

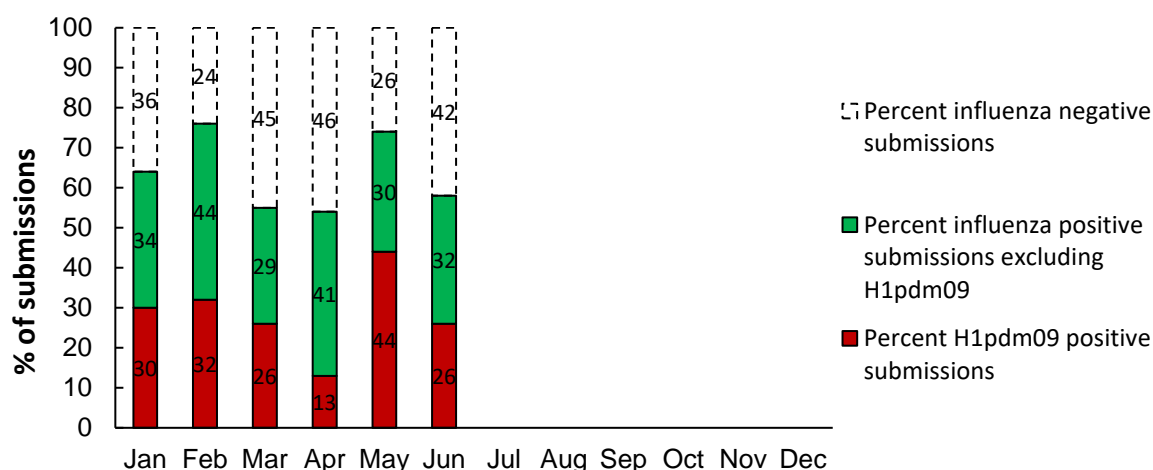
Surveillance of Influenza A virus in Danish pigs

Samples and results 2023

The table illustrates the number of samples, submissions and herds that contributed to the surveillance program each month. In addition, the results of the influenza A virus and H1pdm09 screening are shown.

