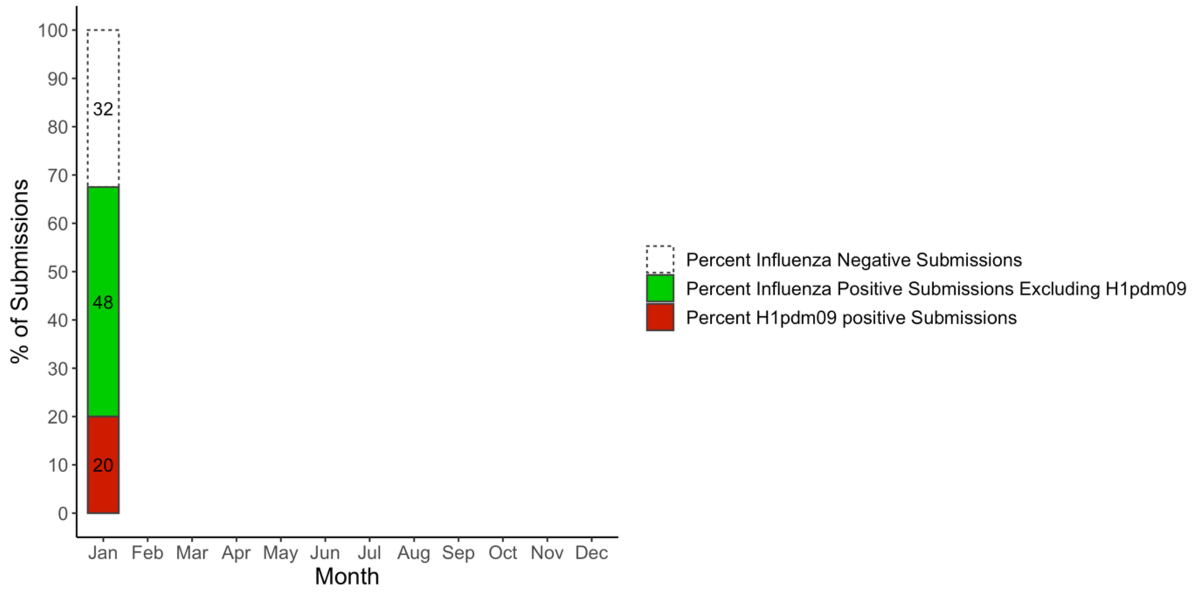
Surveillance of Influenza A virus in Danish pigs

Samples and results 2024

The table illustrate the number of samples, submissions and herds that contributed to the surveillance program each month and for the whole year. In addition, the results of the influenza A virus and H1pdm09 screening are shown.

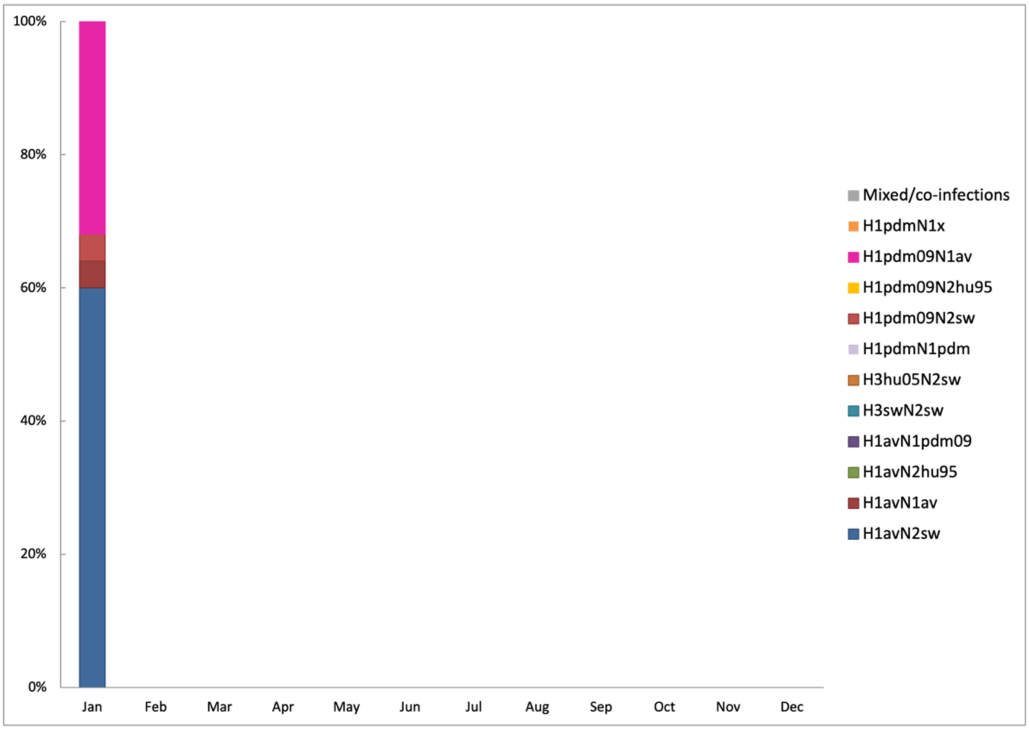
	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
Received												
Samples	156											
Submissions	40											
Herds	40											
Influenza positive												
Samples	70											
Submissions	27											
Herds	27											
H1pdm09 positive												
Samples	24											
Submissions	8											
Herds	8											

