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Resistome analysis of German hunted wildlife animals by capture hybridization enrichment

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Wildlife may act as vehicle for the transfer of AMR bacteria at the human-livestock-wildlife interface. By analyzing resistomes in fecal samples from hunted animals, we aimed to investigate the occurrence of AMR genes in different animal species in order to assess possible transmission pathways.
Fecal swabs were collected directly in the field from hunted animals in Brandenburg and the Harz region. Samples were enriched in buffered peptone water. Cultures from the same animal species were pooled prior to DNA extraction. Sequencing libraries were used to enrich AMR genes by bait-based hybridization capture enrichment followed by NGS with a depth of 162.5 Mbp per sample.
In the season 2024/25, we investigated 73 pooled samples (wild boar n=31; roe deer n=24; red deer n=14; fallow deer n=4) from 284 animals of 21 driven hunts for the presence of AMR genes. Resistance genes were detected in all samples. In total, AMR genes against 16 antimicrobial classes were found. Wild boar had the highest number of resistance genes per sample, with genes for up to 15 antimicrobial classes detected. 42 samples harbored ESBL/AmpC genes, with the most abundant gene families being *bla*ACC (n=19), *bla*CMY (n=18), *bla*ACT (n=12) and *bla*DHA (n=10). Five samples harbored carbapenemase encoding resistance genes belonging to the *bla*OXA, cphA- or cfiA-families. CTX-M, the most abundant ESBL family in livestock and humans, was not detected, indicating a limited anthropogenic impact on the observed patterns.

Keywords

Resistome, wildlife, ESBL

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No, I am not a Junior Scientist.

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