

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

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## Background

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 isolates 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

Nasal swabs from healthy and symptomatic pigs were collected (Fig. 1) and screened for swIAV using qRT-PCR targeting the M gene. Positive samples underwent full genome amplification via one-step RT-PCR with universal primers for all 8 segments.

Amplified genomes were quality-checked using Agilent TapeStation (Fig. 3), then sequenced with Illumina paired-end technology. An in-house pipeline was used for genome assembly, strain subtyping, and mutation analysis.

The hemagglutinin (HA) clade typing was performed using the bv-brc tool for global comparability. A maximum-likelihood phylogeny of the obtained HA segments including three vaccine strains was created using iqtree with 1000 ultrafast bootstraps as parameter. The complete swIAV workflow is shown in Fig. 2.

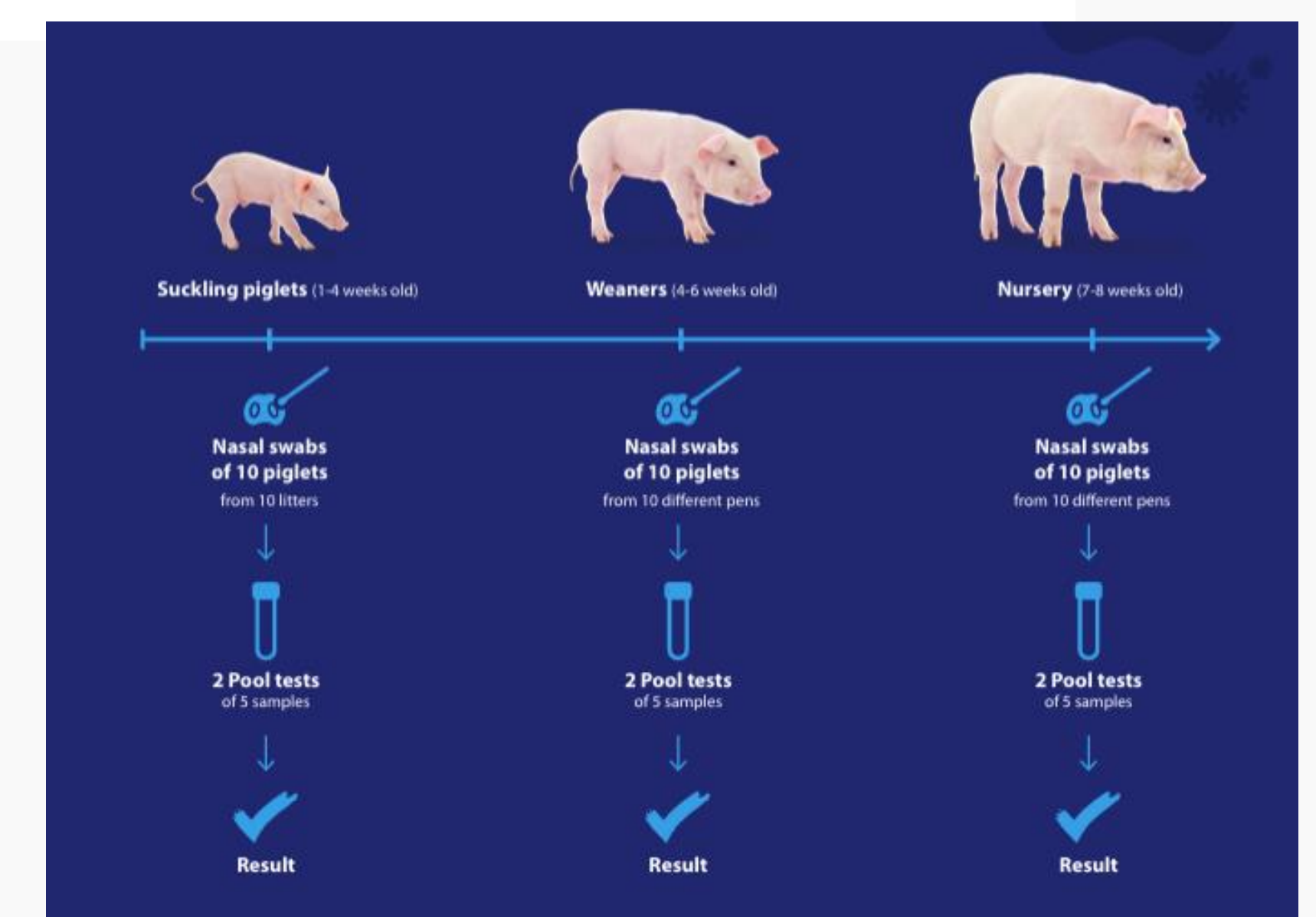


Fig. 1: Sampling approach of porcine nasal swabs (Ceva)

