DOI: 10.21088/jafst.2321.1628.14126.6

Journal of Animal Feed Science and Technology
Volume 14 Number 1 January - June 2026

Review Article

Methicillin-Resistant Staphylococcus Aureus, a Zoonotic Pathogen, in the Dairy - Industry: A Comprehensive Review from Indian Perspective

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How to cite this article:

Anita Tewari, Meena Goswami, Vikas Pathak et. al, Methicillin-Resistant Staphylococcus aureus, a zoonotic pathogen, in the Dairy- industry: A Comprehensive Review from Indian Perspective. Jrl of Ani Feed Sci and Tech 2026; 14(1): 42-51.

ABSTRACT

The dairy industry plays a pivotal role in global food security and rural livelihoods, particularly in countries like India, where smallholder farming dominates milk production. However, the industry faces a significant threat from *Staphylococcus aureus*, a versatile pathogen implicated in both animal disease and public health concerns. While traditionally associated with bovine mastitis, an inflammatory condition of the mammary gland, *S. aureus* has emerged as a zoonotic pathogen, capable of crossing species barriers and contributing to antimicrobial resistance (AMR) globally. Over recent decades, a noticeable rise in methicillin-resistant *Staphylococcus aureus* (MRSA) infections has been observed within healthcare settings and the dairy sector. It is a leading cause of both clinical and subclinical bovine mastitis which significantly impacts milk production and quality. Beyond the economic burden, MRSA has zoonotic potential, with risks of transmission to humans through direct contact or consumption of contaminated milk. The transition

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➤ **Received:** 19-05-2026 ➤ **Accepted:** 23-06-2026

of this organism from hospitals to community environments and subsequently to livestock has exacerbated the situation. Now, with the rise of VRSA and a scarcity of treatment options, it poses a potential threat as one of the pandemics of the 21st century and underscores its relevance as a One Health challenge, demanding integrated surveillance and control strategies. This paper aims to give an overview of the assessment of zoonotic and antimicrobial-resistant S. aureus, particularly emphasizing the dairy industry in India and globally, to enhance awareness of the disease as a critical public health issue.

KEYWORDS:

• Methicillin-Resistant *Staphylococcus Aureus* • Antimicrobial Resistance • Livestock Associated-MRSA • Zoonoses • Dairy • Bovine Mastitis • India

INTRODUCTION

Bovine mastitis is one of the most widespread and economically important diseases in dairy cattle, posing significant risks to animal health, milk production, and public health due to the growing threat of antimicrobial resistance (AMR) (Bardley, 2002). The condition arises when pathogenic microorganisms, primarily bacteria, invade and multiply within the mammary gland, triggering inflammation. To manage these infections, antimicrobials, particularly antibiotics, are routinely administered. However, over time, bacteria have evolved survival mechanisms that render these treatments ineffective, leading to the development of antibiotic-resistant strains (Salam *et al.,* 2023). This phenomenon, known as AMR, occurs not only in the treated animals but can also spread to other animals in the herd and enter the human food chain through contaminated milk and dairy products (Erskine *et al.,* 2002, Tewari *et al.,* 2025). Mastitis is difficult to treat, resulting in reduced milk yield, diminished milk quality, and increased culling rates, thus encourage widespread and sometimes indiscriminate antimicrobial use esp. among small marginal farmers. Consequently, mastitis treatment turned out to be a major source of illegal antibiotic residues in market-sold milk (Erskine *et al.,* 2003).

Among the pathogens implicated, *Staphylococcus aureus* is one of the most common and problematic, responsible for a range of subclinical and chronic infections in dairy cattle (Hegde *et al.,* 2013). S. aureus is a commensal bacterium commonly found on human skin and in the anterior nasal passages of healthy individuals (Pal *et al.,* 2023), as well as in the udders of cows (Aqib *et al.,* 2021). While usually harmless in these natural habitats, it can become a facultative pathogen, causing a wide range of infections- from mild skin conditions to severe invasive diseases in humans, and mastitis in dairy cattle (Annamanedi *et al.,* 2021). Due to its limited ability to provoke a strong immune response in bovines, especially in comparison to *E. coli* or bacterial endotoxins, S. aureus infections typically convert into chronic cases of mastitis, persisting over several months. Besides, it is difficult to treat due to its ability to form biofilms and persist intracellularly within mammary tissue (Bradley, 2002; Tewari *et al.,* 2025). Since the 1940s, S. aureus has demonstrated a remarkable ability to adapt to different antibiotics used in both human and veterinary medicine (ECDC/EFSA/EMA, 2017), making it one of the most resilient and concerning antimicrobial-resistant pathogens today. Of particular concern are methicillin-resistant strains of S. aureus (MRSA), which are resistant to beta-lactam antibiotics and many other commonly used antimicrobials (Pal et al., 2023). In dairy cattle, MRSA infections often lead to chronic or recurrent mastitis cases. The condition is typically managed using various antibiotics; however, emergence of multidrug-resistant (MDR) and MRSA variants has compounded the treatment challenge.

