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## Detection and genetic characterization of *Erysipelothrix rhusiopathiae* in wild birds and poultry

### Inhalt

*Erysipelothrix rhusiopathiae* is a zoonotic, environmentally persistent bacterium causing erysipelas in livestock, wildlife and humans. Although poultry and waterfowl outbreaks are increasingly reported, the role of wild birds at the wildlife–farm interface and fluoroquinolone-resistance markers remain poorly defined. Between 2016 and 2025, we screened liver samples from 553 wild birds representing 31 species, and 205 poultry flocks: 100 chicken, 26 turkey, 38 duck, and 41 goose. Samples were tested by 16S rRNA PCR, and species identification was confirmed by *gyrB* sequencing. In confirmed positives, quinolone-resistance regions of *gyrA* and *parC* were analysed. *E. rhusiopathiae* 16S rRNA was detected in 7/553 wild birds: white storks (4/33), mute swans (2/129) and a raven (1/6). In poultry, 3/41 goose flocks were positive, whereas chicken, turkey and duck flocks were negative. Sequence analysis revealed high genetic similarity to strains previously detected in livestock, poultry and humans. Mutations consistent with fluoroquinolone resistance were detected in both *gyrA* and *parC* in one positive goose flock, while the remaining positives lacked these markers. These results indicate the occurrence of *E. rhusiopathiae* at the interface of wild birds and farmed waterfowl, with geese representing the positive poultry group. Molecular surveillance integrating wildlife, poultry and AMR markers can support risk assessment for this under-monitored zoonosis.

### Keywords

*Erysipelothrix rhusiopathiae*; wild birds; poultry; One Health; fluoroquinolone resistance

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No, I am not a Junior Scientist.

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