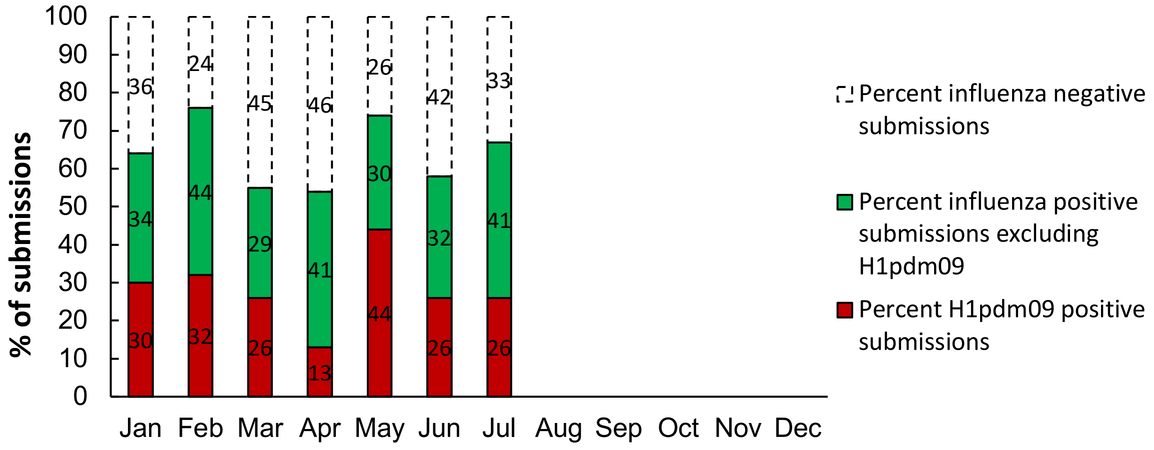
Surveillance of Influenza A virus in Danish pigs

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.

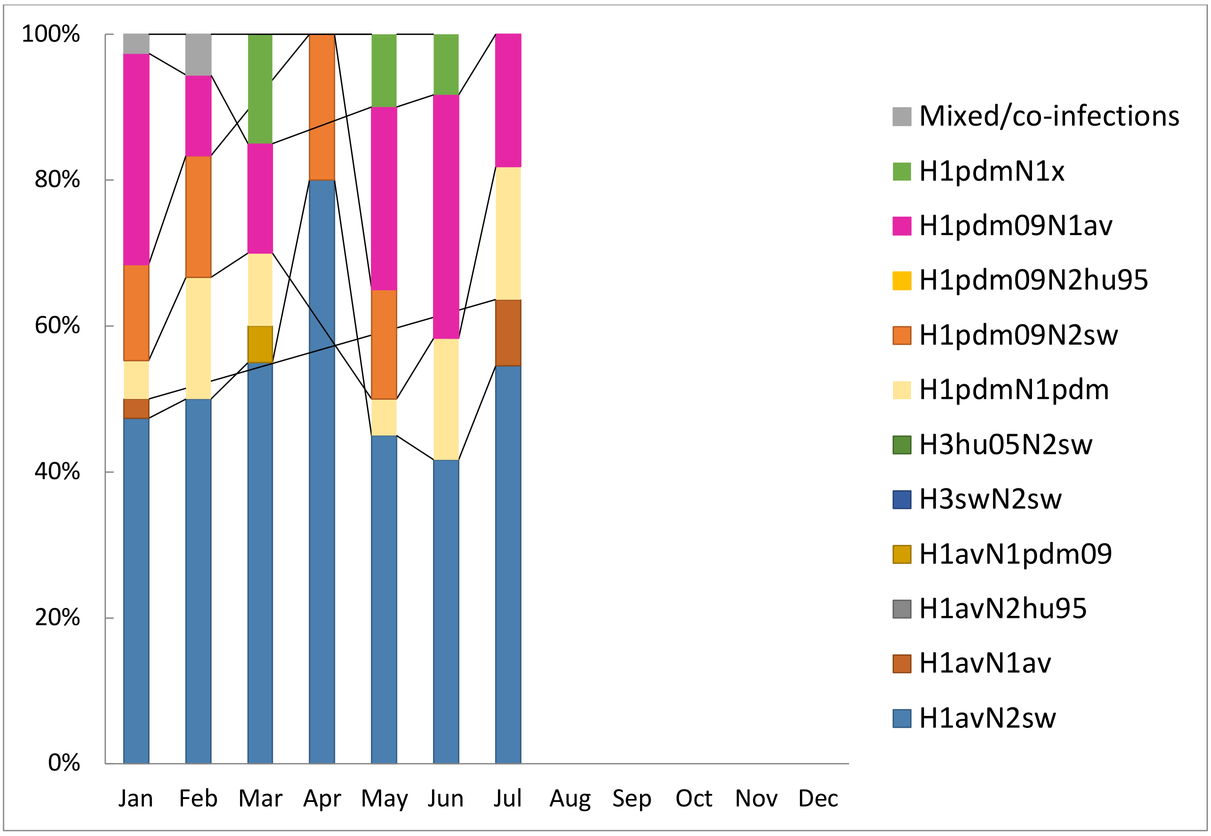
	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
Received												
Samples	169	118	163	143	89	101	97					
Submissions	50	34	49	46	27	31	27					
Herds	46	34	48	45	27	31	27					
Influenza positive												
Samples	84	79	67	61	54	45	44					
Submissions	32	26	27	25	20	18	18					
Herds	31	26	27	25	20	18	18					
H1pdm09 positive												
Samples	36	32	25	12	31	21	15					
Submissions	15	11	13	6	12	8	7					
Herds	15	11	13	6	12	8	7					

