

An overview of Livestock-Associated MRSA: prevalence, lineages, and treatment

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Received 24 November 2025; revised 8 January 2026

The objective of this review is to provide an updated overview of Livestock-Associated MRSA (LA-MRSA), highlighting its global prevalence, clonal lineages, transmission across animal host, and current treatment strategies with One Health perspective. *Staphylococcus aureus* is a Gram-positive, opportunistic, facultative anaerobe found in skin and mucosal layers of the human body. Livestock Associated Methicillin Resistant *Staphylococcus aureus* (LA-MRSA) is one of the three types of MRSA classified based on epidemiological characteristics. Notorious strains of MRSA were found majorly in cities within Eastern Asia, South America, Europe and smaller regions scattered across other continents. Several lineages (like CC398, CC130, CC97 etc.) affect a wide variety of animals and their species along with transfer of infection to humans. LA-MRSA could cause many different issues including contamination of meat sold in markets leading to sickness amongst humans and infection amongst domestic animals which live in the same homes as healthy people. Treatments related to MRSA have been discussed widely from using natural materials to synthesis of new generations of antibiotics. It is stated that antibiotic resistance could emerge as one of the major causes for high mortality rate worldwide by 2050. This review will give an overview on the threat, prevalence, lineages and treatment of LA-MRSA and peek into the future of antibiotic resistance.

Keywords: Antibiotic Microbial Resistance (AMR), Clonal Complexes, One Health Approach, Zoonotic Transmission, MRSA Epidemiology

Introduction

Staphylococcus aureus is a Gram-positive, opportunistic, facultative anaerobe that commonly resides in skin and mucosal surfaces of its host. Over the course of many decades, its epidemiology has been modified¹. A large concern is shifted to the clinical strains that have grown resistant to almost nearly all β -Lactam antibiotics, and other antimicrobials like Fluoroquinolones. Exposures to these strains of pathogens have caused many infections in healthcare workers and nosocomial infections in patients². Since the gene encoding these enzymes is present in transmissible plasmids, they can be easily traded between the cells. MRSA possesses the *mecA* gene, which is located on a mobile genetic element known as the Staphylococcal Cassette Chromosome *mec* (SCC*mec*). The *mecA* gene encodes Penicillin-Binding Protein 2a (PBP2a), an altered version of the normal enzyme required for bacterial cell wall synthesis. Unlike native penicillin-binding proteins, PBP2a has a low affinity for β -lactam antibiotics, allowing MRSA to survive even

in the presence of these drugs. Strains consisting of Panton-Valentine Leukocidin (PVL) toxin are of great concern. The PVL toxin is produced by *Staphylococcus aureus* which can cause tissue necrosis. Due to this, it can cause skin and soft tissue infections, and pneumonia³. MRSA is broadly classified into three types on the basis of source of infection with it being, Hospital-Associated MRSA (HA-MRSA), Community-Associated MRSA (CA-MRSA), and Livestock-Associated MRSA (LA-MRSA)⁵. According to the CDC, a CA-MRSA case is defined as: “a patient with an MRSA infection and no history of the following: surgery, hospitalization, or residence in a long-term care facility within the year before infection, presence of a percutaneous device or indwelling catheter, dialysis within the previous year, hospitalization >48 hrs before MRSA culture, or previous MRSA infection or colonization⁴. According to the NIH, “HA-MRSA is associated with severe infections, with high morbidity and mortality rates, such as ventilator-associated and hospital-associated pneumonia, surgical site infections, as well as catheter-related infections”⁵. CC398 is predominant. CC398 is also said to have no host specificity, so it can infect a wide variety of animals including humans⁶.

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Epidemiology and evolution of different clonal complexes and their associated sequence types

CC398

While studying the CC398 infections and its evolution in both MRSA and MSSA forms, certain links were missing. A study conducted by a group of scientists applied WGST (Whole Genome Sequence Typing) on a diverse group of isolates which then slowly made their way into livestock and later on acquired resistance to β -lactam antibiotics like methicillin⁷. The clonal complex is prevalent in North America and Europe. The clonal complex is seen mainly infecting animals like pigs and veal calves, and is known to have around 43 sequence types with ST398 being the main infectious agent in pigs^{8,9}. Overtime this strain of bacteria gained resistance to methicillin and other antibiotics while also shedding and losing the Φ Sa3 prophage. This prophage carries the IEC (Immune Evasion Cluster) genes like *snc*, *chp* and *sak* which would help the bacteria evade and protect themselves from the human immune system, but due to its shedding, it becomes susceptible to the immune system. Thus, they would be less adapted to infect human beings and would adapt to newer hosts like livestock and domesticated animals¹⁰. Infections caused by CC398 MSSA are much more invasive and severe while CC398 MRSA only causes SSTIs (skin and soft tissue infections) most of the time (Figure 3). Meanwhile, in livestock, infections like wound abscesses, SSTIs, foot and joint infections, mastitis and septicaemia are seen¹¹⁻¹³. In humans, they infect through skin surfaces, mucosal layers like nasopharyngeal regions and wound entries causing infection in those areas. After the host-switch from humans to animals, certain strains of the CC398 lineage of MSSA acquired *tet(M)* gene giving it tetracycline resistance through Tn916 and later acquired *mecA* gene through SCCmec, leading to methicillin resistance¹⁴. This also means the loss of IECs in the livestock, but they remain in the human associated strains (mainly MSSA CC398). Horizontal gene transfer is also efficient; meaning the threat of diversification, adaption and evolution is high¹⁴. CC398 still remains as one of the most crucial lineages in study.

CC130

While most lineages derive their methicillin resistance from the *mecA* gene, CC130 acquires it from the *mecC* gene. Although this lineage infects humans rarely, it is more prevalent among livestock

and animals, making it a vital member of LA-MRSA. This lineage is mostly found in ruminants and was also first described in cattle¹⁵. The lineage carries a specific allele of the exfoliative toxin gene which affects the epidermis, causing skin diseases¹⁶. In an observation made on post mortem tissues of mongoose that was suspected to have septicaemia, Mo4 isolates of ST130 were studied. It was seen that *icaA* and *icaD* genes were present to create the biofilms which helped the bacteria to adhere to their surfaces. This would be a notable characteristic of the Mo4 isolate¹⁷.

CC97

Upon using RS-PCR method to analyse different isolates from different countries, Mastitis has been problematic in Indian dairy industries due to use of milk derived from infected cattle¹⁸. In Italian pig industries, CC97 is the second most prevalent clonal lineage consisting of *spa* types t1730 and t4795 holding 11% of their pig farms¹⁹. CC97 was identified as one of the predominant bovine-adapted *S. aureus* lineages in Ireland, showing diversification mainly through recombination. A distinct ST71-like subgroup with CC97 exhibited large genomic rearrangement near the origin of replication, resulting in the loss of *ica* operon and histidine biosynthesis genes²⁰. Despite this, the subgroup retained biofilm forming ability, suggesting alternative mechanism of adhesion. The frequent recovery of ST71-like isolates compared to typical CC97 strains indicates enhanced adaptation to the bovine mammary environment and ongoing clonal evolution within the lineage²⁰. Along with gene loss and gene diversification to suit their growth in this new host (including improved carbohydrate metabolism like lactose), some STs like ST71 have known to show extensive recombination. This has resulted in evolution of new genes to show potential reverse zoonosis and to evade human immune system during infection²¹.

CC1

Although, it is primarily considered CA-MRSA, CC1 has also widely found in livestock with most of its cases resulting from a human to animal spill over. A study conducted by Noto *et al.* noted that every MRSA strain has an attBscs (i.e. Attachment site B for Staphylococcal Cassette Chromosome *mec* (SCCmec)) which is highly variable across lineages. This makes the transformation into an MRSA strain harder. CC1 and some other lineages are amongst the

few that have better chances of SCCmec integration into the attB_{scc} site, making their transformation into a mecA-mediated MRSA genotype much easier²². In another study, a specific CC1 strain called MSSA476 was found to carry an SCC element, which is the DNA segment responsible for methicillin resistance. Interestingly, this strain did not have the mecA gene, which is the key gene that provides the resistance. However, it still contained ccr genes, which are responsible for its excision and integration²³.

