

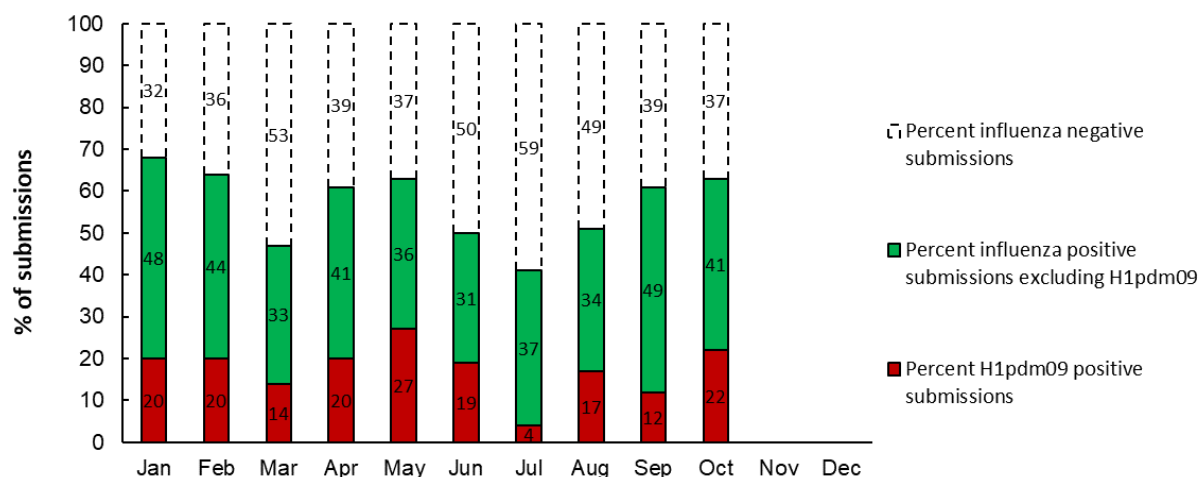
Surveillance of Influenza A virus in Danish pigs

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

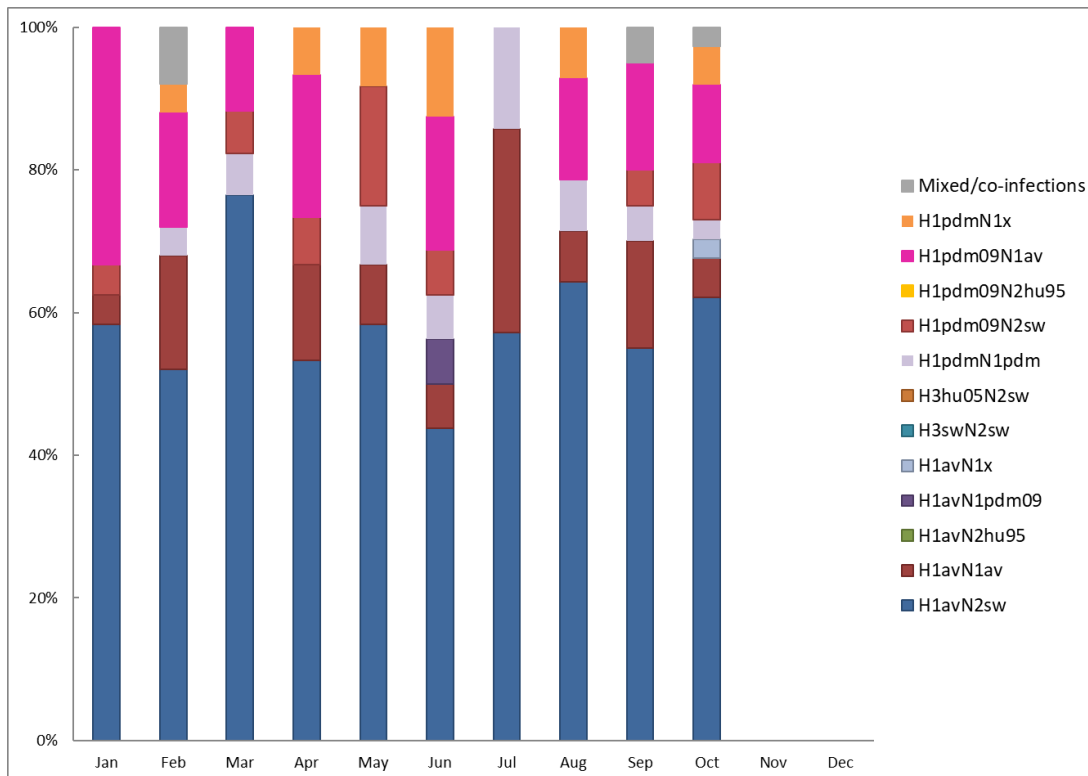
In October, 68 submissions from 67 herds registered with different CHR numbers were received. On average, each submission consisted of 4 samples. The percentage of submissions positive increased this month to 63%, which is similar to the proportion registered April and May. All influenza A virus-positive samples were tested for the presence of H1pdm09. Overall, 35% 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 35%, which is comparable to previous months earlier in the year.