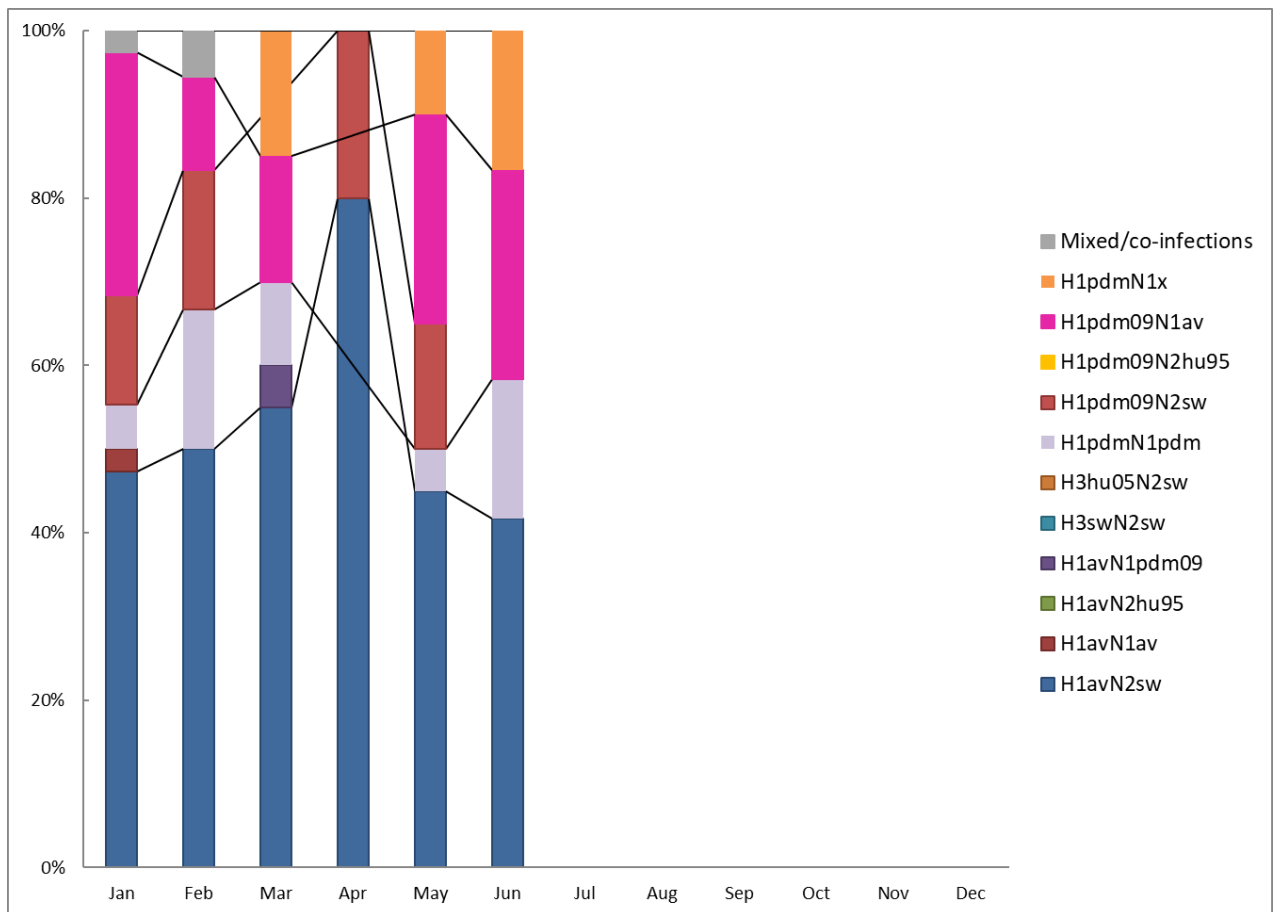
	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
Received												
Samples	169	118	163	143	89	101						
Submissions	50	34	49	46	27	31						
Herds	46	34	48	45	27	31						
Influenza positive												
Samples	84	79	67	61	54	45						
Submissions	32	26	27	25	20	18						
Herds	31	26	27	25	20	18						
H1pdm09 positive												
Samples	36	32	25	12	31	21						
Submissions	15	11	13	6	12	8						
Herds	15	11	13	6	12	8						

In June, 31 submissions from 31 herds registered with different CHR numbers were received. On average one submission included 3.3 samples. The positive percentage for the month of June was 58 %, resembling the level observed in March and April. All influenza A virus positive samples were tested for the presence of H1pdm09. In total, 44 % of the influenza A virus positive submissions were positive for H1pdm09 resembling the proportion observed in January-March.



The figure illustrates the percentage of influenza A virus negative and positive submissions including the proportion of H1pdm09 positive submissions.