These resistant pathogens can persist within herds, reduce treatment effectiveness, and contaminate milk and dairy products, posing serious risks to consumer health. Unpasteurized or unhygienically handled milk can act as a vehicle for bacterial contamination and may facilitate the spread of AMR organisms, as demonstrated in a raw milk quality assessment from Rewa, Madhya Pradesh (Tewari *et al.,* 2017). The horizontal transfer of resistance genes has further facilitated the spread of

AMR within and beyond farm environments. Zoonotic transmission of MRSA between milk handlers and dairy cows has been documented globally, underscoring its One Health implications (ECDC/EFSA/EMA, 2017). While direct or indirect occupational contact with colonized animals is considered the primary route of transmission, contaminated food products may also serve as a source of human colonization or infection. In 2019, the Institute for Health Metrics and Evaluation (IHME) identified MRSA as the leading cause of AMR-related mortality worldwide, attributing approximately 121,000 deaths to MRSA-related AMR. The highest mortality rates were observed in Southeast Asia, East Asia, and Oceania. Alarmingly, newborns (0–28 days old) identified as the most vulnerable group (Buonsenso *et al.,* 2023). In response to the growing AMR crisis, several countries have enacted regulatory measures. European Union banned the use of antibiotics for growth promotion in livestock in 2006. Similarly, the U.S. Food and Drug Administration (FDA) banned the use of medically important antibiotics (used in human medicine) for growth promotion in food-producing animals (Patel *et al.,* 2020). These policies aim to mitigate the rise and spread of antimicrobial resistance in both veterinary and human medicine.

From *S. aureus* to MRSA and then VRSA: The Evolution of *S. aureus* Resistance

Initially, *S. aureus* was susceptible to penicillin, but it rapidly developed resistance through the production of β-lactamase enzymes, rendering it ineffective. In response, methicillin, a β-lactamase-resistant antibiotic, was introduced in 1959. Yet within a year, *S. aureus* acquired the mecA gene, encoding the altered penicillin-binding protein PBP2a with low affinity for β-lactams, resulting in the emergence of methicillin-resistant S. aureus (MRSA). By the 1980s and 1990s, MRSA had become a global concern, with strains spreading across hospitals (HA-MRSA), communities (CA-MRSA), and livestock farms (LA-MRSA) (Lowy, 2003). As MRSA became widespread, vancomycin was adopted as the drug of last resort. Over time, some strains developed intermediate resistance (VISA) via cell wall thickening. Eventually, vancomycin-resistant *S. aureus* (VRSA) strains emerged after acquiring the vanA gene from Enterococcus, altering the cell wall target and reducing vancomycin binding. The first VRSA case was reported in 2002 (CDC, 2002), and sporadic reports have since followed worldwide (Helen & Kaushik, 2019). This evolutionary progression, from penicillin resistance to MRSA and eventually VRSA, demonstrates S. aureus's remarkable adaptability. The bacterium's resistance mechanisms are primarily driven by selective pressure from antibiotic misuse and horizontal gene transfer, facilitated by mobile genetic elements such as plasmids, transposons, bacteriophages, and pathogenicity islands (Culyba *et al.,* 2015).

