

Virulence factors and phylogenetic relationships in *Staphylococcus aureus* from wild ungulates in Brandenburg, Germany

Wednesday, 11 October 2023 13:15 (15 minutes)

Data regarding the occurrence of *Staphylococcus* (S.) *aureus* in wild living animals is rare. The aim of this study was to provide insights into the occurrence and characteristics of *S. aureus* in ungulates from Brandenburg, Germany.

Nasal swabs of wild boars, roe, fallow and red deer were collected in hunting season 2021/2022 and analyzed for *S. aureus* by selective enrichment. Species were determined using matrix assisted laser desorption ionization mass spectrometry. Whole-genome sequencing was conducted for genotyping and analysis of phylogenetic relationships.

S. aureus were recovered from approximately 7% of nasal swabs. *S. aureus* isolates were associated with several sequence types (ST). ST1 isolates clustered closely together in the phylogenetic tree. Genes encoding staphylococcal enterotoxin (SE) or SE-like (SEl) were found in 14/17 isolates. In particular, a *seh* gene was present in 12/17 isolates. Moreover, two isolates harbored a multiplicity of SE or SEl genes. In addition, the toxic shock syndrome toxin encoding *tsst-1* gene was detected in an isolate.

Wild animals may carry potentially virulent *S. aureus*. The close phylogenetic relationship of *S. aureus* isolates indicates a possible spread between animals from the same territory. Handling of animals or their carcasses might contribute to staphylococcal infections in humans. Moreover, food poisoning due to SE producing strains may occur, if recommended hygiene practices are not applied during processing of game meat.

Keywords

Staphylococcus aureus, Wild Ungulates, Virulence, Toxins

Registration-ID code

ZOO23-449

Professional Status of the Speaker

Senior Scientist

Junior Scientist Status

No, I am not a Junior Scientist.

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Session Classification: Session 12: Zoonoses & Wildlife II

Track Classification: Zoonoses & Wildlife