

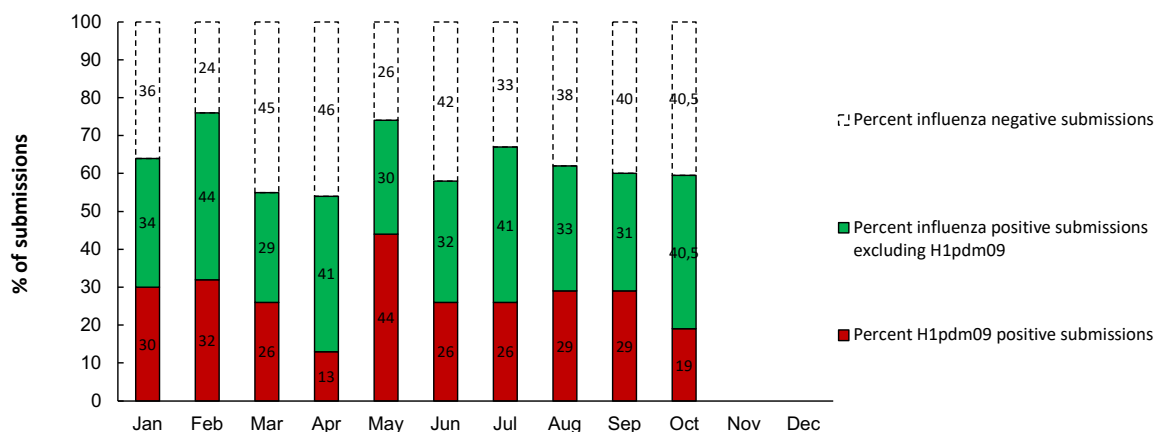
Surveillance of Influenza A virus in Danish pigs

Samples and results 2023

The table illustrate 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	97	136	144	150		
Submissions	50	34	49	46	27	31	27	42	42	42		
Herds	46	34	48	45	27	31	27	41	42	42		
Influenza positive												
Samples	84	79	67	61	54	45	44	52	76	73		
Submissions	32	26	27	25	20	18	18	26	25	25		
Herds	31	26	27	25	20	18	18	26	25	25		
H1pdm09 positive												
Samples	36	32	25	12	31	21	15	16	24	15		
Submissions	15	11	13	6	12	8	7	12	12	8		
Herds	15	11	13	6	12	8	7	12	12	8		

In October, 42 submissions from 42 herds registered with different CHR numbers were received. On average, one submission included 3.6 samples. The positive percentage for the month of September was 59 %, which is comparable to August and September. All influenza A virus positive samples were tested for the presence of H1pdm09. In total, 32 % of the influenza A virus positive submissions were positive for H1pdm09 resembling the proportion observed previously in June.



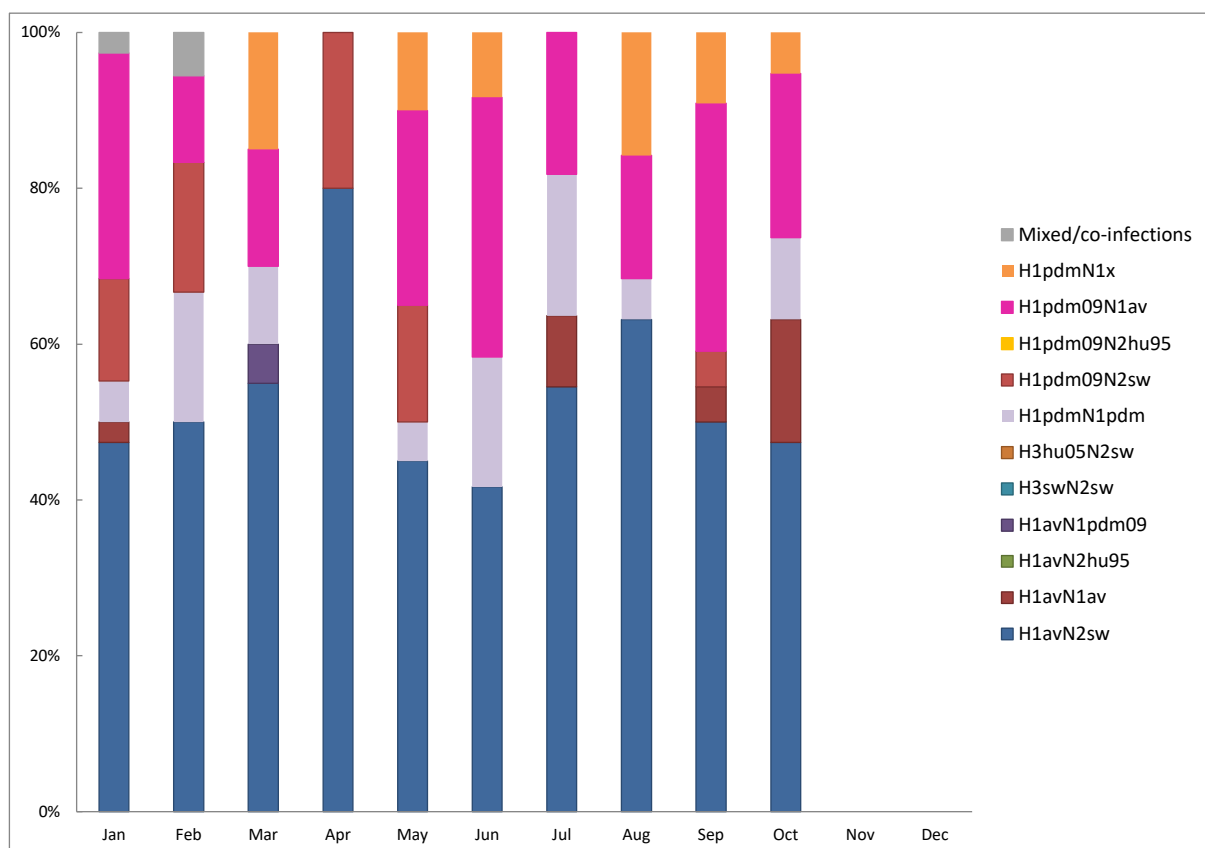
The figure illustrates the percentage of influenza A virus negative and positive submissions including the proportion of H1pdm09 positive submissions. We observed a 10% decrease of H1pdm09 positive submissions compared to the previous months. Overall, the percentage of influenza negative

