



Swine Influenza A virus surveillance in Switzerland from genotype to phenotype

Annual ESFLU meeting Copenhagen, 25 – 27 March 2025 Ronald Dijkman, Ph.D.

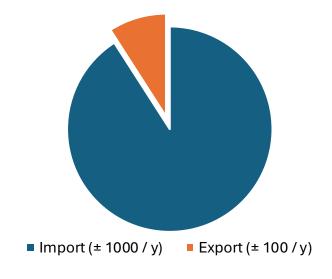


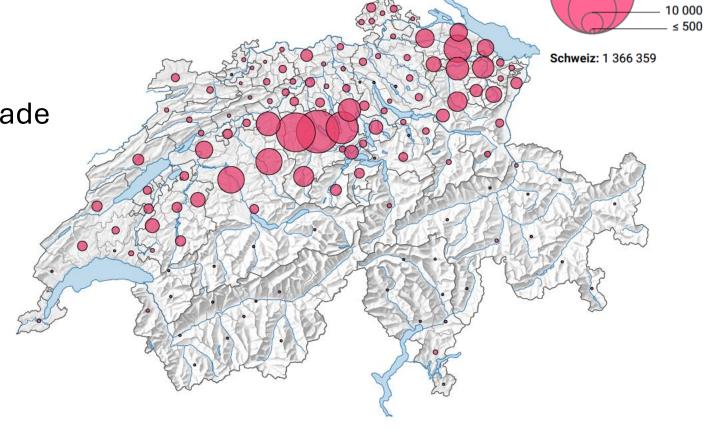


Swine industry in Switzerland

• Strict regulation on live animal trade

Annual Trade (1998-2022)





Distribution of (>5500) pig farms in CH

No. pigs

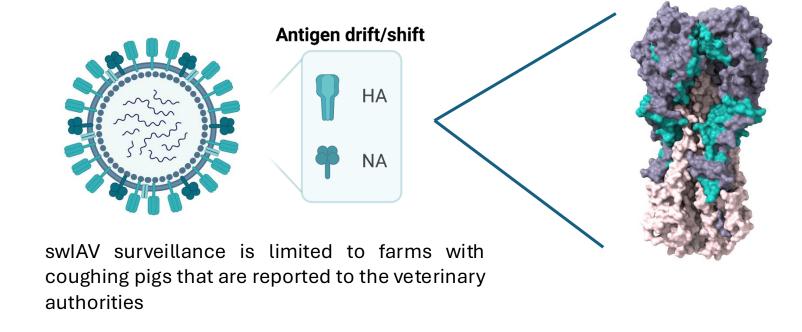
156 277

50 000

No active vaccination program

Sources: Swiss Federal Statistical Office (BFS)
Federal Office for Customs and Border Security (FOCBS)
Federal Food Safety and Veterinary Office (FSVO)

swIAV surveillance in Switzerland



Lechmann et al. medRxiv 2025

Missing information:

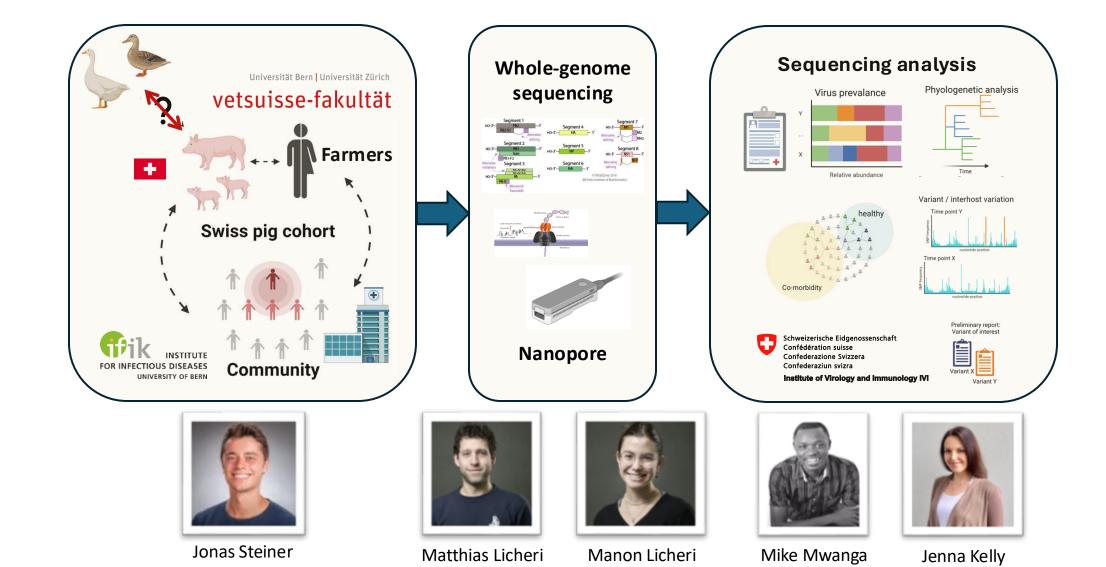
- Antigenic **Sa**, **Sb**, and **Cb** sites
- Receptor binding regions
 - D190/D130 loops

