

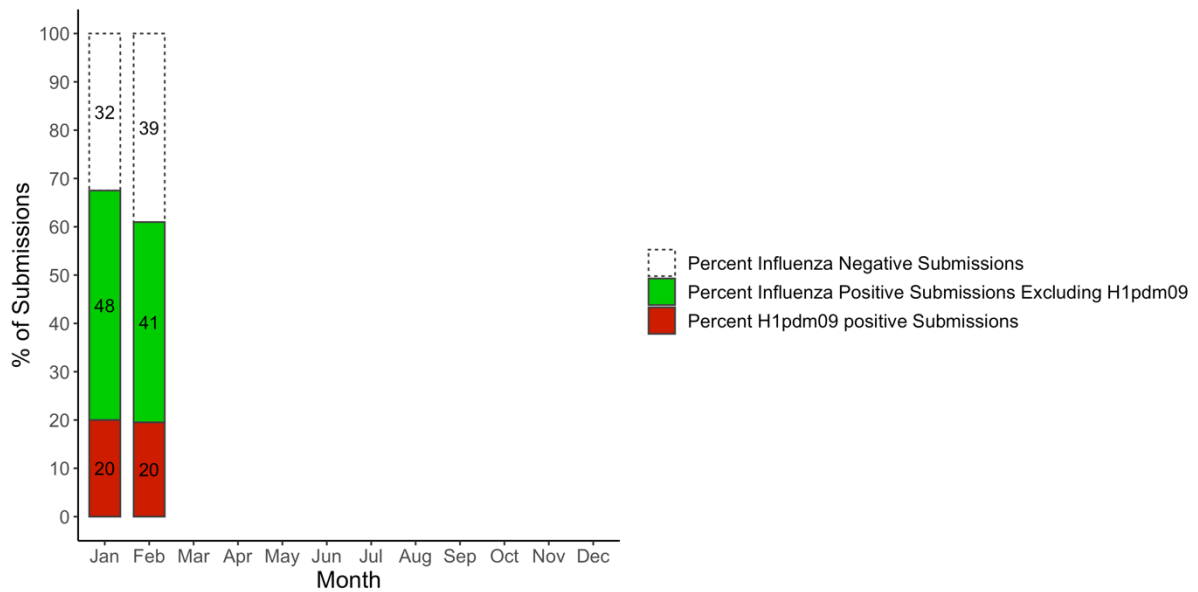
Surveillance of Influenza A virus in Danish pigs

Samples and results 2024

The table illustrates 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.

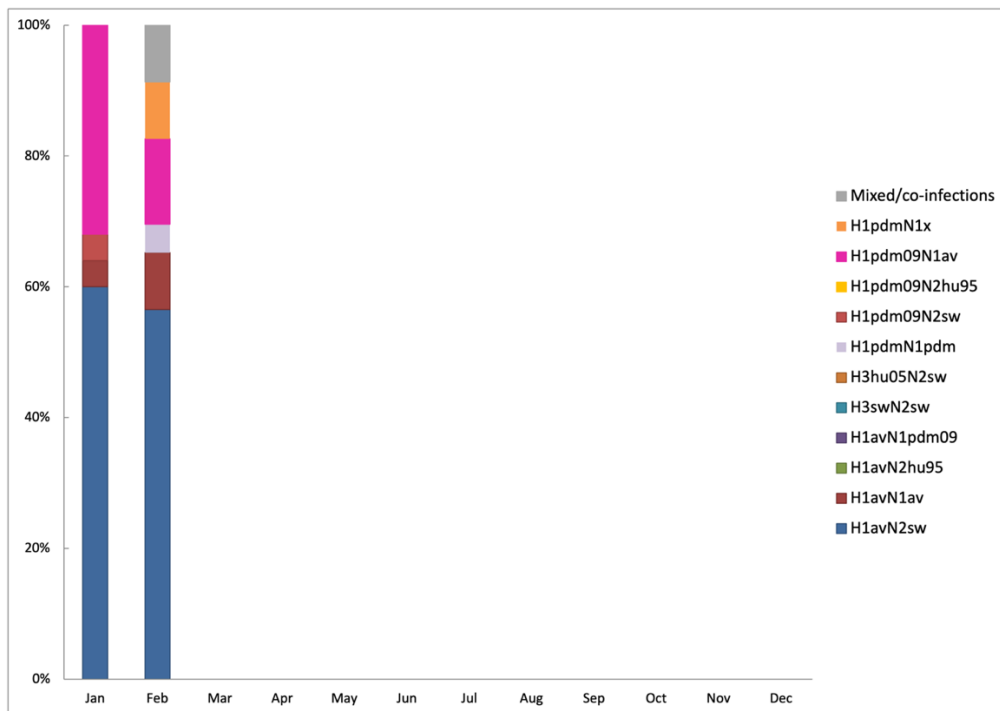
	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
Received												
Samples	156	140										
Submissions	40	41										
Herds	40	41										
Influenza positive												
Samples	70	53										
Submissions	27	25										
Herds	27	25										
H1pdm09 positive												
Samples	24	14										
Submissions	8	8										
Herds	8	8										

In February, 41 submissions from 41 herds registered with different CHR numbers were received. On average, each submission consisted of 3.4 samples. The percentage of the submissions that were positive for Influenza A virus was 60.9%, which is slightly lower compared to the previous month. All influenza A virus positive samples were tested for the presence of H1pdm09. Overall, 32% 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 January 2024 and across 2023.

