

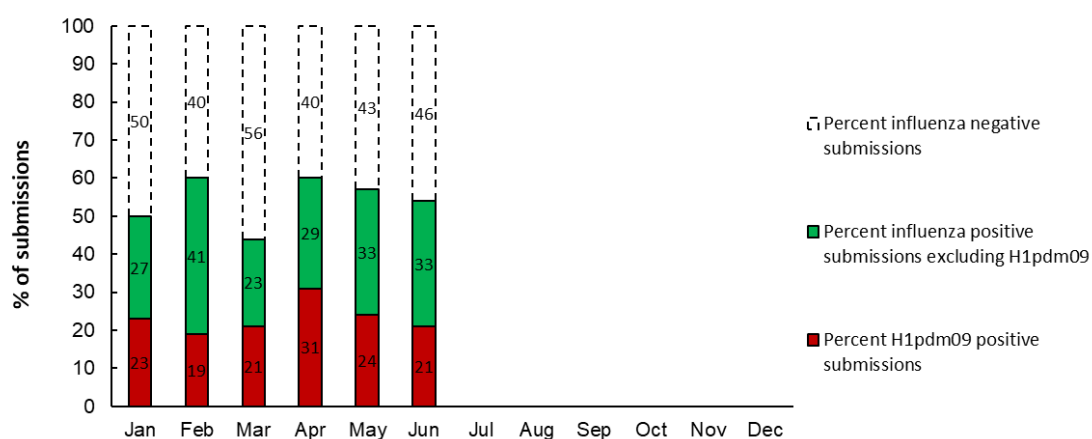
Surveillance of Influenza A virus in Danish pigs

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						
Submissions	22	52	43	42	21	33						
Herds	22	51	41	42	21	29						
Influenza positive												
Samples	28	69	42	60	27	39						
Submissions	11	31	19	25	12	18						
Herds	11	31	19	25	12	18						
H1pdm09 positive												
Samples	13	14	21	25	13	17						
Submissions	5	10	9	13	5	7						
Herds	5	10	9	13	5	7						

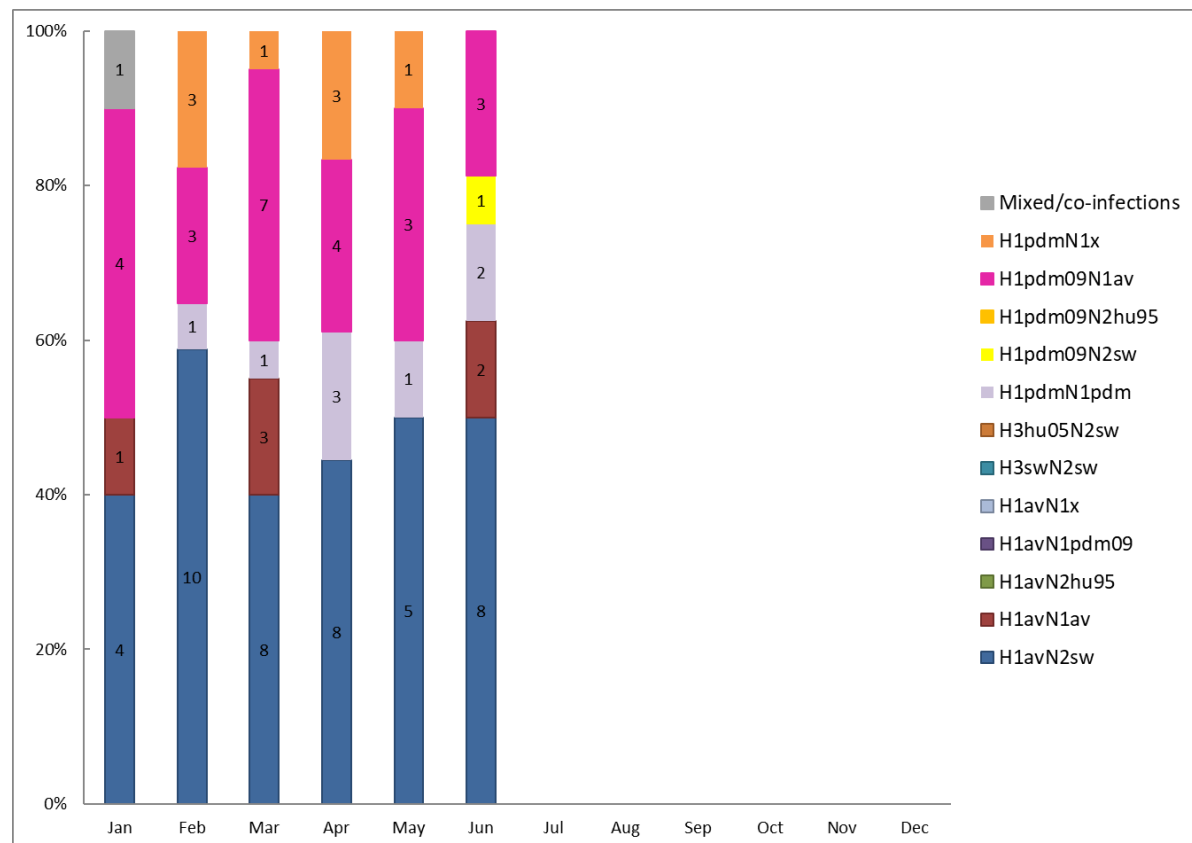
In June, 33 submissions from 29 herds registered with different CHR numbers were received. On average, each submission consisted of 3.3 samples. The percentage of influenza positive submissions was 54 %, which is slightly lower than the level observed in May. All influenza A virus-positive samples were tested for the presence of H1pdm09. Overall, 39 % 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.

