

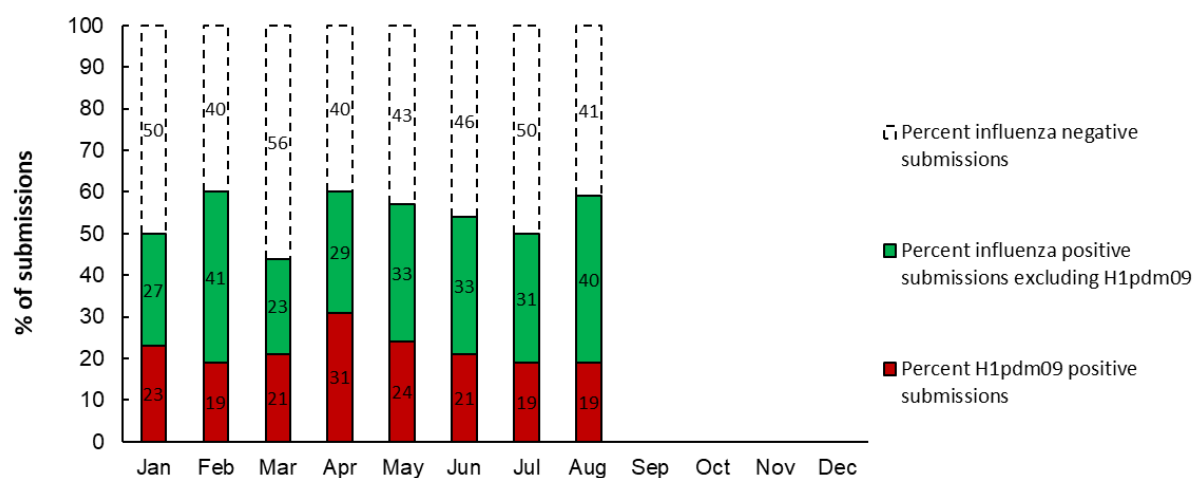
Surveillance of Influenza A virus in Danish pigs

Samples and results 2025

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	Sep	Oct	Nov	Dec
Received												
Samples	60	151	124	148	67	110	93	123				
Submissions	22	52	43	42	21	33	26	37				
Herds	22	51	41	42	21	29	25	36				
Influenza positive												
Samples	28	69	42	60	27	39	25	50				
Submissions	11	31	19	25	12	18	13	22				
Herds	11	31	19	25	12	18	13	21				
H1pdm09 positive												
Samples	13	14	21	25	13	17	11	14				
Submissions	5	10	9	13	5	7	5	7				
Herds	5	10	9	13	5	7	5	7				

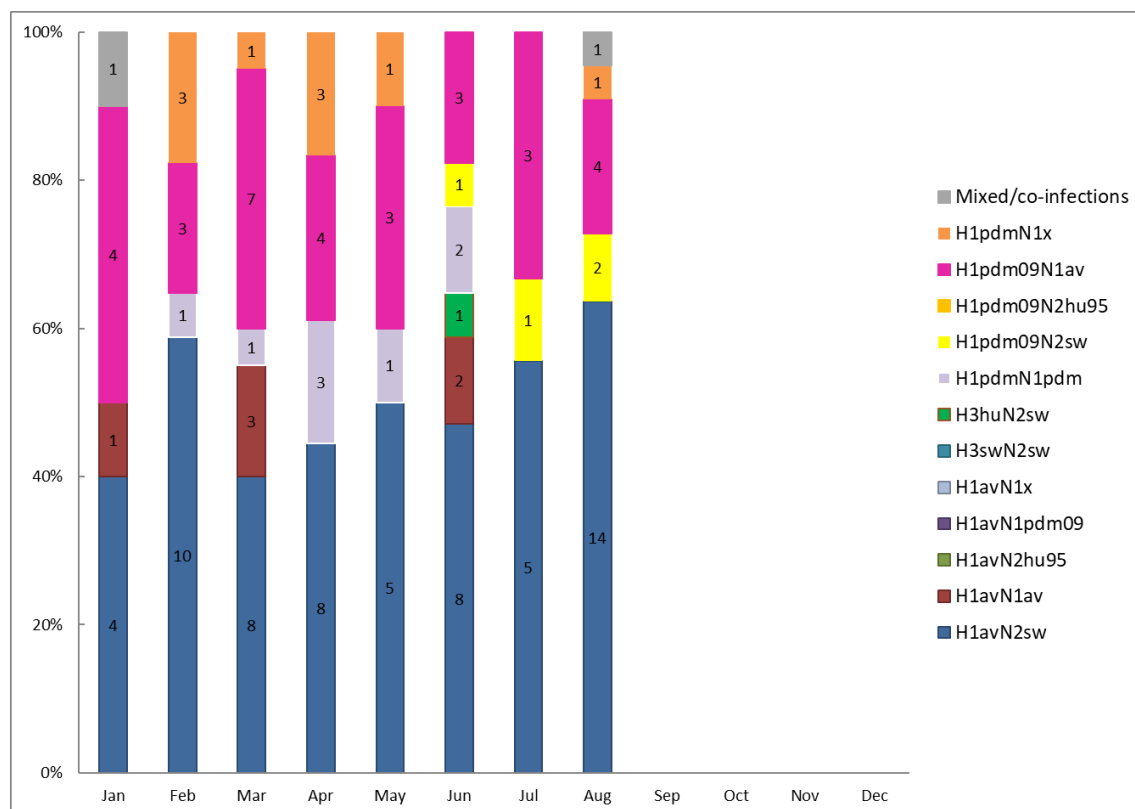
In August, 37 submissions from 36 herds registered with different CHR numbers were received. On average, each submission consisted of 3.3 samples. The percentage of influenza positive submissions was 59 %, which is higher than the last two months but corresponds to the level observed in April and February. All influenza A virus-positive samples were tested for the presence of H1pdm09. Overall, 32 % 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.