CC9

Due to this sporadic knowledge, reports on its epidemiology and infection are also very limited. Over a span of time, CC9 cases were reported describing the infected patient to have not had any contact with a possible host while being in an environment that had plenty of livestock. This could be reasoned by assuming the patient had consumed contaminated meat or contaminated animal products²⁴. A study conducted by Xiaohua Ye *et al.* added to the existing knowledge of LA-MRSA amongst people with occupational exposure to livestock and prevalence of CC9 and other strains amongst them. In the 19 MRSA CC9 isolates, they showed extensive resistance to plethora of antibiotics and absence of IEC genes. The control group who had absolutely no exposure to livestock environment showed no cases of possible infection²⁵. Studies like this underscore the frequency at which CC9 infects people and its prevalence in livestock associated environments compared to community and healthcare associated environments.

Livestock-Associated MRSA: epidemiology in animals

Livestock-associated MRSA in SWINE/PIGS: host susceptibility, transmission routes, clinical manifestations, and zoonotic risk

The spread of LA-MRSA has likely been promoted by the selective pressure of antimicrobials used in veterinary medicine. Zinc oxide (ZnO) has long been used in pig feed to prevent post-weaning diarrhoea caused by enterotoxigenic *Escherichia coli*. However, its use at medicinal levels has been shown to promote the selection and persistence of CC398 in swine populations. The selective pressure is likely due to co-resistance mechanisms involving zinc and antibiotic resistance genes. In response to growing evidence of this association, the European Medicines Agency (EMA) recommended the withdrawal of marketing authorisations for veterinary medicinal products containing zinc oxide in 2022, although its use at low

concentrations as a feed additive remains permitted²⁶. Environmental factors such as contaminated surfaces, pig transportation, and bacterial genetic adaptations are major drivers of LA-MRSA dissemination among pig herds. Mechanical vectors, including house and stable flies, contribute to farm-to-farm transmission; up to 26.5% of house flies exiting contaminated barns carry viable LA-MRSA. LA-MRSA prevalence typically increases during the post-weaning stage and decreases by the finishing phase. However, piglet immune status appears unrelated to colonization risk²⁶. Notably, direct contact remains the primary route of LA-MRSA transmission among pigs. Skin carriage appears more common than nasal, indicating environmental exposure may contribute to spread. LA-MRSA-negative pigs get infected during transportation and stunning at abattoirs. Dust serves as a significant vector, with *S. aureus* being able to survive for weeks. Colonization of piglets from LA-MRSA-negative sows indicates additional transmission routes, making sow colonization status a critical focus for control strategies. These transmission dynamics are not confined to animal populations alone, as the potential for zoonotic transfer of LA-MRSA to humans has been well established. Additionally, food-producing animals serve as reservoirs of resistant bacteria²⁶. For treating bacterial skin infections in livestock, macrolides, aminoglycosides, fluoroquinolones, and agents like florfenicol were also frequently used²⁷.

Livestock-associated MRSA in CATTLES: host susceptibility, transmission routes, clinical manifestations, and zoonotic risk

Though MRSA prevalence in dairy herds is lower, studies report rates ranging from 0 to 4.4% in bulk tank milk. Several environmental factors within the dairy industry have been associated with the transmission of *S. aureus*. Poor milking hygiene further increases the risk of MRSA spread within herds. The predominant bovine-associated MRSA lineage in Europe, CC398, originally emerged in pigs, highlighting their role as a primary reservoir. Additionally, shared farm environments have been shown to facilitate interspecies transmission, including between pigs and cattle. Larger herd sizes and conventional dairy systems are associated with a higher prevalence of MRSA in bulk tank milk. Although bovine and human *S. aureus* strains are often distinct, indicating limited zoonotic and reverse zoonotic transmission under normal, reports of CA and HA-MRSA strains in cattle are increasing. Mastitis is the leading reason for

antibiotic use in dairy cows, with cloxacillin widely used to treat intramammary *S. aureus* infections. The extensive use of β -lactams is considered a potential driver for MRSA emergence. In Thailand, MRSA was more frequently detected in milk from cows treated with high antibiotic doses compared to those on standard regimens²⁸. Direct transmission is suggested by the detection of LA-MRSA in up to 50% of beef calves on a single farm, likely via close contact or exposure to contaminated environments. Whole-genome sequencing has suggested possible spillover from pig to veal calf production systems. Indirect transmission via shared milking equipment and farmers' hands, also likely facilitates LA-MRSA spread in dairy settings. MRSA has been detected in farm environments, which can serve as reservoirs and facilitate transmission. Furthermore, it has been known that purchasing infected replacement heifers and people that have visited many farms per day might introduce new *S. aureus* strains into dairy herd^{28,11}. In Poland, MRSA had not been detected in cattle despite high mastitis rate (17-44%), while neighbouring countries reported MRSA in dairy herds – 6.5% in Ukraine, 5.7% in Germany, and 38% in the Czech Republic²⁹. Bovine mastitis is a significant disease in dairy cows, causing considerable losses due to decreased milk yield and quality. The condition damages mammary gland tissue, often preventing regular milking. Clot formation in milk is common and results from bacterial enzymes such as coagulase, which catalyse the conversion of fibrinogen to fibrin. Among the various pathogens, *Staphylococcus aureus* is the primary causative agent, accounting for approximately 40% of mastitis cases. A skin abscess most commonly develops on the head, neck/dewlap, back, chest, and limbs. Various staphylococcal species, including *S. aureus* (most frequent) and *Staphylococcus hyicus*, are part of the normal skin flora in cattle^{30,31}. Abscess management in dairy cows involves surgical drainage, antiseptic dressing (such as povidone-iodine), and supportive therapy using broad-spectrum antibiotics (e.g., tetracyclines or cephalosporins) along with non-steroidal anti-inflammatory drugs for pain relief. With proper care, most animals recover uneventfully within two weeks³².

Livestock-associated MRSA in horses: host susceptibility, transmission routes, clinical manifestations, and zoonotic risk

LA-MRSA was first identified in horses in 1989. The anterior nares are the primary site of colonization and LA-MRSA has been frequently isolated from

surfaces that come into regular contact with horses' nasal secretions. Several places like gastrointestinal tract can also be colonized. Studies have shown that approximately 10% of healthy horses carry LA-MRSA in their nasal cavities. Although reports of LA-MRSA in horses remain limited, its presence is recognized as a potential public health concern due to transmission risks. LA-MRSA colonization is most commonly detected in the nasal cavity, unlike humans where colonization occurs in multiple areas such as the nose, hair, nails, skin, and perineum. Close interaction with colonized caregivers, including veterinarians, presents a major transmission route for LA-MRSA in horses. Shared handling equipment and stabling conditions further contribute to this risk. Environmental Factors like Suboptimal stable hygiene and poor ventilation significantly increase MRSA risk. This colonized reservoir facilitates the spread of LA-MRSA within equine populations. Although the environment in veterinary hospitals and farms is not typically considered a primary source of LA-MRSA transmission, it can contribute to its spread if hygiene is inadequate. Maintaining strict cleanliness in equine environments is necessary. The movement of horses between facilities, farms, or events may facilitate the spread of LA-MRSA, although direct studies on transportation-related transmission in horses are limited. Although healthy horses typically exhibit low LA-MRSA prevalence, rates are significantly higher in horses treated in veterinary hospitals, which increases the risk for both animals and healthcare personnel. Veterinary staff and caregivers colonized with MRSA can transmit bacteria to horses, highlighting the bidirectional nature of transmission³³. Negative pressure wound therapy (NPWT) involves dressing over an exposed wound and applying controlled suction. This removes exudates and reduces swelling, promoting faster healing by stimulating tissue regeneration and moderating inflammation³⁴. Oral and parenteral antibiotics are commonly employed to treat LA-MRSA infections in horses, while nebulized antimicrobials such as amikacin and enrofloxacin have also shown efficacy in eradicating persistent colonization for individuals in close contact with horses³³. Antimicrobial therapy is essential when systemic infection such as sepsis or cellulitis develops. Doxycycline is often recommended as a first-line treatment, with gentamicin, penicillin, and trimethoprim-sulphadiazine serving as alternative options. In cases of severe dermatitis or folliculitis, antibiotics can be prescribed to manage subcutaneous infections, often

accompanied by anti-inflammatory treatment and tetanus antitoxin administration where necessary³⁵.

