

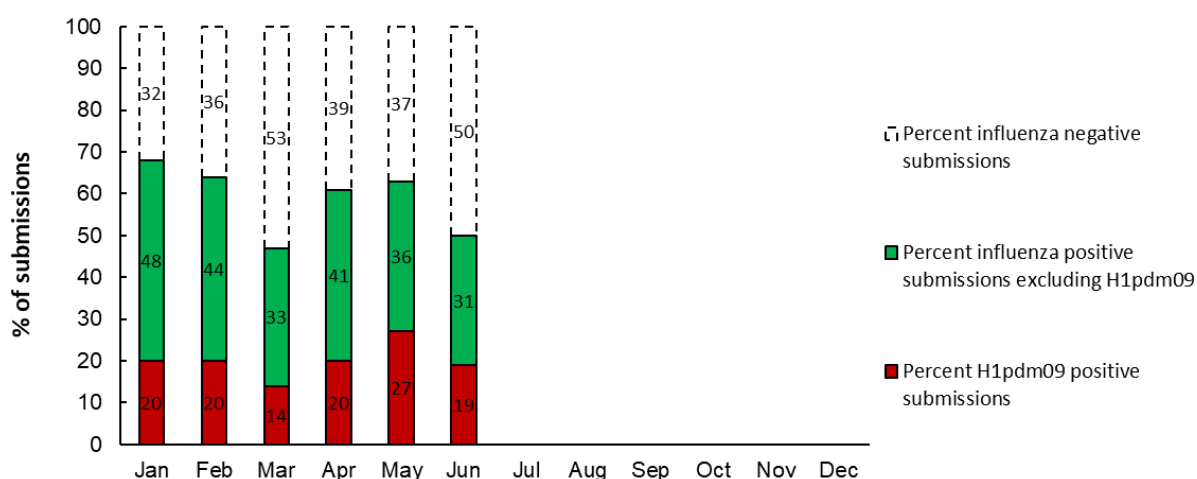
# Surveillance of Influenza A virus in Danish pigs

## 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
<b>Received</b>						
Samples	156	140	121	141	107	84
Submissions	40	41	36	44	30	26
Herds	40	41	34	42	30	24
<b>Influenza positive</b>						
Samples	70	53	43	60	44	38
Submissions	27	25	17	27	19	13
Herds	27	25	17	27	19	13
<b>H1pdm09 positive</b>						
Samples	24	14	10	22	17	10
Submissions	8	8	5	9	8	5
Herds	8	8	5	9	8	5

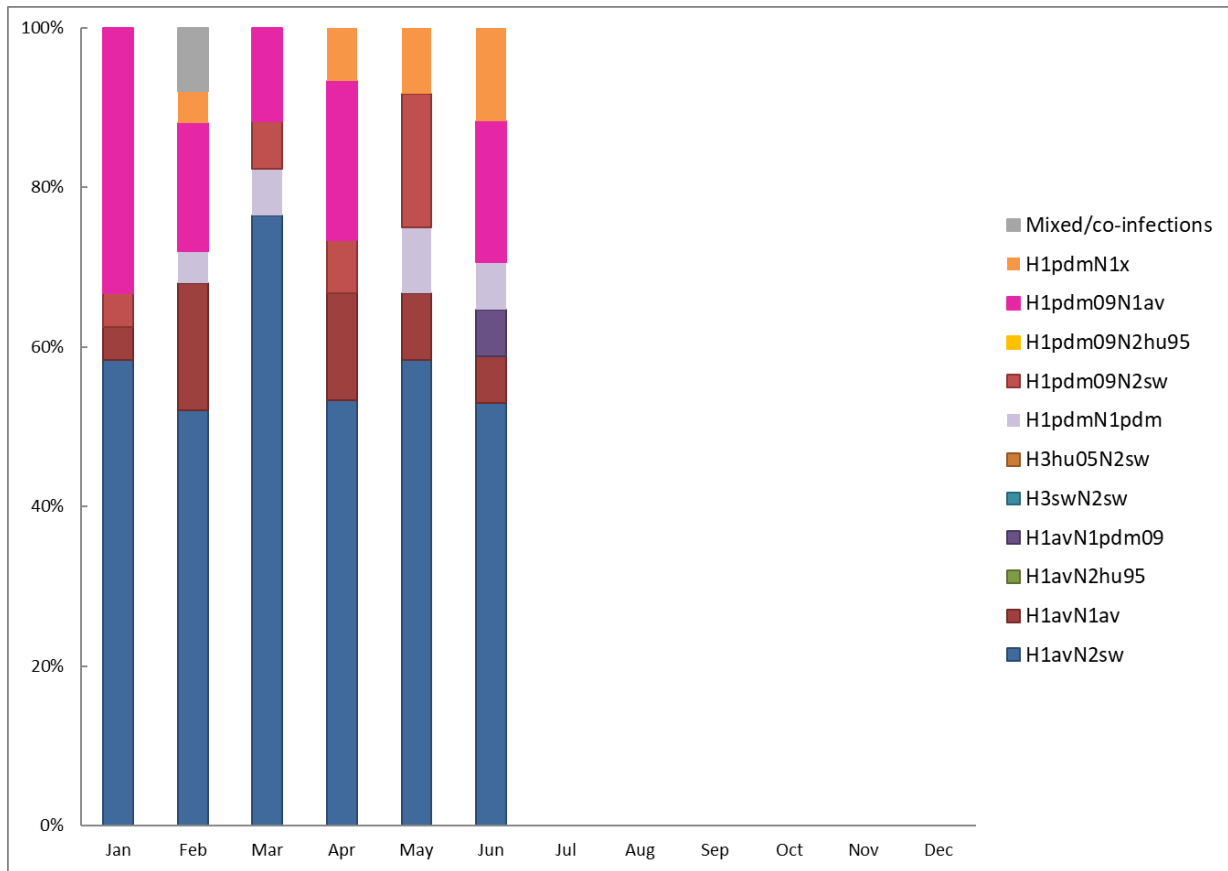
In June, 26 submissions from 24 herds registered with different CHR numbers were received. On average, each submission consisted of 3.2 samples. The percentage of submissions positive for Influenza A virus was 50%, which is lower than the proportion of positive submissions observed in January, February, April and May, but higher than the proportion observed in March. All influenza A virus-positive samples were tested for the presence of H1pdm09. Overall, 38% 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 similar to

