

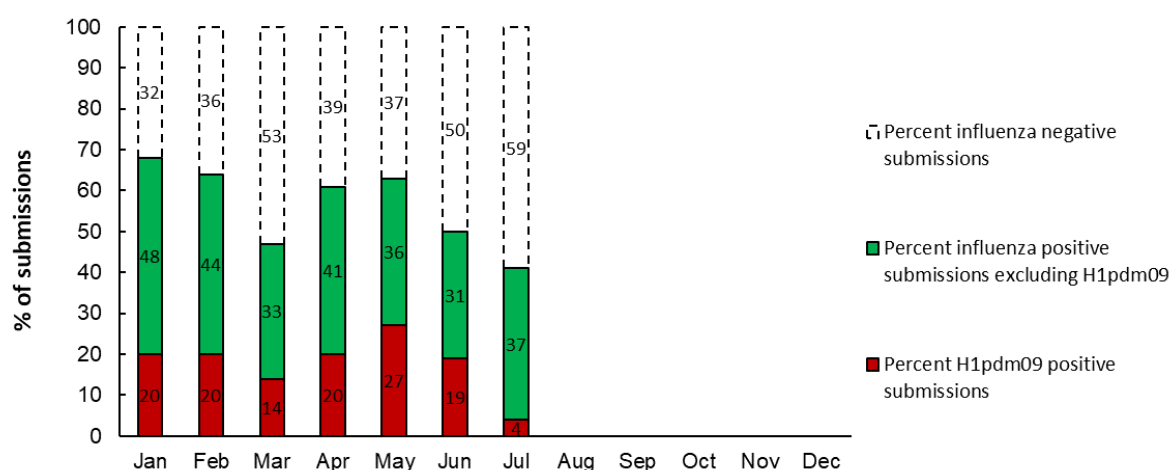
Surveillance of Influenza A virus in Danish pigs

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.

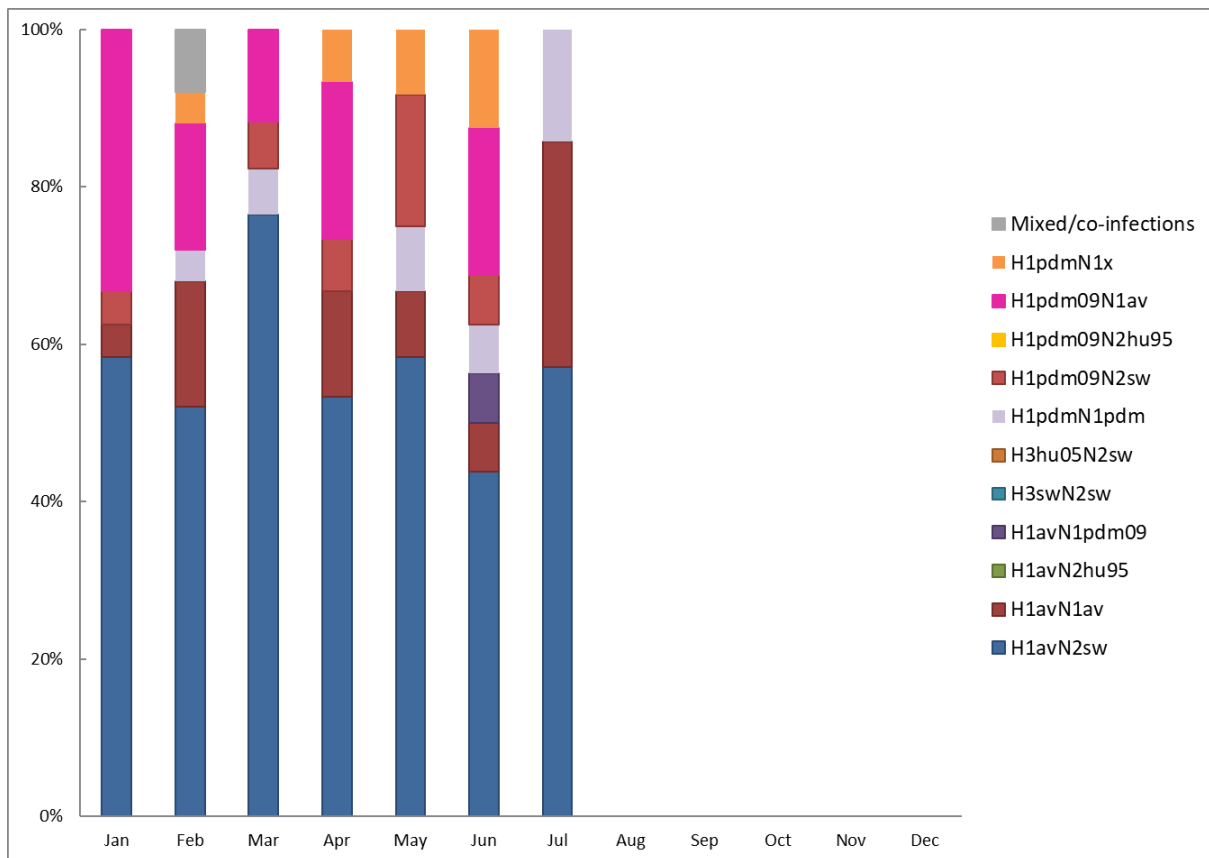
	Jan	Feb	Mar	Apr	May	Jun	Jul
Received							
Samples	156	140	121	141	107	84	68
Submissions	40	41	36	44	30	26	27
Herds	40	41	34	42	30	24	23
Influenza positive							
Samples	70	53	43	60	44	38	19
Submissions	27	25	17	27	19	13	11
Herds	27	25	17	27	19	13	10
H1pdm09 positive							
Samples	24	14	10	22	17	10	2
Submissions	8	8	5	9	8	5	1
Herds	8	8	5	9	8	5	1

