

Animal reservoirs of methicillin-resistant *Staphylococcus aureus*: Implications for veterinary and public health

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ABSTRACT

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a serious antimicrobial-resistant infection that presents serious problems for public and veterinary health. Despite being first identified as a pathogen linked to healthcare, MRSA has spread outside of clinical settings, with a variety of animal species now acting as significant reservoirs that aid in its persistence and spread. MRSA is maintained by livestock, companion animals, wildlife, and aquatic ecosystems through intricate networks of transmission that include direct contact, contaminated food items, and environmental pathways. Concerns about zoonotic transmission and the growing overlap between animal and human MRSA lineages have been raised by the advent and global spread of livestock-associated MRSA (LA-MRSA), especially clonal complexes like CC398 and CC9. The molecular traits, distribution, and epidemiology of animal-associated MRSA are outlined in this review, which also emphasizes the significance of various animal reservoirs and the routes of transmission that connect animals, people, and the environment. The consequences of MRSA for veterinary medicine, food safety, workplace health, and public health are also covered, with a focus on the increasing difficulties caused by antibiotic resistance and the scarcity of efficient treatment alternatives. According to available data, environmental pollution, intense animal production, poor biosecurity, and antibiotic abuse continue to be the main causes of MRSA emergence and spread. There are still significant knowledge gaps about the ecological significance of wildlife, environmental reservoirs, and regional epidemiological differences despite improvements in molecular epidemiology and genomic surveillance. Integrated surveillance systems, appropriate antimicrobial stewardship, improved infection prevention strategies, and interdisciplinary cooperation under the One Health concept are all necessary to address these issues. To mitigate MRSA transmission, maintain antibiotic efficacy, and lessen the worldwide burden of antimicrobial resistance, a coordinated approach including the veterinary, medical, food safety, and environmental sectors is crucial.

Introduction

One of the most urgent global public health issues is antimicrobial resistance (AMR), which poses a danger to the efficient prevention and treatment of infectious illnesses in both humans and animals (Salam *et al.*, 2023). The selection and spread of resistant microorganisms have been accelerated by the extensive and frequently improper use of antimicrobial agents in human medicine, veterinary practice, and food animal production (Caneschi *et al.*, 2023). This has led to an increase in morbidity, mortality, healthcare expenses, and economic losses globally (Patra *et al.*, 2025). Because AMR is complicated and involves interactions between people, animals, food systems, and the environment outside of clinical settings, coordinated and interdisciplinary methods to its prevention and management are required (Velazquez-Meza *et al.*, 2022).

Because of its amazing adaptability, wide host range, and ability to develop resistance to many antibiotic classes, methicillin-resistant *Staphylococcus aureus* (MRSA) continues to be a prominent concern among antimicrobial-resistant organisms (Abebe and Birhanu, 2023). Hospi-

tal-associated MRSA (HA-MRSA), community-associated MRSA (CA-MRSA), and livestock-associated MRSA (LA-MRSA) are some of the various epidemiological groups that have emerged as a result of MRSA's gradual spread into animal and community populations after it was first identified as a pathogen linked to healthcare (Bouali *et al.*, 2023). These lineages' appearance demonstrates MRSA's capacity to spread throughout a variety of ecological settings and represents the dynamic development of *S. aureus* (Jiang *et al.*, 2023).

Animals are essential to the epidemiology of MRSA because they are reservoirs that can sustain and spread resistant strains (Kasela *et al.*, 2023). MRSA has been found in livestock, domestic animals, wildlife, and, to a lesser extent, aquatic creatures (Silva *et al.*, 2022a). Colonization frequently takes place in the absence of clinical illness (Choo, 2017). In addition to facilitating bacterial persistence in home settings and agricultural systems, these animal reservoirs offer chances for transmission through common environmental sources, infected food products, and direct contact (Shoaib *et al.*, 2023). As a result, the contact between people and animals has grown in significance in comprehending the epidemiology

of MRSA and its consequences for public health (Olanipekun *et al.*, 2025).

The significance of the One Health concept, which acknowledges that human, animal, and ecosystem health are inextricably linked, is highlighted by the interwoven spread of MRSA across humans, animals, and the environment (Pitt and Gunn, 2024). A thorough framework for comprehending transmission dynamics and putting into practice efficient control measures is provided by integrating surveillance, antimicrobial stewardship, biosecurity, infection prevention, and molecular epidemiology across sectors (Banwo *et al.*, 2026). In order to prevent the emergence and spread of resistant diseases while maintaining the effectiveness of currently available antimicrobial drugs, such interdisciplinary cooperation is crucial (Liu *et al.*, 2025).

This review aims to provide a comprehensive overview of the role of animals as reservoirs of MRSA and to examine their implications for veterinary and public health. In particular, the review highlights current surveillance systems, prevention strategies, knowledge gaps, and future research priorities within the One Health framework. It also summarizes the molecular characteristics and epidemiology of animal-associated MRSA, investigates transmission pathways between animals, humans, and the environment, and discusses the associated veterinary and public health impacts.

Biology and molecular characteristics of MRSA

The biological and molecular characteristics of MRSA underpin its adaptation, persistence, and dissemination across human and animal populations.

Taxonomy and general characteristics

MRSA is a facultative anaerobic, Gram-positive bacteria that is a member of the *Staphylococcus* genus in the *Staphylococcaceae* family (Touaitia *et al.*, 2025). *S. aureus* is a major opportunistic pathogen that can colonize a variety of hosts, including humans, livestock, companion animals, and wildlife (Martínez-Seijas *et al.*, 2023; Titouche *et al.*, 2024; Afnani *et al.*, 2026). It can also cause a wide range of clinical manifestations, from minor skin infections to serious invasive diseases like osteomyelitis, pneumonia, septicemia, and endocarditis (Kaushik *et al.*, 2026). Its exceptional capacity to adapt to many biological niches has made it easier for persistent reservoirs to form in community and healthcare settings, as well as within animal populations (Li *et al.*, 2025).

S. aureus's wide range of virulence factors, which encourage host colonization, immune evasion, and tissue invasion, are largely responsible for its pathogenic success (Cheung *et al.*, 2021). Surface-associated adhesins, often referred to as microbial surface components recognizing adhesive matrix molecules (MSCRAMMs), facilitate sustained colonization by mediating adhesion to extracellular matrix proteins and epithelial tissues (Foster, 2019). By interfering with host immune responses and causing tissue damage, additional virulence factors such as protein A, capsular polysaccharides, hemolysins, leukocidins, cytolytic toxins, and different extracellular enzymes contribute to bacterial persistence (Thomer *et al.*, 2016). Additionally, the capacity to build biofilms on abiotic surfaces and host tissues increases bacterial survival in harsh environments, decreases resistance to antimicrobial treatments, and contributes to recurring or chronic infections (Peng *et al.*, 2022).

In MRSA epidemiology, colonization is a crucial stage that often comes before clinical infection (Turner *et al.*, 2019). The main ecological niche in humans is the anterior nares, while colonization can also take place on the skin, throat, and perineum (Brown *et al.*, 2014). Depending on the host species, MRSA has been isolated from the gastrointestinal system, skin, mammary gland, nasal cavity, and other mucosal surfaces in animals (Phan *et al.*, 2025). While acting as crucial reservoirs that aid in the spread of bacteria through direct contact, infected fomites, or environmental exposure, colonized persons frequently do not exhibit any

symptoms (Cuny *et al.*, 2010). As a result, MRSA circulation in hospitals, farms, homes, and the larger community is mostly maintained by asymptomatic carriage in both humans and animals (Elbehiry *et al.*, 2026).

Mechanisms of methicillin resistance

MRSA is distinguished by its resistance to almost all β -lactam antibiotics, which is mostly caused by the acquisition of the *mecA* or the less commonly seen *mecC* gene (Tabassum *et al.*, 2025). Penicillin-binding protein 2a (PBP2a), an alternative transpeptidase with a significantly lower affinity for β -lactam antibiotics, is encoded by these genes (Fishovitz *et al.*, 2014). In contrast to native penicillin-binding proteins, PBP2a maintains its functional activity even when β -lactam concentrations are inhibitory (Lade *et al.*, 2022). This allows bacterial cell wall integrity to be preserved and peptidoglycan synthesis to continue after antimicrobial exposure (Yang *et al.*, 2026a).