Livestock-associated MRSA in POULTRY: host susceptibility, transmission routes, clinical manifestations, and zoonotic risk

Staphylococcus aureus is a common pathogen in poultry, found in feed, equipment, and farm environments. It causes a wide variety of conditions including omphalitis, gangrenous dermatitis, abscesses, synovitis, arthritis and endocarditis. Poultry production serves as a potential reservoir for MRSA food borne infections, with reported prevalence rates of 1.2% in raw chicken meat from Tunisia and 38% *mecA*-positive samples from Egypt. In Algeria, 42% of laying hens and 12% of broiler carried *S. aureus*, over half being MRSA, with the highest prevalence observed in turkeys. This may be linked to antibiotic misuse or a common infection source, warranting further investigation³⁶. High stocking densities and intensive farming systems are associated with increased MRSA prevalence due to enhanced transmission opportunities. In contrast, lower prevalence is often reported in small-scale or organic systems, indicating the role of farm scale and bird density as important risk factors³⁷. Airborne spread plays a key role in LA-MRSA dissemination within and between poultry facilities. Dust particles and aerosols, particularly those originating from faeces, feathers, or litter, can carry MRSA and remain viable for extended periods, posing ongoing risks to birds and humans³⁸. Reuse of contaminated litter or the accumulation of faeces between production cycles increases the likelihood of MRSA persistence and transmission to subsequent flocks³⁷. LA-MRSA can enter broiler flocks as early as the hatchery stage, with chicks acquiring the bacterium from contaminated eggshells or incubators. A German study reported 54% colonization within 72 hours of placement³⁷. During growth, shared water troughs and high stocking densities (≥ 30 kg/m²) facilitate rapid transmission, often resulting in near 100% flock prevalence by slaughter³⁹. Implementing closed breeding systems significantly reduces LA-MRSA introduction risks. Post-slaughter barn decontamination using quaternary ammonium compounds has been shown to lower environmental persistence by 78%. Worker decolonization protocols involving mupirocin nasal ointment and chlorhexidine showers reduced occupational colonization rates from 22% to 3% in Dutch poultry facilities. Equipment LA-MRSA can persist on poultry transport crates despite

routine cleaning, posing a risk to slaughterhouse workers. Cross-contamination during processing increases LA-MRSA prevalence on both carcasses and handlers' hands. Farms receiving birds from LA-MRSA-positive sources showed a fourfold increase in transmission rates. Slaughterhouse workers, especially those handling live broilers, exhibited high LA-MRSA colonization, notably with CC398 strains. Chicken meat has been identified as a major reservoir, with LA-MRSA detected in raw and frozen chicken and turkey across various regions. Recovered LA-MRSA patients can also serve as reservoirs in healthcare settings, posing further risks to professionals and the community³⁷. Bumble foot is an inflammatory or degenerative foot disease in poultry, commonly seen between 14-70 days of age, with most cases around 35 days. It ranges from mild redness or swelling to severe abscesses and bone changes. The high isolation rate of *S. aureus* in bumble foot cases is linked to poor farm conditions, such as contaminated litter, humid environments. Injuries to the footpad allow *S. aureus* entry, causing swelling and abscess formation⁴⁰.

LA-MRSA in companion animals

Companion animals including dogs, cats, and horses can acquire LA-MRSA through direct contact with colonized humans, environmental exposure and less commonly from other animals. Compared to other companion animals, dogs showed the highest proportion of MRSA among *S. aureus* isolates (65%). This finding highlights dogs as a significant reservoir for MRSA compared to other hosts in the study⁴¹. MRSA strains recovered from companion animals are often genetically like those isolated from their human owners, indicating possible bidirectional transmission. This is clinically important since House contact clones (HC-MRSA) isolates usually carry more virulence genes and more resistance genes than MRSA originating from companion animals⁴². Preventive strategies focus on proper antibiotic use, improved hygiene and environmental sanitation to reduce cross-species transmission^{43,44}. Integration of a One Health approach, combining efforts from medical, veterinary, and environmental health disciplines is essential for surveillance, public education, and coordinated responses to limit zoonotic transmission of LA-MRSA^{41,44}.

LA-MRSA in Food

Food-producing animals constitute an expanding reservoir of so-called LA-MRSA strains worldwide,

of which CC398 predominates Europe. The analysis also showed that the human-to-livestock host jump was accompanied by the loss of the Φ Sa3 phage encoding proteins that protect *S. aureus* from the human innate immune response⁴⁵. Additional risk arises from cross-contamination during processing or food preparation, particularly with undercooked meat, posing a serious threat to immunocompromised individuals⁴⁶. Although LA-MRSA is not traditionally classified as a foodborne pathogen, its potential depends on the presence of staphylococcal enterotoxin (SE) genes and favourable conditions for growth and toxin production⁴⁷. Between 2007 and 2010, 693 food samples linked to foodborne illness in Alberta were analyzed for common pathogens. *S. aureus* was found in 10.5% of samples, with 59% showing co-contamination by other bacteria⁴⁸. Positive samples mainly included meat and prepared foods, followed by dairy and produce. Although no MRSA was detected, the presence of *S. aureus* highlights the need for continued surveillance to prevent potential outbreaks⁴⁸. Contamination of chicken-based food products further increases the risk of poultry-to-human spread⁵⁴. A study in Riyadh found 62.7% of 150 processed foods, including salami, turkey, and sausages were contaminated with *S. aureus*, with 56.4% identified as MRSA; sausage samples accounted for the majority of isolates (58.5%)⁴⁹. A study in Guangdong, South China (2017-2022) detected *S. aureus* contamination in 8.9% of 824 ready-to-eat food samples, with levels mostly between 0.3-1.0 MPN/g. Among these, 10 isolates were MRSA⁵⁰. In response to the emerging threat, the European Food Safety Authority (EFSA) has recommended enhanced surveillance and routine monitoring of MRSA in food-producing animals and food products to better access and manage the zoonotic transmission risk.

Global prevalence of livestock-associated MRSA

Prevalence of LA-MRSA in ASIA

China

The prevalence of LA-MRSA, particularly ST398, has been increasingly reported across China, with notable geographic and host variability. In Eastern China and Qinghai, swine are the predominant reservoirs, underscoring the significance of pig farming systems. In Hanzhong, most LA-MRSA detections involve humans, especially slaughterhouse workers, indicating occupational exposure risks.

