

## ABSTRACT

Aims: To pheno- and genotypically characterise *Staphylococcus aureus* isolated from raw and fermented camel milk from Kenya and Somali for their antibiotic resistance. Methodology: Microdilution assays to determine minimal inhibitory concentrations (MICs) were done using 20 different antibiotics. Further tests with selected antibiotics were done using disk diffusion test. Genotypic antibiotic resistance was tested using microarray hybridization with selected isolates and consequent screening of antibiotic resistance genes by PCR. Results: Prevalence of antibiotic resistance among the 47 *S. aureus* tested were ampicillin 26% (12), gentamicin 26% (12), streptomycin 11% (5), tetracycline 13% (6), trimethoprim 6% (3) and fusidic acid 2% (1). Multi-resistance was detected with three isolates resistant to two antibiotics, six to three antibiotics and six to four or more antibiotics. Three multi-resistant *S. aureus* isolates were positive for the  $\beta$ -lactamase resistant genes (*blaZ*), the tetracycline resistance gene *tet38* and the Panton-Valentine leukocidin gene *pvl* according to microarray hybridization assays. Two of the three isolates harbored additionally streptomycin resistance gene *ant(6)-Ia*. The tetracycline resistance gene *tet(K)* was also detected by microarray in four isolates. PCR detected *tet(K)* and *blaZ* in 2 and 7 additional isolates respectively. Conclusion: Controlled antibiotic therapy in camels should be introduced to prevent the increase of AB resistant bacteria for this and similar milk and hygienic situations in similar production environment. Detection of the Panton-Valentine leukocidin gene *pvl* by microarray hybridization calls for further research on possibility of community-acquired methicillin-resistant *S. aureus* (CA-MRSA) in the milk as CA-MRSA with high virulence potential has been associated with the gene *lukF-PV* (*pvl*).