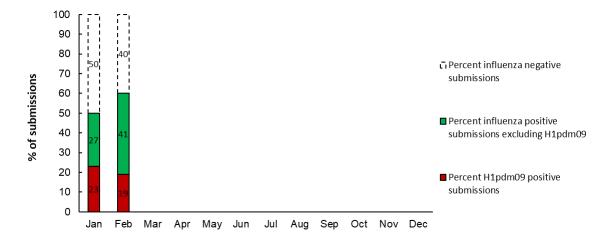
Surveillance of Influenza A virus in Danish pigs

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	151										
Submissions	22	52										
Herds	22	51										
Influenza positive												
Samples	28	69										
Submissions	11	31										
Herds	11	31										
H1pdm09 positive												
Samples	13	14										
Submissions	5	10										
Herds	5	10	•	•			•	•	•			•

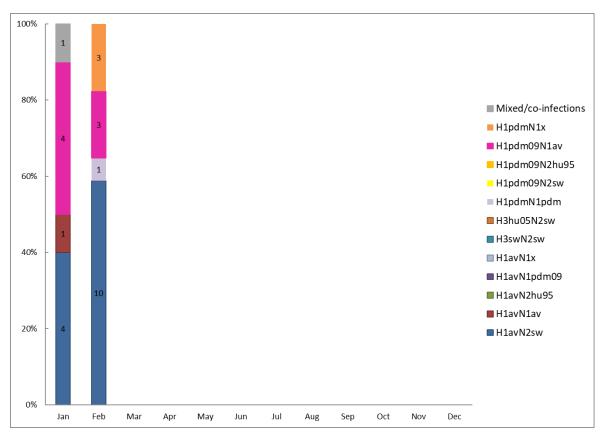
In February, 52 submissions from 51 herds registered with different CHR numbers were received. On average, each submission consisted of 2.9 samples. The percentage of influenza positive submissions was 60 %, which is higher than the previous month. All influenza A virus-positive samples were tested for the presence of H1pdm09. Overall, 32% of the submissions testing positive for the influenza A virus were positive for H1pdm09, which is lower than the level observed in January.



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

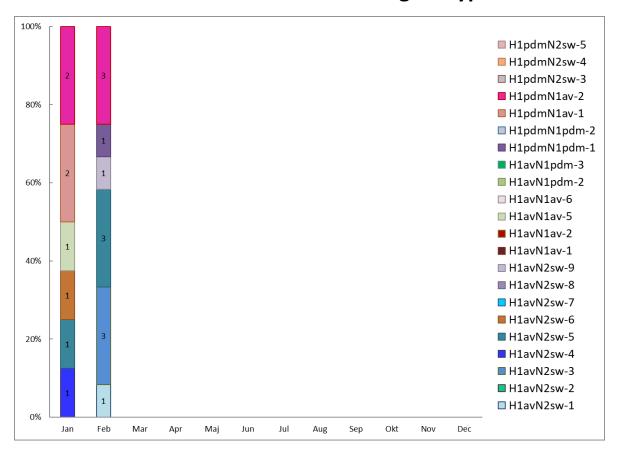
Distribution of swine influenza A virus subtypes

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 February, the full subtype (both HA and NA gene segments) was determined for 17 submissions. The majority of were of the H1avN2sw subtype, and H1pdmN1av or H1pdmN1x were represented in six submission.

Distribution of swine influenza A virus genotypes



For February, 12 submissions were genotyped and included six different genotypes. H1avN2sw-3, H1avN2sw-5 and H1pdmN1av-2, were observed in three submissions, respectively, whereas one H1pdmN1pdm-1 and one H1avN2sw-1 were also observed. In addition, a novel H1avN2sw-9 genotype was identified carrying the PB2, NP and M gene of H1N1pdm09 origin and the PA, PB1 and NS gene of Eurasian avian-like H1N1 origin.

Phylogenetic analysis

