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Environmental characteristics associated with the resistome from wildlife populations of house mice

Monday, October 13, 2025 2:30 PM (15 minutes)

Antimicrobial resistance poses a significant challenge to global health. However, the factors that maintain antimicrobial resistance genes (ARGs) within wildlife microbiomes, particularly in species inhabiting human-dominated landscapes, remain unclear. In this study, we analysed ARGs in 846 faecal samples collected from house mice (*Mus musculus*) on farms in Germany between 2016 and 2022 using metagenomic sequencing. We fitted joint species distribution models to determine which characteristics of the mouse, landscape or climate explain the presence of ARGs within the house mouse microbiome. A model incorporating all identified ARGs revealed that environmental variables and livestock accounted for over 25% of ARG variance, whereas climatic and mouse-associated characteristics accounted for less than 4% each. When differences in genomic localisation, mobility potential and drug class between ARGs are included in the model, agricultural land use and exposure to livestock interacted with genomic mobility potential. In particular, pig density was strongly associated with integron-encoded genes conferring resistance to aminoglycosides and trimethoprim. Our data suggest that landscape conditions influence the presence of specific ARGs with mobility potential within the microbiomes of house mice. A better understanding of the factors impacting ARG prevalence in wildlife species is crucial for determining transmission of antimicrobial-resistant microorganisms from animal reservoirs.

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ARGs, Landscape, Wildlife, Mice

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Professional Status of the Speaker

Postdoc

Junior Scientist Status

No, I am not a Junior Scientist.

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