

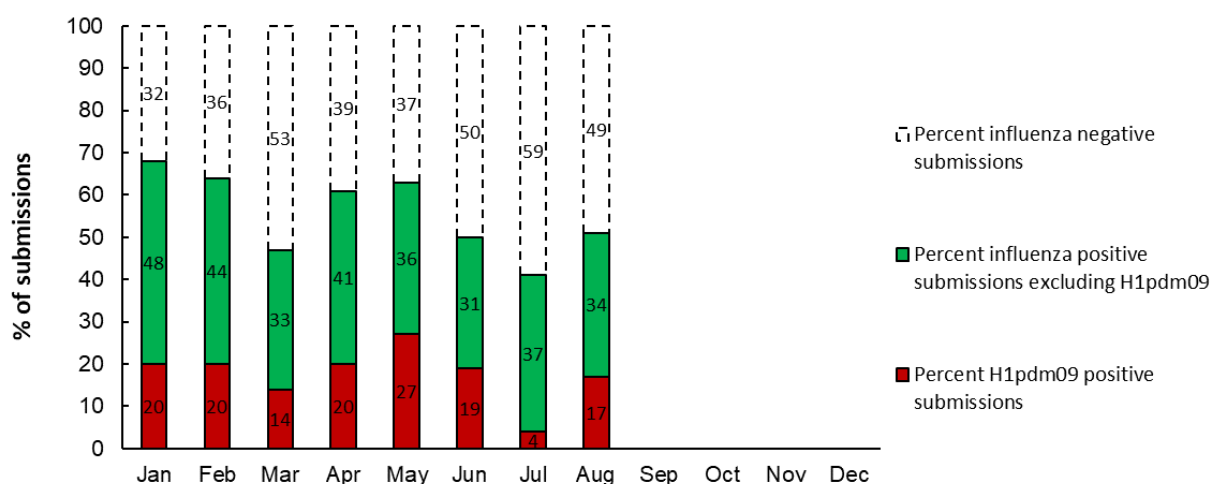
Surveillance of Influenza A virus in Danish pigs

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.

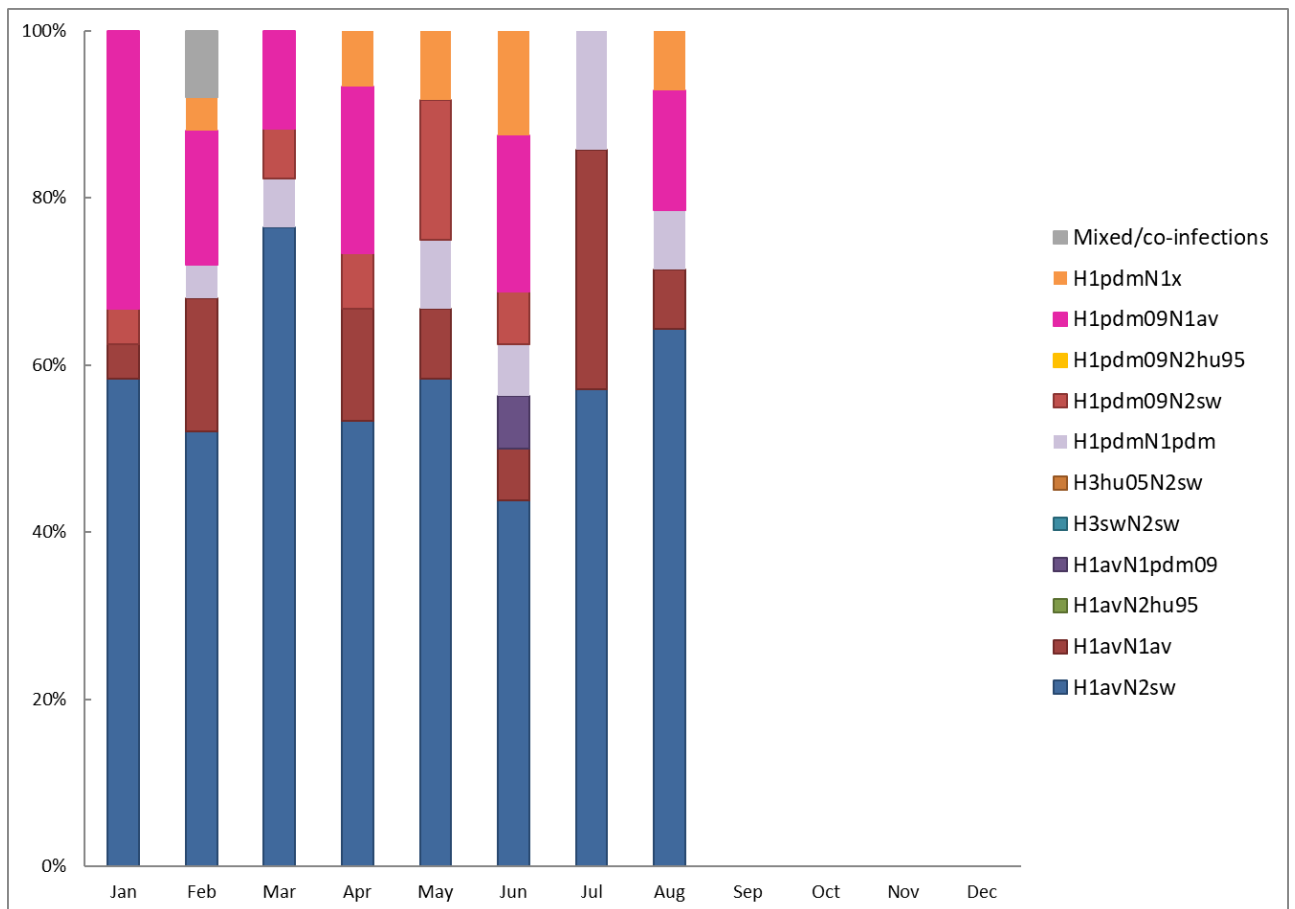
	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug
Received								
Samples	156	140	121	141	107	84	68	115
Submissions	40	41	36	44	30	26	27	35
Herds	40	41	34	42	30	24	23	34
Influenza positive								
Samples	70	53	43	60	44	38	19	42
Submissions	27	25	17	27	19	13	11	18
Herds	27	25	17	27	19	13	10	18
H1pdm09 positive								
Samples	24	14	10	22	17	10	2	14
Submissions	8	8	5	9	8	5	1	6
Herds	8	8	5	9	8	5	1	6

