

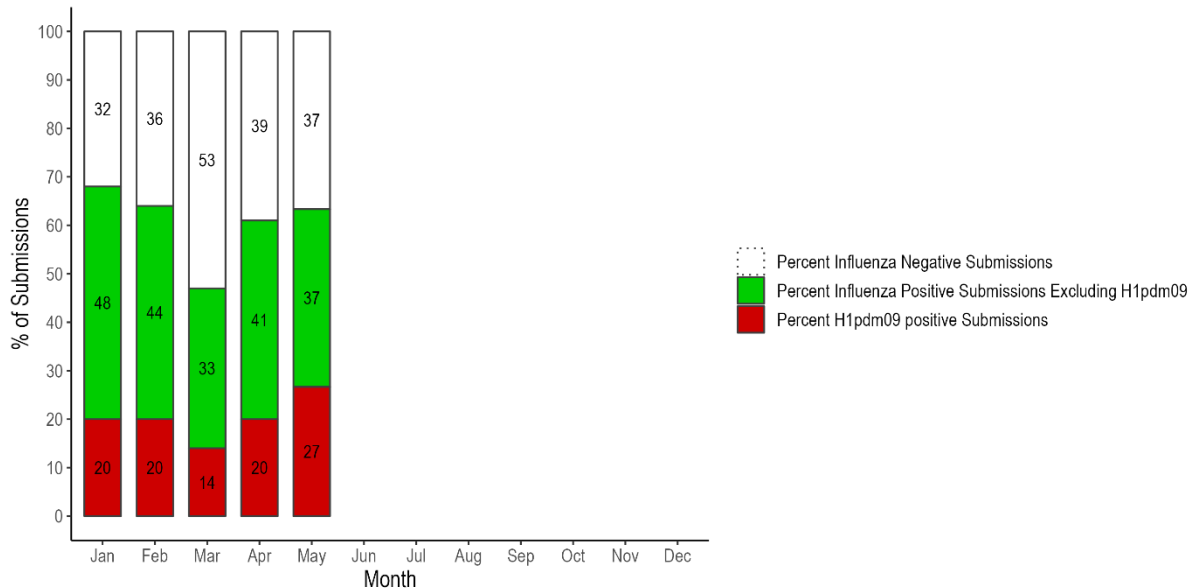
# Surveillance of Influenza A virus in Danish pigs

## 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.

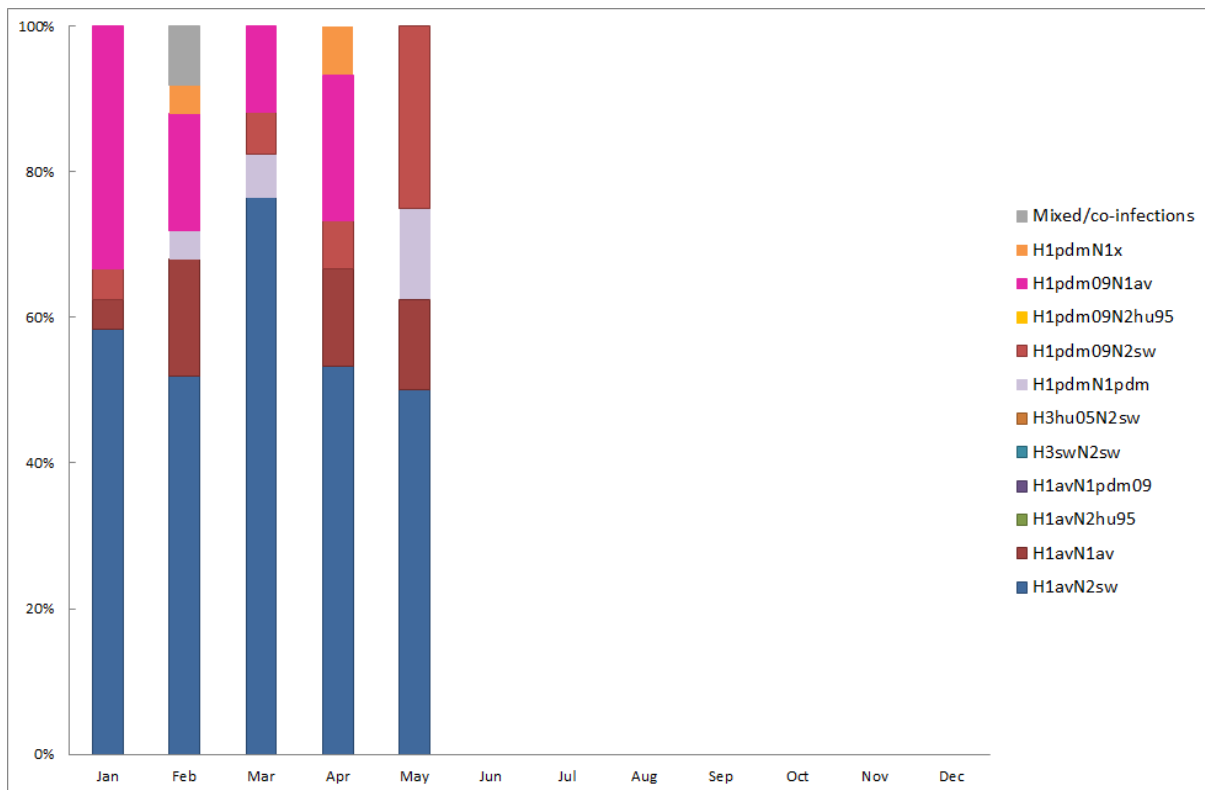
	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
<b>Received</b>												
Samples	156	140	121	141	107							
Submissions	40	41	36	44	30							
Herds	40	41	34	42	30							
<b>Influenza positive</b>												
Samples	70	53	43	60	44							
Submissions	27	25	17	27	19							
Herds	27	25	17	27	19							
<b>H1pdm09 positive</b>												
Samples	24	14	10	22	17							
Submissions	8	8	5	9	8							
Herds	8	8	5	9	8							

