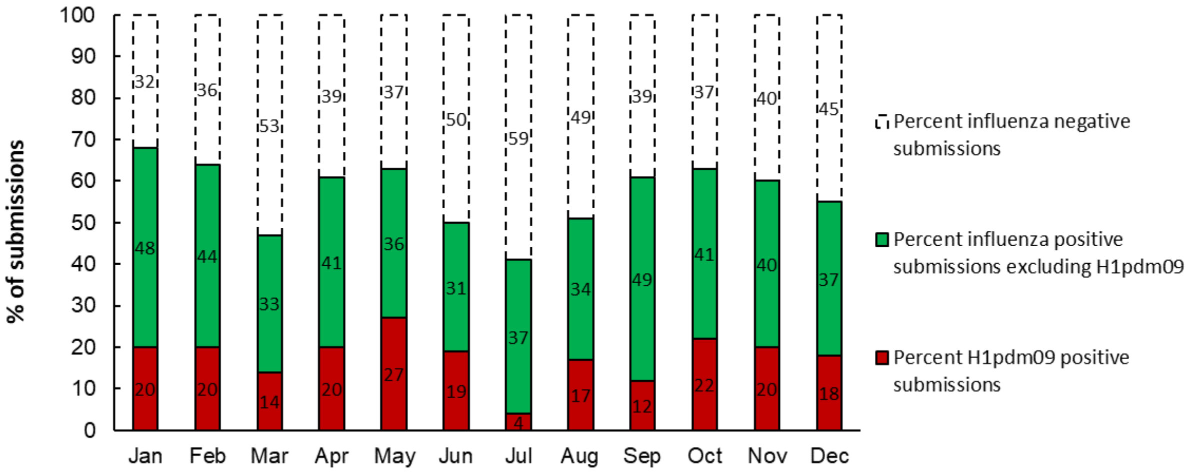
Surveillance of Influenza A virus in Danish pigs

Samples and results 2024

The table illustrate 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	Aug	Sep	Oct	Nov	Dec
Received												
Samples	156	140	121	141	107	84	68	115	141	278	129	128
Submissions	40	41	36	44	30	26	27	35	41	68	40	38
Herds	40	41	34	42	30	24	23	34	37	67	38	36
Influenza positive												
Samples	70	53	43	60	44	38	19	42	58	100	53	55
Submissions	27	25	17	27	19	13	11	18	25	43	24	21
Herds	27	25	17	27	19	13	10	18	23	43	24	19
H1pdm09 positive												
Samples	24	14	10	22	17	10	2	14	17	29	19	18
Submissions	8	8	5	9	8	5	1	6	5	15	8	7
Herds	8	8	5	9	8	5	1	6	5	15	8	6

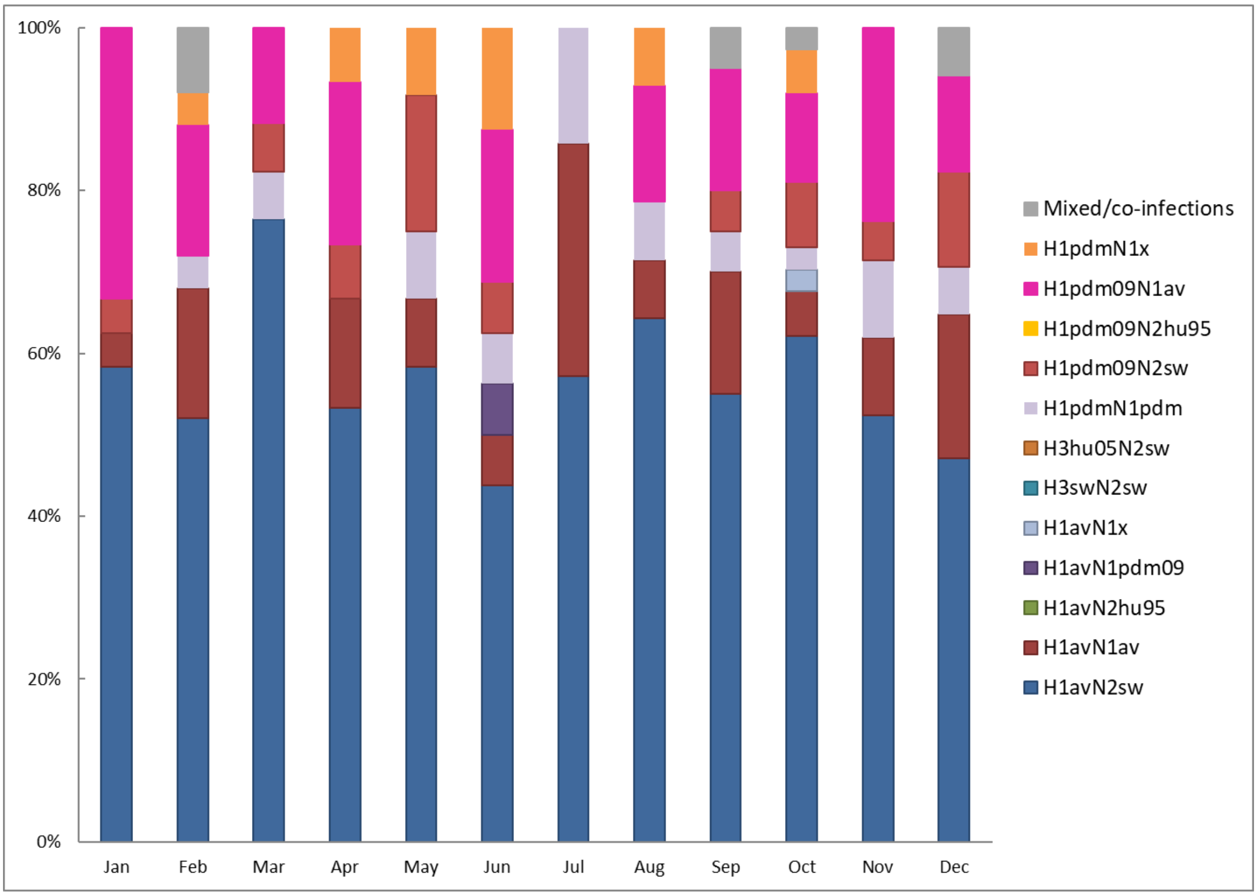
In December, 38 submissions from 36 herds registered with different CHR numbers were received. On average, each submission consisted of 3.4 samples. The percentage of submissions positive was 55 % slightly lower than the three previous months. All influenza A virus-positive samples were tested for the presence of H1pdm09. Overall, 33% of the submissions testing positive for the influenza A virus were positive for H1pdm09, which is similar to the level observed the two previous months.



