

ENCONTRO SCIENTIA

January 16

12h00

Online

Unveiling antimicrobial resistance in wild ungulates: Insights from *Staphylococcus aureus* transmission dynamics under a One Health approach

Antimicrobial resistance (AMR) poses a significant threat to public health and was recently recognized as a One Health issue, emphasizing the interconnectedness of human, animal, and environmental health. The increasing prevalence of AMR bacteria in humans and animals underscores the need for a mechanistic understanding of AMR transmission.

In this work, we used *Staphylococcus aureus* and wild ungulates as models to investigate AMR transmission under the One Health nexus. We explored a large dataset of *S. aureus* draft genomes from multi-host systems to address the hypothesis that wildlife colonization and AMR occurrence are related to human activities. We confirm that human-associated strains – more likely exposed to selective pressure from antimicrobial use – colonize wild ungulates and show that agriculture and livestock farming promote spillover to wildlife. Phylodynamic inferences suggest that several *S. aureus* clonal lineages were widespread among humans before jumping to new hosts, highlighting recent spillover events from livestock to wildlife.



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