The staphylococcal cassette chromosome *mec* (SCC*mec*), a mobile genetic element that integrates into the bacterial chromosome and can spread horizontally among staphylococcal species, contains both *mecA* and *mecC* (Saber *et al.*, 2017). Numerous SCC*mec* types and subtypes with varying structural organization, genetic content, and epidemiological distribution have been discovered to date (Lakhundi and Zhang, 2018). While smaller SCC*mec* variations typically show greater mobility and are more frequently linked to community-acquired strains, larger SCC*mec* elements frequently carry additional antimicrobial resistance determinants (Thacharodi *et al.*, 2025). MRSA populations' genetic heterogeneity and adaptive development are significantly influenced by the diversity of SCC*mec* (Briki *et al.*, 2025).

Through the accumulation of additional chromosomal mutations and horizontally acquired resistance genes, MRSA often displays multi-drug-resistant phenotypes beyond β -lactam resistance (Vestergaard *et al.*, 2019). An increasing number of human and animal isolates have been found to be resistant to macrolides, lincosamides, aminoglycosides, tetracyclines, fluoroquinolones, glycopeptides, and other antimicrobial families (Alghamdi *et al.*, 2023). Plasmids, transposons, pathogenicity islands, and other mobile genetic elements that promote genetic exchange within bacterial communities frequently carry these resistance genes (Malachowa and DeLeo, 2010). The growth and maintenance of multidrug-resistant MRSA clones are thus encouraged by antimicrobial selection pressure in clinical, veterinary, and agricultural contexts, creating serious therapeutic problems (Mehndiratta and Bhalla, 2014). The molecular basis of methicillin resistance in MRSA is illustrated in Figure 1 to clarify the role of *mec* genes, SCC*mec* elements, and PBP2a in β -lactam resistance.

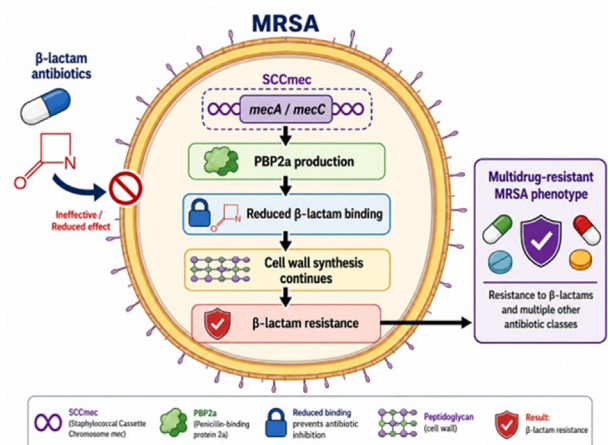


Figure 1. Molecular mechanism of methicillin resistance in MRSA.

Major MRSA Lineages

Over the past few decades, MRSA's epidemiology has changed sig-

nificantly, leading to the formation of multiple epidemiologically diverse lineages with varying antibiotic resistance profiles, transmission dynamics, and major host populations (Hajhamed *et al.*, 2025). MRSA has historically been divided into three categories: hospital-associated (HA-MRSA), community-associated (CA-MRSA), and livestock-associated (LA-MRSA) (Wu *et al.*, 2019). However, because of frequent interspecies transmission and widespread distribution, there has been an increasing amount of overlap between these categories (Belhadj *et al.*, 2026).

Hospital-associated MRSA (HA-MRSA) is mainly connected with hospital settings, where prolonged patient exposure and selective antimicrobial pressure encourage the maintenance of multidrug-resistant clones (Lindsay, 2013). Large *SCCmec* elements and resistance to several non- β -lactam antibiotic classes are typical in these isolates, which restricts the therapy options (Wassanarungroj *et al.*, 2025). HA-MRSA continues to be a significant contributor to infections linked to healthcare, especially in immunocompromised patients and those undergoing lengthy hospital stays or invasive medical procedures (Said *et al.*, 2025).

Community-associated MRSA (CA-MRSA) is typically linked to healthy people who do not have conventional hospital-related risk factors (DeLeo *et al.*, 2010). It first appeared on its own outside of healthcare settings (Otter and French, 2011). CA-MRSA is more transmissible and frequently harbors smaller *SCCmec* components than HA-MRSA, yet it is still susceptible to a number of non- β -lactam antibiotics (Sowash and Uhlemann, 2014). Strong virulence factors, such as Panton-Valentine leukocidin (PVL), which has been linked to necrotizing pneumonia and severe skin and soft tissue infections, are also present in many CA-MRSA strains (Darboe *et al.*, 2019).

From a veterinary and public health standpoint, livestock-associated MRSA (LA-MRSA) has grown in significance (Dweba *et al.*, 2018). LA-MRSA was first found in animals that produced food, but it has now been found in horses, cattle, pigs, poultry, companion animals, and wildlife (Sharma *et al.*, 2016). While CC9 is more common in a number of Asian nations, clonal complex 398 (CC398) is the lineage most commonly linked to livestock in Europe and North America (Butaye *et al.*, 2016). Compared

to the general population, people who deal with livestock, such as farmers, veterinarians, and slaughterhouse employees, have a significantly higher risk of colonization (Crespo-Piazuelo and Lawlor, 2021). Crucially, LA-MRSA can spread outside of agricultural settings through environmental dissemination, contaminated food products, and direct animal interaction, highlighting the interconnectedness of MRSA transmission within the One Health approach (Roy *et al.*, 2024).

Animal reservoirs of MRSA

A wide range of animal species have been identified as reservoirs of MRSA, facilitating its maintenance and transmission within diverse ecological settings. Table 1 summarizes the diversity of animal reservoirs associated with MRSA, including livestock, companion animals, wildlife, and aquatic systems. Figure 2 provides a simplified overview of major animal reservoirs involved in the maintenance and dissemination of animal-associated MRSA.

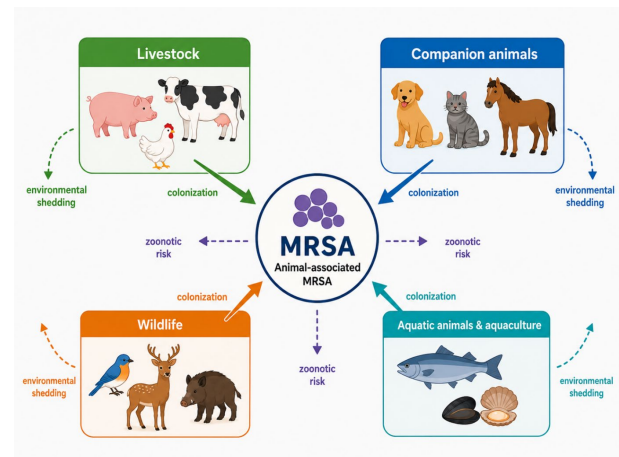


Figure 2. Animal reservoirs of MRSA across ecological interfaces.

Table 1. Animal reservoirs of MRSA, predominant hosts, colonization sites, and epidemiological significance.