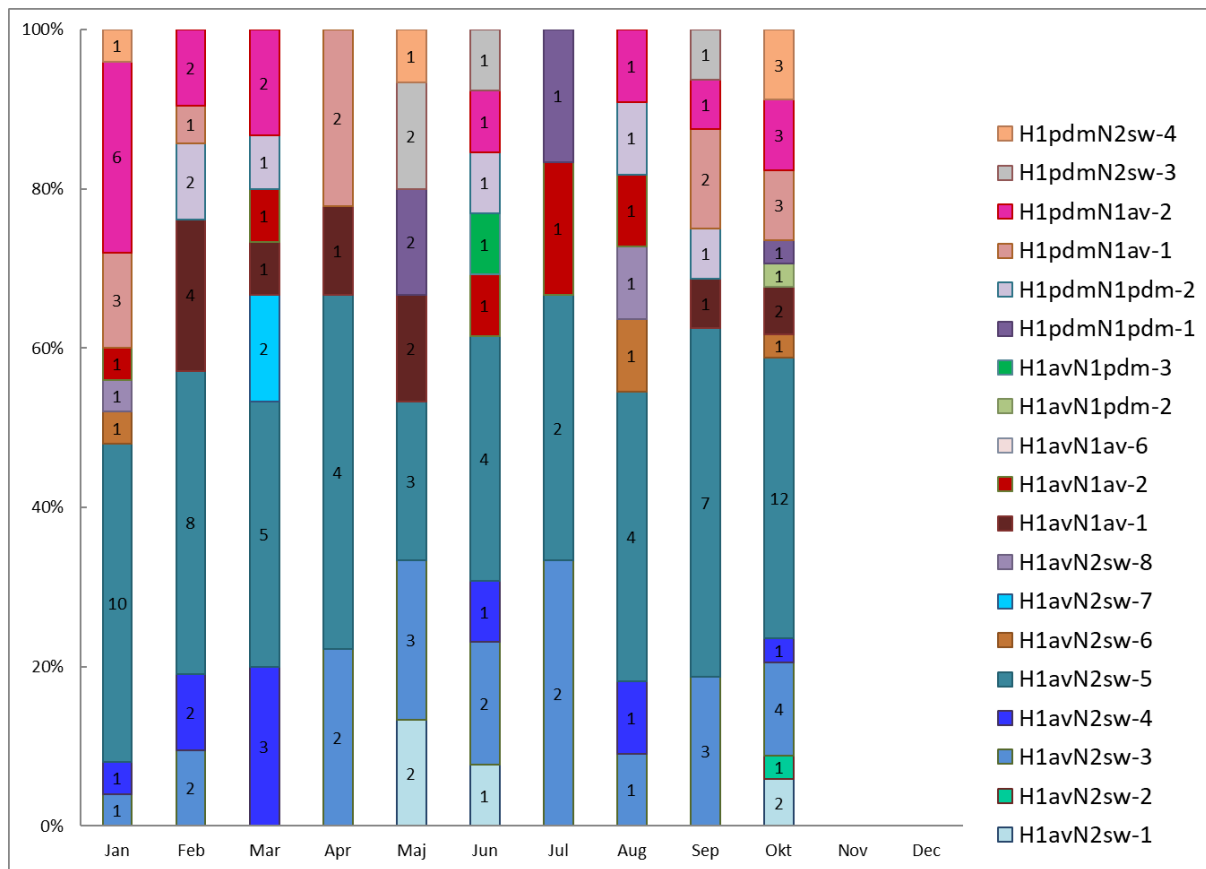
Distribution of swine influenza A virus subtypes

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 October, the full subtype (both HA and NA gene segments) was determined for 37 submissions. The far greatest majority of the submissions were of H1avN2sw origin (n=23), whereas a few submission were positive for H1pdm09N1av, H1pdm09N2sw, H1avN1av and H1pdmN1pdm.

Distribution of swine influenza A virus genotypes



For October, 34 submissions were genotyped. The H1avN2sw-5 viruses with a complete internal cassette of H1N1pdm09 origin were again the most abundant (n=12), but also H1avN2sw3, H1pdmN2sw-4 and H1pdmN1av-2, were observed frequently, all with an internal gene cassette where all but the NS gene were of H1N1pdm09 origin.

Phylogenetic analysis

Fylogenetisk træ - Influenza A virus overvågning i Danske svin Oktober 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 laboratorum, Kjellerup starter med "LF" og er navngivet med Kjellerups sagsnummer.