In July, 27 submissions from 27 herds registered with different CHR numbers were received. On average one submission included 3.6 samples. The positive percentage for the month of July was 66 %, which is a higher than the previous two months. All influenza A virus positive samples were tested for the presence of H1pdm09. In total, 38.8 % of the influenza A virus positive submissions were positive for H1pdm09 resembling the proportion observed previously.



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

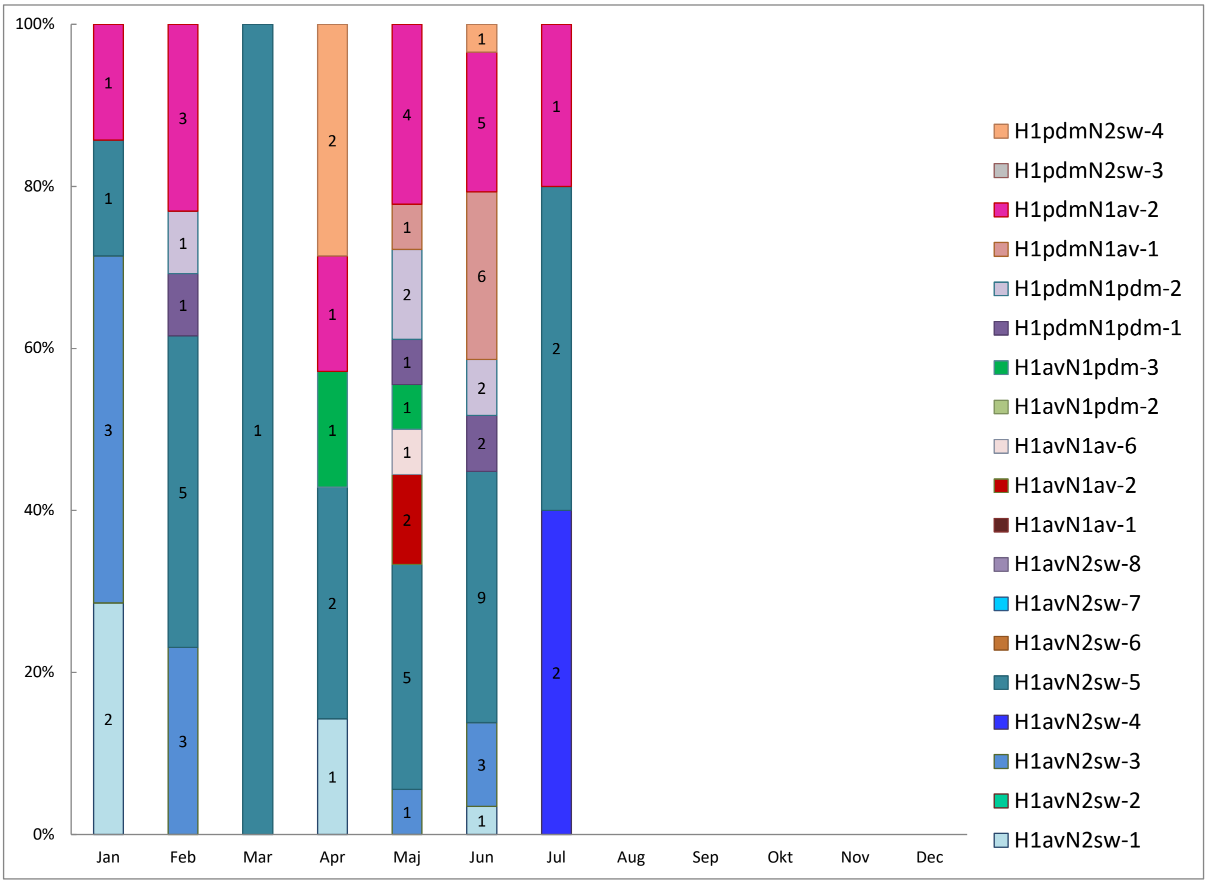
Distribution of swine influenza A virus subtypes



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.