Chongqing contributes emerging data on LA-MRSA in goats and cattle. This regional and species-specific diversity highlights the complex epidemiology of LA-MRSA in China and underscores the need for tailored surveillance approaches. In Eastern China, MRSA has been detected in all surveyed pig farms and slaughterhouses, with a prevalence of 10.44% and 15.29%, respectively. Among 1,318 samples, 150 (11.38%) were positive for *S. aureus*, yielding 63 MRSA isolates, of which 56 belonged to LA-MRSA CC398 and 7 to CC9. Notably, 24.34% of isolates came from faeces and 4.42% from worker gloves, underscoring both animal and occupational reservoirs. LA-MRSA CC398 has been sporadically reported in pork and milk, though CC9 remains dominant. Surveillance reports show regional variation in pig-associated MRSA prevalence with 49% in Shandong, 45% in Shanghai, and only 5.17% in Henan¹⁰. In Qinghai, 68 *S. aureus* strains (48.9%) were recovered from 139 samples collected from pig farms and a slaughterhouse, including 26 MRSA ST398-t011 and 1 ST5-t002⁵¹ (Figure 1). These findings confirm ST398 as a dominant lineage and suggest ongoing transmission between farms and processing facilities. The data highlights the endemic nature of LA-MRSA CC398 in pig farming systems even in remote northwestern regions. A 2024 genome-based surveillance in Hanzhong City revealed high MRSA carriage among humans and retail meat, with 93 isolates from which 67 were from clinical patients and 26 from meat products. The predominant type was ST59-t437 with 70.1% prevalence, with ST398 and

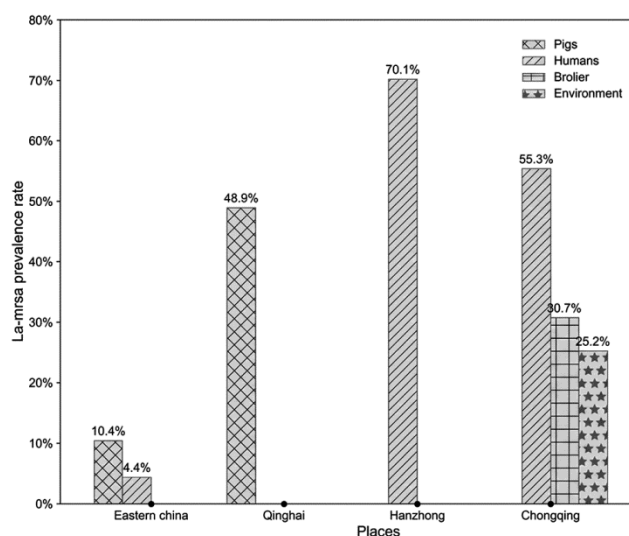


Fig. 1 — La-Mrsa Prevalence by Region and Host in China (2022-2025)

ST9 also identified in human samples, indicating overlap between human and livestock-associated strains. Hanzhong's central location, combined with patient and product data, makes it a hotspot for cross-transmission studies and strains like ST59 are spreading through animal products, raising concern for interspecies transmission⁵². From September 2022 to May 2023, a One Health study across three broiler farms in Chongqing found alarming transmission patterns of *S. aureus* between broilers, the environment, and workers. In stage 1 (before chicks entered), only 1.32% of samples were positive; by stage 2 (before slaughter), this rose to 28.63%. Colonization rates reached 30.74% in broilers, 55.27% in workers, and 25.21% in the environment. This closed-cycle transmission shows how rapidly LA-MRSA can spread during a single production cycle. The multidrug resistance rate among broilers was reported as high as 71.9%, underscoring the urgency of biosecurity and surveillance efforts in poultry systems⁵³.

Taiwan

As of writing this paper, no significant studies have been published in the period between 2020 and 2025 that specifically address the prevalence of LA-MRSA, including ST9 and ST398, in Taiwan. The most recent available data stem from investigations conducted between 2012 and 2020, underscoring a significant gap in current surveillance and highlighting the need for updated research in this region. In Taiwan, ST9 is the most prevalent MRSA sequence type in pigs and

is also common in pig farm workers ST398 is comparatively rare in pigs but appears more frequently in humans. ST9 is dominant in livestock and ST398 has a limited but notable presence in human carriers. Although MRSA has been a major pathogen in both hospital and community settings in Taiwan for decades, LA-MRSA surveillance has been relatively limited (Figure 2). To address this, investigation of MRSA colonization among pigs and pig-exposed individuals across six counties was conducted. Of 641 pig nasal swabs collected, 14.4% were MRSA-positive, with higher prevalence among piglets (18.5%) and grower pigs (15.3%) compared to sows (6.3%). Farms with larger pig populations (>1,000 animals) had a notably higher prevalence (34.3%), suggesting that intensive farming facilitates LA-MRSA spread. Additionally, younger pigs (<3 months) showed the highest carriage rate (25.4%). Human sampling (n=100) revealed a 13% MRSA carriage rate, with farm workers (19.2%) and regular visitors (18.8%) showing the highest positivity. Notably, large-farm workers had the highest risk (36.8%), and women were significantly more likely to be colonized than men (OR: 4.26; 95% CI: 1.18–15.39). These findings underscore the occupational risk of ST9 MRSA transmission in Taiwan's pig farming sector. The MRSA prevalence in Taiwanese pigs (14.4%) was higher than neighbouring China (11.4%), but lower than figures reported in earlier Taiwanese studies, which showed a wide range from 4% to 42.5%. Although ST9 remains the dominant LA-MRSA clone in Taiwan and much

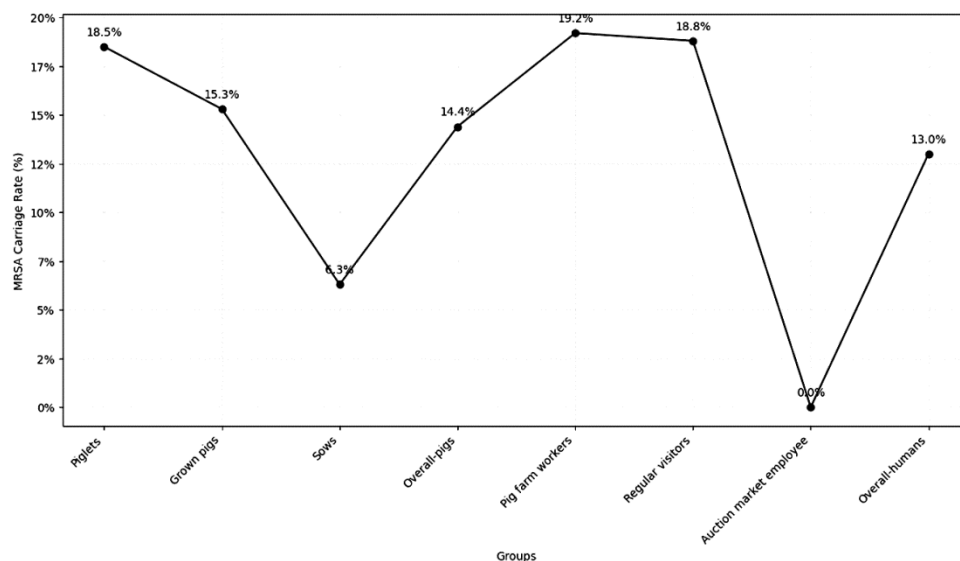


Fig. 2 — St9 Carriage rates Among Pigs and Humans in Taiwan

of Asia, its molecular characteristics can vary significantly between regions, suggesting that continuous monitoring of genomic evolution is essential for effective risk assessment. ST398 MRSA, while a major LA-MRSA clone in Europe, is rarely associated with livestock in Taiwan. It was first detected in Taiwan in 2012 in a MRSA carriage survey among nursing home residents. In a study analysing 6,413 *S. aureus* isolates (collected between 1995 and 2017), only 18 (0.28%) were identified as ST398, including 12 MRSA and 6 MSSA. Out of these, only one isolate was obtained from pork; the remainder were human-associated. Notably, none of the MRSA ST398 isolates were linked to symptomatic infections in livestock, indicating that this clone's presence in Taiwan is primarily human-adapted, with minimal linkage to farm animals or food chains. The few ST398 isolates potentially linked to livestock (one from pork and two MSSA from meat handlers) further support the conclusion that ST398 in Taiwan likely stems from imported human strains. While ST9 dominates Taiwan's LA-MRSA landscape, the sporadic detection of ST398 calls for enhanced genomic surveillance to detect any shift in its zoonotic or nosocomial behaviour^{54,55}.