In July, 27 submissions from 23 herds registered with different CHR numbers were received. On average, each submission consisted of 2.5 samples. The percentage of submissions positive for Influenza A virus was 41%, which is the lowest proportion registered so far in 2024. All influenza A virus-positive samples were tested for the presence of H1pdm09. Overall, 9% 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 was very low this month but it should be noted that the proportion was based on a low number of influenza A virus positive submissions.

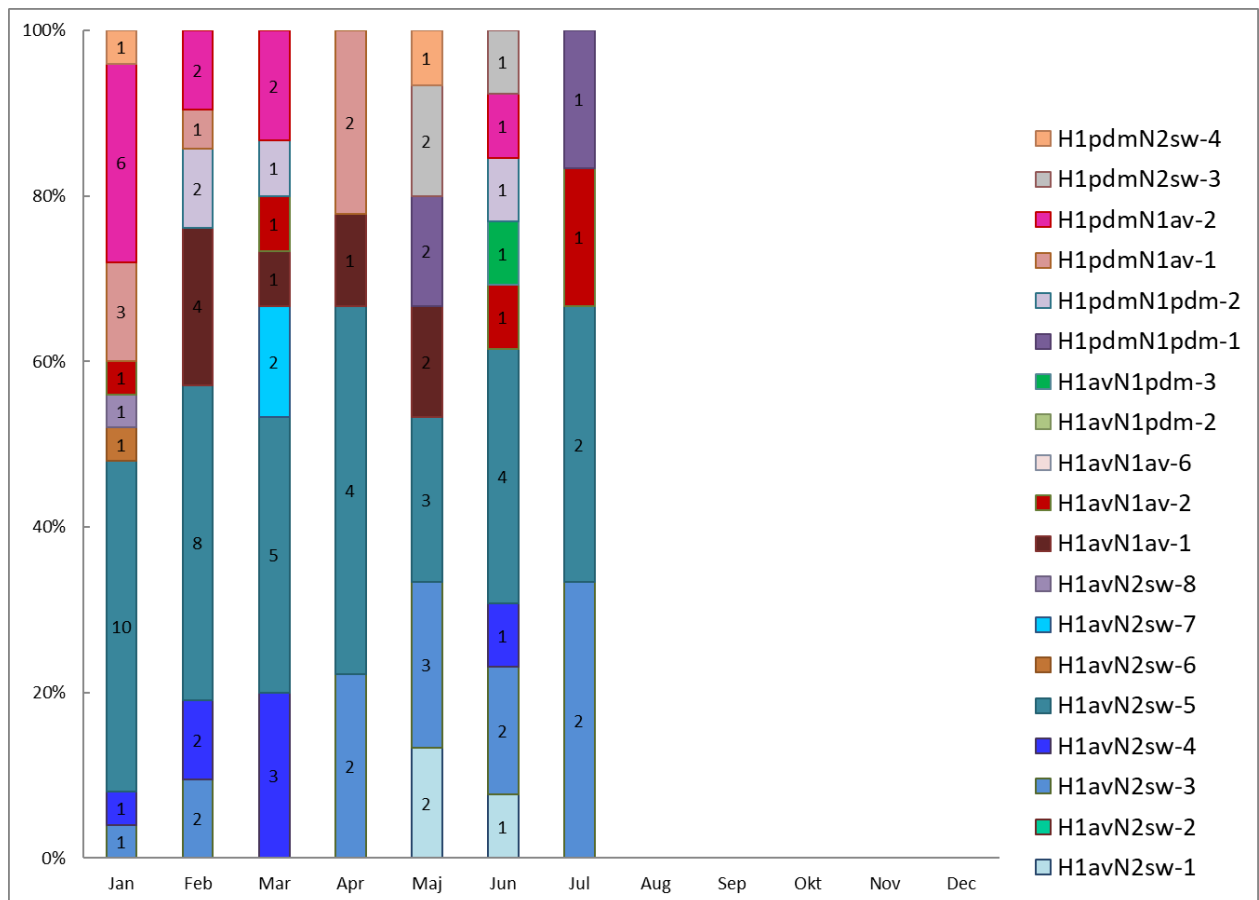
Distribution of swine influenza A virus subtypes



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 July, the full subtype (both HA and NA gene segments) was determined for 7 submissions. The majority of the submissions were of H1avN2sw origin (n=4) followed by H1avN1av (n=2).

Distribution of swine influenza A virus genotypes



For July, six submissions were genotyped. The H1avN2sw-3 and H1avN2sw-5 were again the most abundant genotypes observed.

Phylogenetic analysis

Fylogenetisk træ - Influenza A virus overvågning i Danske svin Juli 2024

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