Animal group	Representative species	Major MRSA lineages (if reported)	Main colonization sites	Epidemiological significance	References
Livestock	Swine, cattle, poultry, sheep, goats	CC398 (Europe and North America), CC9 (Asia), CC97 (cattle)	Nasal cavity, skin, mammary gland, teat surface, respiratory tract, feathers, cloaca	Primary reservoir of livestock-associated MRSA (LA-MRSA); persistence in intensive farming systems; environmental contamination; occupational exposure; zoonotic transmission through direct animal contact and contaminated farm environments	Aklilu and Chia (2020); Köck <i>et al.</i> (2012); Benrabia <i>et al.</i> (2020); Belhout <i>et al.</i> (2022); Khairullah <i>et al.</i> (2020a, 2023a, 2024a); Talim <i>et al.</i> (2024); Tenhagen <i>et al.</i> (2024); Wang <i>et al.</i> (2023); Barua <i>et al.</i> (2025); Bager <i>et al.</i> (2025)
Companion animals	Dogs, cats, horses	Predominantly human-associated and mixed epidemic clones	Nasal cavity, oral cavity, skin, ears, wounds, perineal region, urinary tract, respiratory tract	Bidirectional transmission between humans and animals; household and veterinary hospital reservoirs; source of community- and hospital-associated MRSA dissemination	Petinaki and Spiliopoulou (2015); van Duijkeren <i>et al.</i> (2004); van Balen <i>et al.</i> (2014); Khairullah <i>et al.</i> (2022, 2023b); Ramadhani <i>et al.</i> (2024); Kaben <i>et al.</i> (2024); Kabir <i>et al.</i> (2024); Sarker <i>et al.</i> (2025); Noor <i>et al.</i> (2026); Miszczak <i>et al.</i> (2023); Afnani <i>et al.</i> (2022)
Wildlife	Wild boar, deer, rodents, foxes, non-human primates, wild birds, marine mammals	Diverse lineages, frequently related to livestock- or human-associated clones	Respiratory tract, skin, gastrointestinal tract, nasal cavity (species-dependent)	Ecological sentinels of environmental antimicrobial resistance; facilitate MRSA circulation at the wildlife–livestock–human interface; long-distance dissemination through wildlife movement and migratory birds	Abdullahi <i>et al.</i> (2021); Heaton <i>et al.</i> (2020); Ramos <i>et al.</i> (2022); Kutkowska <i>et al.</i> (2019); Silveira <i>et al.</i> (2021); van Duijkeren <i>et al.</i> (2016); Hamar <i>et al.</i> (2025); Lim <i>et al.</i> (2025); Faires <i>et al.</i> (2009); Foysal <i>et al.</i> (2025); Al-Khalafah <i>et al.</i> (2025); da Silva <i>et al.</i> (2026)
Aquatic animals and aquaculture	Farmed fish, shellfish, cultured aquatic species	Sporadic environmental MRSA isolates; no dominant clonal lineage identified	Skin, gills, gastrointestinal tract, aquaculture water, sediments, biofilms, farming equipment	Secondary environmental reservoir; persistence in aquaculture systems; dissemination of antimicrobial resistance genes through aquatic microbial communities; potential implications for food safety and One Health	Fri <i>et al.</i> (2020); Goldstein <i>et al.</i> (2012); Garlock <i>et al.</i> (2024); Kaushik <i>et al.</i> (2024); Ifedinezi <i>et al.</i> (2024); Alem <i>et al.</i> (2025); Mushtaq <i>et al.</i> (2026); Zvezdanova <i>et al.</i> (2026)

Livestock

Livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA) is mostly found in cattle, which is an important interface for the persistence, amplification, and spread of resistant strains in agricultural production systems (Aklilu and Chia, 2020). MRSA colonization and transmission among food-producing animals are facilitated by selected pressures created by intensive farming practices, high animal density, frequent animal mobility, and widespread use of antimicrobial drugs (Talim et al., 2024). Livestock may serve as long-term carriers, adding to environmental contamination and raising the risk of zoonotic transmission through direct contact or indirectly through contaminated farm supplies, even if colonization is frequently asymptomatic (Wang et al., 2023).

With clonal complex 398 (CC398) predominating in Europe and North America and CC9 more commonly observed in Asian nations, swine are acknowledged as the most thoroughly investigated reservoir of LA-MRSA globally (Lee et al., 2024). Pigs may harbor MRSA for several production stages without showing signs of illness since colonization mostly takes place in the nasal cavity and skin (Köck et al., 2012). Close animal-to-animal contact, herd size, biosecurity procedures, and antibiotic exposure have all been linked to the high frequency of MRSA in intensive pig rearing (Khairullah et al., 2023a).

MRSA has been isolated from both clinically ill and healthy cattle, especially dairy cows with intramammary infections (Tenhagen et al., 2024). Because MRSA-caused bovine mastitis degrades animal comfort, lowers milk output, and raises treatment costs, it is especially concerning (Khairullah et al., 2020a). Colonization has been shown in the skin, teat surfaces, and nasal cavities in addition to breast tissue, enabling continuous circulation across dairy herds (Bouari et al., 2026). If hygiene procedures are not followed, the dairy environment, milking equipment, and human handlers may all contribute to the spread of bacteria (González-Machado et al., 2024).

Additionally, poultry is a significant MRSA reservoir, especially in intensive broiler and layer production systems (Benrabia et al., 2020). Bacterial persistence is facilitated by environmental contamination of litter and chicken houses, and colonization has been found in the respiratory system, skin, feathers, and cloaca (Khairullah et al., 2024a). Due to its potential spread through occupational contact and the food production chain, poultry-associated MRSA has garnered growing interest, despite the fact that prevalence varies significantly among geographic regions and production methods (Belhout et al., 2022).

Compared to pigs and cattle, small ruminants like sheep and goats have gotten less attention, despite the fact that MRSA has been found in these animals more frequently (Barua et al., 2025). Mastitis, cutaneous lesions, and asymptomatic carriage have all been linked to colonization and infection, especially in dairy flocks (Crombé et al., 2013). Bacterial transmission is made possible by the intimate contact between animals, farm laborers, and common husbandry settings, underscoring the necessity of increased surveillance in small-ruminant production systems (Bager et al., 2025).

Companion Animals

Due to their frequent and intimate interactions with humans, companion animals have become important MRSA reservoirs (Kaben et al., 2024). The significance of home environments in the epidemiology of antimicrobial resistance is shown by the fact that MRSA isolates obtained from household pets often reflect bidirectional transmission between people and animals, in contrast to livestock-associated infections (Ramadhani et al., 2024). Although clinical infections of the skin, ears, urinary tract, surgical wounds, and respiratory system have been documented, colonized animals are frequently asymptomatic (Khairullah et al., 2023b).

The most common companion animals found to be MRSA carriers are dogs (Sarker et al., 2025). Frequent physical contact with owners and

veterinary professionals facilitates the spread of colonization, which frequently takes place in the nasal cavity, mouth cavity, skin, and perineal area (Petinaki and Spiliopoulou, 2015). Numerous canine MRSA isolates are genetically identical to modern human strains, according to molecular epidemiology research, supporting the presence of recurrent human-to-dog and dog-to-human transmission (van Duijkeren et al., 2004).

Additionally, cats are accidental MRSA reservoirs, especially in veterinary facilities, animal shelters, and multi-pet families (Noor et al., 2026). Colonized cats may contribute to home transmission by close physical contact, even though the frequency is typically lower than that found in dogs (Miszczak et al., 2023). Their frequent touch with environmental surfaces and grooming habits may contribute to the spread of germs in home environments (Afnani et al., 2022).

Due to their extensive interactions with both veterinary healthcare professionals and animal caregivers, horses constitute a distinct epidemiological niche (Khairullah et al., 2022). In addition to asymptomatic colonization, equine MRSA has been linked to respiratory disorders, septic arthritis, surgical site infections, and wound infections (Kabir et al., 2024). Veterinary hospitals have been identified as significant settings for the development of MRSA in horses, where human contact, contaminated surfaces, and equipment may all contribute to nosocomial dissemination (van Balen et al., 2014).

Wildlife

The role of wildlife as ecological sentinels and possible reservoirs for the spread of MRSA in both natural and man-made environments is becoming more widely acknowledged (Abdullahi et al., 2021). The identification of MRSA in free-ranging wildlife indicates that resistant germs have spread outside of agricultural and medical settings, even if the incidence is often lower than that seen in domesticated animals (da Silva et al., 2026). Through interactions with human activity, contact with domestic animals, or environmental contamination, wildlife can contract MRSA, which then facilitates long-distance spread over geographic regions (van Duijkeren et al., 2016).