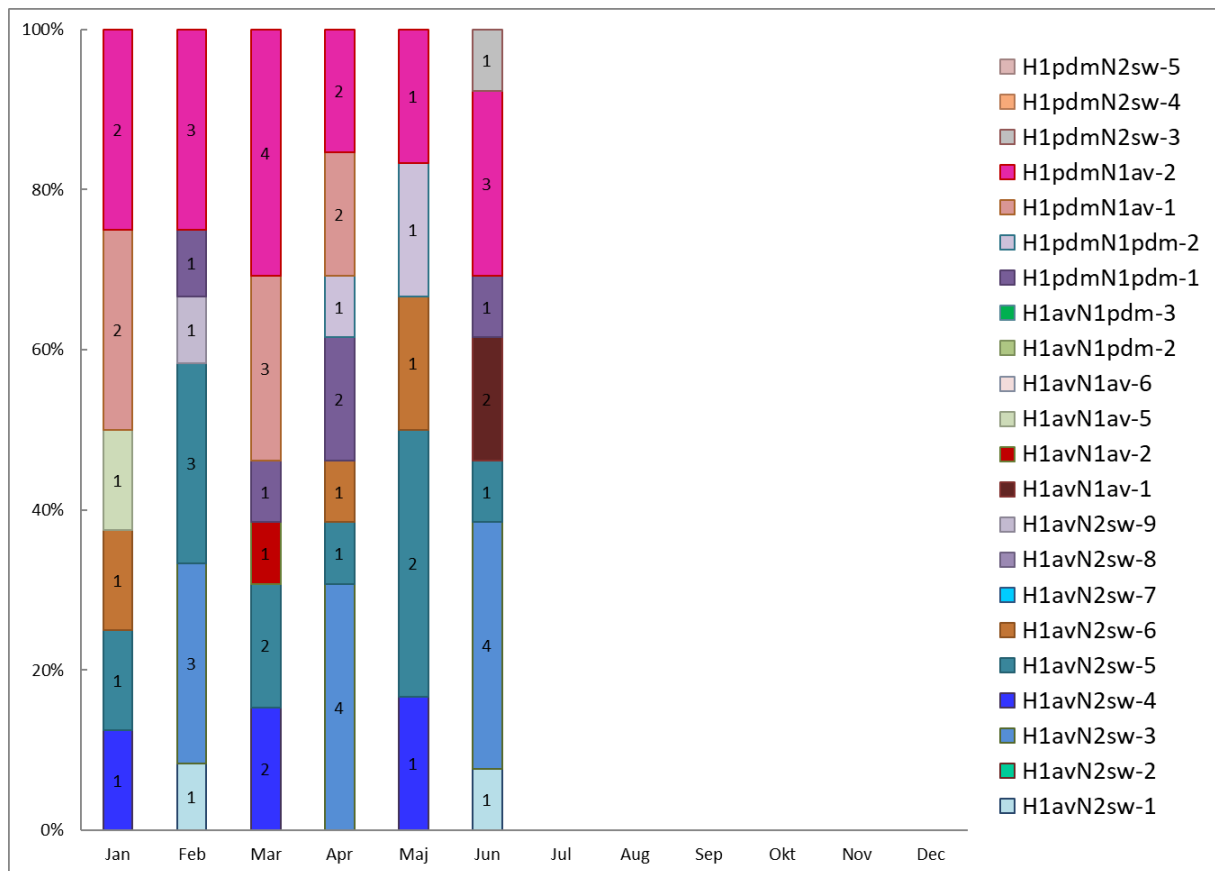
Distribution of swine influenza A virus subtypes

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 June, the full subtype (both HA and NA gene segments) was identified for 16 submissions. The majority were of the H1avN2sw subtype (n=8) while the H1pdmN1av was observed in three submissions. In addition, the following subtypes were identified; two H1pdmN1pdm, two H1avN1av and one H1pdmN2sw.

Distribution of swine influenza A virus genotypes



For June, 13 submissions were genotyped and included seven different genotypes. The most prevalent genotypes were H1avN2sw-3 and H1pdmN1av-2 carrying similar internal gene cassettes.

Phylogenetic analysis

