

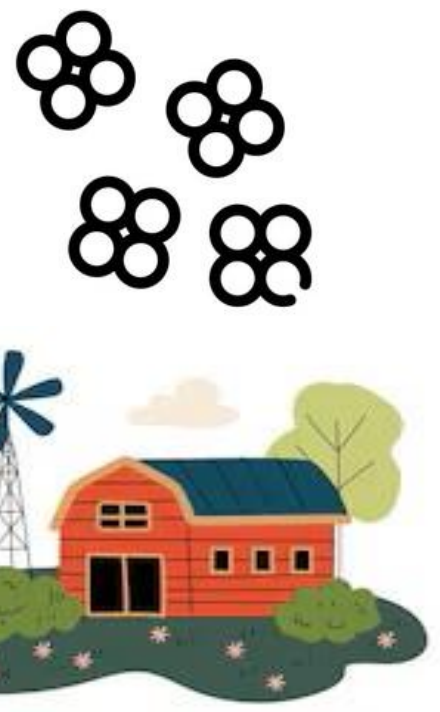


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Antimicrobial resistance in *Staphylococcus aureus* from livestock: a One Health review



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Abstract: *Staphylococcus aureus* remains a major bacterial pathogen at the human–animal interface, with antimicrobial resistance (AMR) posing a critical One Health concern. In livestock, the emergence of methicillin-resistant *S. aureus* (MRSA) and multidrug-resistant strains threatens animal welfare, food safety, and public health. This review compiles data from studies published between 2020 and 2025, summarizing prevalence, resistance mechanisms, and epidemiological trends across main livestock species, cattle, pigs, and poultry. The literature reveals persistent resistant strains in farm environments, dominated by β -lactamase, and *mecA/mecC*, mediated resistance, and a strong link between antimicrobial use and AMR emergence. Despite geographic and host variability, livestock remain a substantial AMR reservoir, facilitating transmission to humans through direct contact and the food chain. Strengthened biosecurity, rational antibiotic use, and integrated One Health surveillance are essential to limit the spread of resistant *S. aureus* and protect both animal and public health.

• Introduction



Staphylococcus aureus is an important pathogen in both humans and animals, causing diseases from localized infections to systemic illness. In livestock, it contributes to major economic losses through mastitis, respiratory, and skin infections. The emergence of methicillin-resistant *S. aureus* (MRSA), carrying *mecA* or *mecC*, has become a critical One Health issue.

Recent evidence (2020–2025) shows persistent antimicrobial resistance (AMR) across livestock species. Dairy herds harbor β -lactamase-producing and multidrug-resistant strains, while LA-MRSA CC398 predominates in pigs, showing high β -lactam and tetracycline resistance linked to *mecA* and *tetM*. Poultry isolates also exhibit MDR profiles associated with *blaZ*, *erm(B)*, and *tet(K/M)* genes. Comparative studies reveal the long-term stability of these determinants and interspecies transmission between animals, humans, and the environment. Livestock thus represent a key AMR reservoir requiring integrated surveillance and responsible antimicrobial use.

• Material and method



This review was based on a structured literature search across PubMed, ScienceDirect, Scopus, and ResearchGate to synthesize recent data (2020–2025) on *Staphylococcus aureus* antimicrobial resistance in livestock. The keywords included *S. aureus*, MRSA, livestock, antimicrobial resistance, and specific species terms (dairy cattle, pigs, poultry, sheep, goats).

Twenty-two peer-reviewed studies were selected according to strict inclusion criteria: isolates of animal origin, antimicrobial susceptibility testing, and molecular characterization of resistance determinants. Extracted data covered country, species, sample type, resistance rates, genes (*mecA*, *mecC*, *blaZ*, *tetK*, *tetM*, *erm* family), and molecular typing (ST/CC, *spa*, *SCCmec*). Results were compared qualitatively and, where available, quantitatively to identify interspecies and regional AMR patterns within a One Health context.

