese dairy herds exhibited a markedly higher burden of AMR genes among *S. aureus* isolated from clinical mastitis. Qu et al. (2019) reported that 95% of isolates carried the β -lactamase gene *blaZ*, while 16% harboured *mecA*. Tetracycline resistance genes (*tetM*, *tetK*) and macrolide resistance determinants (*ermT*) were also prevalent. Notably, non-*aureus* staphylococci (NAS) displayed even higher resistance gene frequencies, acting as potential reservoirs for multidrug resistance. The molecular epidemiology revealed the dissemination of specific random amplification of polymorphic DNA (RAPD) types within herds, suggesting clonal spread and udder adaptation of successful genotypes (Qu et al., 2019).

In New Zealand's pasture-based dairy system, Greening et al. (2021) found a distinct population structure dominated by ST-1 (61.4%), a lineage often associated with human infections but now prevalent in bovine mastitis. AMR gene prevalence was low, with *blaZ* detected in only 33% of isolates and a single ST-5 isolate carrying *mecA*. Phenotypic resistance to penicillin was observed in 36% of isolates, but no clear association was found between dry cow therapy regimens and AMR gene carriage. Interestingly, virulence gene profiles varied considerably, with staphylococcal enterotoxin genes present in 70.2% of isolates, yet human-associated virulence factors such as Panton–Valentine leukocidin (PVL) were largely absent (Greening et al., 2021).

Together, these studies underscore the geographic and management-driven variability in the molecular ecology of dairy-associated *S. aureus*. While US and New Zealand populations show lower AMR gene prevalence—possibly reflecting more conservative antimicrobial use—Chinese herds face significant multidrug resistance challenges. The persistence of specific clonal complexes (e.g., CC97, ST-1) across regions highlights the successful adaptation of certain lineages to the bovine mammary niche. Furthermore, the widespread carriage of enterotoxin and other virulence genes across all regions emphasises the ongoing zoonotic and food safety risks, independent of AMR status. Continued genomic surveillance is essential to track the evolution of these populations, understand drivers of resistance, and inform targeted mastitis control and antimicrobial stewardship strategies in dairy production worldwide.

Mechanisms of AMR in Dairy-Associated *Staphylococcus aureus*

Staphylococcus aureus is a significant foodborne pathogen commonly isolated from raw milk and dairy products, posing a substantial public health risk due to its ability to acquire and disseminate antimicrobial resistance (AMR) (Jamali et al., 2015). The mechanisms underlying AMR in dairy-associated *S. aureus* are multifaceted,

involving both intrinsic and acquired genetic determinants that enable survival against commonly used antibiotics in veterinary and human medicine.

One of the primary mechanisms of resistance in dairy *S. aureus* is the production of β -lactamases, enzymes that hydrolyze β -lactam antibiotics such as penicillin. This resistance is frequently encoded by the *blaZ* gene, often found on mobile genetic elements like plasmids and transposons (Mlynarczyk-Bonikowska et al., 2022). In a study of raw milk and traditional dairy products in Iran, the *blaZ* gene was detected in 46% of *S. aureus* isolates, correlating with high phenotypic resistance to penicillin G (47.3%) (Jamali et al., 2015). More critically, methicillin resistance, mediated by the *mecA* gene (or its homolog *mecC*), leads to the production of an altered penicillin-binding protein (PBP2a) with low affinity for nearly all β -lactams (Mlynarczyk-Bonikowska et al., 2022). These genes are housed within staphylococcal cassette chromosome *mec* (SCC*mec*) elements, which can be transferred between strains. In dairy samples, methicillin-resistant *S. aureus* (MRSA) prevalence has been reported, with 16.2% of isolates in one study showing oxacillin resistance, all confirmed to carry the *mecA* gene (Jamali et al., 2015).

Resistance to tetracyclines, frequently used in animal husbandry, is also prevalent in dairy *S. aureus*. The primary mechanisms include active efflux of the drug, mediated by genes such as *tet(K)* and *tet(L)*, and ribosomal protection, mediated by *tet(M)* (Mlynarczyk-Bonikowska et al., 2022). Jamali et al. (2015) found that 56.1% of dairy isolates were resistant to tetracycline, with the *tetM* gene being the most common (34.8%), often found in combination with *tetK* or *tetL*. This high prevalence is likely driven by the widespread use of tetracyclines for disease treatment and growth promotion in dairy farms, selecting for resistant strains that enter the food chain via raw milk.