Korea

A 2023 survey collected 320 swab samples across ten farms in five provinces, identifying *S. aureus* in 50.9% of samples, specifically 55% of pigs, 42% of environmental surfaces, and 55% of farm workers. Among the 163 *S. aureus* isolates, 31.3% were MRSA and 68.7% MSSA. Notably, 100% of MRSA and 98.2% of MSSA isolates belonged to the CC398 lineage, mainly ST398, with minor representation of ST541 and ST3370 demonstrating its overwhelming predominance. The CC398 lineage in Korea is associated with high multidrug resistance, including widespread chloramphenicol resistance (98% of MRSA isolates) and the presence of the linezolid resistance gene *clf*⁵⁶. A prior study reported MDR rates of 87.5% in MRSA and 58.5% in MSSA from Korean pig farms. The increasing prevalence of CC398 from 2018 to 2023, rising from 81.1% to 100% in MRSA, and 32.0% to 98.2% in MSSA, underscores the urgent need for targeted antimicrobial stewardship and continued surveillance to mitigate zoonotic transmission risks, particularly among high-risk occupational groups such as farmers and veterinarians⁵⁶.

India

In a cross-sectional study conducted in Madurai district, Tamil Nadu, a total of 255 nasal swab samples were collected from bovines ($n = 129$) and small ruminants ($n = 126$) to assess the prevalence of *Staphylococcus aureus* (SA) and methicillin-resistant *S. aureus* (MRSA). The overall prevalence of SA across all samples was found to be 35.6%, with bovine samples showing a significantly higher prevalence (42.63%) compared to small ruminants (28.57%). Among the SA-positive isolates, 28 were confirmed as MRSA based on the presence of the *mecA* gene, with MRSA prevalence in bovines and small ruminants recorded as 12.4% and 9.5% respectively; however, this difference was not statistically significant. These results emphasize that while bovines appear to serve as a more consistent reservoir for SA, small ruminants cannot be overlooked as potential MRSA carriers. The environmental context of sample origin was also considered, with samples categorized into urban and rural settings. SA prevalence was significantly higher in urban samples (53.97%) than in rural ones (29.69%), likely due to higher animal density and closer human-animal interaction. While MRSA rates did not significantly differ between settings, slightly higher urban counts suggest that urban livestock management may enhance colonization and zoonotic risk. Additionally, the study highlights the presence of multi-drug resistant (MDR) *S. aureus* isolates and their potential to act as reservoirs for zoonotic pathogens, underscoring the need for enhanced surveillance and control measures in high-risk livestock environments⁵⁷. In a comprehensive cross-sectional study in Bangalore, designed within a One Health framework, a total of 666 samples were collected to monitor methicillin resistance in staphylococci from dairy cattle. Out of these, 66 isolates were confirmed as *mecA*-positive staphylococci using multiplex PCR, indicating the presence of methicillin resistance. Among these *mecA*-positive isolates, 24% ($n = 16$) were identified as MRSA, while the remaining 76% ($n = 50$) were classified as methicillin-resistant coagulase-negative staphylococci (MRCoNS). Notably, 15 of the 16 MRSA isolates were obtained from cattle milk samples, and one was from cattle wound sample, confirming that the majority of MRSA was associated with milk, a critical route of potential exposure to humans. No MRSA was detected in any of the other collected sample types. The overall MRSA prevalence

based on total sample size was approximately 2.4% (16 out of 666 samples), reflecting the presence of drug-resistant *S. aureus* in the dairy production environment. The study emphasizes the role of dairy cattle, particularly through milk, as a reservoir of MRSA, raising significant concerns for public health and food safety. Monitoring such resistance patterns not only helps contain animal infections but also mitigates the zoonotic risk of MRSA transmission to humans through direct contact or consumption of contaminated dairy products⁵⁸. A comprehensive study conducted in Assam during the summer seasons of 2019 and 2021 found that the region's high humidity and fluctuating warm temperatures may promote *Staphylococcus aureus* growth on skin, increasing MRSA burden., a total of 611 samples were collected, including 204 livestock-associated specimens such as bovine milk, animal wound swabs, and meat samples from poultry slaughterhouses. Among the 63 *S. aureus* isolates identified from livestock-associated samples, 82.53% (52/63) were confirmed as LA-MRSA, based on phenotypic resistance and the presence of the *mecA* gene (Figure 4). This prevalence is notably higher than the global average (0.028%–9.3%) and consistent with prior Indian studies reporting LA-MRSA rates ranging from 5.4% to 29.41% in dairy cattle. Earlier findings from Assam also indicated MRSA prevalence in animal meat between 28.6% and 48.57%, further confirming a significant regional burden. The study revealed that raw bovine milk was the dominant source of LA-MRSA isolates, with 14 out of 18 lukPV-positive isolates derived from milk, suggesting a strong link between traditional hand-milking practices and pathogen transmission. The mean MAR index (Multiple Antibiotic Resistance index) for LA-MRSA was 0.289, which was lower than that observed in human-associated MRSA strains. Nonetheless, the resistance profile included commonly used antibiotic classes such as β -lactams, cephamycin's, macrolides, and tetracyclines. The lukPV gene, associated with virulence and tissue invasion, was frequently detected in bovine-origin isolates, reinforcing concerns of zoonotic potential⁵⁹.

Prevalence of LA-MRSA in Europe

Netherlands

Over the past two decades, the Netherlands has emerged as one of the European countries with the highest prevalence of LA-MRSA, particularly linked

to CC398. Occupational contact with pigs, veal calves, and dairy cattle remains the primary risk factor for MRSA carriage, especially among farmers and farm workers. In a national study, MRSA was detected on 75.8% of fattening pig farms, establishing pigs as a major reservoir. Comparatively lower prevalence was reported on veal calf farms (25.4%), dairy farms (6.2%), and sheep farms (4.5%), while no MRSA was found on broiler farms via dust sampling. However, some broiler farm workers tested positive, indicating potential under detection. Among animal samples, 15.2% of nasal swabs from veal calves were MRSA-positive, with higher prevalence in white veal operations. MRSA colonization was found in 33% of farmers, 26% of employees, and 8% of family members, reflecting exposure risk from close animal contact. In addition to farm prevalence, MRSA contamination in meat products was consistently reported (Figure 3). The Netherlands observed a slight fall in general MRSA occurrence in meat, from 7.2% in 2022 to 6.9% in 2023⁶⁰. In meat from cattle, processing plant samples showed higher MRSA rates (9.1% in 2022 and 13.6% in 2023), compared to retail meat (6.1% and 3.9% respectively). In 2023, 4.6% of sheep meat samples also tested positive. Turkey meat had particularly high detection rates, with 28.6% to 50% of samples testing positive across 2022 and 2023 (Figure 5). While meat is not considered a primary route of MRSA transmission to the general population, its presence across multiple meat types

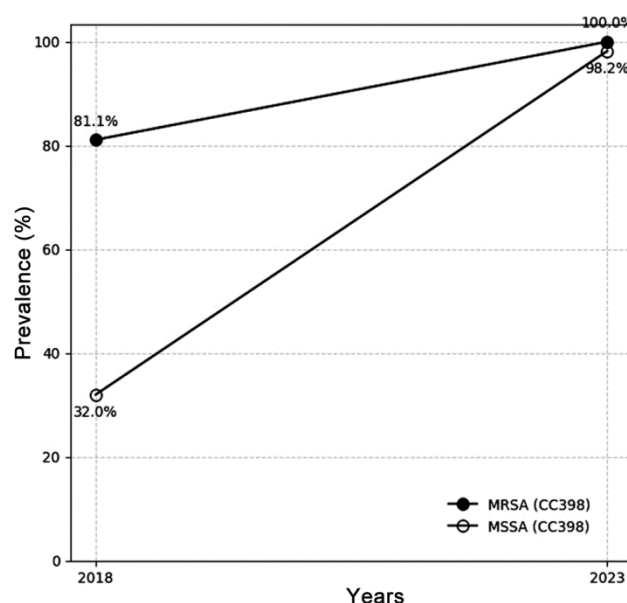


Fig. 3 — Cc398 Prevalence in Mrsa and Mssa (2018 Vs 2023)