Whole genome information

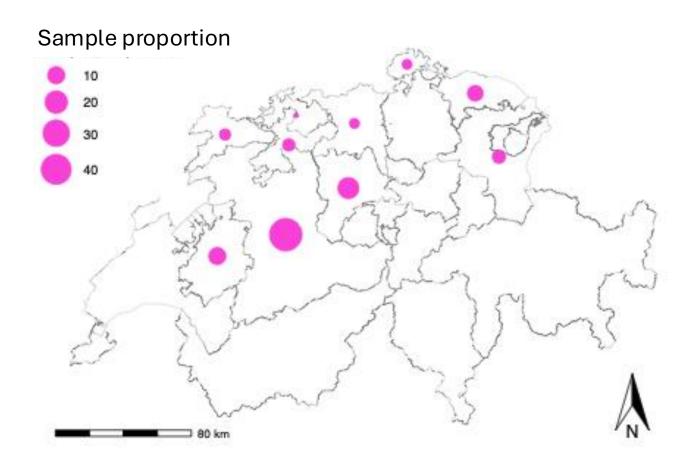
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PB2 = Viral replication activity
PB1 = PB1-F2 (pathogenicity marker)
PA = resistance to Baloxovir marboxil
HA = receptor tropsim & pH stability
NP = resistance to human MxA
NA = resistance to Zanamivir / Oseltamivir
M = viral morphology - respiratory transmission
NS = supression host response
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Detailed genomic, molecular, and biological characterisation for swIAV is incomplete.

Genomic Surveillance of IAV in Humans and Swine



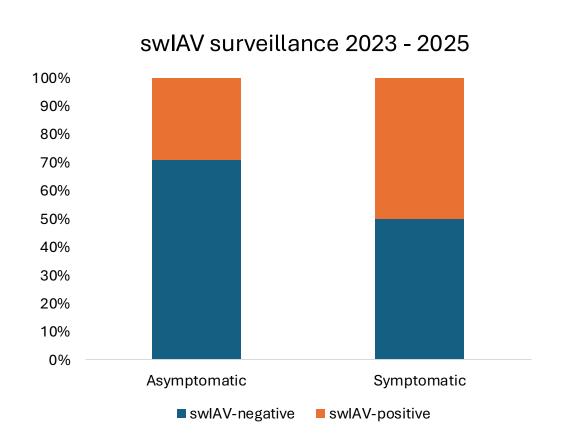
Active swIAV surveillance



≥1600 samples from 102 farms analysed (2023 – 2025)

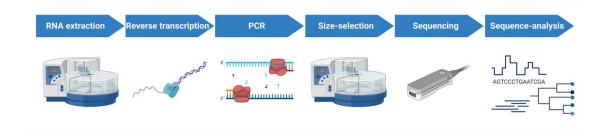
- Voluntarily nasal swab of farm personnel
- Fatteners and weaners

Active swIAV surveillance

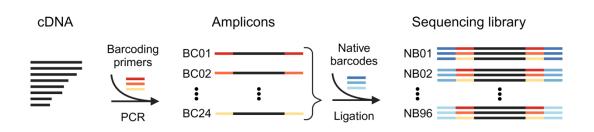


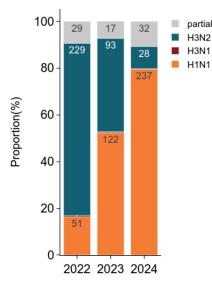
- Prevalence of swIAV in asymptomatic pigs
 - ~ 30% of Swine farms are positive
- First description of swIAV prevalence in asymptomatic pigs in Switzerland
- 143 qRT-PCR swIAV-positive samples
 - 40 have been analysed with WGS

