

Surveillance of Influenza A virus in Danish pigs

Samples and results 2026

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	161											
Submissions	48											
Herds	45											
Influenza positive												
Samples	92											
Submissions	31											
Herds	31											
H1pdm09 positive												
Samples	43											
Submissions	13											
Herds	13											

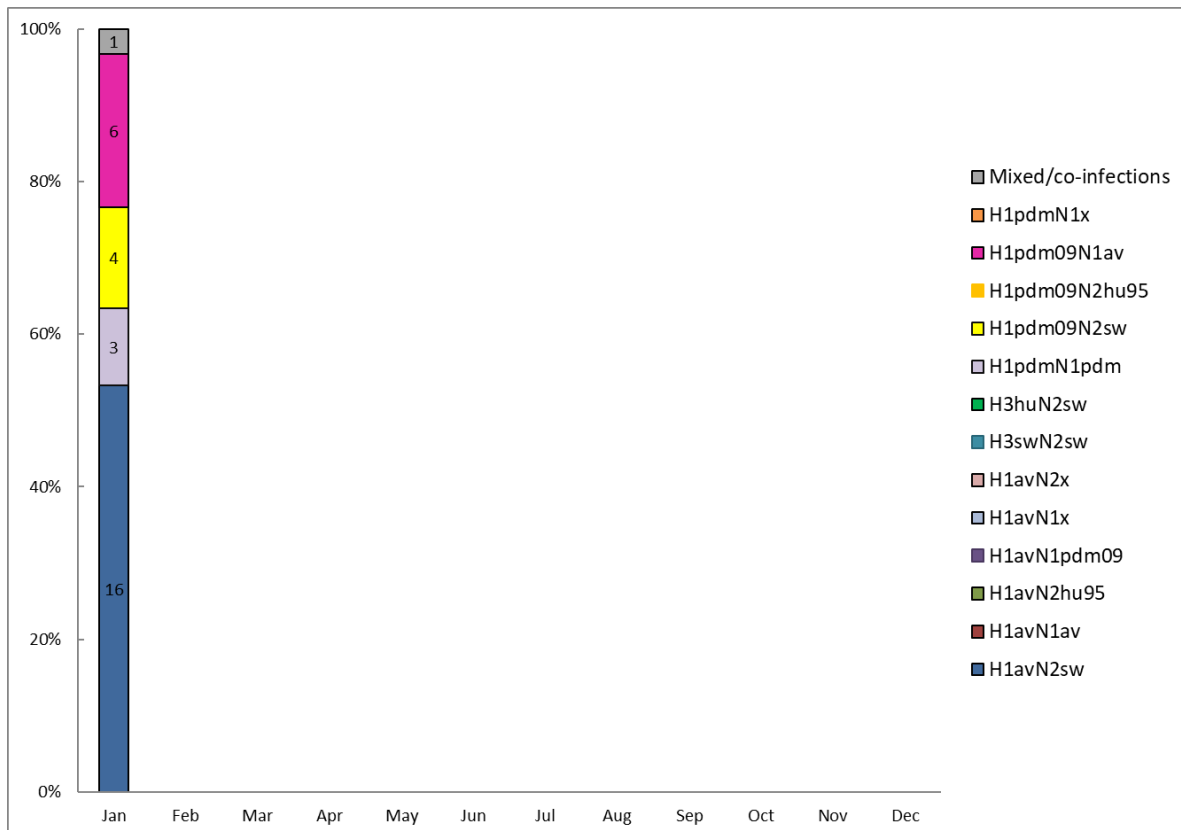
In January, 48 submissions from 45 herds registered with different CHR numbers were received. On average, each submission consisted of 3.3 samples. The percentage of influenza positive submissions was 65 %, that is slightly higher than the level observed in December 2025. All influenza A virus-positive samples were tested for the presence of H1pdm09. Overall, 42 % of the submissions testing positive for the influenza A virus were positive for H1pdm09, again similar to the level observed in December 2025.



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 identified for 30 submissions. The majority were of the H1avN2sw subtype (n=16) while the H1pdm09N1av was observed in six submissions. In addition, H1pdmN2sw and H1pdmN1pdm and were observed in four and three submissions, respectively. This month one submission had two different subtypes circulating in different age groups within the same herd (CHR-number).

Distribution of swine influenza A virus genotypes



For January, 29 submissions were genotyped. In total eleven different genotypes were observed, with H1avN2sw-5 being most often detected (n=6). H1avN2sw-3 and H1pdmN1av-1 were observed in four submissions, respectively, and H1avN2sw-4 and H1pdmN2sw-4 were observed in three submissions, respectively, whereas the remaining detected genotype were only observed in one-two submissions.

Phylogenetic analysis

Fylogenetisk træ - Influenza A virus overvågning i danske grise

Januar 2026

FIND DIN PRØVE: Tryk "ctrl + f" og søg på dit sagsnummer: fx "25-03138-4"

Vær opmærksom på at prøver indsendt til SSI starter med "SIO" og er navngivet med SSI's sagsnummer, mens prøver indsendt til Veterinært laboratorium, Kjellerup starter med "LF" og er navngivet med Kjellerups sagsnummer.

1A, 1B og 1C clades (i følge BV-BRC.org) er angivet på referencesekvenser som suffix i sekvensnavnet

