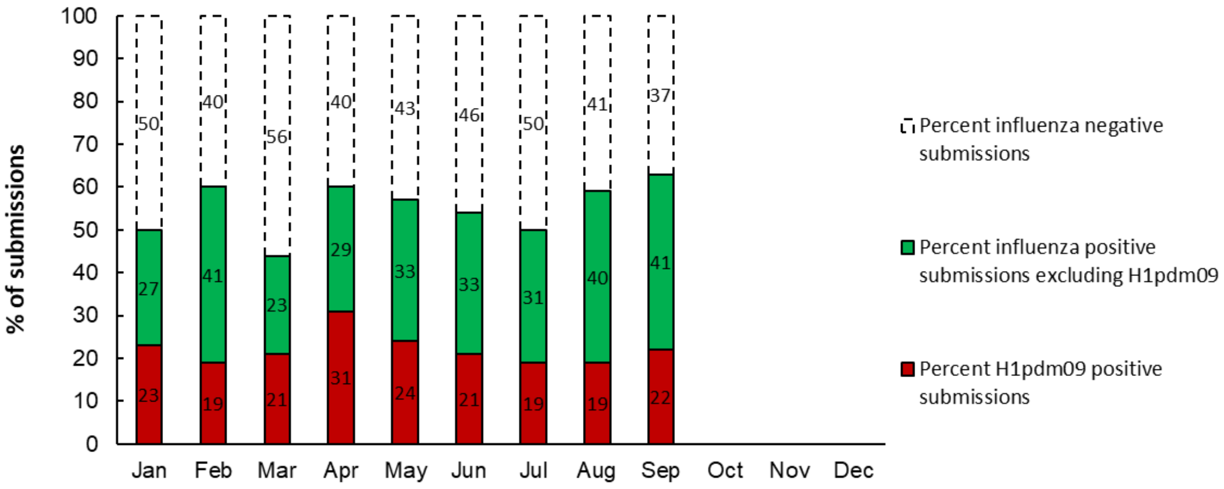
Surveillance of Influenza A virus in Danish pigs

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	172			
Submissions	22	52	43	42	21	33	26	37	46			
Herds	22	51	41	42	21	29	25	36	44			
Influenza positive												
Samples	28	69	42	60	27	39	25	50	72			
Submissions	11	31	19	25	12	18	13	22	29			
Herds	11	31	19	25	12	18	13	21	28			
H1pdm09 positive												
Samples	13	14	21	25	13	17	11	14	23			
Submissions	5	10	9	13	5	7	5	7	10			
Herds	5	10	9	13	5	7	5	7	10			

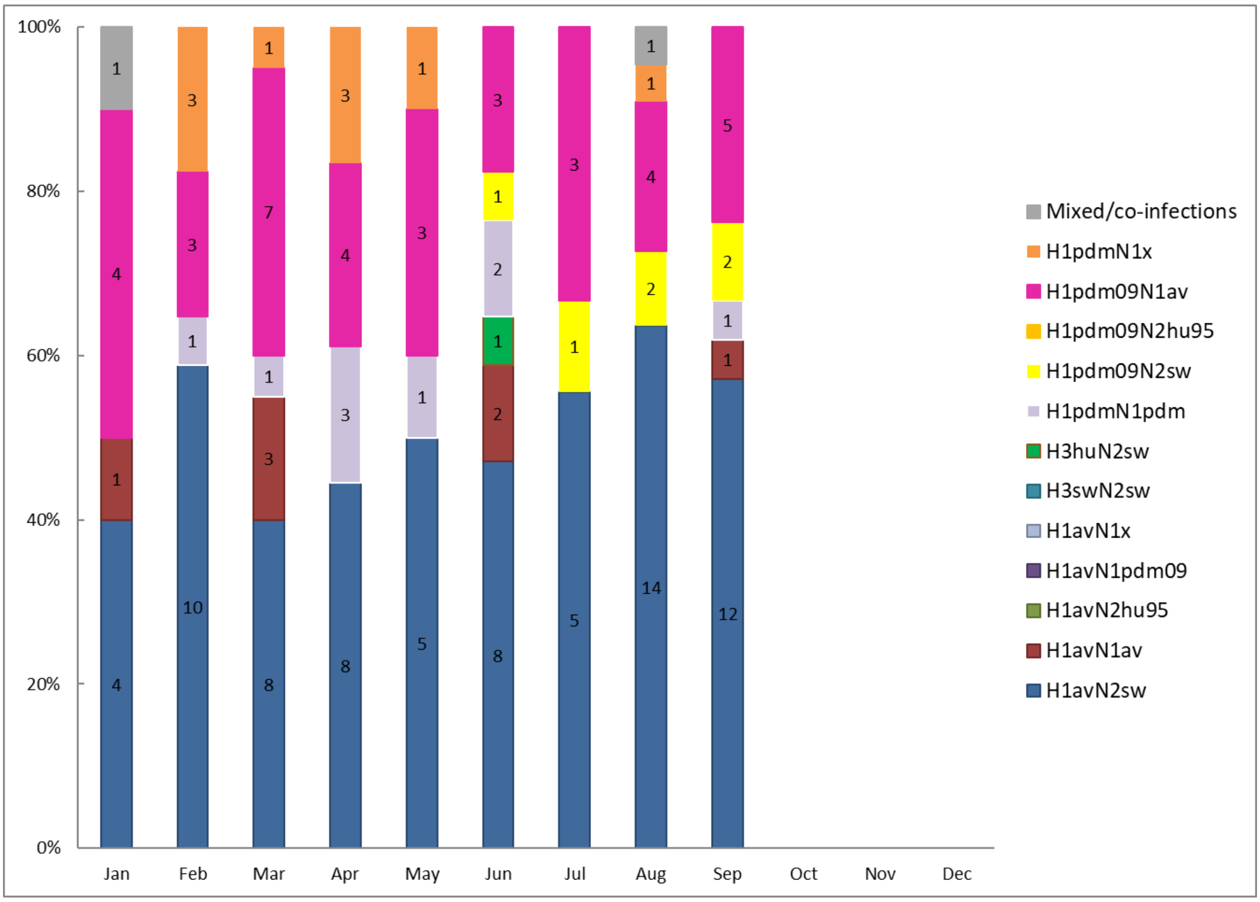
In September, 46 submissions from 44 herds registered with different CHR numbers were received. On average, each submission consisted of 3.7 samples. The percentage of influenza positive submissions was 63 %, which is higher than the last two months but corresponds to the level observed in April and February. All influenza A virus-positive samples were tested for the presence of H1pdm09. Overall, 34.5 % 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.