In recognition of the growing AMR crisis, the European Union enacted new regulations in 2022, requiring member states to track antibiotic sales and usage, proposing restrictions on medically important antibiotics for veterinary use, and banning the import of meat from animals raised with growth promoters (Simjee & Ippolito, 2022). However, countries like India, despite hosting the world's largest livestock population (535.78 million; 20th Livestock Census, AHS), have invested minimally in AMR research focused on animals and the One Health approach. A review found that only 3% of 2,152 AMR-related studies from Indian institutions addressed animal health, and just 1% integrated a One Health perspective (Gandra *et al.,* 2017). Many other countries similarly lack comprehensive AMR surveillance systems or enforceable regulations on antimicrobial use (Kirchhelle, 2018). While S. aureus continues to be a major cause of bovine mastitis (Patil *et al.,* 2020; Sentitula *et al.,* 2012), efforts to monitor and understand livestock-associated MRSA (LA-MRSA) and its zoonotic potential remain limited. The public health risk is further exacerbated by the co-occurrence of enterotoxigenic and other virulence factors—such as biofilm-associated genes, adhesins, and protein A-alongside MRSA in milk, livestock, and dairy farm environments (Huber *et al.,* 2010; Badawy *et al.,* 2022). Recognizing its major public health implications, the World Health Organization has listed MRSA as a high-priority pathogen for research and the development of new antimicrobial therapies (WHO, 2017). The rising rates of MRSA colonization and infection (Shrestha *et al.,* 2021), along with the emergence of VRSA, underscores the urgent need for responsible antibiotic stewardship, improved surveillance, and the development of novel treatment strategies to mitigate the global impact of antimicrobial resistance.

MRSA and Dairy Industry: Economic impact:

Bovine mastitis leads to substantial economic losses, both directly through reduced milk yield and indirectly through increased veterinary costs and culling (Aqib *et al.,* 2021). Globally, the average annual financial loss has been estimated at US $200 per cow (Costello, 2004). In Asia, the impact is similarly severe. Thai dairy farms reported average three-month losses of US $557, with over 89% of losses attributed to discarded milk (Dejyong *et al.,* 2022). In China, large commercial farms experienced monthly losses of US $15,000–$76,000 across seven provinces (He *et al.,* 2020). In India, the total annual loss due to mastitis, clinical and subclinical, is estimated at US $98,228 million (□71.655 billion) (Krishnamoorthy *et al.*, 2021), with subclinical mastitis alone contributing 58% (□41.511 billion) (Sentitula *et al.,* 2012). The disease significantly affects productivity, reducing milk yield from 9–10 kg to 6–7 kg per cow per day, and decreasing income from □413–458 to □306–335 per cow per day (Wani *et al.,* 2022).

MRSA now accounts for up to 40% of mastitis cases, leading to higher treatment costs, prolonged infections, and increased culling (Bradley, 2002; Shah *et al.,* 2025). While MRSA-specific data are more limited, its multidrug-resistant nature often leads to higher treatment costs, increased culling rates, and prolonged recovery times compared to methicillin-susceptible strains. For instance, European studies show MRSA-infected cows may experience 15–20% reductions in milk yield, resulting in significant loss of income over time.

MRSA in clinical vs subclinical mastitis:

Subclinical mastitis, often overlooked due to the absence of visible symptoms in milk, is more prevalent and economically burdensome than clinical mastitis (Hegde *et al.,* 2013). It is estimated to occur 15 to 40 times more frequently, making it significantly harder to detect and control, and contributing to greater cumulative milk production losses. In contrast, clinical mastitis—which presents with noticeable signs—represents only "the tip of the iceberg" in the overall mastitis burden (Krishnamoorthy *et al.,* 2021). A comprehensive global meta-analysis by Krishnamoorthy *et al.,* (2021), analyzing data from 1967 to 2019, reported global pooled prevalence rates of 42% for subclinical mastitis and 15% for clinical mastitis. In India, these figures were even higher, at 45% and 18%, respectively, highlighting the widespread and underestimated impact of subclinical infections on dairy economics. Similar patterns have been observed in Pakistan, where 75.31% of mastitis cases were subclinical, compared to 24.69% clinical cases (Javed *et al.,* 2022), underscoring the widespread and often underestimated impact of subclinical mastitis in South Asia's dairy sector.

A global meta-analysis reported an overall MRSA prevalence of 3.81% in dairy cattle farms (Khanal *et al.,* 2022), and another covering 77,644 mastitis samples found 4.3% MRSA prevalence, with significantly higher rates in Asia (6.47%) than in Europe (1.18%) (Zaatout and Hezil, 2022). Country-specific studies focusing on subclinical mastitis, show varying MRSA rates: 3.88% in Iran (Khazaie & Ahmadi, 2021), approximately 11–12% in Vietnam and Indonesia, 17.89% in Malaysia (Aklilu & Chia, 2020) and around 35.7% in Egypt (Elhaig *et al.,* 2015). MRSA prevalence in mastitic milk varies widely across regions, from less than 1% in countries like Nepal and Hungary to over 70% in parts of Egypt and China (Shrestha *et al.,* 2021). Deddefo *et al.,* (2022) reported an overall MRSA prevalence of 0.73% across all dairy products, with a significantly higher pooled prevalence of 15.9% in mastitic milk samples. This elevated rate is attributed to the frequent use of antibiotics in treating mastitis, which can select for resistant strains like MRSA.