Numerous wild species, such as deer, wild boars, rats, foxes, and non-human primates, have been found to have MRSA (Heaton et al., 2020). These species might help maintain microorganisms at the wildlife-livestock interface, especially in places where agricultural activity and natural habitats coexist (Ramos et al., 2022). Because of their ecological overlap with domestic pigs and their growing proximity to human populations, wild boars are particularly interesting (Hamar et al., 2025).

Additionally, wild birds contribute significantly to the spread of antimicrobial-resistant microorganisms in the environment (Kutkowska et al., 2019). MRSA has been found in waterfowl, migratory birds, raptors, and scavenging animals, most likely as a result of contact with contaminated water bodies, landfills, livestock facilities, and wastewater (Silveira et al., 2021). Birds may contribute to the regional and global spread of resistant clones due to their migratory habits, albeit their exact epidemiological role is still unknown (Lim et al., 2025).

The increasing impact of anthropogenic contamination on aquatic environments is reflected in the discovery of MRSA in marine animals and other aquatic creatures (Foysal et al., 2025). Seals, dolphins, and other marine animals have resistant bacteria, which raises the possibility that coastal pollution and wastewater discharge could introduce clinically significant infections into marine settings (Faires et al., 2009). These results highlight the environmental aspect of MRSA ecology within the One Health concept, despite the paucity of available data (Al-Khalaifah et al., 2025).

Aquatic Animals and Aquaculture

The growing intensification of aquatic food production and the extensive interaction between farmed animals, water supplies, and sur-

rounding habitats have made aquaculture a possible ecological niche for microorganisms resistant to antibiotics (Mushtaq *et al.*, 2026). Although fish are not thought of as *S. aureus*' primary hosts, MRSA has occasionally been identified from aquaculture-associated settings, farmed fish, and shellfish, suggesting that aquatic systems may operate as secondary reservoirs for resistant germs (Fri *et al.*, 2020).

Numerous environmental factors, like as water quality, stocking density, biosecurity procedures, and antibiotic exposure, affect the prevalence of MRSA in aquaculture (Zvezdanova *et al.*, 2026). While wastewater from hospitals, livestock farms, and municipal sources can bring resistant microbes into aquatic habitats, contaminated feed, equipment, sediments, and processing facilities may promote bacterial persistence (Goldstein *et al.*, 2012). The horizontal spread of antimicrobial resistance genes among aquatic microbial populations is made possible by several interrelated processes (Alem *et al.*, 2025).

Aquaculture habitats are significant environmental reservoirs in addition to farmed fish (Garlock *et al.*, 2024). Bacterial survival and genetic exchange are facilitated by biofilms that grow on tanks, pipes, cages, and other submerged surfaces (Kaushik *et al.*, 2024). The continued growth of aquaculture worldwide emphasizes the need for integrated surveillance to better understand its contribution to the environmental epidemiology of MRSA and its potential implications for food safety and public health, even though the overall prevalence of MRSA in aquatic production systems is still relatively low when compared to terrestrial livestock (Ifedinezi *et al.*, 2024).

Epidemiology and distribution of animal-associated *Staphylococcus aureus*

Animal-associated MRSA exhibits considerable epidemiological diversity, reflecting differences in host species, geographic regions, and production systems.

Global Prevalence

Over the past 20 years, the epidemiology of animal-associated MRSA has changed significantly, reflecting the intricate interactions between the use of antibiotics, livestock production systems, international trade, and animal transportation (Cuny *et al.*, 2015). The dissemination of MRSA is influenced by local management methods, monitoring intensity, and antimicrobial stewardship programs, as seen by the significant variation in MRSA prevalence between animal species, geographic regions, and industry sectors (Hanamoto *et al.*, 2025). MRSA has been continuously found in cattle, companion animals, wildlife, and aquaculture habitats throughout all inhabited continents, despite significant variation among published research, highlighting its extensive ecological dispersion (Khan *et al.*, 2026).

Variations in farming practices and dominant circulating lineages are the main causes of regional variations in MRSA prevalence (Alkuraythi and Alkhulaifi, 2024). In Europe, intensive pig production is mostly linked to livestock-associated MRSA, where clonal complex 398 (CC398) has gained widespread recognition (Narongpun *et al.*, 2025). On the other hand, a number of Asian nations report a greater diversity of MRSA lineages, with CC9 being one of the most common livestock-associated clones, especially in poultry and pigs (Crombé *et al.*, 2013). While studies from South America and Africa show a relatively lower but rapidly rising incidence, epidemiological data from these locations are still few (Belhout *et al.*, 2022). North America has also demonstrated widespread circulation of CC398 in commercial pig farms (Alt *et al.*, 2011). These regional differences highlight how crucial region-specific surveillance techniques are to comprehending the epidemiology of MRSA linked to animals (González *et al.*, 2025).

High animal density and constant animal turnover are characteristics of production methods that indicate conditions with a higher risk of

MRSA spread (Casey *et al.*, 2014). The most well-documented high-risk industry is still intensive pig production, which is followed by commercial dairy and poultry businesses (Pedersen *et al.*, 2024). Concentrating vulnerable animals in small spaces makes it easier for germs to spread through direct touch, contaminated housing, equipment, aerosols, and farm workers (Stein, 2009). On the other hand, MRSA can still be introduced by animal replacement, human interaction, or environmental exposure, but infection rates are often lower in large or pasture-based production systems (Shoaib *et al.*, 2023). Therefore, one of the main factors influencing MRSA persistence at the herd or flock level is production intensity (Dweba *et al.*, 2018).

Dominant Clonal Complexes

Numerous clonal complexes (CCs) that are crucial to the worldwide spread of animal-associated MRSA have been found by molecular epidemiology studies (Bouiller *et al.*, 2020). The host adaption, geographic spread, antimicrobial resistance profiles, and zoonotic potential of these lineages vary, demonstrating the dynamic development of MRSA in various ecological contexts (Lei *et al.*, 2026).

It is commonly acknowledged that the most common MRSA lineage linked to cattle globally is clonal complex 398 (CC398) (Sharma *et al.*, 2016). CC398 was first found in swine populations, but it has since been found in cattle, poultry, horses, companion animals, and people who work with livestock (Laumay *et al.*, 2021). This lineage's exceptional flexibility has made it possible for it to successfully spread across various production methods and international borders (Narongpun *et al.*, 2025). Despite being initially thought to be animal-adapted, growing reports of human infections unconnected to direct interaction with cattle point to continued evolutionary diversification and wider public health significance (Smith and Wardyn, 2015).

Another significant lineage linked to cattle, especially in East and Southeast Asia, is Clonal Complex 9 (CC9) (Monecke *et al.*, 2022). This clone, which is commonly isolated from pigs and poultry, has significant genetic variation and fluctuating patterns of antibiotic resistance (Elbehiry *et al.*, 2026). The coexistence of CC9 with other livestock-associated lineages in intensive farming systems emphasizes the impact of local agricultural practices on clonal distribution and the regional heterogeneity of MRSA epidemiology (Lamamy *et al.*, 2013).

Another lineage of epidemiological significance is Clonal Complex 97 (CC97), which has historically been linked to bovine populations and intramammary infections (Campos *et al.*, 2022). Molecular data suggests that CC97 has experienced host adaptation events that promote transmission between animals and humans, despite being mostly associated with dairy cattle (Elbehiry and Marzouk, 2025). This ability to spread across species highlights MRSA's evolutionary flexibility and heightens worries about the zoonotic potential of clones linked to animals (Matuszewska *et al.*, 2022).

In addition to these dominant lineages, several newly formed clonal complexes have been observed more frequently in both domestic and wild animals (Silva *et al.*, 2022a). The identification of clonal complexes including CC1, CC5, CC8, CC22, CC30, and CC130 in a variety of animal hosts shows that MRSA epidemiology goes beyond the clones that are often associated with cattle (Cuny *et al.*, 2024). The worldwide population structure of MRSA is constantly changing due to the formation of new lineages through mutation, recombination, and horizontal gene transfer, underscoring the need for ongoing molecular surveillance utilizing high-resolution genomic techniques (Jiang *et al.*, 2023).