In January, 40 submissions from 40 herds registered with different CHR numbers were received. On average, each submission consisted of 3.9 samples. The percentage of the submissions that were positive for Influenza A virus was 67.5%, which is slightly higher compared to the previous months, but similar to January 2023 (64%). All influenza A virus positive samples were tested for the presence of H1pdm09. Overall, 30% of the submissions testing positive for the influenza A virus were found to be positive for H1pdm09.



The figure illustrates the percentage of influenza A virus negative and positive submissions including the proportion of H1pdm09 positive submissions. The proportion of influenza positive submissions and the proportion hereof of H1pdm09 are more or less consistent with the numbers observed in 2023.

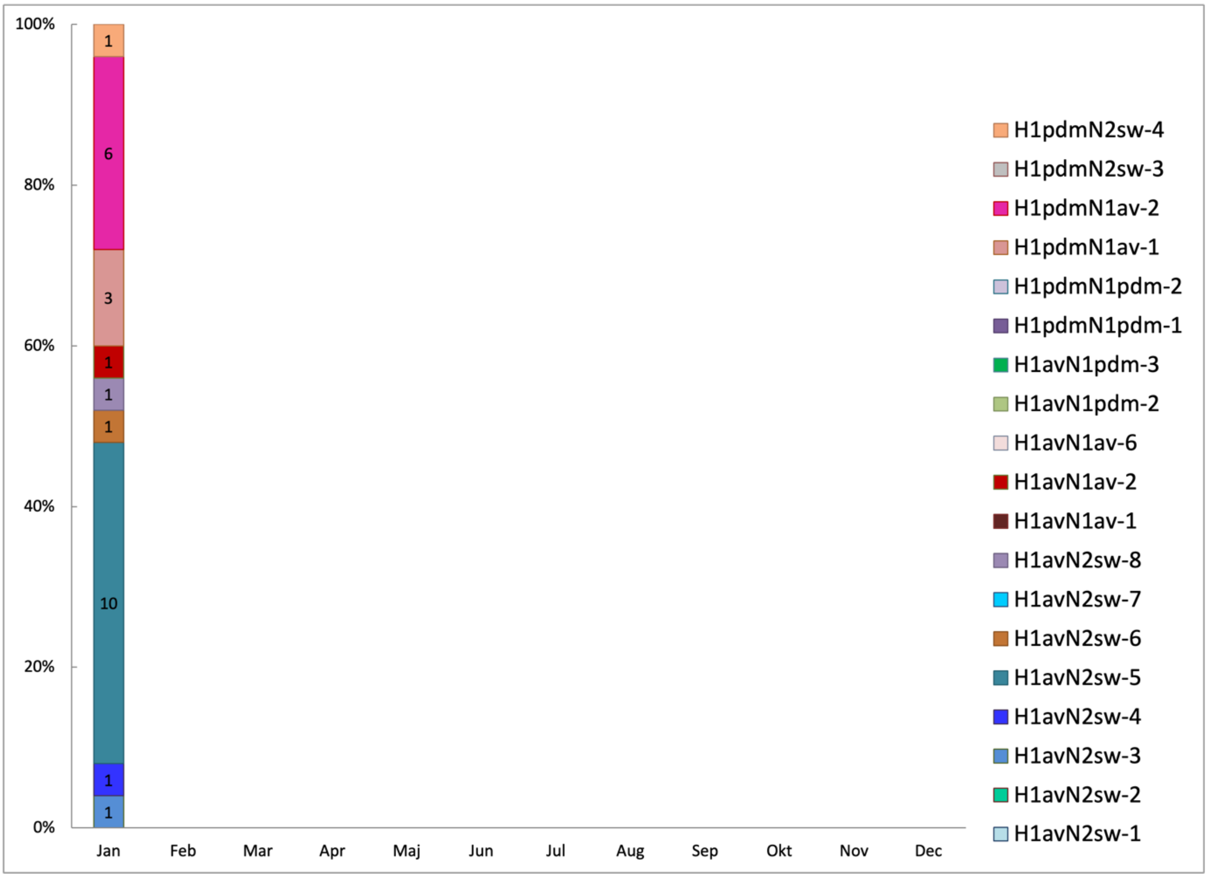
Distribution of swine influenza A virus subtypes