In India, MRSA prevalence is particularly high (Table 1). Clinical isolates have shown resistance rates ranging from 32% to 80% across studies (Van Boeckel et al., 2015). A meta-analysis covering 2015–2020 reported a pooled MRSA prevalence of 37% among S. aureus isolates in India (Patil *et al.,* 2022). According to CDDEP (2015), MRSA prevalence among S. aureus isolates rose from 29% in 2009 to 47% in 2014, based on a major private lab network's data, indicating a rapid escalation in antimicrobial resistance within the dairy sector. Multiple studies suggest MRSA is more common in subclinical mastitis than clinical cases. For example, in Andhra Pradesh, India, 35.7% of subclinical cases were MRSA-positive, compared to 22.2% in clinical cases (Chinta Siva *et al.,* 2017a). Similarly, Shrivastava *et al.,* (2017) found MRSA in 28% of subclinical vs.

17% of clinical samples in Madhya Pradesh. Neighboring countries show similar patterns, may be because of similar climate and geography. In Bangladesh, 60.7% of subclinical mastitis cases were caused by S. aureus, with 21.8% of isolates demonstrating methicillin resistance (Islam et al., 2025). Another study by Rahman *et al.,* (2024) in Bangladesh also found that sub-clinical mastitis (27.19%) was more common than clinical mastitis (17.49%) among dairy animals. In Pakistan's Narowal District, S. aureus prevalence was 45.8% in subclinical and 37.5% in clinical cases (Shah *et al.,* 2025), while in the Pothohar region, 21% of subclinical cases were MRSA-positive compared to previously reported rates i.e. 4–6% in clinical mastitis (Shahzad et al., 2024). Similarly, in Northwest Cameroon, MRSA contamination demonstrating slight predominance in subclinical cases (20.4%) than clinical mastitis (24.2%) (Esemu *et al.,* 2024). These data collectively highlight that subclinical mastitis serves as a hidden reservoir for MRSA, complicating detection and control efforts. The ability of MRSA to persist asymptomatically, withstand antibiotic treatments, and cross species barriers makes it a formidable economic and public health threat in the global dairy sector.

MRSA in Dairy Milk Across Indian States:

The prevalence of MRSA in milk and dairy products in India varies across regions and studies, reflecting differences in farming practices, antibiotic usage, and surveillance efforts. A study in Gujarat found a 13.1% MRSA prevalence in bovine mastitis cases (Mistry *et al.,* 2016), while in Haryana, Roshan *et al.,* (2022) reported a significantly higher rate of 75% MRSA among S. aureus strains isolated from mastitic milk (Roshan *et al.,* 2022). In Uttarakhand, a 2022 investigation involving samples from cows and goats documented a 19.6% MRSA prevalence (Begum & Mir, 2024). In Chennai, Deepak *et al.,* (2023) examined 259 raw milk samples and found 34.4% positive for S. aureus, with 27% of these confirmed as MRSA, exhibiting both community-associated traits and multidrug resistance. Bardhan et al., (2024) identified 30.8% MRSA positivity among 146 S. aureus isolates collected from cattle milk across three agro-climatic zones in South Bengal, with a notable ability to form biofilms. Of the *S. aureus* isolates, 42.11% exhibited oxacillin resistance, and 7.89% were cefoxitin-resistant MRSA strains. Similarly, Mahanti *et al.,* (2020) found a 9.6% MRSA prevalence among 450 composite milk samples from West Bengal.