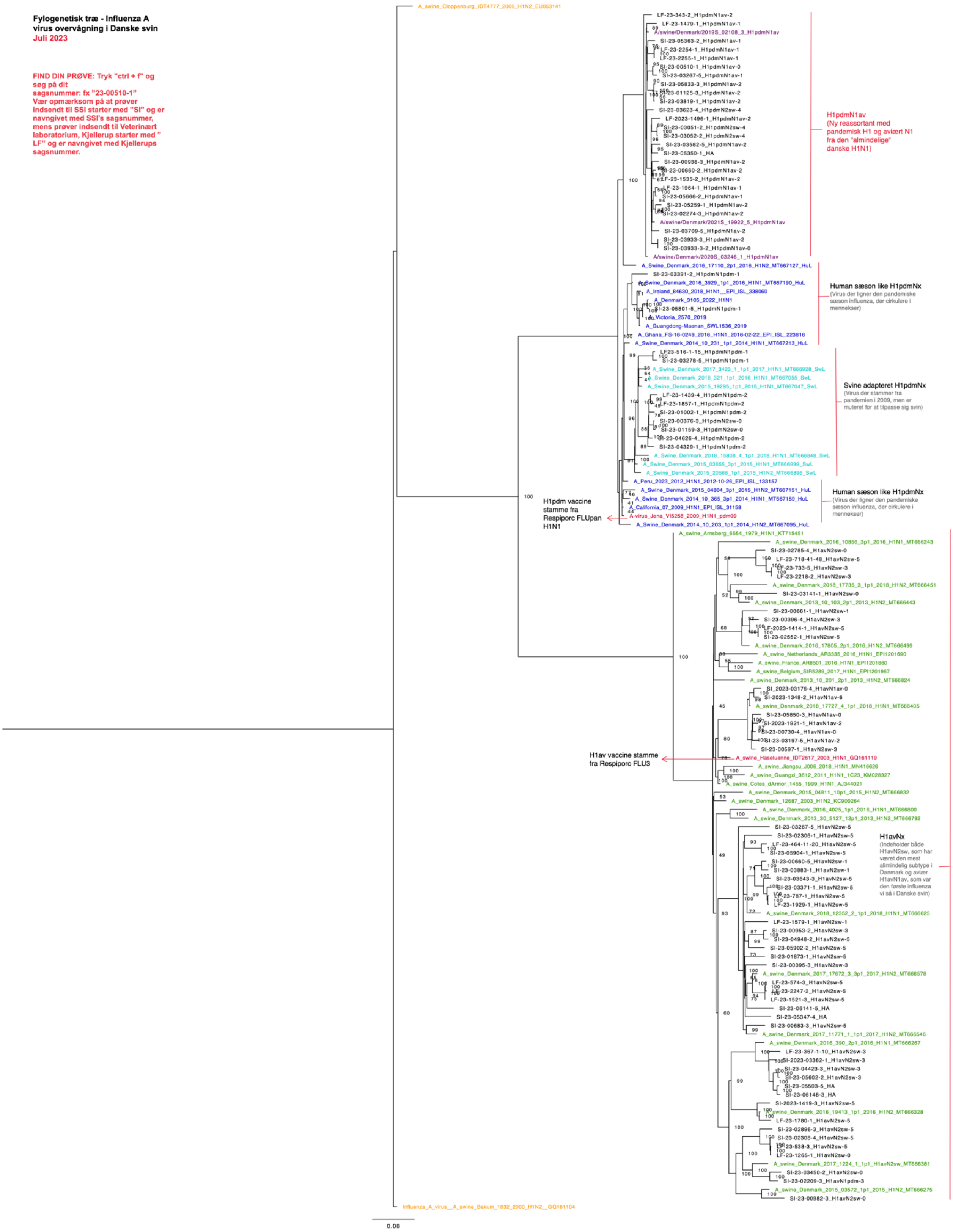
In July, the subtype (HA and HA gene segments) was determined for 11 submissions. The H1avNx viruses were dominating, with H1avN2sw being the most prevalent. In addition, a major proportion of the submissions included H1pdm09N1av and H1N1pdm09 viruses, similar to the pattern observed in previous months.

Distribution of swine influenza A virus genotypes



For July, five submissions were genotyped. For the H1avN2sw viruses, the dominating genotype was H1avN2sw-4 and H1avN2sw-5 which contained a complete internal gene cassette of H1N1pdm09 origin (except for PB1 in H1avN2sw-4). For the H1pdmNx viruses (H1pdmN1av, H1pdmN1pdm, H1pdmN2sw), only one sample was genotyped with H1pdmN1av-2 which 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

FIND DIN PRØVE: Tryk "ctrl + f" og søg på dit sagsnummer: fx "23-00510-1" Vær opmærksom på at prøver indsendt til SSI starter med "SI" og er navngivet med SSI's sagsnummer, mens prøver indsendt til Veterinært laboratorium, Kjellerup starter med " LF" og er navngivet med Kjellerups sagsnummer.

H1pdmN1av
(Ny reassortant med pandemisk H1 og aviært N1 fra den "almindelige" danske H1N1)

Human sæson like H1pdmNx
(Virus der ligner den pandemiske sæson influenza, der cirkulere i mennekser)

Svine adapteret H1pdmNx
(Virus der stammer fra pandemien i 2009, men er muteret for at tilpasse sig svin)

Human sæson like H1pdmNx
(Virus der ligner den pandemiske sæson influenza, der cirkulere i mennekser)

H1pdm vaccine stamme fra Respiporc FLUpan H1N1

H1av vaccine stamme fra Respiporc FLU3

H1avNx
(Indeholder både H1avN2sw, som har været den mest alimindelig subtype i Danmark og aviær H1avN1av, som var den første influenza vi så i Danske svin)