Swine influenza A virus can be classified into subtypes and genotypes. The subtype describes the combination of HA and NA surface gene segments, and the genotype describes the combination of all eight segments based on their genetic origin. Information on the contemporary circulating swine influenza A virus subtypes is essential for the update of vaccination protocols, optimization of the diagnostic assays and for evaluation of the zoonotic risk.

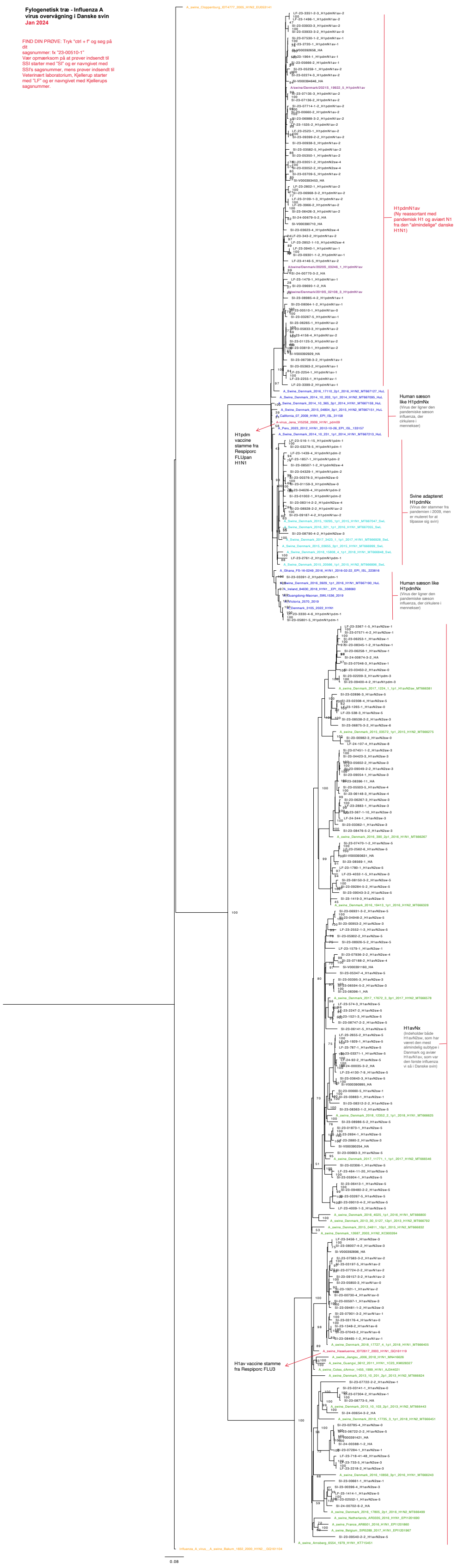
In January, the full subtype (both HA and NA gene segments) was determined for 25 submissions. The H1avNx viruses were slightly dominating over H1pdm09 subtype, with H1avN2sw (n=15 submissions) being the most prevalent. The determined H1pdm09 subtypes were H1pdmN1av (n=8 submissions) and H1pdmN2sw (n=1).

Distribution of swine influenza A virus genotypes



For January, 25 submissions were genotyped. For the H1avN2sw viruses, the dominating genotypes was H1avN2sw-5 (n=10) with a mix of avian-like swine and H1pdm origin internal genes. Additionally, one submission was genotyped H1avN1av-2, which contained mainly gene segments of avian-like swine origin and the MP segment from pandemic origin. For the H1pdmNx viruses, we genotyped six submissions with H1pdmN1av-2, three with H1pdmN1av-1 and one with H1pdmN2sw-4.

Phylogenetic analysis



Fylogenetisk træ - Influenza A virus overvågning i Danske svin
Jan 2024

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sagsnummer: fx "23-00510-1"
Vær opmærksom på at prøver indsendt til SSI starter med "SI" og er navngivet med SSI's sagsnummer, mens prøver indsendt til Veterinært laboratorium, Kjellerup starter med "LF" og er navngivet med Kjellerups sagsnummer.