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FIRST IDENTIFICATION OF SWINE INFLUENZA A VIRUS CLADES IN SIX AUSTRIAN PIG HERDS IN 2024

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Background and Objectives

Swine influenza viruses (swIAV) are a common cause of respiratory disease in pigs, leading to production losses and posing zoonotic risk. Despite the burden associated with swIAV, surveillance in Europe, including Austria, is limited and fragmented. This study aims to identify and characterize swIAV in Austrian pig farms to raise awareness of the need for better surveillance and control. Notably, this is the first study to report the identification and sequence analysis of swIAV in Austrian pig farms.

Material and Methods

Pooled nasal swabs were collected from healthy pigs, as well as from pigs with influenza-like symptoms and screened using RT-qPCR. Influenza A genomes were amplified by one-step RT-PCR, subjected to Illumina paired-end sequencing and processed with an in-house bioinformatics pipeline. Phylogenetic analysis of the hemagglutinin (HA) and neuraminidase (NA) gene segments was performed to genotype the swIAV variants.

Results

In 2024, nasal swabs were collected from 15 pig farms in Styria and Upper Austria, yielding a total of 58 samples for analysis. Among these, 11 samples from six different farms yielded high-quality swine influenza virus sequences. Two subtypes via phylogenetic analysis were identified: H1N1, HA clade 1C.2.2, was detected in 8 samples, while H1N2, HA Clade 1C.2.4 was found in 3 samples.

Discussion and Conclusion

This study represents the first surveillance effort to document the circulation of swIAV strains in Austrian pig farms, identifying Eurasian avian lineage 1C strains, specifically H1avN1 clade 1C.2.2 and H1avN2 clade 1C.2.4, in six farms across two federal states in 2024.