Resistance to aminoglycosides (e.g., gentamicin, kanamycin) in dairy *S. aureus* is commonly due to enzymatic modification of the drug. The bifunctional aminoglycoside-modifying enzyme AAC(6')-Ie/APH(2'')-Ia, encoded by the *aacA-aphD* gene, confers resistance to gentamicin and tobramycin (Mlynarczyk-Bonikowska et al., 2022). All gentamicin-resistant isolates in the study by Jamali et al. (2015) carried this gene. Similarly, resistance to macrolides (e.g., erythromycin) and lincosamides (e.g., clindamycin) is often due to rRNA methylation by Erm methylases (e.g., *ErmA*, *ErmC*) or drug efflux pumps (Mlynarczyk-Bonikowska et al., 2022). Inducible clindamycin resistance, detectable by the D-test, was observed in 44% of erythromycin-resistant, clindamycin-susceptible isolates, highlighting the importance of accurate phenotypic testing to avoid therapeutic failure (Jamali et al., 2015).

The emergence of multidrug-resistant (MDR) *S. aureus* in dairy products is a major concern. These strains accumulate multiple resistance genes on plasmids, transposons, or SCC*mec* cassettes, leading to co-resistance to several antibiotic classes (Mlynarczyk-Bonikowska et al., 2022). Jamali et al. (2015) reported that 12.8% of *S. aureus* isolates from milk and dairy products were resistant to more than two antimicrobial classes. The genetic plasticity of *S. aureus*, facilitated by mobile genetic elements, allows for the rapid horizontal transfer of resistance genes not only within the species but also between different bacterial genera present in the farm environment (Mlynarczyk-Bonikowska et al., 2022).

Transmission Dynamics at the One Health Interface of AMR

The global rise of antimicrobial resistance (AMR) is a typical One Health challenge, intricately linking human, animal, and environmental health. Dairy production systems, where humans and animals interact closely, serve as critical interfaces for the bidirectional transmission of pathogens like *Staphylococcus aureus* and their associated resistance genes, a risk elevated by the increasing intensification of farming and routine antimicrobial use (Mengistu et al., 2024; Roy et al., 2024). The transmission dynamics are complex and multifactorial, operating at the intersection of all three One Health spheres. The primary cycle involves infected cattle, often with mastitis, shedding *S. aureus* into milk and contaminating the farm environment, including equipment and housing. Workers then become colonized through direct contact during milking and can subsequently transfer bacteria back to animals or further contaminate equipment, perpetuating a continuous infection cycle. This is evidenced by a meta-analysis in Ethiopian dairy systems which found a pooled *S. aureus* prevalence of 22% across workers, animals, and equipment, with nearly equal contamination levels among these categories (Mengistu et al., 2024).

This transmission is fundamentally bidirectional. Zoonotic spillover from cattle to humans is well-documented, primarily through direct contact and contaminated dairy products. Molecular studies provide strong evidence, such as the identification of genetically indistinguishable *S. aureus* strains belonging to the common bovine lineage CC97 in both bovine mastitis milk and the nasal swabs of farm personnel in South Africa (Schmidt et al., 2017). Conversely, transmission is not unidirectional, as human-adapted clones can also spill over into cattle populations. The same South African study identified a strain of sequence type ST8—a lineage frequently associated with humans—that was genetically identical in a mastitic cow and a human nasal swab from the same farm, indicating that human-origin clones can transfer, adapt, and cause disease in livestock (Schmidt et al., 2017). A critical driver of these dynamics is the antimicrobial selection pressure in veterinary medicine, which promotes resistance. For instance, in Ethiopian smallholder systems, *S. aureus* isolates exhibited 100% resistance to beta-lactam antibiotics like ampicillin and penicillin, reflecting their common use for mastitis treatment (Marami et al., 2022). The genomic plasticity of *S. aureus*, facilitated by mobile genetic elements like plasmids and SCCmec, enables the horizontal transfer of these resistance genes not only among staphylococci but also across different bacterial species within the farm ecosystem, amplifying the overall resistance pool (Elbehiry & Marzouk, 2025).

The environment itself acts as a major reservoir and transmission bridge, a role often underestimated. *S. aureus* and associated resistance genes can be disseminated through farm wastewater, manure, and bioaerosols, contaminating soil and water systems where genetic exchange can occur (Ibekwe et al., 2023). The significance of this environmental compartment is highlighted by research from Bangladesh, which reported the highest MRSA prevalence in environmental samples (19.3%), with phylogenetic analysis revealing high genetic similarity among isolates from cows, humans, and the farm environment, suggesting clonal transmission across this interface (Roy et al., 2024). Furthermore, raw milk and unpasteurized dairy products contaminated with *S. aureus*, including enterotoxigenic and multidrug-resistant strains, represent a direct foodborne transmission route to consumers, posing risks of both acute intoxication and long-term resistance gene dissemination (Silva et al., 2023).