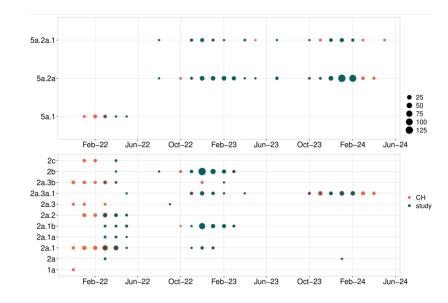
Optimized IAV WGS approach



Increased sensitivity, works on diverse avian, swine and human subtypes







Scalable and high throughput WGS of IAV

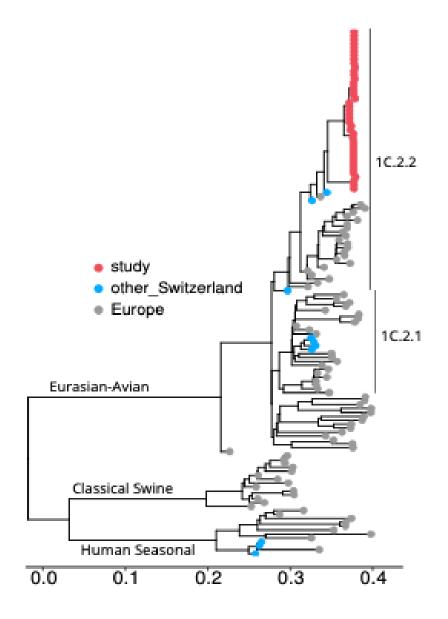
• NGS cost reduction ≥ 8-fold

Phylogenetic analysis

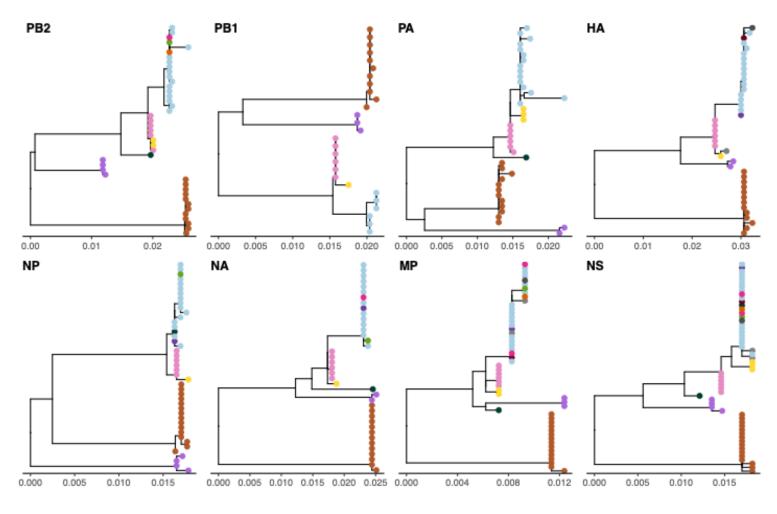
 Phylogenetically distinct swIAV strains from the rest of Europe

Two distinct 1C.2.2 clusters

Unique swIAV evolution

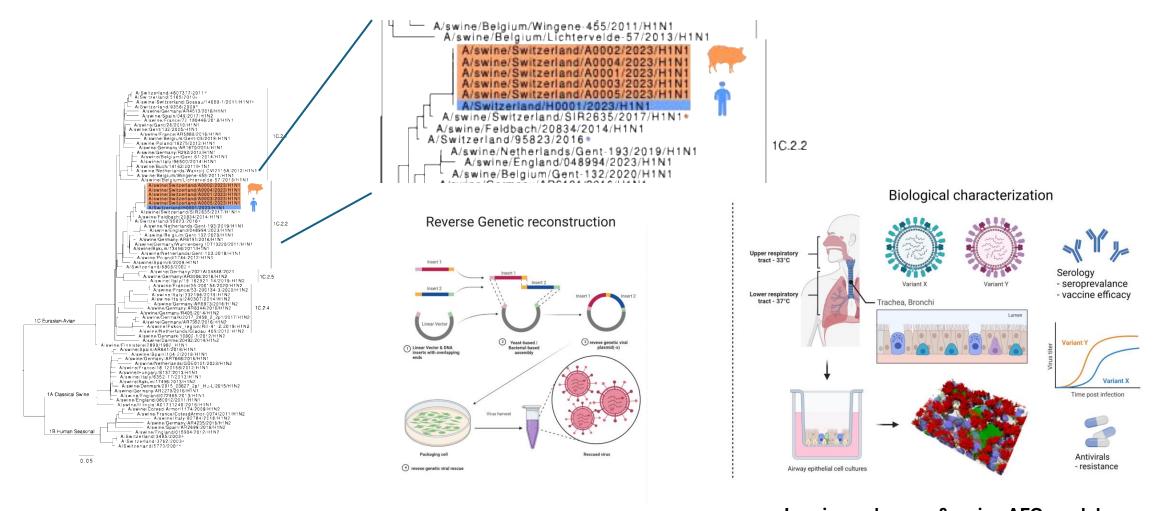


Phylogenetic analysis



Heterogeneity among genomic segments and swine farms

A curious case of swIAV



In primary human & swine AEC models

Summary

- Active genomic surveillance of swIAV with WGS genotypic characterization
- Circulation of swIAV in symptomatic and asymptomatic pigs
- Swiss-specific swIAV evolution
 - With possible Cantonal differences
- Identification of a potential zoonotic event
- Characterising IAV from genotype to phenotype to generation of a biologically accurate risk profile.

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