• Results and discussions



Between 2020 and 2025, over 45,000 samples from cattle, pigs, poultry, goats, and farm environments were analyzed across Africa, Asia, and Europe. The reviewed data revealed clear differences in *Staphylococcus aureus* and MRSA prevalence among livestock species and regions.

Swine production consistently showed the highest MRSA rates, reaching up to 15% in pigs and 8% among slaughterhouse workers in China, while European dairy herds recorded <4% prevalence and sporadic MRSA detection. In contrast, African farms reported markedly higher rates, 57% in cattle and 46% in pigs. Environmental studies confirmed MRSA persistence in air and dust, with bacteria detected several kilometers from farms, underlining the One Health relevance of airborne spread. Across species, β -lactams (64–100%) and tetracyclines (>50%) showed the highest resistance levels, particularly in pigs and poultry. Macrolide and lincosamide resistance ranged from 30–75%, being highest in pigs and poultry and lowest in cattle and goats.

Small ruminants and European dairy isolates displayed much lower AMR levels, penicillin 17%, erythromycin 8%, MDR 3.6%, while resistance in German dairy herds declined substantially (erythromycin 53% → 8%).

In contrast, studies from South and Southeast Asia still reported alarming MDR levels, up to 85% in mastitic milk isolates and 43% in caprine respiratory isolates.

At the opposite end, environmental and retail surveys confirmed >95% MDR among MRSA from swine, carcasses, and workers in China, while certain drugs such as linezolid, vancomycin, and rifampin remained fully effective across all regions.

Genetic data showed that resistance is primarily driven by *mecA*, *blaZ*, *tetM*, and *tetK*, characteristic of LA-MRSA CC398 (Europe) and ST9 (Asia). Recently detected genes *cfr*, *optrA*, and *poxA* indicate emerging resistance to linezolid and enhanced genomic adaptability.

Figure 1 illustrates comparative resistance by livestock species, showing the highest levels in pigs, followed by poultry, cattle, and goats.

The reviewed studies (2020–2025) confirm that livestock remain a major reservoir of *Staphylococcus aureus* antimicrobial resistance, with methicillin-resistant strains (MRSA) posing persistent One Health risks.

MRSA prevalence varies widely by species and geography, highest in pigs (up to 15%) and poultry, and lower in cattle and small ruminants (<5%), reflecting differences in antimicrobial use and biosecurity.

Resistance to β -lactams and tetracyclines remains dominant across species, followed by macrolides and lincosamides, consistent with long-term antimicrobial use in intensive livestock production. Despite regional progress in antibiotic stewardship, multidrug resistance (MDR) persists in both animal and environmental isolates.