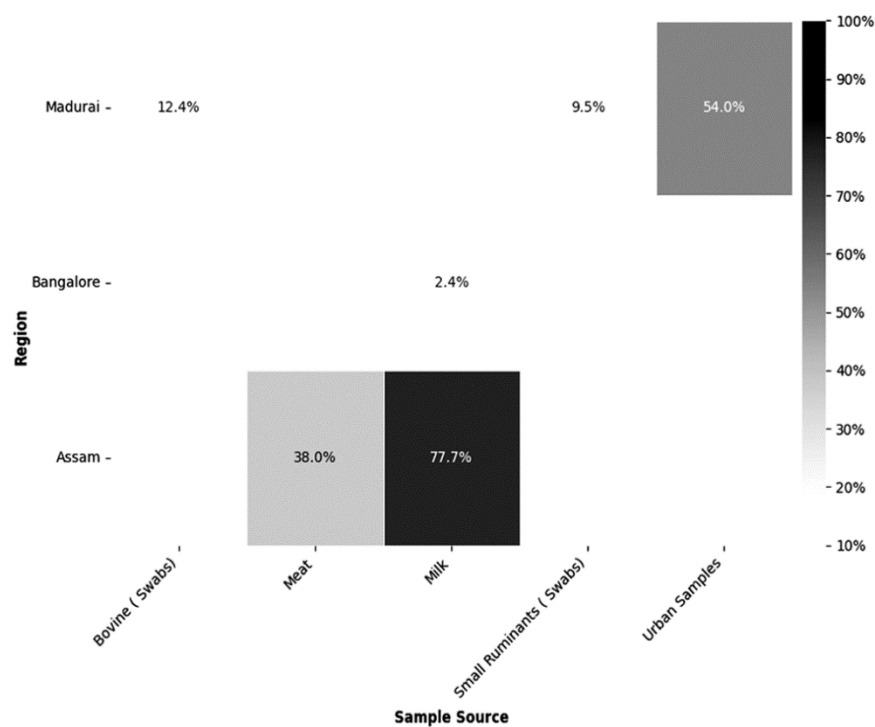


Fig. 4 — Heatmap of La-Mrsa Prevalence by Region and Source in India (2019-2023)

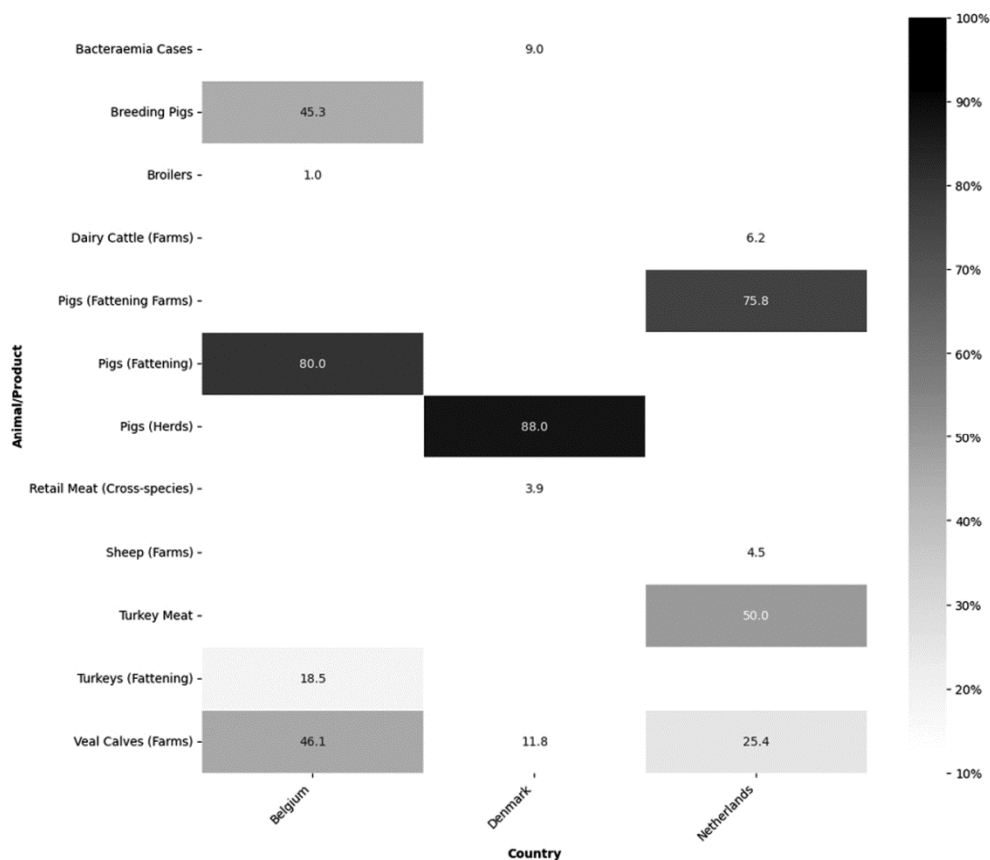


Fig. 5 — La-Mrsa Prevalence Across European Countries and Animal reservoirs (2016-2023)

and supply stages underscores the importance of hygiene practices and proper cooking⁶¹.

Belgium

In Belgium, LA-MRSA has been a long-standing concern, particularly in pig and veal farming. As early as 2009, a study found that 37.8% of persons on 49 swine farms carried MRSA ST398, with risk factors including pig contact and use of protective clothing⁶². By 2011, Belgium ranked among the highest in Europe for human MRSA ST398 isolates, comprising 4.7% of all human MRSA cases⁶³. In bovine farms, a 2014 study estimated MRSA herd prevalence at 19.8%, with substantial variation by production type—9.9% in dairy, 10.2% in beef, and 46.1% in veal calf farms. Consistently, ST398 remained the dominant clone across studies and livestock species and showed high multidrug resistance⁶⁴. Recent surveillance reports confirm continued high prevalence. In 2022, MRSA was detected in up to 80% of fattening pigs and 45.3% of breeding pig herds in Belgium, the highest rates reported in the EU⁶¹. In 2023, MRSA was also found in 18.5% of fattening turkeys and 1.0% of broilers⁶⁵. The consistently high levels of MRSA in Belgian livestock underscore a sustained reservoir with zoonotic potential. These findings reinforce the need for robust surveillance, hygiene measures, and targeted control strategies to mitigate the risk of transmission to humans, particularly among farm workers, veterinarians, and slaughterhouse personnel.

Denmark

Denmark has seen a steady and concerning rise in LA-MRSA, particularly CC398, over the past decade. The first reported bloodstream infection (BSI) caused by LA-MRSA CC398 occurred in 2010 in an 11-year-old boy whose father owned a pig farm. That same year, only 16% of Danish pig farms tested positive for LA-MRSA CC398. By 2014, this number had grown to over 60%, coinciding with a sharp rise in skin and soft tissue infections (sstis) caused by the same strain. Interestingly, many patients with LA-MRSA had no direct livestock contact but lived in rural areas, suggesting environmental exposure or indirect community transmission⁶⁶. Surveillance of veal calf farms in 2015 revealed a low prevalence, with MRSA detected in just 11.8% of farms, and very few isolates overall, suggesting limited spill over into other livestock sectors⁶⁷. LA-MRSA was first identified in Danish pig farms in 2005 (from 2 separate studies by

Bagcigil and Guardabassi in 2007) and has since spread rapidly. In 2010-2011, LA-MRSA was found in 16% of tested pig herds (from DANMAP study in 2011 and 2012). By 2014, prevalence had risen sharply to 66% in nucleus/multiplier herds and 68% in production herds, reaching 88% of production herds by 2016 (taken from the study of DANMAP in 2017). This trend highlights the swift and widespread establishment of LA-MRSA within Denmark's pig population over a decade⁶⁸. MRSA spa type t4549 is increasing reported in Denmark, with unclear sources of transmission. A nationwide study (2022-2023) revealed higher infection rates among males, often affecting the foot and toe. Possible risk factors include contact with pheasants, indoor team sports, and swimming. The rising prevalence highlights the need for targeted preventive measures and further investigation into environmental and wildlife-related transmission routes⁶⁹. According to recent EU surveillance data, Denmark remains among the countries with the highest farm-level LA-MRSA prevalence, though community spread has been relatively contained through effective monitoring programs⁶⁵. Pigs continue to be the most affected reservoir, highlighting the need for sustained surveillance and biosecurity to mitigate further spread.