In August, 35 submissions from 34 herds registered with different CHR numbers were received. On average, each submission consisted of 3.3 samples. The percentage of submissions positive increased this month to 51%, which is similar to the proportion registered in March and June. 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.



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 33%, which is again similar to previous months.

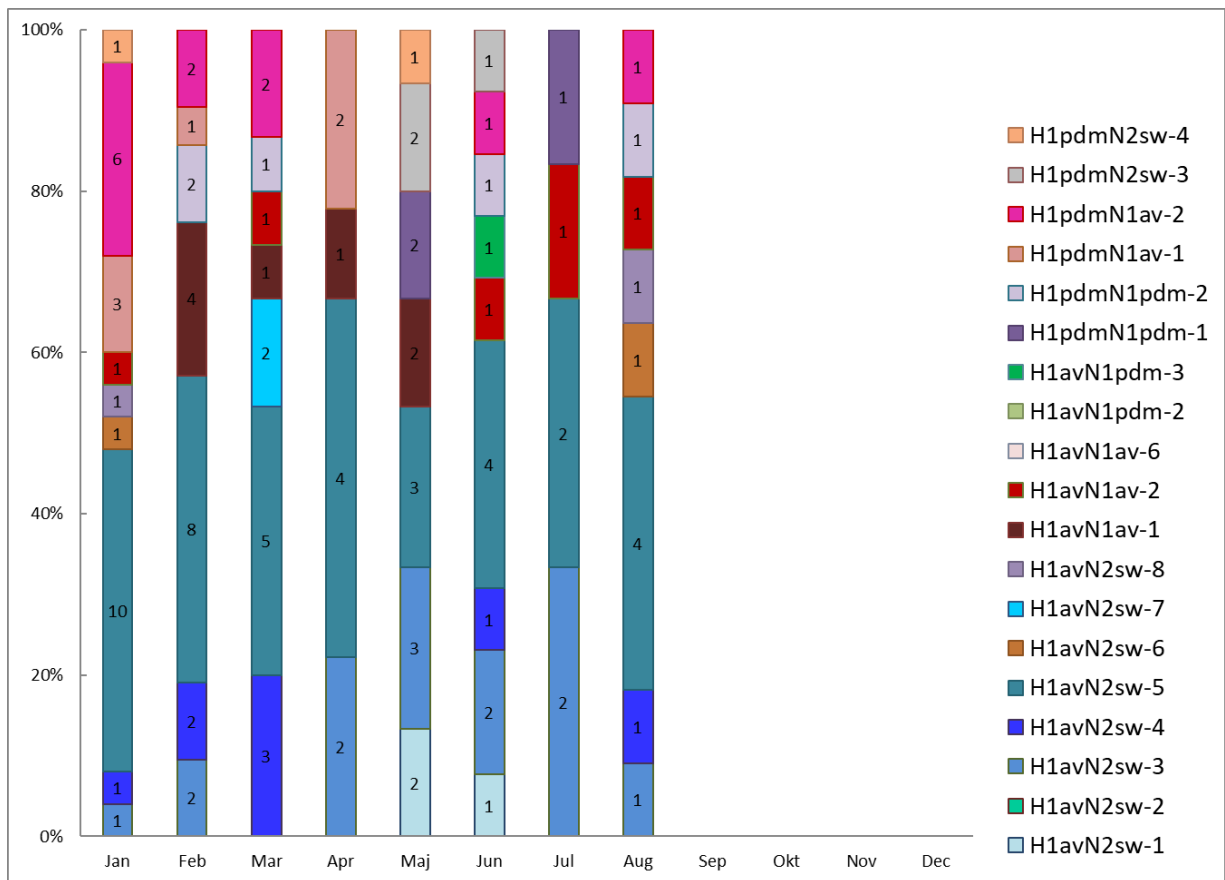
Distribution of swine influenza A virus subtypes