Genotypic characterizations of bovine mastitis-associated S. aureus have also been conducted in Andhra Pradesh, Telangana, and Karnataka (Venugopal *et al.,* 2019; Brahma *et al.,* 2022). Further studies across the country reported MRSA rates ranging from 9.6% to 31.7% in mastitis milk samples (Mahanti et al., 2020; Hamid *et al*., 2017). A broader multi-state analysis by Annamanedi *et al.,* (2021) across six states- Karnataka, Gujarat, Telangana, Uttar Pradesh, and Maharashtra-revealed that 14.46% of 166 S. aureus isolates were oxacillin-susceptible MRSA. In the southern districts of Tamil Nadu, earlier findings indicated that 31.1% of S. aureus isolates were methicillin-resistant (Rajaduraipandi *et al.,* 2006). Alarmingly, Bhattacharyya *et al.,* (2016) identified vancomycin-resistant (VRSA) and intermediate (VISA) *S. aureus* in bovine and caprine milk, linking the emergence to possible antibiotic overuse in healthcare and its environmental spillover into livestock systems. Scattered reports from other regions of India also indicate the presence of VRSA-for example, in Bangalore (Abeysooriya & Temitayo, 2019), and Tirupati (Chinta Siva *et al.,* 2017b). Thus, robust MRSA/VRSA tracking, responsible antimicrobial use, and strict hygiene in dairy systems are essential to safeguard human health.

Such disparities in MRSA prevalence across Indian states may be driven by diverse factors, including heterogeneous antibiotic practices, differences in hospital and livestock management, environmental conditions (humidity and temperature), and clonal strain diversity, compounded by variation in surveillance capabilities. Socioeconomic factors, such as self-medication, public awareness, and sanitation practices, further shape local epidemiology.

Table 1: Studies reporting MRSA/VRSA in dairy milk and bovine mastitis in India

State/Region	Study/Year	Sample/Focus	Major Findings	Key Highlights
Tamil Nadu	Rajaduraipandi *et al.*, 2006	*S. aureus* isolates	31.1% isolates were methicillin resistant	Early evidence of MRSA emergence in southern India
Gujarat	Mistry *et al.*, 2016	Bovine mastitis isolates	13.1% MRSA prevalence	Presence of oxacillin-susceptible mecA-positive MRSA
Andhra Pradesh (Tirupati)	Chinta Siva *et al.*, 2017a	Clinical and subclinical mastitis	35.7% MRSA in subclinical mastitis and 22.2% in clinical mastitis	Higher MRSA burden in subclinical mastitis
Andhra Pradesh (Tirupati)	Chinta Siva *et al.*, 2017b	Raw milk samples	Detection of MRSA and VRSA in milk	Highlighted zoonotic importance of resistant strains
Madhya Pradesh (Jabalpur)	Shrivastava *et al.*, 2017	Dairy cattle mastitis	MRSA prevalence higher in subclinical (28%) than clinical mastitis (17%)	Suggested hidden reservoir role of subclinical mastitis
Karnataka	Venugopal *et al.*, 2019	Cattle, handlers and environment	Molecular detection and typing of MRSA and MR-CoNS	Demonstrated possible environmental and occupational transmission
Karnataka, Gujarat, Telangana, UP and Maharashtra	Annamanedi *et al.*, 2021	Bovine mastitis-associated S. aureus	14.46% oxacillin-susceptible MRSA detected	Multi-state molecular fingerprinting study
West Bengal	Mahanti et al., 2020	Composite milk samples	9.6% MRSA prevalence	Enterotoxigenic and methicillin-resistant strains identified
Haryana	Roshan *et al.*, 2022	Mastitic milk isolates	75% MRSA among S. aureus isolates	High prevalence with virulence and enterotoxin genes
Andhra Pradesh, Telangana and Karnataka	Brahma *et al.*, 2022	Clinical bovine mastitis isolates	Molecular profiling and antimicrobial resistance characterization	Reported multidrug-resistant S. aureus strains
Chennai, Tamil Nadu	Deepak *et al.*, 2023	Retail raw milk samples	34.4% samples positive for S. aureus; 27% confirmed MRSA	Community-associated traits and multidrug resistance observed
Uttarakhand	Begum & Mir, 2024	Cow and goat milk samples	19.6% MRSA prevalence	Demonstrated MRSA circulation in bovine and caprine milk
South Bengal	Bardhan *et al.*, 2024	Cattle milk isolates across agro-climatic zones	30.8% MRSA positivity among S. aureus isolates	Strong biofilm-forming ability reported
Bangalore	Abeysooriya & Temitayo, 2019	Hospital and environmental settings	Presence of VRSA strains	Suggested possible spillover of resistance into livestock ecosystems
India (Meta-analysis)	Patil *et al.*, 2022	MRSA prevalence studies	Pooled MRSA prevalence of 37% among S. aureus isolates	Demonstrated rising MRSA burden nationally

Host specific-MRSA *S. aureus* evolving to cross species barrier: Emerging zoonotic agent

Although humans and animals are natural reservoirs of *S. aureus*, epidemiological studies suggest that bovine and human *S. aureus* strains typically belong to different sequence types (Schnitt and Tenhagen, 2020). *S. aureus* comprises multiple host-specific lineages that are generally associated with particular host species, including cattle, poultry, cats, and humans (Lowder *et al.,* 2009). However, over the past two decades, significant shifts in MRSA epidemiology have been observed. Once regarded solely as a human pathogen, MRSA has now demonstrated the ability to cross species barriers, adapting from humans to animals and vice versa.

