

# Understanding the molecular epidemiology of mastitis-associated *S. aureus* through genomics

Bovine mastitis is a serious concern for dairy industries across the globe due to economic challenges faced by the stakeholders including declined milk production, animal culling, and the treatment costs associated with it. The leading causative agent behind this condition is the well-known pathogen *Staphylococcus aureus*, which triggers intramammary infections (IMI), eventually developing into subclinical (SCM) and clinical mastitis (CM). Although the basic processes of bacterial entry and replication dynamics are understood, there is a lack of elaborated molecular mechanisms underlying *S. aureus* IMI. To bridge this gap, researchers at the National Institute of Animal Biotechnology have performed whole-genome sequencing and comparative genomic analysis of 41 Indian strains of mastitis-associated *S. aureus*. They have delivered critical insights into the pathogen's molecular epidemiology for enhancing livestock health and dairy industry management.

The study identified 15 sequence types (STs) grouped into five clonal complexes (CCs), with CC8 and CC97 being the most prevalent ones. CC8 displayed genetic links to human-associated strains, raising concerns about potential zoonotic transmission. However, CC97 was shown to be exclusive to bovine origins. These complexities highlighted the significance of monitoring the spread of *S. aureus*.

Further, the researchers discovered the presence of a total of 17 antimicrobial resistance (AMR) genes, although all the strains under investigation were methicillin-sensitive. Genes associated with biofilm formation, such as the *ica* operon, were widespread, enabling the pathogen's persistence in the host and treatment resistance. Virulence factors supporting bacterial adhesion, colonization, and immune escape were also prevalent, highlighting their role in causing infection.

Overall, the genomic and phylogenetic analysis shed light on the limited variability, the nearly consistent genetic makeup of *S. aureus*, and a possible human-to-cattle host shift for some strains. These implications are crucial for devising focused interventions, reiterating the need for improved surveillance, and developing integrated approaches to curb mastitis-related losses and prevent potential public health threats from zoonotic pathogens. The above study opens up research avenues for future studies that may explore pathogen's genetic and functional characteristics, evolutionary course of adaptation and resistance mechanisms for better therapeutic and preventive measures.