submission remains the same while the numbers of influenza positive submissions, excluding H1pdm09, increased compared to August and September.

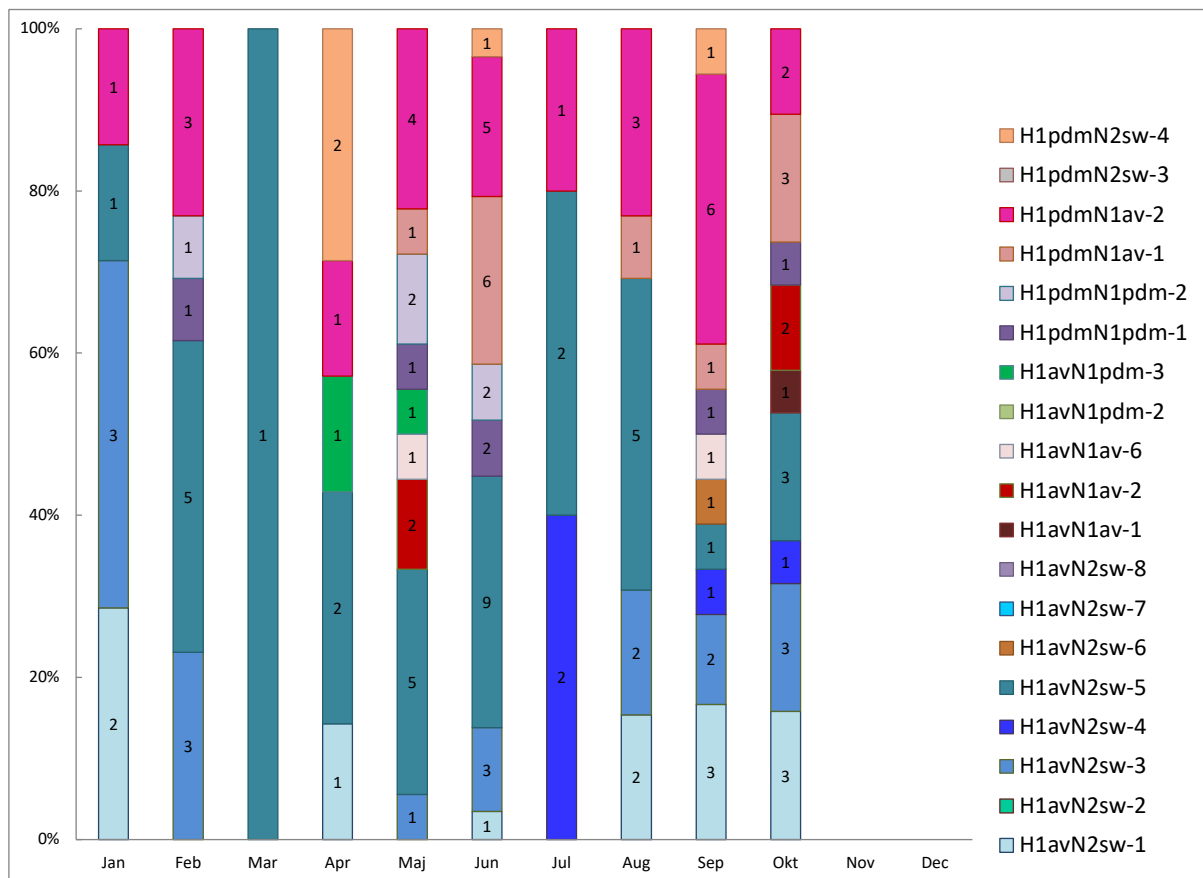
Distribution of swine influenza A virus subtypes

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 October, the subtype (HA and NA gene segments) was determined for 19 submissions. The H1avNx viruses were dominating, with H1avN2sw being the most prevalent. In addition, a major proportion of the submissions included H1pdm09N1av followed by other H1pdm09N1x viruses, similar to the pattern observed in September, August and March.



Distribution of swine influenza A virus genotypes



For October, 19 submissions were genotyped. For the H1avN2sw viruses, the dominating genotypes were H1avN2sw-1, which contained all gene segments of avian-like swine origin, and H1avN2sw-3 and H1avN2sw-5 with a mix of avian-like swine and H1pdm origin internal genes. For the H1pdmNx viruses, H1pdmN1av-1 and H1pdmN1av-2 were dominating with three and two submissions having those genotypes, respectively. H1pdmN1av-1 has an internal gene cassette of H1N1pdm09 origin, while H1pdmN1av-2 have an internal gene cassette of H1N1pdm09 origin except from the NS segment that is of avian-like swine H1N1 origin.

Phylogenetic analysis

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

FN0 DN PROVE: Tryk "ctrl + f" og søg på dit sagsnummer: fx "23-00510-1"
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