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 August, the full subtype (both HA and NA gene segments) was determined for fourteen submissions. The majority of the submissions were of H1avN2sw origin (n=9) followed by H1pdmO9N1av (n=2).

Distribution of swine influenza A virus genotypes

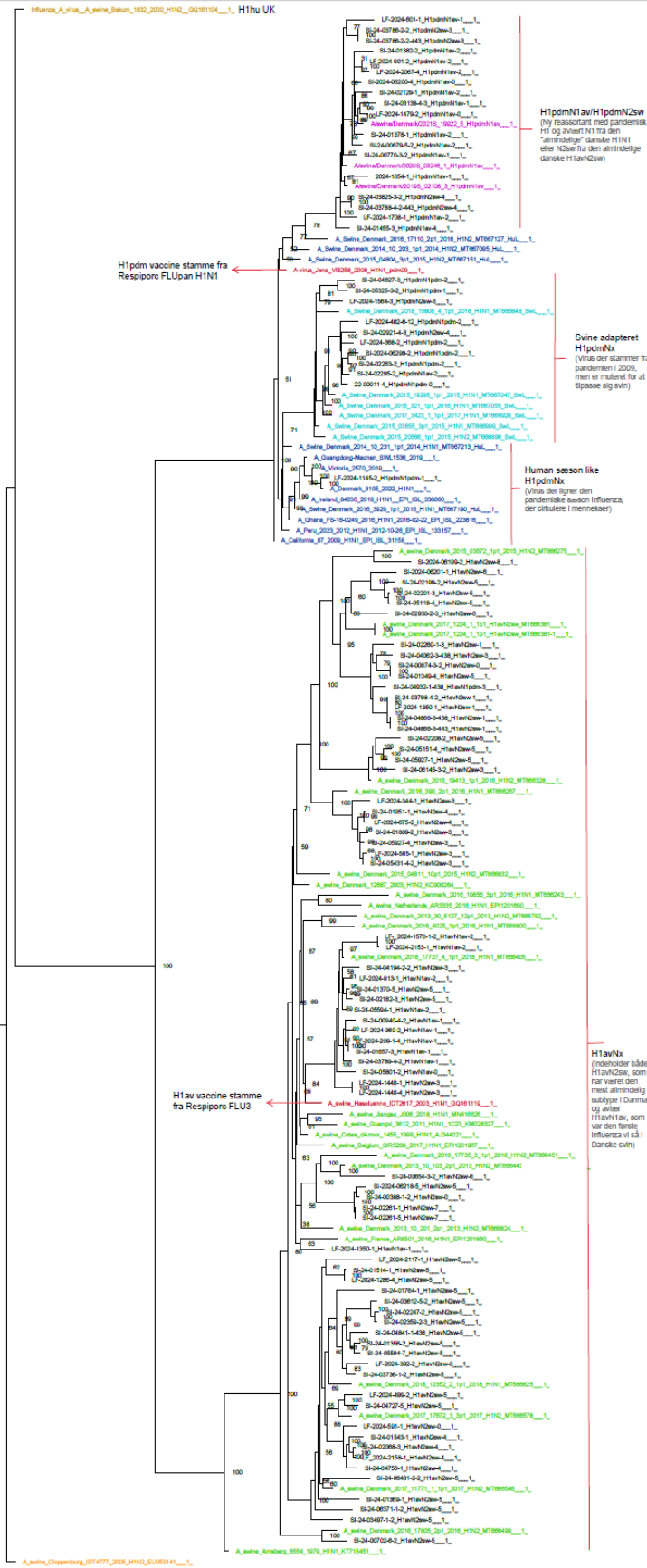


For august, eleven submissions were genotyped. The H1avN2sw-5 viruses with a complete internal cassette of H1N1pdm09 were the most abundant (n=4).

Phylogenetic analysis

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

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H1pdmN1av/H1pdmN2sw (Ny reassortant med pandemisk H1 og avlært N1 fra den "almindelige" danske H1N1 eller N2sw fra den almindelige danske H1avN2sw)

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 dominerende sæson influenza, der cirkulerer i mennesker)

H1avNx (Indoliserede H1avN2sw, som har været den mest almindelige subtype i Danmark og avlært H1avN1av, som var den første influenza vi så i Danske svin)