Distribution of swine influenza A virus subtypes

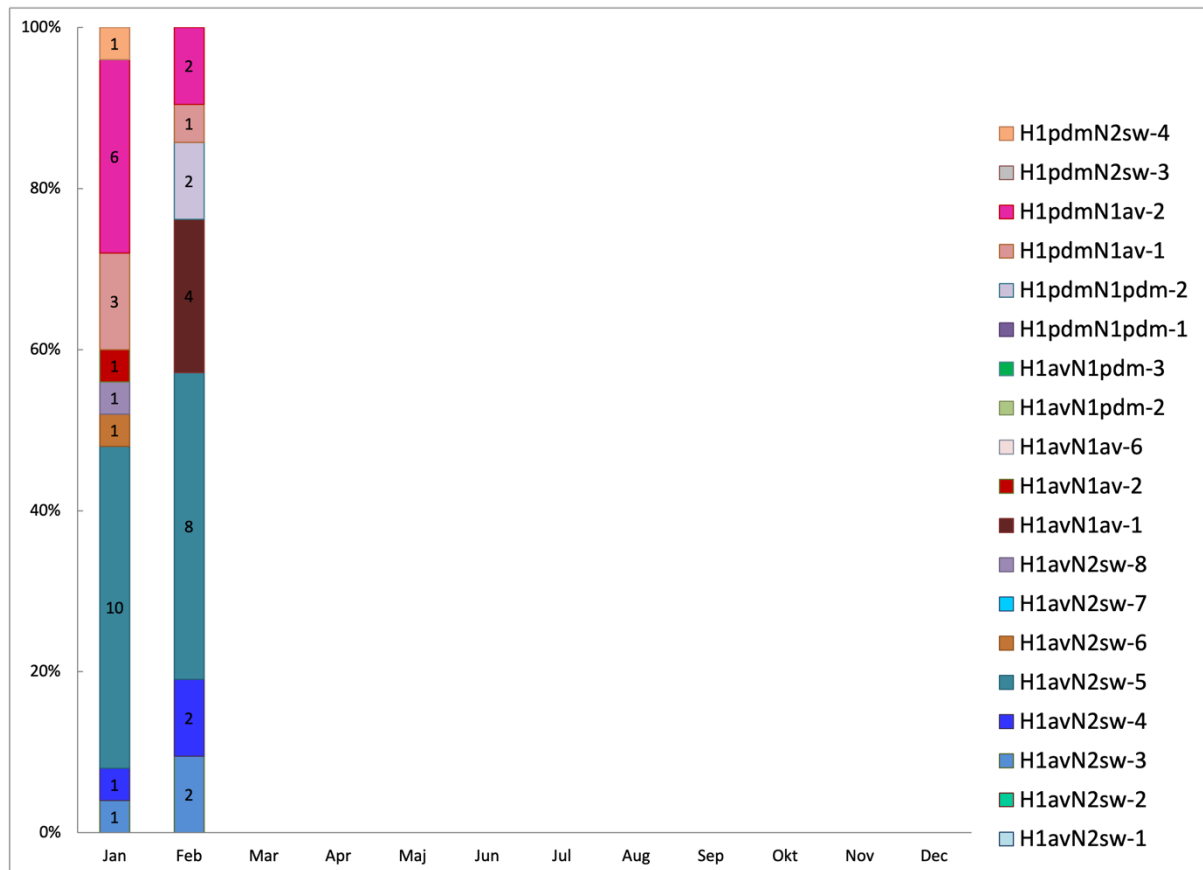


Swine influenza A virus can be classified into subtypes and genotypes. The subtype describes the combination of HA and NA surface gene segments, and the genotype describes the combination of all eight segments based on their genetic origin. Information on the contemporary circulating swine

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 February, the full subtype (both HA and NA gene segments) was determined for 23 submissions. The H1avNx viruses were slightly dominating over H1pdm09 subtype, with H1avN2sw (n=13 submissions) being the most prevalent. The determined H1pdm09 subtypes were H1pdmN1av (n=3 submissions), H1pdmN1pdm (n=1) and H1pdmNx (n=2). Furthermore, two samples were identified as mixed/co-infected.

Distribution of swine influenza A virus genotypes



For February, 21 submissions were genotyped. For the H1avN2sw viruses, the dominating genotypes was H1avN2sw-5 (n=8), with a mix of avian-like swine and H1pdm origin internal genes, followed by H1avN2sw-3 (n=2) and H1avN2sw-4 (n=2). Additionally, four submissions were genotyped H1avN1av-1, which contained all gene segments of avian-like swine origin. For the H1pdmNx viruses, we genotyped five submissions: one with H1pdmN1av-1, two with H1pdmN1av-2 and one with H1pdmN1pdm-2.

Phylogenetic analysis

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

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