Prevalence of LA-MRSS in North America

Khanna *et al.* (2008) first reported LA-MRSA in North America, detecting the bacterium in 25% of pigs and 20% of swine workers in Ontario, predominantly spa type t034. Subsequent studies revealed notable regional variability: Smith *et al.* (2009) identified 70% within-herd prevalence in U.S. pigs, while Weese *et al.* (2011) found a much lower prevalence in pigs on small, non-intensive farms in Canada, suggesting that production practices significantly influence LA-MRSA occurrence⁷⁰. LA-MRSA ST398 is now widespread in North American livestock, but other strains, including human-associated ST8 and ST5, have also been detected on pig farms⁷¹. In pork processing plants, a study found MRSA prevalence was 61.9% in pigs at slaughter, which dropped to 1.2% in retail pork. Most isolates were ST398, though human-associated ST002 was also present. All isolates were resistant to β -lactams and tetracycline, and 10% showed tigecycline resistance⁷². Occupational exposure to livestock continues to pose a significant zoonotic risk. A large study of over 14,000 people found that those working

with livestock in North America are much more likely to carry LA-MRSA, with the highest risk seen in pig and cattle workers. Veterinarians, horse workers, poultry workers, and slaughterhouse workers also had increased risk, highlighting the clear link between animal contact and LA-MRSA in humans⁷¹ (Figure 6). Livestock-exposed individuals demonstrated a significantly higher rate of LA-MRSA carriage than non-exposed individuals (Bayesian OR ≈ 7.6 for CC398), providing strong evidence of zoonotic transmission from swine to humans in North America⁷³. Poultry appears to be a limited reservoir for LA-MRSA. A prevalence study in Quebec found LA-MRSA in only 1.3% of retail chicken samples and none in live broilers, suggesting limited transmission through poultry⁷⁴. Spa type t571 and t034 predominated in Farm A, while t1451 and t011 were most common in Farm B; all isolates carried *mecA*, exhibited 100% resistance to β -lactams and tetracycline, and showed farm-specific multidrug resistance profiles⁷⁵. In North Carolina, the second-largest hog producer in the U.S., industrial hog operations (IHOs) are a key setting for exposure to livestock-associated pathogens, including LA-MRSA and multidrug-resistant *S. aureus* (MDRSA). Studies have detected these strains in pigs, air samples near workers, and the ambient environment of IHOs. Frequent contact with swine increases the risk of colonization, and IHO workers carrying these strains report more skin and soft tissue infections. Evidence suggests livestock-associated MRSA and (MDRSA) strains may be more harmful than community strains⁷⁶.

Prevalence of LA-MRSA IN South America

LA-MRSA is abundant in South America, making up for around 27% of poultry tested in the continent being infected¹¹. In a study conducted, it was noted that 14% of chicken meat sold in a number of retail outlets in Brazil and 7% of chicken meat found in hospitals were contaminated with MRSA⁷⁷. In a study done to study infection in meat of hamburgers and sandwiches sold in retail, around 50 of frozen hamburgers and 50 ready-to-eat sandwiches were tested (both of the 50 hamburgers and sandwiches having 25 chicken burgers/sandwiches and 25 beef burgers/sandwiches). After testing and isolation, 34 hamburger and 7 sandwich samples were contaminated with coagulase-positive Staphylococci⁴. A 2023 study first isolated strains of CC398 and CC1 from pig farms in Argentina, and another study conducted in the State of Rio De Janeiro isolated Staphylococci from 14 of the 230 pig farms tested⁷⁸ (Figure 7). This makes up for 6% of pig farms in the state. Additionally, in 4 of 27 workers from eleven farms from which they had also tested, had shown positive results for infection⁷⁹.

Prevalence of LA-MRSA in Africa

A large population of Africa is non-vegetarian. This demographic feature puts the inhabitants of this continent at risk of infection. Nigeria, a country with a large meat-eating population, was taken as a subject of study. The *IcaA* gene was located in 76% of the bio-film producing strains. These bio-films can help the strains survive adversely unfavourable conditions like antibiotics, immune system, and antiseptic etc⁸⁰. It is rather difficult to study the prevalence of LA-MRSA

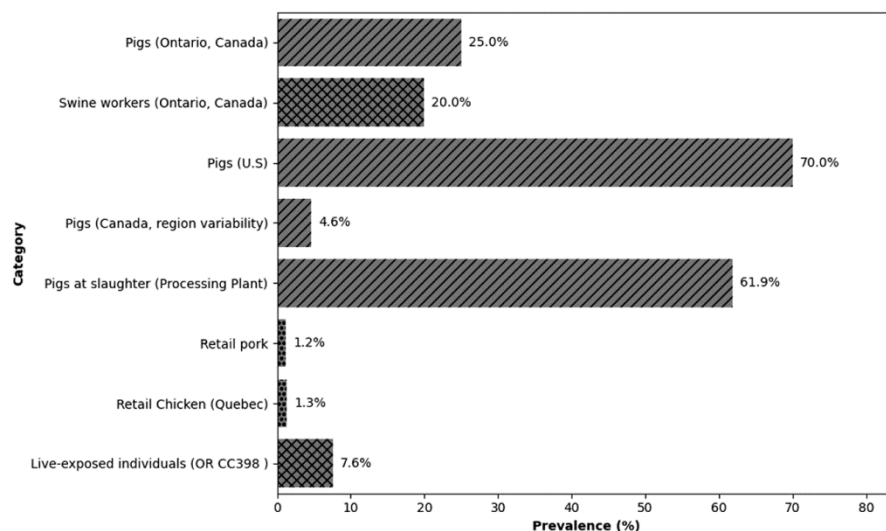


Fig. 6 — Summary of La-Mrsa Prevalence and Risk Factors in North America (2008-2024)

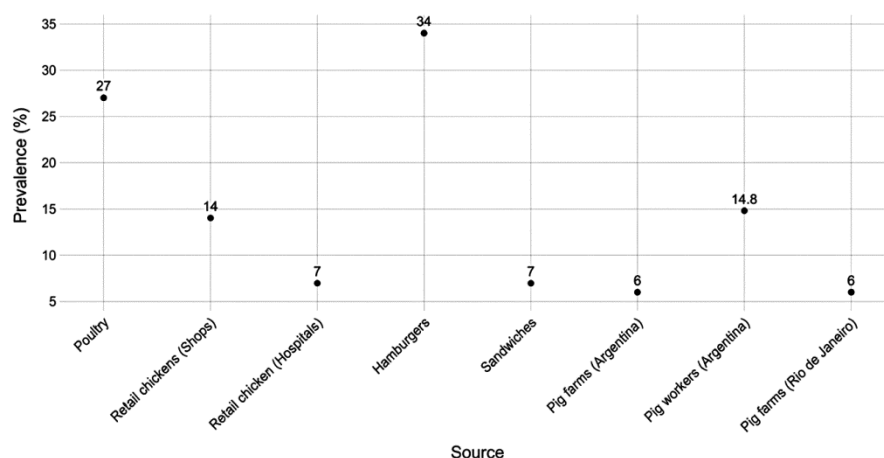


Fig. 7 — La-Mrsa Contamination Rates in Food, Poultry, Meat, and Pig Farms in South America

panning an entire continent as the smallest difference in data can change the results and different studies have different values taken in consideration. In one study conducted in Sub-Saharan Africa, certain STs have been recorded in species of monkeys like ST1874, ST2058, and ST2071. Overall, the infection rate of MRSA in Africa is very low but studies in Nigeria tell us that a 16% colonisation rate was seen among cattle⁸¹. In Egypt, 3% of analysed dog samples recorded colonisation and no tested cat samples showed any traces of MRSA⁸². A notable characteristic in the African studies is the interspecies transmission of certain strains. CC72 was one of the strains that were observed to have colonized three gorillas from a human-to-gorilla transmission. The milk produced by mammals like cattle that have been diseased was studied and it was noted that mastitis-causing MRSA strains were observed in some cases⁸³.