In May, 30 submissions from 30 herds registered with different CHR numbers were received. On average, each submission consisted of 3.6 samples. The percentage of submissions positive for Influenza A virus was 63%, which is on par with January, February and April, and greater than March. 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 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 is higher than for previous months, while the total share of positive submissions is normalized after the low numbers for March.

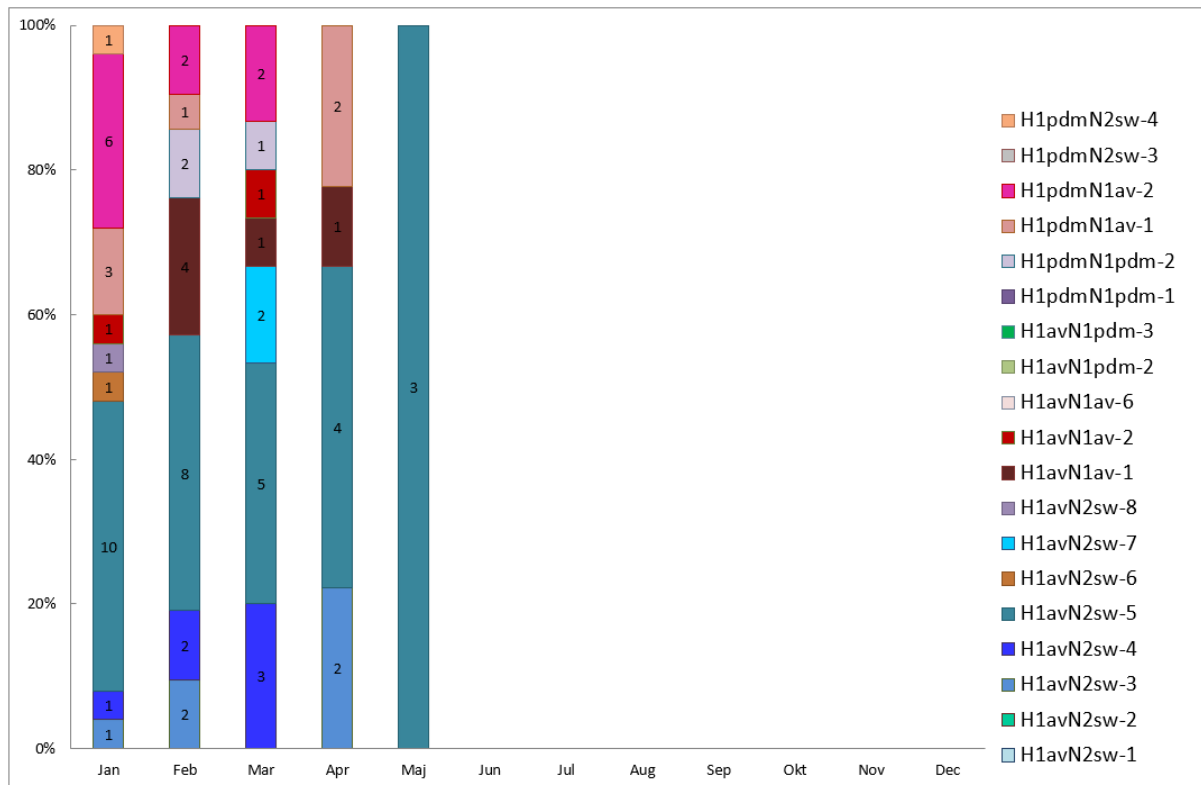
## Distribution of swine influenza A virus subtypes



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 May, the full subtype (both HA and NA gene segments) was determined for 8 submissions. The H1avNx viruses were slightly dominating over H1pdm09 subtype, with H1avN2sw (n=4 submissions) being the most prevalent followed by H1avN1av (n=1). The determined H1pdm09 subtypes were H1pdmN1pdm (n=1 submissions), and H1pdmN2sw (n=2).

## Distribution of swine influenza A virus genotypes



For May, 3 submissions were genotyped. All submissions were genotyped to H1avN2sw-5 (n=3), with a mix of avian-like swine and H1pdm origin internal genes.

# Phylogenetic analysis