Risk Factors for Colonization

The possibility of bacterial introduction, persistence, and transmission in animal populations is determined by a variety of microbiological, environmental, and management-related factors (Guo *et al.*, 2021). In an-

imal production systems, these factors often work together to create optimal conditions for sustained circulation rather than working separately (Simeanu and Matei, 2025).

One of the key factors influencing the establishment and maintenance of MRSA is still the use of antimicrobial drugs (Abebe and Birhanu, 2023). Whether for medicinal, metaphylactic, or preventive objectives, the repeated or improper use of antimicrobial medications creates selective pressure that promotes the survival and growth of resistant bacterial populations (Li *et al.*, 2025). While methicillin resistance is directly connected to β -lactam antibiotics, co-selection mechanisms involving genetically linked resistance determinants may also encourage the preservation of multidrug-resistant MRSA when exposed to other antimicrobial classes (Rosado *et al.*, 2025).

By increasing animal density, contact frequency, and environmental contamination, intensive farming techniques greatly increase the likelihood of bacterial transmission (Petinaki and Spiliopoulou, 2012). Continuous animal movement, shared housing, and centralized management techniques are common in large-scale commercial enterprises, all of which speed up the spread of colonizing germs (Kasela *et al.*, 2023). Bacterial survival in production facilities may be further supported by inadequate ventilation, high humidity, and the buildup of organic matter, increasing the danger of exposure for both farm personnel and animals (Michels *et al.*, 2009).

Another important route for the spread of MRSA is the movement of animals between farms, breeding facilities, live markets, and slaughterhouses (Crombé *et al.*, 2013). Successful epidemic clones can spread

geographically through international trade and transboundary cattle movement, whereas colonized animals may bring resistant strains into previously unaffected populations (Pirolo *et al.*, 2020). The quiet spread of MRSA across regional and national borders may be made easier by the lack of routine screening during animal movement (Stein, 2009).

Farm management techniques have a significant impact on MRSA prevalence at the flock and herd levels (Geenen *et al.*, 2013). Reduced transmission risk is linked to effective biosecurity measures, such as quarantining recently introduced animals, routinely cleaning housing facilities, maintaining proper stocking densities, and enforcing stringent hygiene standards for staff (Bager *et al.*, 2025). On the other hand, frequent human-animal interaction, poor cleaning and disinfection, and shortcomings in infection control may promote bacterial persistence in production settings (Lucian-Daniel *et al.*, 2026). When taken as a whole, our findings highlight the necessity of integrated management approaches that combine careful antibiotic use, improved biosecurity, and ongoing epidemiological surveillance in order to restrict the spread of animal-associated MRSA within the One Health framework (Shoaib *et al.*, 2023).

Transmission pathways between animals, humans, and the environment

MRSA spreads through dynamic transmission pathways involving animals, humans, and environmental reservoirs, reflecting its complex epidemiological ecology. Table 2 summarizes the principal transmission pathways of MRSA across animal, human, and environmental interfaces.

Table 2. Transmission pathways of MRSA across animals, humans, and environmental interfaces.

Transmission pathway	Main sources	Mechanisms of spread	Key risk settings	Epidemiological significance	References
Animal-to-animal transmission	Livestock (swine, cattle, poultry, sheep, goats), companion animals	Direct contact between colonized and susceptible animals; shedding through nasal secretions, skin squames, saliva, feces, and wound exudates; indirect transmission via contaminated housing, feeding equipment, bedding, transport vehicles, and husbandry tools	Intensive livestock farms, dairy production systems, poultry houses, kennels, breeding facilities, veterinary clinics	Maintains MRSA circulation and clonal persistence within animal populations; promotes amplification and dissemination through intensive production systems and animal movement	Khairullah <i>et al.</i> (2024a); Petinaki and Spiliopoulou (2015); Olanipekun <i>et al.</i> (2025); Crespo-Piazuelo and Lawlor (2021); Belhout <i>et al.</i> (2022); Craft <i>et al.</i> (2019); Cuny <i>et al.</i> (2015); Locatelli <i>et al.</i> (2016); Ferreira <i>et al.</i> (2011); Silva <i>et al.</i> (2022a)
Animal-to-human transmission	Colonized livestock, companion animals, contaminated carcasses and animal products	Direct animal contact, inhalation of contaminated aerosols or dust, contact with contaminated surfaces, occupational exposure during animal handling, slaughtering, veterinary procedures, and household contact	Livestock farms, veterinary clinics and hospitals, slaughterhouses, meat-processing plants, households	Principal zoonotic transmission pathway; increased MRSA carriage among farmers, veterinarians, slaughterhouse workers, and pet owners; facilitates secondary transmission in households and healthcare settings	Aires-de-Sousa (2017); Hanselman <i>et al.</i> (2006); Hogan <i>et al.</i> (2020); Anjum <i>et al.</i> (2019); Hamar <i>et al.</i> (2025); Barua <i>et al.</i> (2025); Wulf <i>et al.</i> (2006); Magalhães <i>et al.</i> (2010); Turabelidze <i>et al.</i> (2006); Ivbulle <i>et al.</i> (2017); Xing <i>et al.</i> (2025); Elbehiry <i>et al.</i> (2026); Khairullah <i>et al.</i> (2023b); Chan (2025); Silva <i>et al.</i> (2022b); Weese <i>et al.</i> (2006)
Human-to-animal transmission (reverse zoonosis)	Colonized or infected humans (farm workers, veterinarians, pet owners, veterinary personnel)	Direct contact during animal care, veterinary procedures, husbandry activities, contaminated medical equipment, and inadequately disinfected clinical environments	Veterinary hospitals, farms, households, animal shelters	Introduces human-associated MRSA lineages into animal populations; enables adaptation and sustained circulation of human-derived clones; highlights the interconnectedness of human and animal health under the One Health framework	Heaton <i>et al.</i> (2020); Stein (2009); Petinaki and Spiliopoulou (2015); Fetsch <i>et al.</i> (2021); Abebe and Birhanu (2023); Olanipekun <i>et al.</i> (2025); Nandimpalli <i>et al.</i> (2020); Lucian-Daniel <i>et al.</i> (2026); Al Noman <i>et al.</i> (2024); Kasela <i>et al.</i> (2023); Tesema and Birhanu (2024)
Environmental transmission	Soil, dust, manure, water, wastewater, farm environments, food production chain products	Environmental contamination through bacterial shedding; indirect exposure via contaminated surfaces, feed, water, aerosols, biofilms, wastewater, agricultural runoff, and contaminated food products	Livestock buildings, dairy farms, wastewater treatment plants, aquatic environments, slaughterhouses, food-processing facilities	Functions as an intermediate reservoir supporting long-term MRSA persistence; facilitates indirect transmission, environmental dissemination, and horizontal transfer of antimicrobial resistance genes across human, animal, and environmental sectors	da Silva <i>et al.</i> (2026); Alhmidi <i>et al.</i> (2017); Turner <i>et al.</i> (2019); Shoaib <i>et al.</i> (2023); Khairullah <i>et al.</i> (2020b); Madsen <i>et al.</i> (2018); Dos Santos <i>et al.</i> (2025); Casey <i>et al.</i> (2013); Goldstein <i>et al.</i> (2012); Lena <i>et al.</i> (2021); Bouchami <i>et al.</i> (2020); Xing <i>et al.</i> (2025); González-Machado <i>et al.</i> (2024); Roy <i>et al.</i> (2024)

Animal-to-Animal Transmission

One of the main mechanisms behind the maintenance of resistant strains in both companion animal settings and livestock production systems is the spread of MRSA among animal populations (Khairullah *et al.*, 2024a). The main method of transmission is direct contact between colonized and vulnerable animals, especially in settings with high stocking numbers and extended close contacts (Petinaki and Spiliopoulou, 2015). Herds, flocks, and kennels can spread bacteria more easily because colonized animals constantly release MRSA through nasal secretions, skin squames, saliva, feces, and wound exudates (Olanipekun *et al.*, 2025).

