

## Letter to the Editor

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# Current landscape of antimicrobial resistance genes in *Staphylococcus aureus* from milk: a thousand genome-based analysis

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## To the editor

The use of antibiotics in dairy farming is a common practice to treat and prevent bacterial infections in cows, including mastitis caused by *Staphylococcus aureus* (Rajamanickam *et al.*, 2020). However, the widespread use of antibiotics in agriculture is believed to have contributed to the dissemination of antimicrobial resistance (AMR) in bacteria, including *S. aureus*. This organism can cause chronic intramammary infections and antimicrobial resistant strains can play a role as sources of antimicrobial resistant genes in milk. Furthermore, certain *S. aureus* strains can be associated with infections in humans, such as livestock associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA). MRSA strains are resistant to virtually all beta-lactam antibiotics, posing an increasing threat to public health (Paramasivam *et al.*, 2023). In this regard, we analyzed 1103 publicly available *S. aureus* genomes to understand the current landscape of AMR genes distributed in milk.

We uncovered a high prevalence of *S. aureus* carrying *tet* (99.7%), *mepA* (95.4%), *blaZ* (31.4%), and *fosB* (25.7%) genes. Moreover, the clinically important AMR gene *mecA* (7.6%) was identified. Most interestingly, several *S. aureus* strains isolated from milk phylogenetically clustered with clinical strains from different years and countries. The clustering of milk-derived *S. aureus* strains with clinical strains from diverse geographic regions and time periods suggests a genetic relatedness between these isolates. This raises questions about how these strains are transmitted and whether certain strains have a broader distribution than previously thought. In addition, the data raise questions about the genetic factors that allow these strains to persist in different environments and hosts. We should convey that anthropological actions might be the major significant factor that contributes to contamination of milk in dairy production, especially in low-income countries.

In summary, the presence of AMR genes in *S. aureus* isolated from milk highlights the need for stringent antibiotic use in dairy farming, improved hygiene practices and ongoing efforts to monitor and address antimicrobial resistance in both animal and human health contexts.

## References

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