Regional studies illustrate how local context shapes these transmission dynamics. In a high-prevalence setting like Bangladesh, MRSA shows strong genetic links across cows, humans, and the environment, pointing to active zoonotic spillover mediated by environmental contamination (Roy et al., 2024). In contrast, research from New Zealand, where antimicrobial use is more regulated and MRSA is uncommon, found that *S. aureus* transmission remained mostly within species, largely confined to animals within the same management unit. However, even in this low-prevalence setting, the detection of an extended-spectrum beta-lactamase gene (*bla*TEM-116) in a bovine isolate indicates an underlying risk of emerging resistance (Straub et al., 2024). In conclusion, curbing the spread of AMR *S. aureus* in dairy systems requires integrated One Health strategies that acknowledge its interconnected transmission web. Effective interventions must include improving on-farm hygiene and biosecurity to break direct contact cycles, enforcing prudent antimicrobial use to reduce selection pressure, ensuring the pasteurization of dairy products to sever the foodborne route, and implementing coordinated molecular surveillance across human, animal, and environmental compartments to track transmission pathways and inform targeted measures.

Public health Implications of AMR of *S. aureus* in Dairy

The emergence and spread of antimicrobial-resistant (AMR) *Staphylococcus aureus*, particularly methicillin-resistant *S. aureus* (MRSA) and multidrug-resistant (MDR) strains, within the dairy production chain pose a significant and escalating threat to global public health (Badawy et al., 2022; Algammal et al., 2020). This threat operates through two primary, interconnected routes: foodborne transmission and zoonotic occupational exposure.

The consumption of contaminated raw milk or inadequately processed dairy products serves as a direct conduit for resistant and virulent strains into the human food supply (Normanno et al., 2007; Paramasivam et al., 2023). Studies from diverse regions, including Egypt, South Africa, India, and Ethiopia, consistently document a high prevalence of enterotoxigenic and MRSA strains in these products (Badawy et al., 2022; Akindolire et al., 2015; Bharathy et al., 2015; Geletu et al., 2022). For instance, research in Egypt found 80% of *S. aureus* isolates from cheese were enterotoxigenic, with 60% carrying the *mecA* gene (Badawy et al., 2022), while studies in Ethiopia

reported MDR rates as high as 98.4% in farm isolates (Geletu et al., 2022). This is particularly concerning given *S. aureus*'s ability to cause staphylococcal food poisoning via heat-stable enterotoxins (Hennekinne et al., 2012).

Simultaneously, the dairy farm environment acts as an ecological amplifier for AMR. Dairy cattle, especially those with mastitis, are reservoirs, and resistant bacteria can spread to farmers, milkers, and veterinarians through direct contact with animals or contaminated environments (Algammal et al., 2020; Phiri et al., 2022). Molecular evidence from Zambia confirms strain transmission between milkers and milk, with some isolates carrying virulence genes like PVL associated with severe human infections (Phiri et al., 2022).

The driver of this crisis is the widespread misuse and overuse of antimicrobials in dairy farming for therapy, prophylaxis (e.g., blanket dry cow therapy), and growth promotion, which exerts powerful selective pressure (Silbergeld et al., 2008; Paramasivam et al., 2023). Common practices like self-administration by farmers and disregard for withdrawal periods, as noted in Ethiopia, exacerbate the problem (Geletu et al., 2022). This selects for MDR strains with resistance to critical drugs like beta-lactams, macrolides, fluoroquinolones, and even last-resort options like vancomycin (Algammal et al., 2020; Paramasivam et al., 2023).

The public health consequences are severe. Infections caused by livestock-associated MRSA and MDR *S. aureus* are more challenging to treat, leading to higher treatment costs, longer hospital stays, increased morbidity, and greater mortality (Cosgrove, 2006). This creates a substantial economic burden and represents a quintessential "One Health" crisis where agricultural practices directly impact human medicine (Haag et al., 2019).

Mitigating this threat requires a coordinated, multifaceted approach. Key interventions include: implementing strict hygiene and biosecurity protocols throughout the production chain; promoting antimicrobial stewardship and judicious use in veterinary practice; enforcing regulations on antibiotic use and milk quality; enhancing surveillance of AMR in animals, food, and humans; and educating consumers on the risks of raw milk and the importance of pasteurization (Badawy et al., 2022; Algammal et al., 2020; Geletu et al., 2022). Addressing AMR in dairy-derived *S. aureus* is therefore a critical imperative for safeguarding public health.

Integrated Strategies for the Mitigation and Control of Staphylococcus aureus Antimicrobial Resistance in Dairy Production

The emergence and dissemination of antimicrobial-resistant (AMR) *Staphylococcus aureus*, particularly methicillin-resistant strains (MRSA), in dairy cattle represents a significant One Health challenge, jeopardizing animal welfare, farm productivity, and public health (Gogoi-Tiwari et al., 2020; Rollin et al., 2015). Effective mitigation requires a multifaceted, integrated strategy that prioritizes prevention, reduces antimicrobial use (AMU), and employs targeted control measures. A foundational pillar is the rigorous implementation of biosecure herd management and milking hygiene, as the primary route of transmission is from cow to cow during milking (Petersson-Wolfe et al., 2010). Practices such as milkers wearing gloves, systematic pre- and post-milking teat disinfection, and maintaining optimal teat-end condition are strongly associated with reduced incidence, acquisition, and herd prevalence of *S. aureus* intramammary infections (IMIs) (Dufour et al., 2012). Crucially, the identification and culling of chronically infected animals, which act as persistent reservoirs, is also recommended to break the transmission cycle (Vanderhaeghen et al., 2015).