that observed in previous months of 2024 with the exception of May where a higher proportion of H1pdm positive submissions were observed.

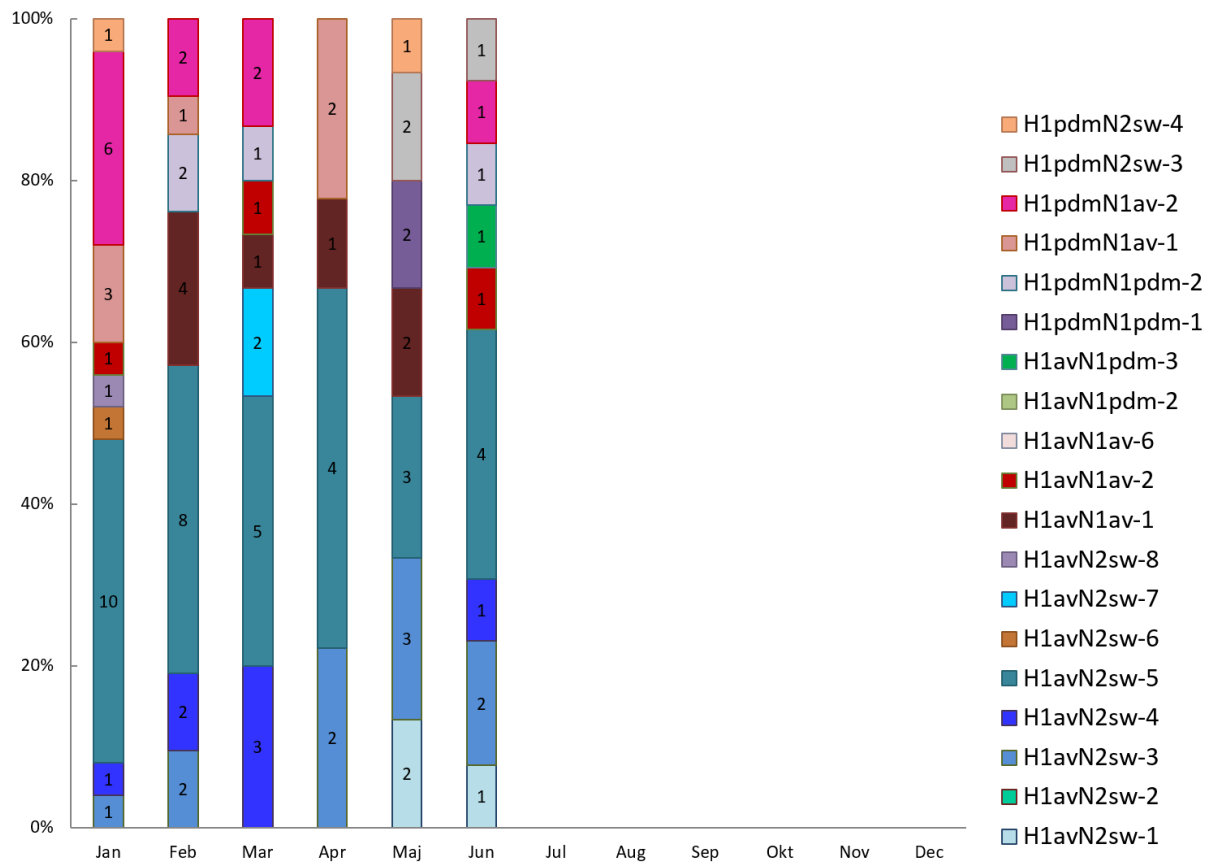
## Distribution of swine influenza A virus subtypes



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 June, the full subtype (both HA and NA gene segments) was determined for 17 submissions. The majority of the submissions were of H1avN2sw origin (n=9) followed by H1pdm09N1av (n=3).

## Distribution of swine influenza A virus genotypes



For June, 13 submissions were genotyped. A wide range of genotypes were identified. However, H1avN2sw-3 and H1avN2sw-5 were most abundant. In general, viruses with an internal gene cassette where all segments except the NS segment is of H1N1pdm09 origin and the NS segment is of Eurasian avian-origin are increasing.