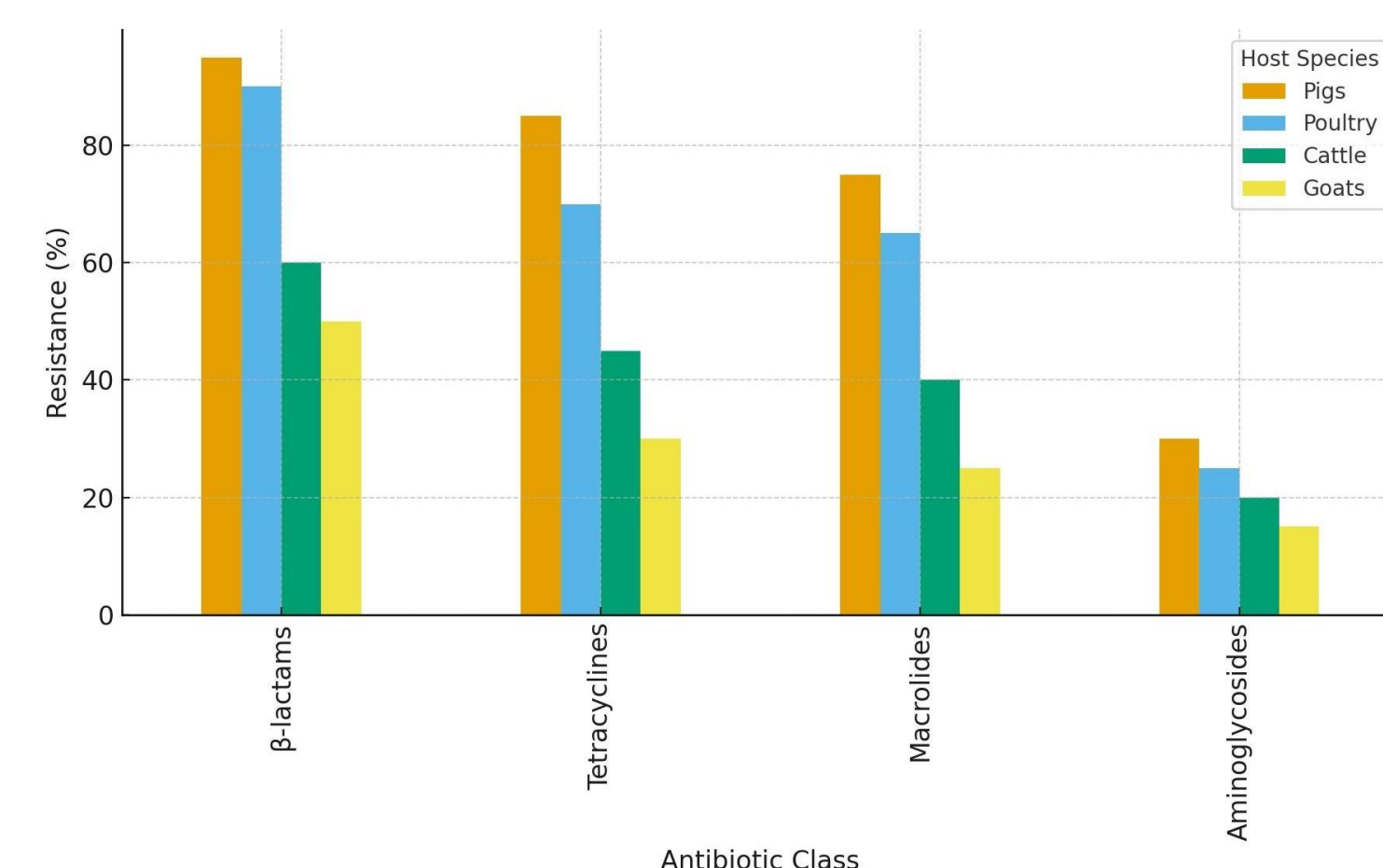


Figure 1. Comparative antimicrobial resistance (%) of *Staphylococcus aureus* isolates by livestock species (2020–2025)



Figure 2. One Health conceptual framework showing zoonotic transmission

• Conclusions

This review confirms *Staphylococcus aureus*, particularly livestock-associated MRSA, as a key antimicrobial resistance (AMR) threat at the human–animal–environment interface.

Across 22 recent studies (2020–2025), resistance to β -lactams, tetracyclines, and macrolides remained widespread among livestock species. Pigs and poultry represent the main MRSA reservoirs, dominated by CC398 and ST9 lineages, while methicillin resistance in dairy herds remains low but persistent. The consistent detection of *mecA*, *blaZ*, *tet(M/K)*, and *erm(B)* genes highlights the stability of AMR within and beyond farms. From a One Health perspective, resistant *S. aureus* circulates through the environment, food chain, and direct or indirect human contact. Reducing AMR in livestock demands rational antibiotic use, improved hygiene, environmental monitoring, and integrated surveillance connecting animal, human, and ecological health sectors. Sustainable, harmonized strategies are essential to curb the spread of resistant *S. aureus* and protect both animal welfare and public health.