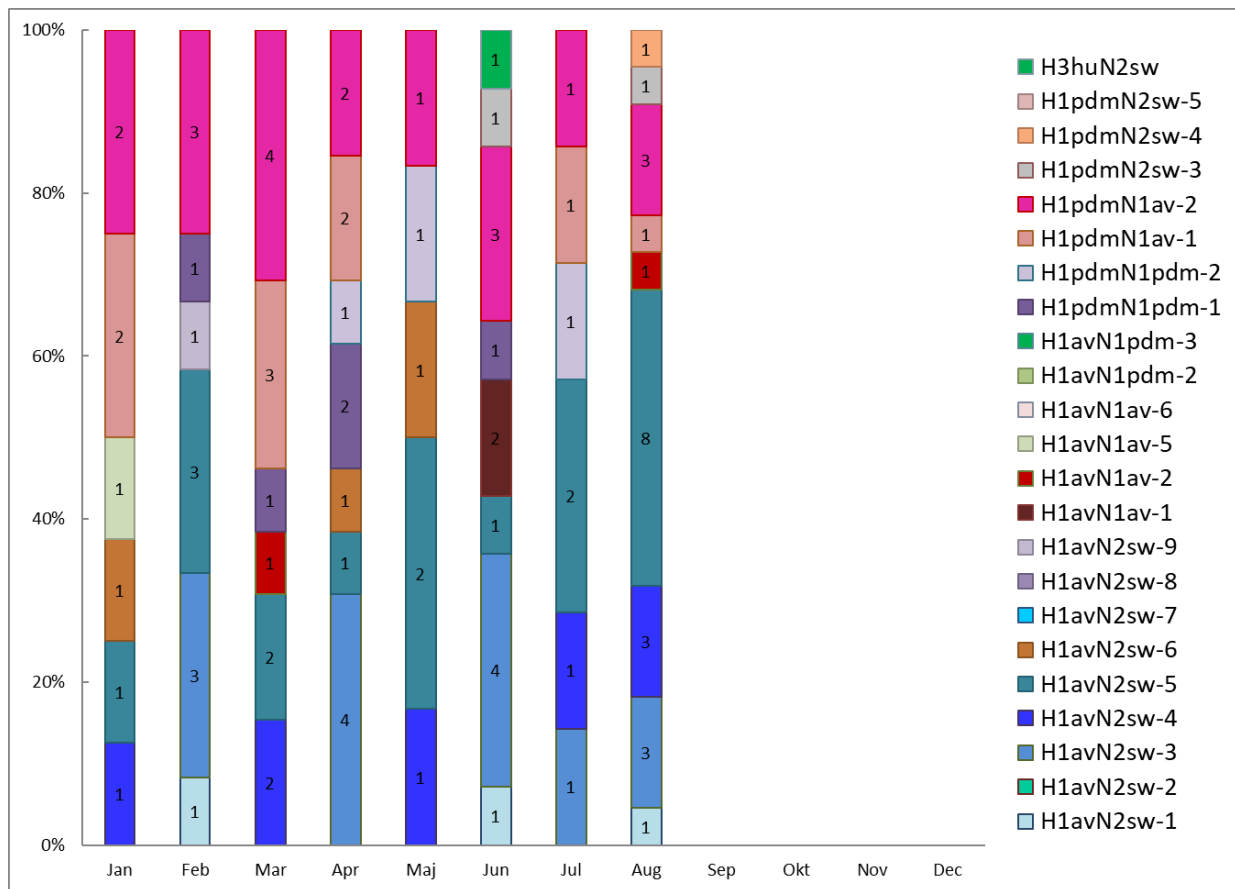
Distribution of swine influenza A virus subtypes

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 identified for 22 submissions. The majority were of the H1avN2sw subtype (n=14) while the H1pdm09N1av and the H1pdm09N2sw were observed in four and two submissions, respectively. In addition, one submission showed signs of multiple subtypes, and one was positive for H1pdmN1, where the origin of the N1 could not be determined.

Distribution of swine influenza A virus genotypes



For August, 22 submissions were genotyped and included nine different genotypes. H1avN2sw-5 were the most observed genotype represented in eight submissions. H1avN2sw-3, H1avN2sw-4 and H1pdmN1av-2 were all observed in three submissions, whereas the remaining genotypes (H1avN2sw-1, H1avN1av-2, H1pdmN1av-1, H1pdmN2sw-3 and H1pdmN2sw-4) were only observed in single submissions.

Phylogenetic analysis

Fylogenetisk træ - Influenza A virus overvågning i danske grise
August 2025

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