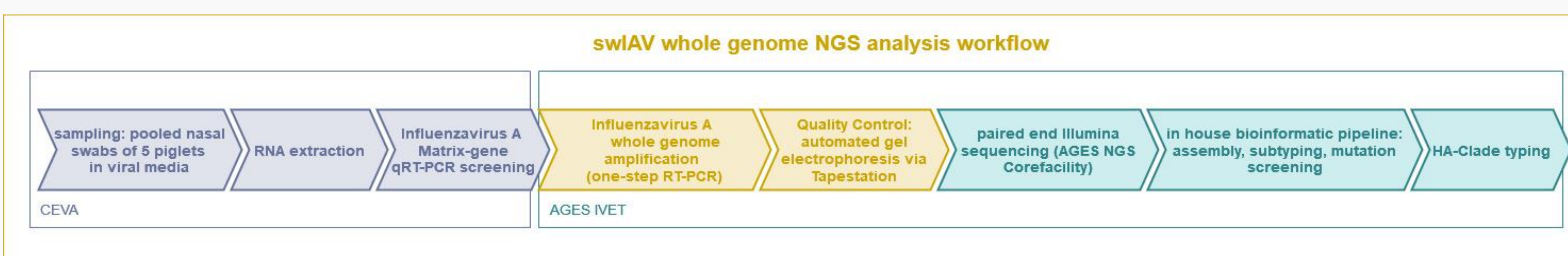


Fig. 2: Schematic illustration of the swIAV whole genome NGS analysis workflow

## 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: Eurasian avian-like (EA) H1N1, HA clade 1C.2.2, was detected in 8 samples, while EA H1N2, HA clade 1C.2.4 was found in 3 samples. In summary, HA clade 1C.2.2 was detected in 4 farms and HA clade 1C.2.4 was detected in two farms.

The identified HA-segments cluster closely to sequences used by commercial vaccines (e.g. RESPIORRC FLUPANH1N1 for H1pdm and FLU3 for H1av and H1 seasonal), indicating a good genetic coverage (Fig. 4). For the detected strains respiratory symptoms like sneezing, coughing, pneumonia and dyspnea were described by the veterinarians. Moreover, fever was also reported.

