

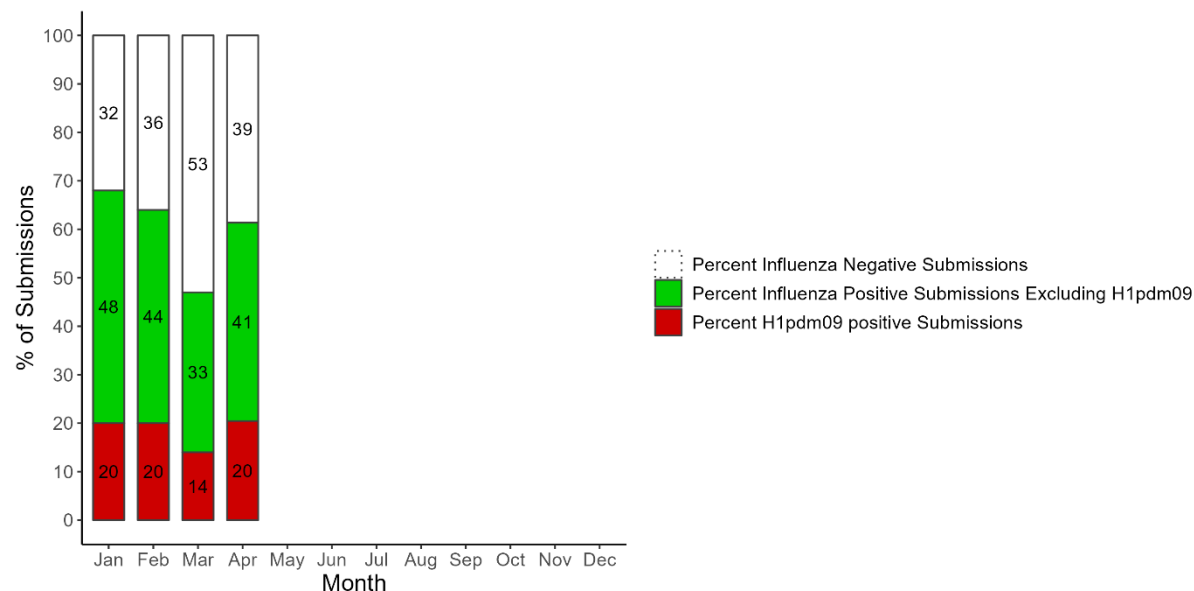
Surveillance of Influenza A virus in Danish pigs

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.

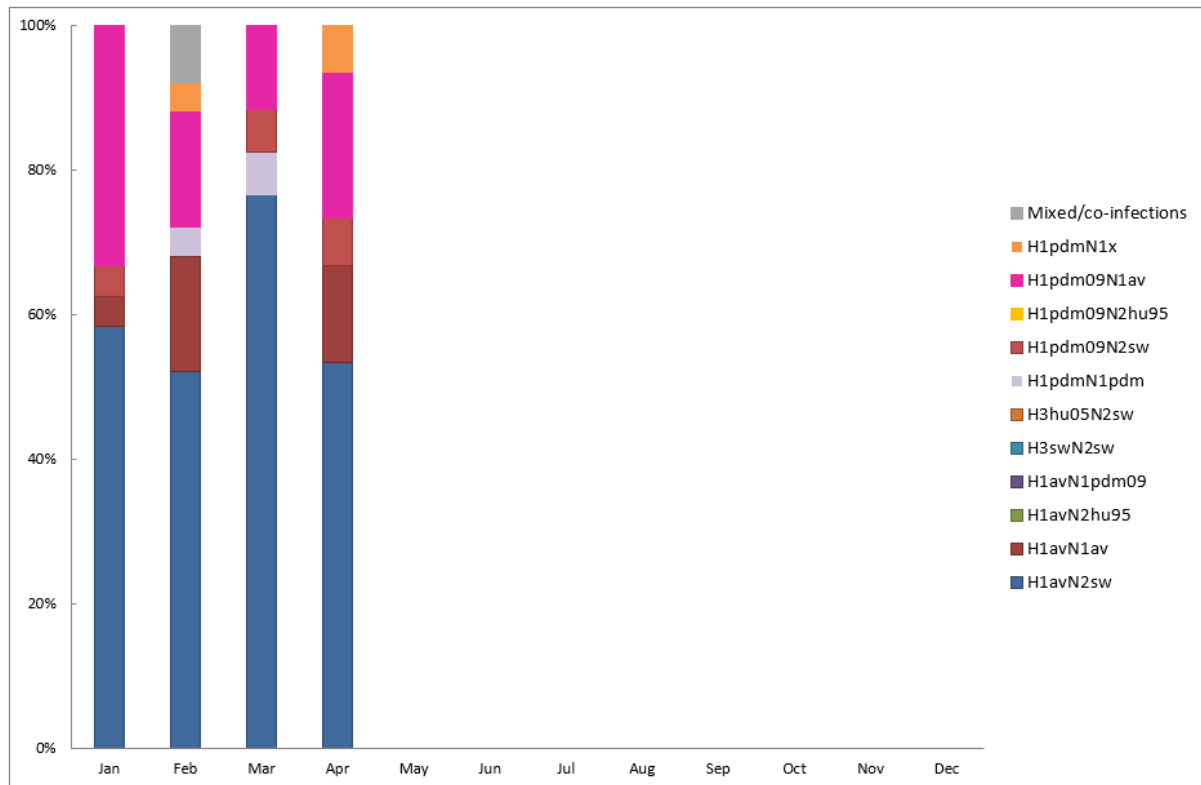
	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
Received												
Samples	156	140	121	141								
Submissions	40	41	36	44								
Herds	40	41	34	42								
Influenza positive												
Samples	70	53	43	60								
Submissions	27	25	17	27								
Herds	27	25	17	27								
H1pdm09 positive												
Samples	24	14	10	22								
Submissions	8	8	5	9								
Herds	8	8	5	9								