MRSA circulation is also sustained in large part via indirect transmission (Crespo-Piazuelo and Lawlor, 2021). Bacterial transmission between consecutive animal groups may be facilitated by contaminated housing facilities, food equipment, bedding materials, transport vehicles, and husbandry instruments (Belhout *et al.*, 2022). MRSA's ability to last on abiotic surfaces for prolonged periods of time increases its persistence in animal production settings, particularly in situations when cleaning and disinfection protocols are inadequate (Craft *et al.*, 2019). Furthermore, the introduction of replacement stock, transportation, and animal mixing are management measures that increase the likelihood of established MRSA clones spreading throughout farms and production networks (Cuny *et al.*, 2015).

Animal species and industrial systems have different transmission dynamics (Chen and Wu, 2021). Dairy cattle may have prolonged circulation due to shared equipment and milking practices, but intensive swine and poultry enterprises often show higher transmission efficiency due to frequent animal interaction and continuous production cycles (Locatelli *et al.*, 2016). Close contact between animals in homes, breeding facilities, and veterinary clinics promotes the spread of pathogens in companion animal populations, especially when infection control measures are insufficient (Ferreira *et al.*, 2011). These findings show that MRSA is maintained over time in animal populations through both direct and indirect transmission mechanisms (Silva *et al.*, 2022a).

Animal-to-Human Transmission

One of the most important public health issues related to animal-associated MRSA is animal-to-human transfer (Aires-de-Sousa, 2017). MRSA colonization is regularly found to be more common in people who have regular contact with colonized animals at work or at home than in the general population (Hanselman *et al.*, 2006). Persistent carriage raises the risk of recurrent infection and creates potential for secondary transmission within homes, healthcare facilities, and the larger community, even if colonization is frequently asymptomatic (Hogan *et al.*, 2020).

Due to their ongoing contact to colonized animals, polluted housing, and dust produced by ordinary husbandry operations, livestock producers are among the occupational categories most at risk (Anjum *et al.*, 2019). Several epidemiological studies have shown that swine, cattle, and poultry farmers have higher MRSA carriage, especially in intensive production systems where bacterial contact is frequent and persistent (Hamar *et al.*, 2025). The length and frequency of animal contact are highly correlated with the risk of colonization, highlighting the significance of biosecurity and occupational hygiene protocols (Barua *et al.*, 2025).

Clinical examination, surgery, diagnostic sampling, and ordinary animal handling expose veterinarians and veterinary staff in similar ways (Wulf *et al.*, 2006). Veterinary clinics and hospitals are settings where MRSA can spread across various animal species, infected equipment, and medical personnel, resulting in circumstances that promote occupational acquisition and subsequent transmission (Magalhães *et al.*, 2010). Therefore, to reduce workplace exposure, appropriate infection control practices, such as hand hygiene, personal protection equipment, and environmental cleanliness, are crucial (Turabelidze *et al.*, 2006).

Employees who work in slaughterhouses, meat processing plants,

and animal transportation frequently come into touch with contaminated carcasses and colonized livestock (Ivbule *et al.*, 2017). Bacterial contamination during slaughter and processing may add to environmental spread and enhance opportunities for human exposure, even though foodborne transmission of MRSA tends to occur less frequently than direct occupational contact (Xing *et al.*, 2025). To lower contamination across the food supply chain, sanitary slaughtering practices and efficient processing controls must be implemented (Elbehiry *et al.*, 2026).

Companion animals may serve as temporary sources of MRSA transmission to pet owners in residential environments (Khairullah *et al.*, 2023b). Bacterial exchange between humans and animals is facilitated by close physical contact, such as stroking, grooming, and shared living spaces (Chan, 2025). Bidirectional household transmission has been supported by the frequent identification of genetically identical MRSA isolates in dogs and their owners by molecular epidemiology studies (Silva *et al.*, 2022b). However, companion animals are typically regarded as secondary reservoirs, and transmission frequently happens after MRSA is first introduced from contaminated people (Weese *et al.*, 2006).

Human-to-Animal Transmission

Reverse zoonosis, also known as human-to-animal transmission, has gained recognition as a significant aspect of MRSA epidemiology in addition to zoonotic transmission (Heaton *et al.*, 2020). Through regular husbandry, veterinary care, or close home contact, infected or colonized individuals may transmit MRSA into animal populations, enabling human-associated lineages to establish permanent colonization in vulnerable animal hosts (Stein, 2009).

Companion animals often pick up MRSA strains that are genetically identical to those found in their owners or veterinarians, according to data from whole-genome sequencing and molecular typing (Petinaki and Spiliopoulou, 2015). Similar transmission events have been reported in cattle, where human-associated MRSA clones may be introduced into production systems by farm workers, animal handlers, and veterinarians (Fetsch *et al.*, 2021). Once established, these strains might adapt locally before spreading on their own among animal groups (Abebe and Birhanu, 2023).

Another significant environment for reverse zoonotic transmission is veterinary clinics (Olanipekun *et al.*, 2025). Through direct touch, compromised medical equipment, or improperly cleaned clinical settings, colonized workers may unintentionally spread MRSA to hospitalized animals (Nadimpalli *et al.*, 2020). These incidents are especially significant during surgery, critical care, and extended hospital stays, when vulnerable animals are exposed to more microorganisms linked to healthcare (Lucian-Daniel *et al.*, 2026).

The increasing awareness of reverse zoonosis emphasizes how human and animal health are intertwined (Al Noman *et al.*, 2024). Therefore, efforts that restrict the introduction of human-associated MRSA into animal populations should be included in infection prevention strategies in addition to preventing animal-to-human transmission (Kasela *et al.*, 2023). Therefore, to properly describe transmission dynamics under the One Health paradigm, integrated surveillance encompassing both the human and veterinary sectors is crucial (Tesema and Birhanu, 2024).

Environmental Reservoirs

The environment serves as a crucial intermediate reservoir that promotes the persistence and spread of MRSA in both humans and animals (da Silva *et al.*, 2026). Continuous bacterial shedding from colonized hosts into soil, dust, water, manure, wastewater, and other environmental matrices causes environmental pollution (Alhmidi *et al.*, 2017). Long-term persistence outside the host is made possible by MRSA's capacity to endure a variety of environmental circumstances, which increases the likelihood of indirect transmission (Turner *et al.*, 2019).

Due to the accumulation of bacteria from infested animals, contaminated equipment, and human activity, farm environments are important ecological reservoirs of MRSA (Shoaib *et al.*, 2023). When hygienic precautions are insufficient, bacterial persistence may be supported by animal housing, feeding systems, bedding materials, milking equipment, and transport facilities (Khairullah *et al.*, 2020b). Because it may include live MRSA germs that can spread across production facilities and expose personnel and animals through surface contamination or inhalation, airborne dust produced within livestock buildings has drawn special attention (Madsen *et al.*, 2018).

The spread of MRSA is also facilitated by aquatic habitats (Dos Santos *et al.*, 2025). Manure application, animal operations, and agricultural runoff can contaminate surface water, groundwater, and irrigation systems (Casey *et al.*, 2013). Antimicrobial-resistant bacteria are also introduced into municipal treatment systems by wastewater from homes, hospitals, veterinary clinics, slaughterhouses, and the pharmaceutical industry (Goldstein *et al.*, 2012). Even while wastewater treatment significantly lowers bacterial burdens, resistant species and antimicrobial resistance genes may still exist in treated effluents, opening the door for horizontal gene transfer within aquatic microbial communities and environmental spread (Lena *et al.*, 2021).

Another possible route connecting environmental contamination and human exposure is the food production chain (Bouchami *et al.*, 2020). As a result of contamination during slaughter, processing, handling, or distribution, MRSA has been found in raw meat, milk, chicken products, shellfish, and other commodities of animal origin (Xing *et al.*, 2025). Inadequate food hygiene and cross-contamination during preparation may promote bacterial transmission, even while well prepared food poses little risk (González-Machado *et al.*, 2024). When taken as a whole, these interrelated environmental routes highlight how crucial it is to implement a thorough One Health strategy that incorporates public health, food safety, environmental management, and animal health in order to successfully stop the spread of MRSA (Roy *et al.*, 2024).

