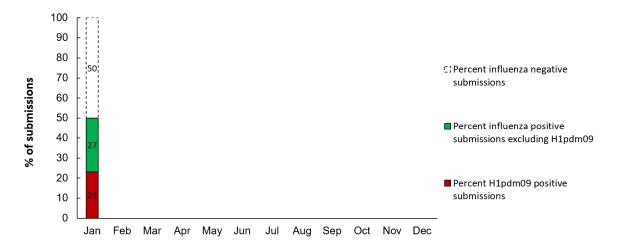
Surveillance of Influenza A virus in Danish pigs

Samples and results 2025

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	60											
Submissions	22											
Herds	22											
Influenza positive												
Samples	28											
Submissions	11											
Herds	11											
H1pdm09												
positive												
Samples	13											
Submissions	5			•		•						
Herds	5											

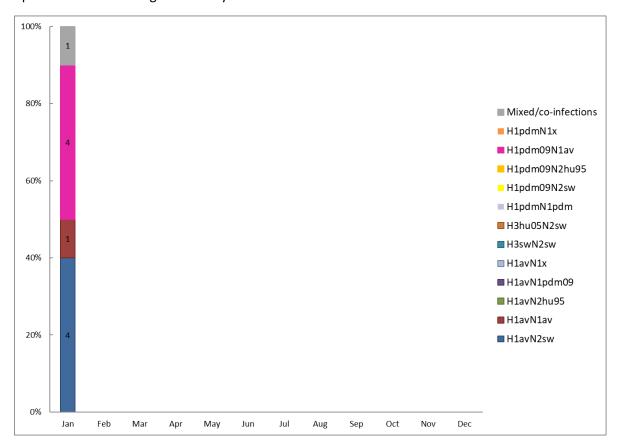
In January, 22 submissions from 22 herds registered with different CHR numbers were received. On average, each submission consisted of 2.7 samples. The percentage of influenza positive submissions was 50 %, which is slightly lower than the previous month (December 2024). All influenza A virus-positive samples were tested for the presence of H1pdm09. Overall, 45% of the submissions testing positive for the influenza A virus were positive for H1pdm09, which is markedly higher than the level observed the last semester of 2024.



The figure illustrates the percentage of influenza A virus negative and positive submissions including the proportion of H1pdm09 positive submissions.

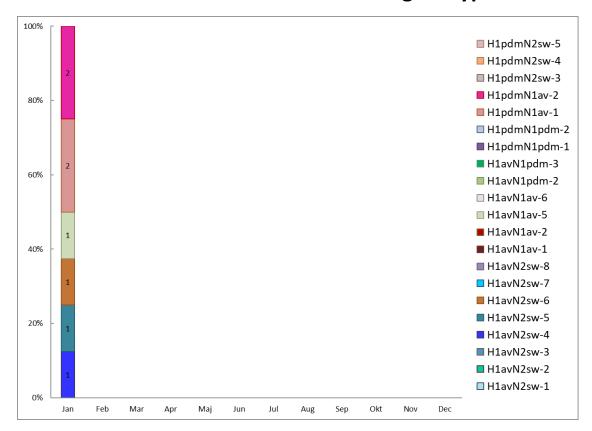
Distribution of swine influenza A virus subtypes

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 genome 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 10 submissions. There was an equal distribution between the H1avN2sw (n= 4) and H1pdmN1av (n=4) viruses, and additionally one H1avN1av virus and one mixed infection were detected.

Distribution of swine influenza A virus genotypes



For January, 8 submissions were genotyped and included six different genotypes. H1pdmN1av-1 and 2 were found in two submissions, respectively, whereas H1avN2sw-4, -5 and -6 were detected in one submissions respectively along with a single case of H1avN1av-6.

Phylogenetic analysis