Concurrent with improved management is the imperative of antimicrobial stewardship (AMS), mandating the prudent and judicious use of antibiotics. This involves a shift from empirical therapy to a culture and susceptibility-guided treatment approach, given the highly variable antibiotic susceptibility patterns of *S. aureus* (Aqib et al., 2018). The use of narrow-spectrum beta-lactamase-stable penicillins is favoured over critically important antimicrobials (CIAs) for susceptible infections (WOAH, 2023). Furthermore, the strategic use of dry cow therapy (DCT) should transition from blanket administration to a selective approach based on individual cow somatic cell count history and culture results, thereby minimizing unnecessary antibiotic exposure during the dry period (Ruegg, 2017; Dufour et al., 2012).

Given the challenges of antibiotic resistance, significant research has focused on developing alternative and adjunctive therapies. Plant-derived phenolic compounds, such as extracts from *Eucalyptus globulus*, show

promising antibacterial activity against mastitis-derived *S. aureus* strains (Gomes et al., 2018). Similarly, innovations like bacteriophages, nanoparticles, and lysostaphin offer pathogen-specific lytic activity and biofilm disruption, presenting targeted non-antibiotic tools (Aqib et al., 2018; Cardoso et al., 2019; Fan et al., 2016). The use of probiotics (e.g., *Lactocaseibacillus casei*) to competitively exclude pathogens and modulate the local immune response also represents a valuable preventive strategy (Aqib et al., 2018; Rainard & Foucras, 2018).

Vaccination remains a critical proactive strategy for primary prevention, though developing an effective vaccine has proven challenging due to the pathogen's complex virulence factors. Research continues to focus on targets such as surface proteins, toxins, and biofilm components, with some commercial and autogenous vaccines showing promise in reducing the rate of new IMIs and clinical severity (Aqib et al., 2018; Pereira et al., 2011; Côté-Gravel & Malouin, 2019). Finally, comprehensive herd management which includes regular monitoring, economic assessments that factor in the hidden costs of mastitis, and education for all stakeholders is vital for the sustainable adoption of these integrated measures and the long-term control of AMR in dairy-associated *S. aureus* (Hagnestam-Nielsen & Østergaard, 2009; Seegers et al., 2003).

CONCLUSION

The global challenge of antimicrobial resistance (AMR) in dairy-related *Staphylococcus aureus* is marked by the widespread distribution of resistant strains, with regional variations shaped by local practices. The evidence presented demonstrates a clear and present danger: the convergence of multidrug resistance (MDR), methicillin resistance (MRSA), and a suite of potent virulence genes in dairy-derived strains creates a significant One Health threat. This threat is amplified by the bidirectional transmission of pathogens and resistance genes between animals and humans, facilitated by occupational contact, environmental contamination, and the consumption of unpasteurized dairy products. The routine use of antibiotics in livestock exerts a powerful selective pressure, driving the evolution and persistence of resistant clones, while the genetic plasticity of *S. aureus* ensures the rapid dissemination of resistance determinants. Addressing this escalating crisis requires an integrated, One Health approach that acknowledges the inseparable links between animal health, human health, and environmental integrity. Coordinated actions across veterinary, agricultural, and public health sectors are essential. Key interventions must include the promotion of stringent antimicrobial stewardship and judicious use in veterinary practice, the rigorous implementation of biosecure herd management and milking hygiene to break transmission cycles, and the enforcement of food safety regulations, particularly regarding pasteurization. Furthermore, enhancing and harmonizing surveillance systems to track resistance trends and strain movement, alongside supporting molecular research to understand resistance gene flow, is critical for informed policy-making. The development and adoption of alternative therapies, such as vaccines, bacteriophages, and phytochemicals, offer promising avenues to reduce reliance on conventional antibiotics. Without such sustained and coordinated efforts, the continued spread of multidrug-resistant *S. aureus* will persistently jeopardize animal welfare, dairy industry sustainability, and public health security worldwide.

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This review was created with the assistance of generative AI tools (Deepseek ai). The AI was used for tasks such as editing and data synthesis. The author reviewed, edited, and validated all output, and assumes full responsibility for the accuracy, integrity, and implications of the final content

REFERENCES

1. Akindolire, M. A., Babalola, O. O., & Ateba, C. N. (2015). Detection of antibiotic resistant *Staphylococcus aureus* from milk: A public health implication. *International Journal of Environmental Research and Public Health*, 12(9), 10254–10275.
2. Algammal, A. M., Hetta, H. F., Elkelish, A., Alkhalifah, D. H. H., Hozzein, W. N., Batiha, G. E.-S., El Nahhas, N., & Mabrok, M. A. (2020). Methicillin-resistant *Staphylococcus aureus* (MRSA): One Health perspective approach to the bacterium epidemiology, virulence factors, antibiotic-resistance, and zoonotic impact. *Infection and Drug Resistance*, 13, 3255–3265.

