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Genomic analysis of *Staphylococcus aureus* in the Zambian dairy value chain reveals a pandemic clone with high virulence potential

Inhalt

Raw milk is a key exposure route for zoonotic pathogens including *Staphylococcus* (*S.*) *aureus* in low- and middle-income countries. *S. aureus* causes food intoxication and severe infections; pandemic clones circulate across human and animal reservoirs, raising One Health concerns. We characterised genomic diversity, AMR, and virulence potential of *S. aureus* from the Zambian dairy value chain and assessed global phylogenetic context.

Whole-genome sequencing (Illumina) data from 94 isolates collected across farms, collection centres, processors, traders, and markets (Lusaka, Southern, Western Provinces) were analysed. Analyses comprised MLST, cgMLST, AMR/virulence gene detection, and maximum-likelihood phylogenetics using 7,054 global assemblies of bovine and human origin.

Predominant local sequence types were ST97 (23.4%), ST152 (16.0%), and ST7344 (13.8%). AMR genes were detected in 69.1% of isolates. All ST152 carried PVL genes; local ST152 were closely related to human blood culture isolates from Malawi. The *tsst-1* gene was present in all ST7344 and four ST152 isolates. cgMLST revealed identical or near-identical isolates spanning multiple supply chain levels and provinces, indicating active transmission.

Circulation of the pandemic clone ST152, carrying PVL genes and *tsst-1*, across the Zambian dairy supply chain poses a direct One Health risk. Targeted control measures are needed.

Keywords

S. aureus; dairy milk chain; Zambia; whole-genome sequencing; phylogeny; toxic shock syndrome toxin (TSST); Pantone-Valentine leucocidin (PVL)

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Professional Status of the Speaker

Senior Scientist

Junior Scientist Status

No, I am not a Junior Scientist.

Author: Dr. MENDES, Ângelo J.F. (University of Glasgow)

Co-Autoren: Dr. PHIRI, Bruno S.J. (University of Zambia); Dr. BIGGEL, Michael (University of Zurich); Prof. HANG'OMBE, Bernard M. (University of Zambia); Dr. SCHAARSCHMIDT, Sara (German Federal Institute for Risk Assessment); Dr. FETSCH, Alexandra (LMU Munich)

Vortragende(r): Dr. FETSCH, Alexandra (LMU Munich)

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Eingereicht von **FETSCH, Alexandra** <alexandra.fetsch@lmu.de> am **Dienstag, 16. Juni 2026**