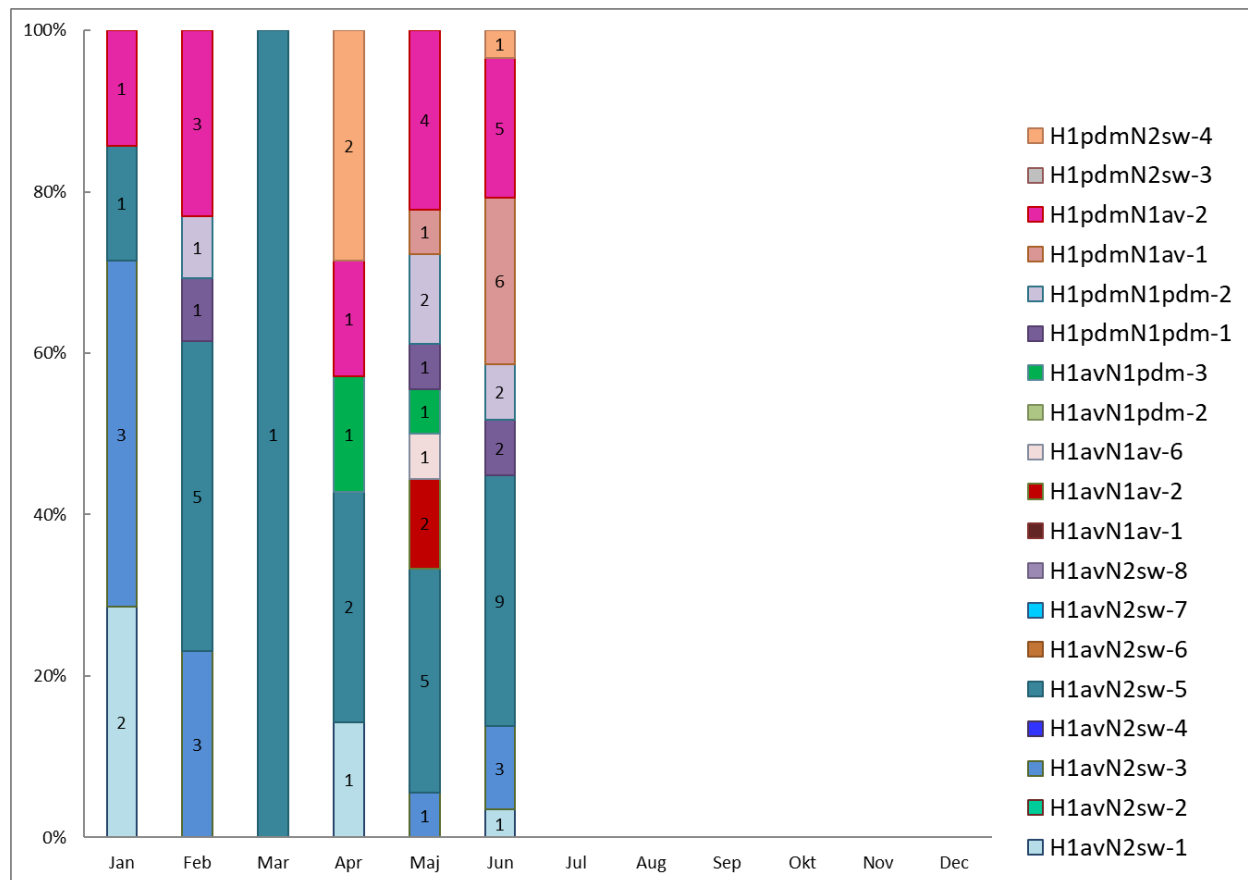
Distribution of swine influenza A virus subtypes



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 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 subtype (HA and NA gene segments) was determined for 12 submissions. In June, the H1pdmNx viruses were dominating, with H1pdm09N1av and H1N1pdm09 being prevalent. In addition, a major proportion of the submissions still included H1avN2sw viruses, similar to the pattern observed in the previous months.

Distribution of swine influenza A virus genotypes



For June, 29 submissions were genotyped. For the H1avN2sw viruses, the dominating genotype was H1avN2sw-5 containing a complete internal gene cassette of H1N1pdm09 origin. In addition, three submissions had an internal gene cassette of H1N1pdm09 origin, with the exception of the NS segment that was of avian-like H1N1 origin, and one submission had a complete internal gene cassette of avian-like H1N1 origin. For the H1pdmNx viruses (H1pdmN1av, H1pdmN1pdm, H1pdmN2sw), 50 % of the genotypes had a complete internal gene cassette of H1N1pdm09 origin, whereas the other 50 % had an internal gene cassette of H1N1pdm09 origin except from the NS segment that was of avian-like H1N1 origin.

Phylogenetic analysis

Fylogenetisk træ - Influenza A virus overvågning i Danske svin Juli 2023

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