3. Aqib, A. I., Ijaz, M., Farooqi, S. H., & Raza, A. (2018). Dairy Staphylococcus aureus: Epidemiology, drug susceptibilities, drug modulation, and preventive measures. In *Staphylococcus aureus*. IntechOpen. <http://dx.doi.org/10.5772/intechopen.74552>
4. Aqib, A. I., Ijaz, M., Farooqi, S. H., Ahmed, R., Shoaib, M., Ali, M. M., & Naseer, M. A. (2018). Emerging discrepancies in conventional and molecular epidemiology of methicillin resistant Staphylococcus aureus isolated from bovine milk. *Microbial Pathogenesis*, 116, 38–43.
5. Aqib, A. I., Saqib, M., Khan, S. R., Ahmad, T., Shah, S. A., Naseer, M. A., ... & Shoaib, M. (2021). Non-steroidal anti-inflammatory drugs, plant extracts, and characterized microparticles to modulate antimicrobial resistance of epidemic mecA positive S. aureus of dairy origin. *Applied Nanoscience*. Advance online publication.
6. Badawy, B., Elaffy, M., Farag, A. M. M., Moustafa, S. M., Sayed-Ahmed, M. Z., Moawad, A. A., Algammal, A. M., Ramadan, H., & Eltholth, M. (2022). Ecological distribution of virulent multidrug-resistant Staphylococcus aureus in livestock, environment, and dairy products. *Antibiotics*, 11(11), 1651.
7. Batool, S., Masood, Z., Ullah, A., Khan, W., Said, M. B., Belkahia, H., Ismael, A. B., & Swelum, A. A. (2025). Isolation of antibiotic-resistant strains of Staphylococcus aureus from raw milk produced by dairy cows with subclinical bovine mastitis. *Journal of Advanced Veterinary and Animal Research*, 12(1), 252–259.
8. Bharathy, S., Gunaseelan, L., Porteen, K., & Bojiraj, M. (2015). Prevalence of Staphylococcus aureus in raw milk: Can it be a potential public health threat? *International Journal of Advanced Research*, 3(2), 801–806.
9. Bonnedahl, J., & Järhult, J. D. (2014). Antibiotic resistance in wild birds. *Upsala Journal of Medical Sciences*, 119(2), 113–116. <https://doi.org/10.3109/03009734.2014.905663>
10. Cardoso, C. V., Barbosa, E. V., Liberal, M. I. T., & das Chagas, E. F. (2019). Transgenic technology: the strategy for the control and prevention of bovine staphylococcal mastitis? *Biotechnology Research and Innovation*, 3(2), 291–297.
11. Cosgrove, S. E. (2006). The relationship between antimicrobial resistance and patient outcomes: Mortality, length of hospital stay, and health care costs. *Clinical Infectious Diseases*, 42(Suppl 2), S82–S89.
12. Côté-Gravel, J., & Malouin, F. (2019). Symposium review: Features of Staphylococcus aureus mastitis pathogenesis that guide vaccine development strategies. *Journal of Dairy Science*, 102(5), 4727–4740.
13. Dufour, S., Dohoo, I. R., Barkema, H. W., DesCôteaux, L., DeVries, T. J., Reyher, K. K., Roy, J.-P., & Scholl, D. T. (2012). Manageable risk factors associated with the lactational incidence, elimination, and prevalence of Staphylococcus aureus intramammary infections in dairy cows. *Journal of Dairy Science*, 95(3), 1283–1300. <https://doi.org/10.3168/jds.2011-4711>
14. Elbehiry, A., & Marzouk, E. (2025). Staphylococci in livestock: Molecular epidemiology, antimicrobial resistance, and translational strategies for One Health protection. *Veterinary Sciences*, 12(8), 757. <https://doi.org/10.3390/vetsci12080757>
15. Fan, J., Zeng, Z., Mai, K., Yang, Y., Feng, J., Bai, Y., & Ma, X. (2016). Preliminary treatment of bovine mastitis caused by Staphylococcus aureus, with trx-SA1, recombinant endolysin of S. aureus bacteriophage IME-SA1. *Veterinary Microbiology*, 191, 65–71.
16. Fang, H., Han, L., Zhang, H., Long, Z., Cai, L., & Yu, Y. (2018). Dissemination of antibiotic resistance genes and human pathogenic bacteria from a pig feedlot to the surrounding stream and agricultural soils. *Journal of Hazardous Materials*, 357, 53–62. <https://doi.org/10.1016/j.jhazmat.2018.05.066>
17. Gadde, U., Kim, W. H., Oh, S. T., & Lillehoj, H. S. (2017). Alternatives to antibiotics for maximizing growth performance and feed efficiency in poultry: A review. *Animal Health Research Reviews*, 18(1), 26–45.
18. Ge, B., Zhao, P., Li, H., Sang, R., Wang, M., Zhou, H., & Zhang, X. (2020). Taraxacum mongolicum protects against Staphylococcus aureus-infected mastitis by exerting anti-inflammatory role via TLR2-NF-κB/MAPKs pathways in mice. *Journal of Ethnopharmacology*, 263, 113595.
19. Geletu, U. S., Usmael, M. A., & Ibrahim, A. M. (2022). Isolation, identification, and susceptibility profile of E. coli, Salmonella, and S. aureus in dairy farm and their public health implication in central Ethiopia. *Veterinary Medicine International*, 2022, Article 1887977.