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

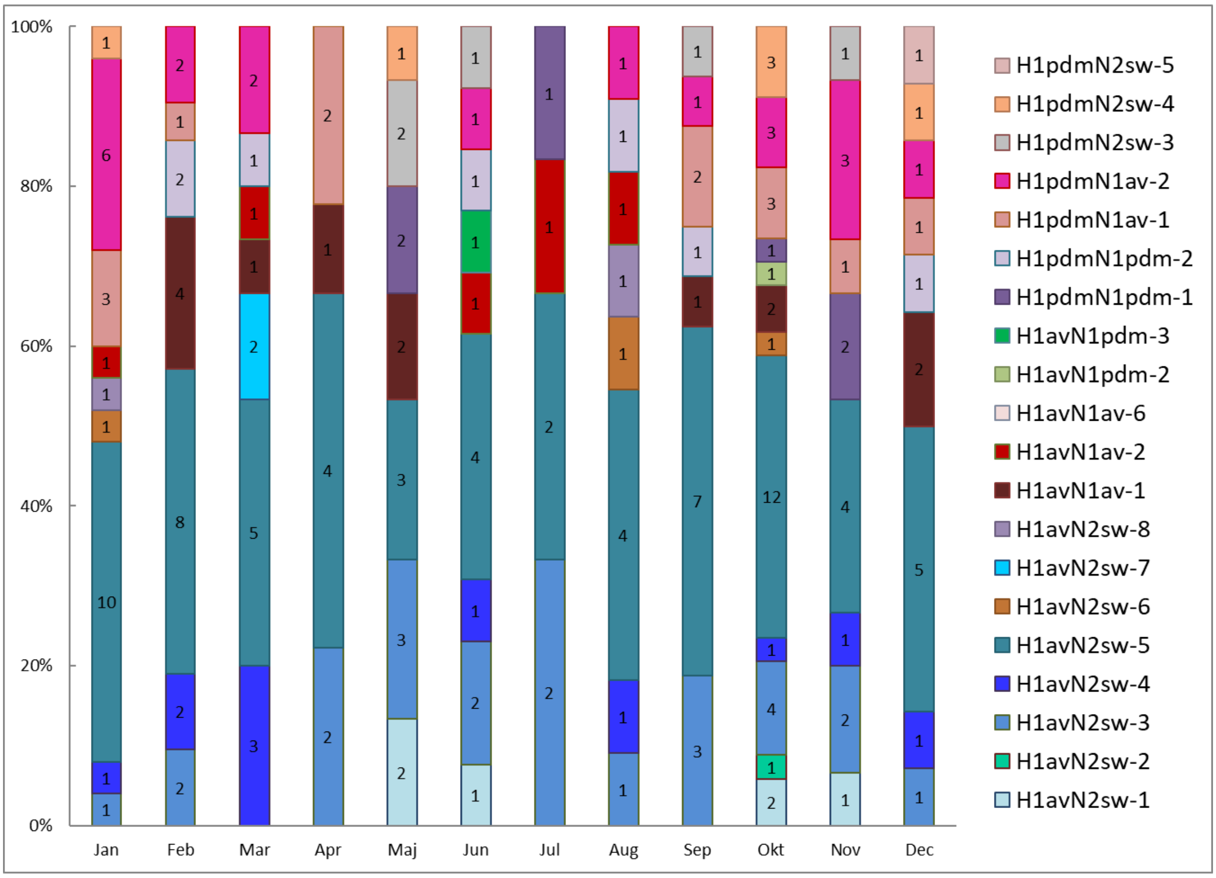
Distribution of swine influenza A virus subtypes

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 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 December, the full subtype (both HA and NA gene segments) was determined for 17 submissions. The far greatest majority of the submissions were of H1avN2sw origin (n=8), whereas a few submissions were positive for H1pdm09N1av, H1pdm09N2sw, H1avN1av and H1pdmN1pdm.