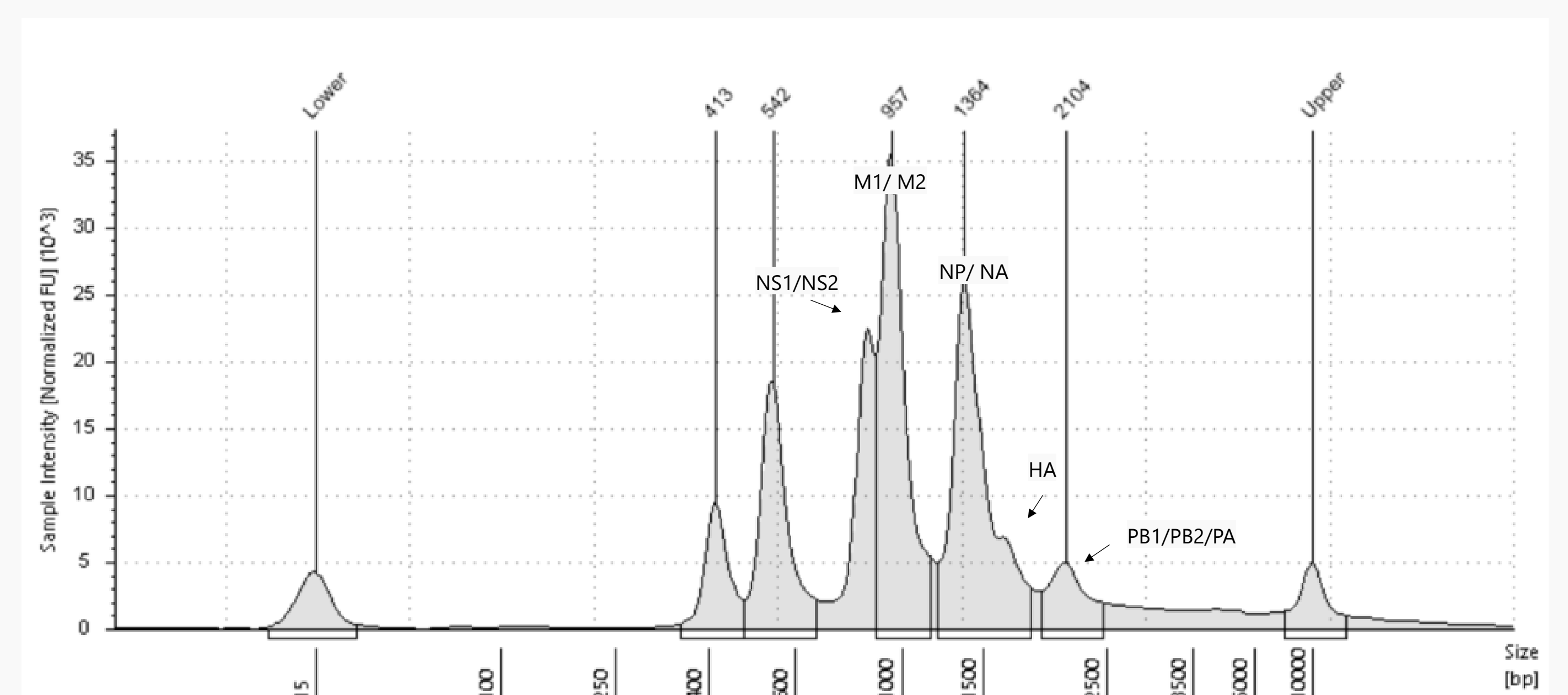


Fig. 3: TapeStation electropherogram of amplified full genome swIAV sample with corresponding segments

## Discussion & 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.

The success of this study highlights the advantages of genetically characterizing and surveilling circulating swIAV in an effort to stay on top of viral developments such as genetic reassortments and genetic drift. This is especially crucial for vaccine development and improvement.

## Funding

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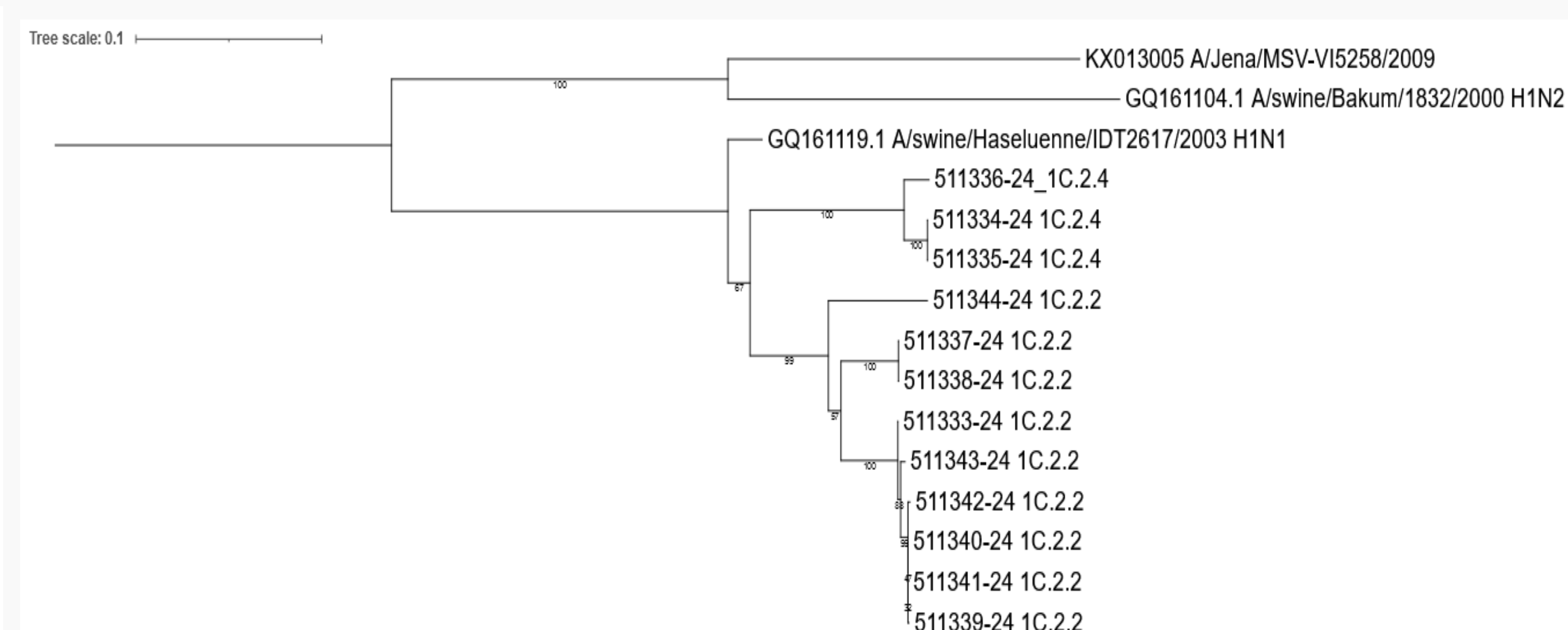


Fig. 4: Phylogeny of HA segments annotated with the respective clades in comparison to vaccine HA-segments: KX013005.1 (H1N1pdm), GQ161104.1 (H1avN1), GQ161119.1 (H1seasonalN2)

## References

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