20. Gogoi-Tiwari, J., Williams, V., & Tiwari, H. K. (2020). Methicillin-resistant *Staphylococcus aureus* (MRSA) in dairy animals and the need for a One Health approach. *Journal of Applied Microbiology*, 129(5), 1101-1114. <https://doi.org/10.1111/jam.14715>
21. Gomes, F., Martins, N., Barros, L., Rodrigues, M. E., Oliveira, M. B. P. P., Henriques, M., & Ferreira, I. C. F. R. (2018). Plant phenolic extracts as an effective strategy to control *Staphylococcus aureus*, the dairy industry pathogen. *Industrial Crops and Products*, 112, 515–520. <https://doi.org/10.1016/j.indcrop.2017.12.027>
22. Greening, S. S., Zhang, J., Midwinter, A. C., Wilkinson, D. A., McDougall, S., Gates, M. C., & French, N. P. (2021). The genetic relatedness and antimicrobial resistance patterns of mastitis-causing *Staphylococcus aureus* strains isolated from New Zealand dairy cattle. *Veterinary Sciences*, 8(11), 287
23. Gutama, K. P., & Anberber, M. (2025). Epidemiological investigation and antimicrobial sensitivity of *Staphylococcus aureus* in dairy farms of selected towns in Western Oromia, Ethiopia. *BMC Veterinary Research*, 21(420), 1–12.
24. Haag, A. F., Fitzgerald, J. R., & Penadés, J. R. (2019). *Staphylococcus aureus* in animals. *Microbiology Spectrum*, 7(3).
25. Hagnestam-Nielsen, C., & Østergaard, S. (2009). Economic impact of clinical mastitis in a dairy herd assessed by stochastic simulation using different methods to model yield losses. *Animal*, 3(2), 315–328.
26. Hennekinne, J. A., De Buyser, M. L., & Dragacci, S. (2012). *Staphylococcus aureus* and its food poisoning toxins: Characterization and outbreak investigation. *FEMS Microbiology Reviews*, 36(4), 815–836.
27. Ibekwe, A. M., Bhattacharjee, A. S., Phan, D., Ashworth, D., Schmidt, M. P., Murinda, S. E., Obayiuwana, A., Murry, M. A., Schwartz, G., & Lundquist, T. (2023). Potential reservoirs of antimicrobial resistance in livestock waste and treated wastewater that can be disseminated to agricultural land. *Science of The Total Environment*, *872*, 162194. <https://doi.org/10.1016/j.scitotenv.2023.162194>
28. Islam, M. M., Hossain, M. I., Islam, M. S., Azam, M. G., & Sultana, S. (2025). Prevalence, antibiotic resistance patterns, and virulence factors of *Staphylococcus aureus* isolates associated with bovine mastitis in northern Bangladesh. *Heliyon*, 11(3), e42107.
29. Jamali, H., Paydar, M., Radmehr, B., Ismail, S., & Dadrasnia, A. (2015). Prevalence and antimicrobial resistance of *Staphylococcus aureus* isolated from raw milk and dairy products. *Food Control*, 54, 383–388.
30. Landin, H., Jansson Mörk, M., Larsson, M., & Waller, K. P. (2015). Vaccination against *Staphylococcus aureus* mastitis in two Swedish dairy herds. *Acta Veterinaria Scandinavica*, 57(1), 81.
31. Leitner, G., Krifucks, O., Kiran, M. D., & Balaban, N. (2011). Vaccine development for the prevention of staphylococcal mastitis in dairy cows. *Veterinary Immunology and Immunopathology*, 142(1–2), 25–35.
32. Marami, L. M., Berhanu, G., Tekle, M., Agga, G. E., Beyene, T. J., Tufa, T. B., Beyi, A. F., & Edao, B. M. (2022). Antimicrobial resistance of staphylococci at animal human interface in smallholders and dairy farms in Central Oromia, Ethiopia. *Infection and Drug Resistance*, 15, 3767–3777.
33. Mengistu, B. A., Getnet, K., Mebratu, A. S., & Fenta, M. D. (2024). Occurrence, multidrug resistance and potential risk factors for *Staphylococcus aureus* infection at worker-animal and working equipment interfaces: A systematic review and meta-analysis of the Ethiopian literature. *Frontiers in Public Health*, 12, 1403012.
34. Mlynarczyk-Bonikowska, B., Kowalewski, C., Krolak-Ulinska, A., & Marusza, W. (2022). Molecular mechanisms of drug resistance in *Staphylococcus aureus*. *International Journal of Molecular Sciences*, 23(15), 8088.
35. Nhatsave, N., Garrine, M., Messa, A. J., Massinga, A. J., Cossa, A., Vaz, R., Ombí, A., Zimba, T. F., Alfredo, H., Mandomando, I., & Tchamo, C. (2021). Molecular characterization of *Staphylococcus aureus* isolated from raw milk samples of dairy cows in Manhica District, Southern Mozambique. *Microorganisms*, 9(8), 1684.
36. Normanno, G., La Salandra, G., Dambrosio, A., Quaglia, N. C., Corrente, M., Parisi, A., Santagada, G., Firinu, A., Crisetti, E., & Celano, G. V. (2007). Occurrence, characterization and antimicrobial resistance