Public health implications

The public health significance of MRSA has expanded beyond clinical settings due to the growing understanding of animals as MRSA reservoirs (Kasela *et al.*, 2023). A One Health approach to antibiotic resistance surveillance and control is crucial because of the strong relationships between humans, animals, and the environment that allow MRSA to spread across several ecological niches (Aslam *et al.*, 2021). MRSA colonization is more common in those who work with livestock, companion animals, or animal-derived goods on a regular basis, such as farmers, veterinarians, animal handlers, and slaughterhouse employees (Hanselman *et al.*, 2006). Even while colonization is frequently asymptomatic, it can act as a prelude to clinical infection and help spread MRSA to homes, hospitals, and the general public (Bes *et al.*, 2025). To reduce occupational transmission, it is crucial to follow biosecurity protocols, practice good personal hygiene, and wear personal protective equipment appropriately (Turabelidze *et al.*, 2006).

MRSA has been found in a range of animal-derived commodities, such as meat, milk, and poultry products, in addition to direct animal contact (Yang *et al.*, 2026b). Rather than systemic infection of animals that produce food, contamination is mostly linked to food handling, transportation, processing, and killing (Elbehiry *et al.*, 2026). Inadequate food hygiene may promote cross-contamination during preparation and handling, even if the risk of contracting MRSA from eating properly cooked food is thought to be minimal (Diaa *et al.*, 2026). Therefore, preventing the spread of bacteria throughout the food supply chain continues to depend on the application of excellent agricultural practices, sanitary processing techniques, and efficient food safety management systems (Song *et al.*, 2024).

Because it can cause infections ranging from minor skin and soft tis-

sue infections to serious invasive illnesses like pneumonia, bacteremia, infective endocarditis, and osteomyelitis, animal-associated MRSA is also a significant clinical problem (Dryden *et al.*, 2010). Because MRSA is multidrug resistant, there are fewer treatment options available, which could result in longer hospital stays, higher medical expenses, and worse clinical outcomes (Gould *et al.*, 2010). Furthermore, the growing genetic overlap across MRSA lineages linked to livestock, communities, and healthcare suggests that transmission happens across conventional epidemiological borders, underscoring the connection between human and animal health (Briki *et al.*, 2025).

Beyond its clinical ramifications, MRSA has a significant financial impact on the animal agriculture and healthcare sectors (Touaitia *et al.*, 2025). Laboratory diagnosis, antibiotic therapy, extended hospital stays, and infection control measures all result in extra expenses in human medicine (Gurusamy *et al.*, 2013). MRSA causes productivity losses, higher treatment costs, stricter biosecurity regulations, and continuous surveillance in the veterinary industry (Sawodny *et al.*, 2025). In order to slow the spread of MRSA and lessen its effects on veterinary and public health, integrated One Health strategies that incorporate antimicrobial stewardship, coordinated surveillance, enhanced biosecurity, and interdisciplinary collaboration are essential (Syah *et al.*, 2025).

Veterinary significance

Because MRSA can colonize a variety of animal species and cause infections that are clinically relevant, it has grown in importance as a pathogen in veterinary medicine (Leonard and Markey, 2008). MRSA is linked to a number of illnesses that jeopardize the health, welfare, and production of animals, despite the fact that asymptomatic carrying is frequent (Cuny *et al.*, 2015). MRSA has been linked to bovine mastitis, wound infections, dermatitis, and septic diseases in animals raised for food, which has decreased productivity and raised veterinary expenses (Barua *et al.*, 2025). MRSA has been isolated from skin and soft tissue infections, surgical wound infections, otitis, urinary tract infections, and musculoskeletal diseases in companion animals, especially dogs, cats, and horses (Petinaki and Spiliopoulou, 2015). In addition to having an impact on clinical results, these infections raise the risk of bacterial persistence and transmission in veterinary facilities and animal populations (Vincze *et al.*, 2014).

Effective disease management and surveillance depend on prompt and accurate diagnosis (Harbarth *et al.*, 2011). Antimicrobial susceptibility testing is required to verify methicillin resistance and direct treatment choices, but conventional bacteriological culture is still the principal technique for isolating *S. aureus* (Putra *et al.*, 2023). Molecular methods that target the *mecA* and *mecC* genes, such as polymerase chain reaction (PCR), have significantly increased diagnostic accuracy and made it possible to quickly identify resistant bacteria (Mohammed *et al.*, 2025). Additionally, whole-genome sequencing has become a useful epidemiological technique for identifying virulence factors, clonal lineages, antibiotic resistance determinants, and transmission channels between humans, animals, and the environment (Khairullah *et al.*, 2024b).

Multidrug resistance restricts the effectiveness of routinely used antimicrobial drugs and reduces treatment options, making the management of MRSA infections in veterinary practice increasingly difficult (Sarker *et al.*, 2025). Antimicrobial stewardship is crucial in veterinary medicine because improper or overuse of antibiotics can hasten the selection and spread of resistant strains (Mehndiratta and Bhalla, 2014). Therefore, an integrated strategy that incorporates precise laboratory diagnosis, evidence-based antibiotic medication, stringent infection prevention measures, and ongoing surveillance is necessary for effective MRSA management (Khalid *et al.*, 2025). These tactics are crucial for enhancing the health and welfare of animals as well as lowering the danger of zoonotic transmission and supporting larger One Health programs meant to manage antibiotic resistance (Sawodny *et al.*, 2025).

Surveillance and one health approaches

To comprehend the epidemiology of MRSA and create evidence-based plans to stop its spread, effective surveillance is essential (Vittorakis *et al.*, 2024). Surveillance systems in veterinary settings offer important data on the distribution, prevalence, and patterns of antibiotic resistance of MRSA circulating in cattle, companion animals, and wild-life (Barua *et al.*, 2025). Antimicrobial susceptibility testing in conjunction with routine animal population monitoring makes it easier to identify emerging resistant clones early on and helps the application of focused infection control strategies (Afnani *et al.*, 2026). In intensive production systems, where frequent animal movement and exposure to antibiotics may hasten the establishment and spread of resistant strains, ongoing surveillance is especially crucial (Waruwu *et al.*, 2023).

Because MRSA spreads throughout the human-animal-environment interface, surveillance should use an integrated One Health approach and go beyond specific sectors (Ramirez-Plascencia *et al.*, 2025). The detection of transmission channels is improved, and a more thorough understanding of MRSA epidemiology is provided by coordinated data collecting and information sharing across veterinary, medical, food safety, and environmental agencies (Rahmaniar *et al.*, 2020). In addition to facilitating prompt risk assessment, this kind of interdisciplinary cooperation aids in the creation of unified guidelines for infection control, biosecurity, and antimicrobial stewardship (Dickmann *et al.*, 2017).

By making it possible to characterize bacterial populations at high resolution, developments in molecular epidemiology have reinforced MRSA surveillance (Lakhundi and Zhang, 2018). Methods including whole-genome sequencing, *spa* typing, staphylococcal cassette chromosome *mec* (SCC*mec*) typing, and multilocus sequence typing (MLST) offer comprehensive details on virulence genes, resistance factors, clonal relationships, and transmission patterns (Wang *et al.*, 2021). These molecular tools have improved the capacity to detect interspecies transmission events, differentiate between endemic and emerging lineages, and track the local, regional, and global evolution of antibiotic resistance (Abebe and Birhanu, 2023).

In order to combat the transboundary nature of MRSA, international surveillance programs are also essential (Li *et al.*, 2025). Standardized data collection, cross-national comparison, and the quick detection of new resistance patterns are all made possible via collaborative monitoring networks (Thacharodi *et al.*, 2025). Additionally, global readiness against antimicrobial resistance is strengthened and coordinated control tactics are developed through international cooperation (Mayers *et al.*, 2026). Therefore, enhancing MRSA control within a thorough One Health framework requires integrating veterinary and public health surveillance with molecular epidemiology and international cooperation (Fungwithaya *et al.*, 2025).