In April, 44 submissions from 42 herds registered with different CHR numbers were received. On average, each submission consisted of 3.2 samples. The percentage of the submissions that were positive for Influenza A virus was 61%, which is on par with January and February and greater than March. All influenza A virus positive samples were tested for the presence of H1pdm09. Overall, 33% 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 share of submissions with H1pdm are back to 20 % like the first two months of the year and the total share of positive submissions are also normalized after the low numbers for March.

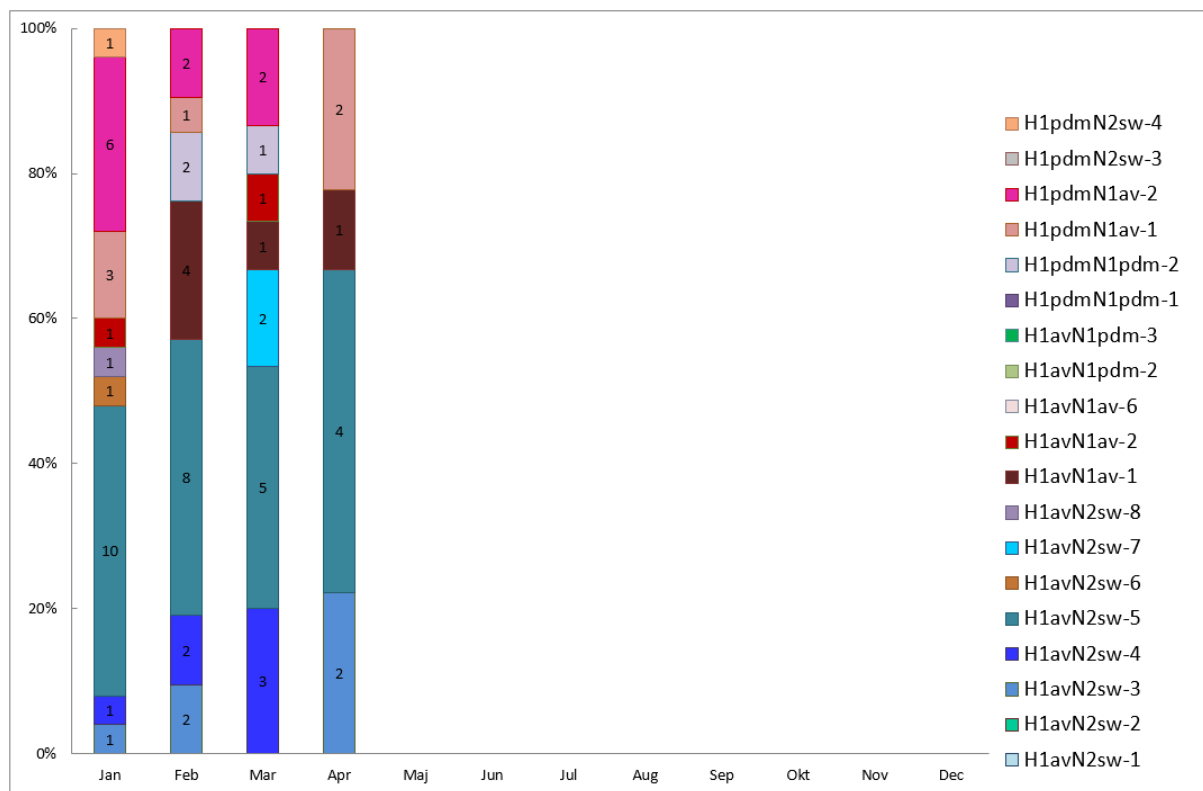
Distribution of swine influenza A virus subtypes



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 April, the full subtype (both HA and NA gene segments) was determined for 15 submissions. The H1avNx viruses were dominating over H1pdm09 subtype, with H1avN2sw (n=8 submissions) being the most prevalent followed by H1avN1av (n=2). The determined H1pdm09 subtypes were H1pdmN1av (n=3 submissions), and H1pdmN2sw (n=1).

Distribution of swine influenza A virus genotypes



For April, 9 submissions were genotyped. For the H1avN2sw viruses, the dominating genotypes was H1avN2sw-5 (n=4), with a mix of avian-like swine and H1pdm origin internal genes, followed by H1avN2sw-3 (n=2). H1avN1av-1 (n=1), which contained all gene segments of avian-like swine origin was also detected. For the H1pdmNx viruses, we genotyped two submissions both with H1pdmN1av-1.

Phylogenetic analysis