- of enterotoxigenic *Staphylococcus aureus* isolated from meat and dairy products. *International Journal of Food Microbiology*, 115(3), 290–296.
37. Oliveira, R., Pinho, E., Almeida, G., Azevedo, N. F., & Almeida, C. (2022). Prevalence and diversity of *Staphylococcus aureus* and staphylococcal enterotoxins in raw milk from Northern Portugal. *Frontiers in Microbiology*, 13, 846653.
38. Paramasivam, R., Gopal, D. R., Dhandapani, R., Subbarayalu, R., Elangovan, M. P., Prabhu, B., Veerappan, V., Nandheeswaran, A., Paramasivam, S., & Muthupandian, S. (2023). Is AMR in dairy products a threat to human health? An updated review on the origin, prevention, treatment, and economic impacts of subclinical mastitis. *Infection and Drug Resistance*, 16, 155–178.
39. Patel, K., Godden, S. M., Royster, E. E., Crooker, B. A., Johnson, T. J., Smith, E. A., & Sreevatsan, S. (2021). Prevalence, antibiotic resistance, virulence and genetic diversity of *Staphylococcus aureus* isolated from bulk tank milk samples of U.S. dairy herds. *BMC Genomics*, 22, 367
40. Pekana, A., & Green, E. (2018). Antimicrobial resistance profiles of *Staphylococcus aureus* isolated from meat carcasses and bovine milk in abattoirs and dairy farms of the Eastern Cape, South Africa. *International Journal of Environmental Research and Public Health*, 15(10), 2223.
41. Peralta, O. A., Carrasco, C., Vieytes, C., Tamayo, M. J., Muñoz, I., Sepúlveda, S., ... & Tadich, T. A. (2020). Safety and efficacy of a mesenchymal stem cell intramammary therapy in dairy cows with experimentally induced *Staphylococcus aureus* clinical mastitis. *Scientific Reports*, 10(1), 2843.
42. Pereira, U. P., Oliveira, D. G. S., Mesquita, L. R., Costa, G. M., & Pereira, L. J. (2011). Efficacy of *Staphylococcus aureus* vaccines for bovine mastitis: A systematic review. *Veterinary Microbiology*, 148(2–4), 117–124.
43. Petersson-Wolfe, C. S., Mullarky, I. K., & Jones, G. M. (2010). *Staphylococcus aureus* mastitis: Cause, detection, and control. Virginia Cooperative Extension.
44. Phiri, B. S. J., Hang'ombe, B. M., Mulenga, E., Mubanga, M., Maurischat, S., Wichmann-Schauer, H., Schaarschmidt, S., & Fetsch, A. (2022). Prevalence and diversity of *Staphylococcus aureus* in the Zambian dairy value chain: A public health concern. *International Journal of Food Microbiology*, 375, 109737.
45. Piepers, S., De Visscher, A., & Haesebrouck, F. (2022). Vaccination as a tool to combat *Staphylococcus aureus* mastitis in dairy cows: A systematic review and meta-analysis. *Journal of Dairy Science*, *105*(7), 6225–6245. <https://doi.org/10.3168/jds.2021-21567>
46. Price, L. B., Stegger, M., Hasman, H., Aziz, M., Larsen, J., Andersen, P. S., Pearson, T., Waters, A. E., Foster, J. T., & Schupp, J. (2012). *Staphylococcus aureus* CC398: Host adaptation and emergence of methicillin resistance in livestock. *mBio*, 3(1), e00305-11.
47. Qu, Y., Zhao, H., Nobrega, D. B., Cobo, E. R., Han, B., Zhao, Z., Li, S., Li, M., Barkema, H. W., & Gao, J. (2019). Molecular epidemiology and distribution of antimicrobial resistance genes of *Staphylococcus* species isolated from Chinese dairy cows with clinical mastitis. *Journal of Dairy Science*, 102(2), 1571–1583.
48. Rainard, P., & Foucras, G. (2018). A critical appraisal of probiotics for mastitis control. *Frontiers in Veterinary Science*, 5, 251.
49. Reed, S. G., Bertholet, S., Coler, R. N., & Friede, M. (2009). New horizons in adjuvants for vaccine development. *Trends in Immunology*, 30(1), 23–32.
50. Rollin, E., Dhuyvetter, K. C., & Overton, M. W. (2015). The cost of clinical mastitis in the first 30 days of lactation: An economic modeling tool. *Preventive Veterinary Medicine*, 122(3), 257–264.
51. Roy, M. C., Chowdhury, T., Hossain, M. T., Hasan, M. M., Zahran, E., Rahman, M. M., Zinnah, K. M. A., Rahman, M. M., & Hossain, F. M. A. (2024). Zoonotic linkage and environmental contamination of Methicillin-resistant *Staphylococcus aureus* (MRSA) in dairy farms: A one health perspective. *One Health*, 18, 100680. <https://doi.org/10.1016/j.onehit.2024.100680>
52. Ruegg, P. L. (2017). A 100-year review: Mastitis detection, management, and prevention. *Journal of Dairy Science*, 100(12), 10381–10397. <https://doi.org/10.3168/jds.2017-13023>
53. Russo, N., Fazio, N. A., Licitra, F., Gajewska, J., Stamilla, A., Salonia, R., Chajęcka-Wierchowska, W., Randazzo, C. L., Caggia, C., Antoci, F., & Cascone, G. (2025). Clonality, virulence genes, and antimicrobial resistance of dairy ruminants in mastitic milk-associated *Staphylococcus aureus* in Sicily. *Antibiotics*, 14(2), 188.