Prevention and control strategies

A comprehensive approach that considers the interdependent roles of humans, animals, and the environment is necessary for the effective prevention and control of MRSA (Cimolai, 2008). Interventions should go beyond treating affected animals and focus on strategies that stop bacterial colonization, transmission, and the development of antibiotic resistance because MRSA survives in a variety of ecological niches (Touaitia *et al.*, 2025). Therefore, to lessen the impact of MRSA in both veterinary and public health settings, an integrated strategy integrating antimicrobial stewardship, biosecurity, infection prevention, food safety, and One Health collaboration is crucial (Sawodny *et al.*, 2025).

The cornerstone of MRSA control continues to be the prudent use of antibiotics (Fiore *et al.*, 2025). To maximize therapeutic efficacy and reduce needless selection pressure, antimicrobial medicines should be administered in accordance with clinical indications and, whenever feasible, supported by antimicrobial susceptibility testing (Sarcaoğlu and

Yörük, 2024). Antimicrobial stewardship initiatives can prevent improper antimicrobial usage, encourage ethical prescription practices, and maintain the efficacy of vitally important antimicrobials in veterinary practice and cattle production (Mugyabuso *et al.*, 2026). Simultaneously, preventing the emergence and spread of resistance bacteria requires tightening regulatory oversight of antimicrobial use in animals raised for food (Mehndiratta and Bhalla, 2014).

In order to stop the entry and spread of MRSA within animal populations, biosecurity measures are equally crucial (Kovács *et al.*, 2025). Transmission can be significantly decreased by utilizing good farm management techniques, including as quarantining recently introduced animals, regularly cleaning and disinfecting housing buildings and equipment, maintaining suitable stocking densities, and limiting needless animal movement (Barua *et al.*, 2025). To reduce nosocomial transmission and occupational exposure in veterinary healthcare settings, standard infection prevention protocols—such as hand hygiene, wearing personal protective equipment, maintaining environmental sanitation, and isolating infected animals when necessary—must be followed (Weese, 2004).

Another essential element of MRSA prevention is food hygiene (González-Machado *et al.*, 2024). The danger of bacterial contamination is decreased throughout the food supply chain by using sanitary slaughtering techniques, good agricultural and manufacturing practices, and proper handling, storage, and processing of goods obtained from animals (da Silva *et al.*, 2020). Continuous surveillance should be used in conjunction with these techniques to track contamination trends and assess how well control measures are working (Kavanagh *et al.*, 2014).

A One Health approach that incorporates veterinary medicine, human healthcare, environmental management, and food safety is the only way to accomplish sustainable control of MRSA due to its complicated epidemiology (Sarker *et al.*, 2025). Coordinated antimicrobial stewardship, interdisciplinary research, and collaborative surveillance make it easier to identify newly developing resistance clones early on and enhance comprehension of the dynamics of transmission across sectors (Oliveira *et al.*, 2024). Increasing collaboration between researchers, physicians, veterinarians, legislators, and public health officials will improve the application of evidence-based interventions and help lessen the worldwide impact of MRSA while maintaining the long-term efficacy of antimicrobial treatments (Nandhini *et al.*, 2022). The integrated One Health strategy for MRSA surveillance and control is summarized in Figure 3.

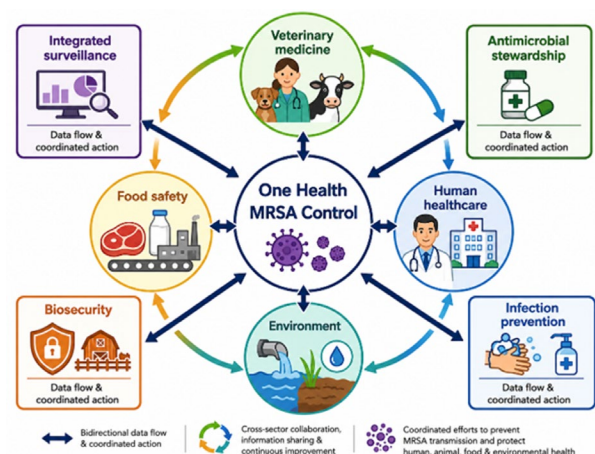


Figure 3. One Health framework for MRSA surveillance and control.

Current knowledge gaps and future perspectives

There are still a number of significant knowledge gaps about the spread of MRSA in humans, animals, and the environment, despite significant advancements in our understanding of its epidemiology (Abebe and Birhanu, 2023). The majority of the evidence now available comes from research done in high-income nations, whereas there is still a dearth

of epidemiological data from many low- and middle-income areas (Bashabsheh *et al.*, 2024). This unequal distribution of monitoring data limits comparisons of prevalence, clonal diversity, and transmission patterns across various production systems and geographical areas and makes it difficult to accurately quantify the worldwide impact of animal-associated MRSA (Cordero *et al.*, 2025).

The lack of knowledge about how wildlife and environmental reservoirs contribute to the persistence and spread of MRSA is another significant drawback (Olanipekun *et al.*, 2025). The ecological relevance of these reservoirs and their role in interspecies transmission are still poorly understood, despite the fact that resistant strains have been found in environmental matrices and free-ranging animals (da Silva *et al.*, 2026). To elucidate transmission pathways and pinpoint elements that promote MRSA persistence in complex ecosystems, longitudinal studies incorporating animal, environmental, and human samples are required (Shoaib *et al.*, 2023).

Characterizing MRSA lineages, antibiotic resistance determinants, and host adaptation has become easier thanks to recent developments in molecular epidemiology, especially whole-genome sequencing and other high-resolution genomic techniques (Geoffrey *et al.*, 2024). However, due to technical and economical limitations, these technologies continue to be underutilized in many monitoring projects (Yunita *et al.*, 2020; Li *et al.*, 2025). Global monitoring efforts would be strengthened and early detection of new clones with increased zoonotic or multidrug-resistant potential would be improved by increasing access to genomic surveillance, standardizing data gathering, and facilitating international data sharing (Briki *et al.*, 2025).

The creation of sustainable intervention techniques that lessen dependency on antimicrobial drugs should also be a top priority for future study (Shao *et al.*, 2025). In order to avoid MRSA colonization and infection in animal populations, research into vaccinations, immunomodulatory strategies, bacteriophage therapy, antimicrobial peptides, probiotics, and other alternative control mechanisms may offer supplementary tools (Tyasningsih *et al.*, 2019; Khan *et al.*, 2026). Additionally, assessing how well integrated biosecurity and antimicrobial stewardship programs work under various production systems will yield important data for enhancing disease control (Elmongui *et al.*, 2025).

Future initiatives should be directed by a thorough One Health framework that encourages cooperation between the veterinary, medical, environmental, and food safety sectors due to the interconnectedness of MRSA epidemiology (Velazquez-Meza *et al.*, 2022). Enhancing multidisciplinary research, standardizing surveillance techniques, and fostering international collaboration would advance knowledge of MRSA ecology and facilitate the creation of evidence-based local, regional, and global antibiotic resistance mitigation policies (Elbehiry *et al.*, 2026).

Conclusion

As MRSA reservoirs, animals are essential to the persistence and spread of resistant strains throughout the human–animal–environment interface. The growing prevalence of MRSA linked to animals draws attention to the pathogen's complicated epidemiology and emphasizes how crucial it is to comprehend the dynamics of its transmission within the context of One Health. Integrated surveillance, careful use of antibiotics, improved biosecurity, and interdisciplinary cooperation across the veterinary, medical, food safety, and environmental sectors are all necessary for effective MRSA mitigation. To enhance MRSA prevention and control methods and lessen the effects of antibiotic resistance on veterinary and public health, further research and concerted international efforts are crucial.

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Conflict of interest

The authors declare that there is no conflict of interest.

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