Distribution of swine influenza A virus genotypes

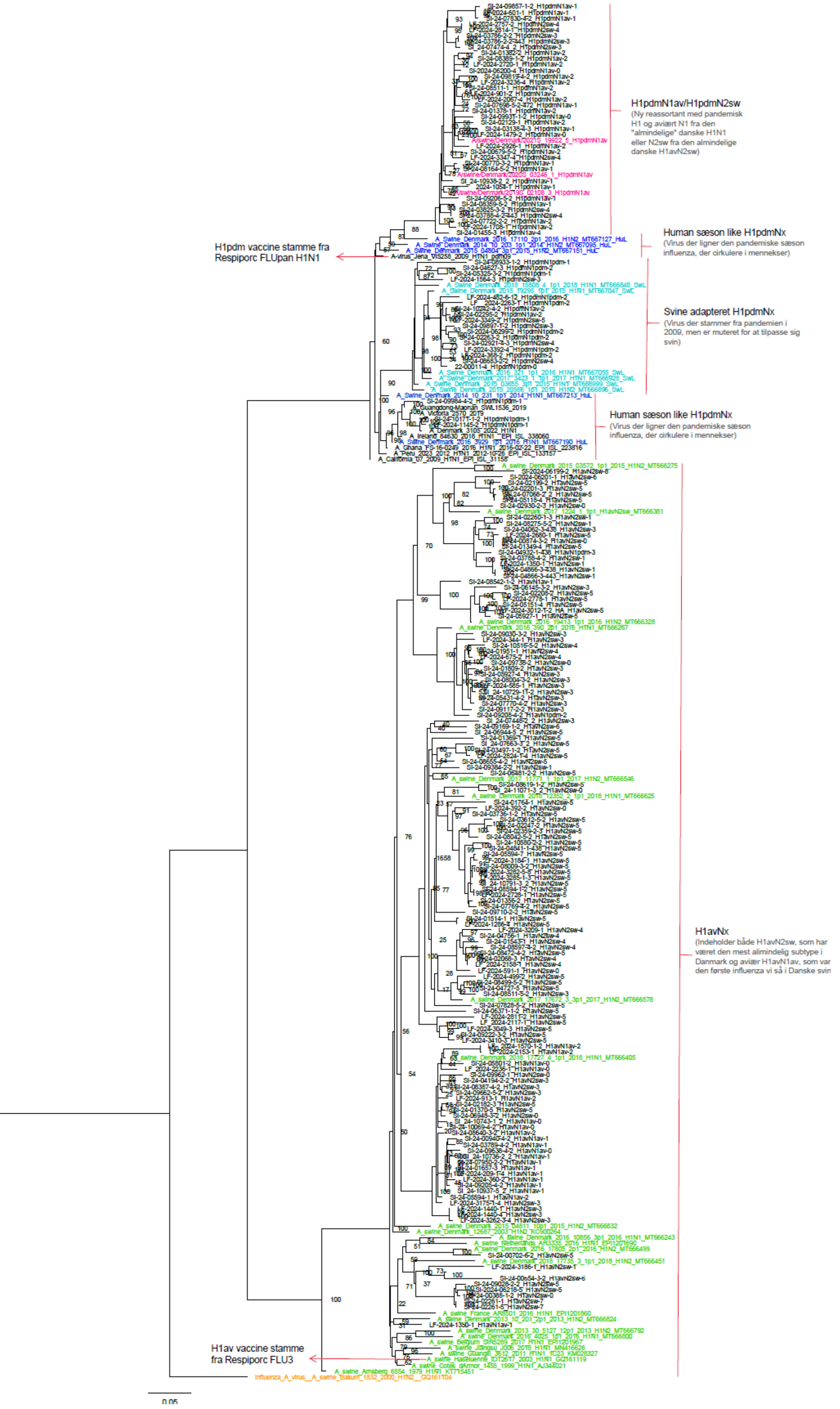


For December, 14 submissions were genotyped. The H1avN2sw-5 viruses with a complete internal cassette of H1N1pdm09 origin were again the most abundant (n=5).

Phylogenetic analysis

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

FIND DIN PRØVE: Tryk "ctrl + f" og søg på dit sagsnummer: fx "24-03138-4" 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/H1pdmN2sw
(Ny reassortant med pandemisk H1 og aviært N1 fra den "almindelige" danske H1N1 eller N2sw fra den almindelige danske H1avN2sw)

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

H1pdm vaccine stamme fra Respiporc FLUpan H1N1

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)

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

H1av vaccine stamme fra Respiporc FLU3