The widespread colonization of livestock with a specific lineage of MRSA, and emerging human infections (Golding *et al* 2010) showed that the animal reservoir of S. aureus can potentially harm human health care (Sakwinska *et al.,* 2011). People living in areas with a higher livestock density (pigs, cattle, and veal calves) or in proximity to areas where manure is applied to crop fields are also at a higher risk of being colonized by LA-MRSA (Schnitt and Tenhagen, 2020). Livestock and companion animals are particularly important considering the relatively high usage of antimicrobials in these species. Additionally, the host range of pathogens is a dynamically evolving trait, enabling bacteria to adapt to new hosts over time (Sakwinska *et al.*, 2011). Early studies demonstrated that MRSA prevalence in bovine mastitis was significantly lower than in human infections (Zaatout & Hezil, 2022). For example, MRSA detection in mastitic milk was rare, with reported prevalence rates of just 0.4% in South Korea (Kang *et al.,* 2024) and 1.4% in Switzerland (Huber *et al.,* 2010). In contrast, MRSA rates in human clinical settings—particularly hospital-associated infections—were substantially higher during the same period. This disparity suggested that methicillin resistance was initially uncommon in bovine isolates, likely due to differences in antibiotic usage, transmission dynamics, and ecological reservoirs between livestock and humans. However, more recent studies have shown a concerning trend toward increased MRSA prevalence in dairy cattle.

CONCLUSION

MRSA is now endemic in India and once it becomes endemic in a setting, it is difficult for other bacteria to compete and displace resistant strains. Studies have documented MRSA prevalence ranging from 13% to 47% in various regions of India, highlighting its widespread presence (Mehta *et al.,* 2020). Infections and disease dynamics caused by the same pathogen differ from host to host and from one geographical location to another. For instance, the incidence of both CA-and HA-MRSA varies from 25% in the western part of India to 50% in South India (INSAR, 2013). Some clonal lineages of a particular pathogen tend to be specific to a host, and others appear to transmit easily between hosts (INSAR, 2013). The MRSA lineage ST5 is highly adapted to humans and rarely found in animals (Challagundla *et al.,* 2018). In contrast, ST398, originally considered pig-specific has also been increasingly reported as a major clone in other livestock such as cattle (Bardiau *et al.,* 2013) and occupationally exposed persons (e.g., farmers, veterinarians). This example highlights host specificity and plasticity of MRSA clones. Similarly, CC130, a mecC-positive (mecC-CC130 MRSA), bovine-adapted lineage commonly associated with cattle mastitis, has been linked to sporadic human cases in rural areas, suggesting occasional zoonotic spillover with limited sustained transmission (Harrison *et al.,* 2013).

Future perspective and One health outlook: The emergence of vancomycin resistance in *S. aureus* has prompted the medical community to explore alternative treatment options and combination therapies. Newer antibiotics like daptomycin, linezolid, and ceftaroline have been developed to combat resistant strains, although their use must be carefully monitored to prevent further resistance development. Ongoing research focuses on understanding the mechanisms of vancomycin resistance and developing novel strategies to overcome it. This includes investigating the potential of antibiotic adjuvants, which can enhance the effectiveness of existing antibiotics, as well as exploring innovative approaches such as bacteriophage therapy, nanoparticles and antimicrobial peptides.

In countries like India, where close human–animal interaction, smallholder dairy farming, over-the-counter antibiotic access, and inadequate antimicrobial stewardship are common, the risk of MRSA transmission is particularly high. Furthermore, the lack of integrated surveillance systems, limited molecular epidemiological data, and poor coordination between veterinary and public health sectors complicate effective control measures. Therefore, combating MRSA requires a comprehensive One Health approach involving prudent antimicrobial use, improved farm biosecurity, routine surveillance, public awareness, and collaborative efforts among medical, veterinary, and environmental health professionals.

Conflicts of Interest: The authors declare no conflicts of interest.

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