54. Schmidt, T., Kock, M. M., & Ehlers, M. M. (2017). Molecular characterization of *Staphylococcus aureus* isolated from bovine mastitis and close human contacts in South African dairy herds: Genetic diversity and inter-species host transmission. *Frontiers in Microbiology*, 8, 511.
55. Seegers, H., Fourichon, C., & Beaudeau, F. (2003). Production effects related to mastitis and mastitis economics in dairy cattle herds. *Veterinary Research*, 34(5), 475–491.
56. Silbergeld, E. K., Graham, J., & Price, L. B. (2008). Industrial food animal production, antimicrobial resistance, and human health. *Annual Review of Public Health*, 29, 151–169.
57. Silva, V., Araújo, S., Monteiro, A., Eira, J., Pereira, J. E., Maltez, L., Igrejas, G., Lemsaddek, T. S., & Poeta, P. (2023). *Staphylococcus aureus* and MRSA in livestock: Antimicrobial resistance and genetic lineages. *Microorganisms*, 11(1), 124.
58. Straub, C., Taylor, W., French, N. P., Murdoch, D. R., Priest, P., Anderson, T., & Scott, P. (2024). Zoonotic transmission of asymptomatic carriage *Staphylococcus aureus* on dairy farms in Canterbury, New Zealand. *Microbial Genomics*, 10(12), 001318. <https://doi.org/10.1099/mgen.0.001318>
59. Titze, I., Lehnher, T., Lehnher, H., & Krömker, V. (2020). Efficacy of bacteriophages against *Staphylococcus aureus* isolates from bovine mastitis. *Pharmaceuticals*, 13(3), 35.
60. Vanderhaeghen, W., Piepers, S., Leroy, F., Van Coillie, E., Haesebrouck, F., & De Vliegher, S. (2015). Invited review: Effect, persistence, and virulence of coagulase-negative *Staphylococcus* species associated with ruminant udder health. *Journal of Dairy Science*, 98(8), 5279–5294. <https://doi.org/10.3168/jds.2014-9205>
61. Veloo, Y., Abu Thahir, S. S., Zakaria, Z., Abdul Rahman, S., Mansor, R., & Rajendiran, S. (2025). A scoping review unveiling antimicrobial resistance patterns in the environment of dairy farms across Asia. *Antibiotics*, 14(5), 436.
62. World Organisation for Animal Health. (2023). Terrestrial Animal Health Code: Section 6.10. on responsible and prudent use of antimicrobial agents in veterinary medicine. <https://www.woah.org/en/what-we-do/standards/codes-and-manuals/terrestrial-code-online-access/>
63. Zaatout, N., Ayachi, A., & Kecha, M. (2020). *Staphylococcus aureus* persistence properties associated with bovine mastitis and alternative therapeutic modalities. *Journal of Applied Microbiology*, 129(5), 1102–1119.