Prevalence of LA-MRSA in Australia

In Australia, the emergence and expansion of LA-MRSA have become increasingly evident in pig production systems, particularly involving ST93 and ST398 clones. While MRSA in pigs was first reported in 2014, recent studies have documented a high carriage rate among pigs (75.2%) and piggery workers (59.6%), indicating frequent asymptomatic colonization and bidirectional transmission between humans and animals⁸⁴. Interestingly, the dominant clone identified was ST93, a highly virulent community-associated (CA-MRSA) strain in Australia, marking its unusual adaptation to swine, previously undocumented in pig settings⁸⁵. ST398, a more classical LA-MRSA, was less prevalent but still present. Among pigs, weaners showed the highest

MRSA prevalence (97.8%), suggesting age-specific risk patterns and underscoring the role of antibiotic exposure and weaning stress in resistance development⁸⁴. A 2022 national surveillance further confirmed the presence of both Livestock-Associated and Community-associated CC398 clones in bloodstream infections, highlighting their potential spillover into human healthcare⁸⁶. Beyond livestock, MRSA and methicillin-resistant *Staphylococcus pseudintermedius* (MRSP) have been identified in companion animals, particularly dogs and cats, with ST496 and ST749 being the most common clones in Australia⁸⁷. These findings suggest that pets, too, may serve as secondary reservoirs or indicators of broader community transmission, likely influenced by pet migration between Australia and New Zealand. Together, these studies emphasize the zoonotic and reverse zoonotic potential of LA-MRSA in Australia and call for integrated One Health surveillance encompassing livestock, humans, and companion animals.

Treatment

The overuse of antimicrobials as growth promoters and prophylactics has surged globally, with estimates reaching 131,109 tons in 2013 and projected to exceed 200,000 tons annually by 2030. This poses significant public health risks, with the potential to cause 10 million deaths annually by 2050⁸⁸. Despite policies and recommendations, high volumes of antibiotics such as tetracycline and penicillin are still used in food-producing animals⁸⁹. Zinc oxide nanoparticles (zno-nps), approved by the FDA for their biocompatibility, exhibit strong antibacterial activity mainly through reactive oxygen species

(ROS) generation. Ecofriendly synthesis using natural biotemplates such as albumin and eggshell via the sol-gel method produces stable, uniform nanorods suitable for biomedical use. In MRSA, zno nanorods (zno-nrs) effectively inhibited growth and biofilm formation, with an MIC of 23µg/ml and > 75% biofilm reduction at 32µg/ml. At 2xm (46µg/ml), zno-nrs significantly downregulated resistance genes (*mecA*, *mecr1*, *blaz*, *blar1*) and biofilm genes (*icaA*, *icaB*, *icaD*, *fnbA*), while markedly reducing PBP2a expression. These findings demonstrate that green-synthesized zno-nrs effectively suppress both antibiotic resistance and biofilm formation in MRSA⁹⁰. Similar concerns were raised in Japan following risk assessments of colistin and zinc use in pig feed⁹¹. Alternative strategies like phage therapy have been explored; a 2021 trial using a triple-phage cocktail showed safety and persistence but failed to reduce LA-MRSA levels due to low bacterial loads⁹². Natural products like curcumin, garlic, oregano, Manuka and Tualang honey, and apple cider vinegar show strong antibacterial effects against drug resistant *S. aureus*, highlighting the potential of phytochemicals in managing MRSA infections. Synthetic agents such as methicillin, vancomycin, daptomycin, mupirocin and linezolid effectively target MRSA through cell wall or protein synthesis inhibition. Newer drugs like tigecycline, oritavancin, iclaprim, cethromycin and deflazacin also exhibit strong anti-MRSA activity. Combining natural compounds (eg., tiliroside, tomatidine, piperine) with antibiotics enhances drug uptake and potency against MRSA. Synergistic antibiotic pairs, such as vancomycin or daptomycin with β -lactams, rifampin, gentamicin or fosfomycin and linezolid with carbapenems further improves treatment efficacy. Antibiotic-loaded nanoparticles provide targeted and sustained delivery, strengthening resistance control⁹³. There is no single, lasting solution for LA-MRSA, as every current treatment has its own limitations and fails to provide long-term control. Combining prudent antibiotic use, risk factor management, improved farm practices, and innovative therapies offers the best approach, yet even integrated strategies have drawbacks. Ongoing research and region-specific interventions remain essential to achieve sustainable LA-MRSA control.

Future of antibiotic resistance

As the years pass by, antibiotic resistance poses a huge threat to humanity. With microbes quickly

evolving and passing down resistance genes, overtime this could become a much larger threat than it already is. One of the ways to counter antibiotic resistance in our world is through *Antibiotic Resistance Breakers (ARBs)*. These compounds counter the resistance mechanism of the organism, failing it⁹⁴. One of the important ARBs classes is the class of *BLIs (Beta Lactamase Inhibitors)*. These inhibit the action of enzymes that resist action of β -lactam antibiotics (Beta Lactamases). One potential drug can be used against Gram-positive pathogens like MRSA, Berberine. This plant-derived isoquinoline alkaloid was used in traditional medicine in different countries across Europe, Asia, North America and South America. This is used to treat symptoms like Diarrhoea and others. It is observed that this alkaloid is ten times more potent and effective against Gram-positive bacteria than Gram-negative bacteria, which makes it a suitable contender for MRSA treatment⁹⁶. Vaccines are another proposed theoretical solution to the resistance issue but this might cause the resistant strains to be replaced by other bacteria in an ecological niche and it is a risk to be sure that the newer bacteria aren't worse than the ones exterminated⁹⁵. Other concepts include sensitization, the act of combining classic antibiotics which could work under synergy, and use of newer generation antibiotics⁹⁶. Mandatory Pan-European MRSA Surveillance has been effective in reducing HA-MRSA and LA-MRSA, lowering the rates by 10-76% over the span of 6-12 years. These policies demonstrate that coordinated surveillance and antibiotic stewardship can significantly curb MRSA prevalence⁹⁷. The severity of antibiotic resistance can either be major or minor depending on how communities and society react to it in the present. If organisations, governments and influencers can take the initiative to spread awareness, a major amount of progress is in the horizon for us.

Conclusion

LA-MRSA has emerged as a globally distributed and actively evolving zoonotic pathogen, catalysed by intensive livestock production, antimicrobial use, and close human-and-animal contact. Dominant lineages such as CC398, CC9, and CC130 exhibit host adaptation, enabling interspecies transmission and re-entry into human populations, especially among individuals in direct contact with animals or the food-production chain. To effectively control such an adversity, monitoring routine antibiotic administration,

metal co-selection, overcrowding, and hygiene is important.

Antimicrobial stewardship and exploration of alternative strategies to treat such infections is dire and necessary due to the limited therapeutic options available. Some alternative strategies include vaccines, phytochemicals, nanoparticles, phage therapy etc. Implementation of a coordinated One health framework is essential to manage LA-MRSA. If proper knowledge on its origins, survival in the environment and prevention methods is known, strategies to control further transmission to other living beings can be formulated.

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