

Avian influenza virus detection and genetic characterization in domestic duck flocks through slurry analysis.

Inhalt

Avian influenza viruses (AIVs) circulate widely in domestic and wild birds and pose major risks to animal and public health, in particular those of high pathogenicity (HP). Ducks play a key role in AIV ecology due to frequent subclinical infections and high viral shedding. Efficient environmental surveillance approaches are needed to complement costly individual testing, especially in the context of large-scale anti-H5 vaccination as implemented in France. We evaluated the slurry produced in duck fattening units as a matrix for AIV detection and optimized molecular protocols for molecular detection and genetic characterization. Slurry samples (n = 172) were collected from 37 duck farms in southwestern France between May 2024 and February 2025. Among several extraction strategies, RNA extraction from the solid fraction using TRIzol LS followed by magnetic bead purification yielded the highest sensitivity. Using this protocol, 82% of samples tested positive for AIV RNA, with 30% of positives being H5-positive; no H7 viruses were detected. Whole-segment RT-PCR and sequencing were successful for shorter genomic segments, enabling subtype determination. Virus isolation consistently failed. These findings demonstrate that slurry is a promising matrix for AIV detection, providing valuable molecular data. Slurry-based surveillance may therefore complement individual testing and improve early warning capacities for influenza surveillance in a One Health perspective.

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Professional status of the speaker

Senior Scientist

Junior scientist status

No, I am not a junior scientist.

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