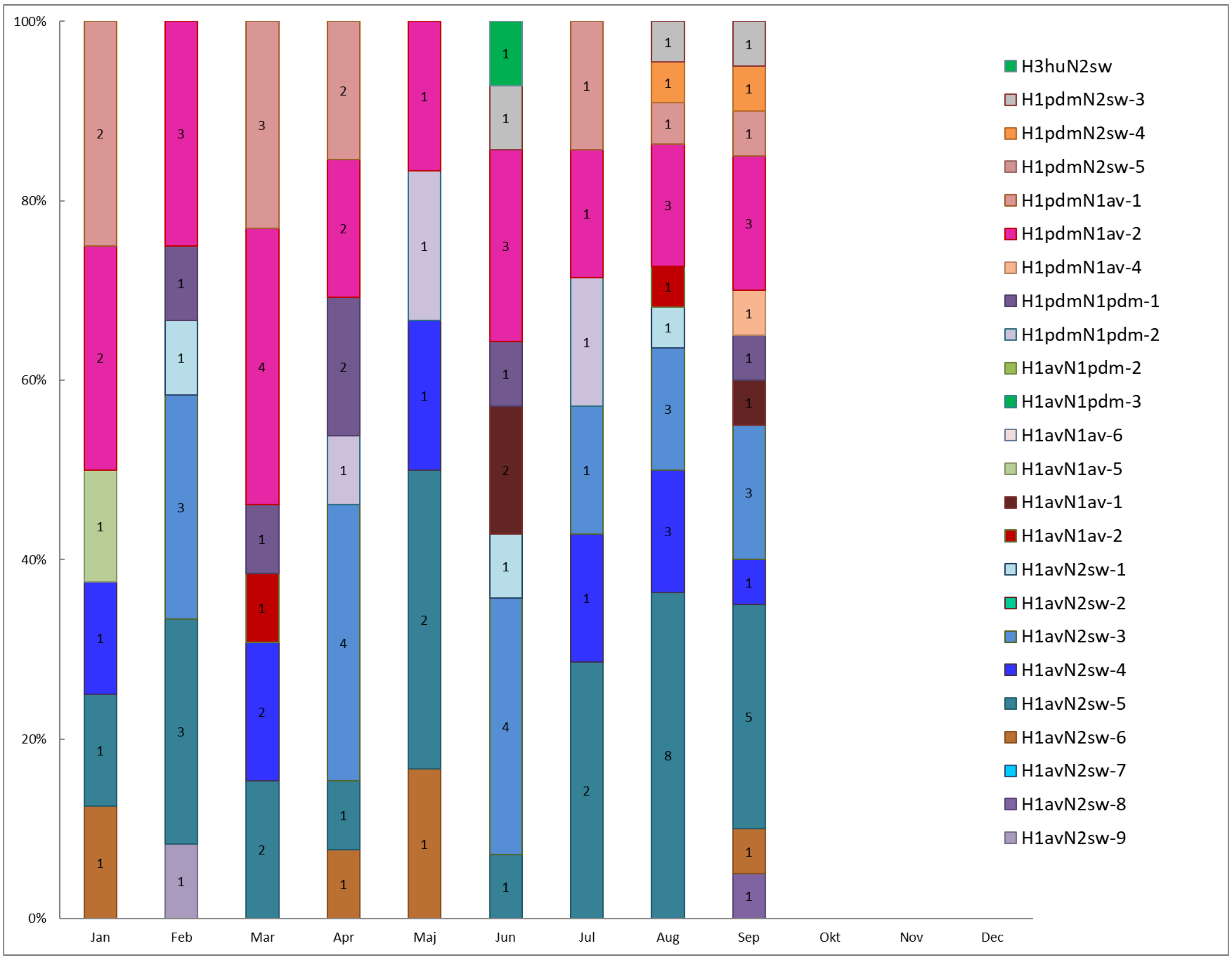
Distribution of swine influenza A virus subtypes

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 September, the full subtype (both HA and NA gene segments) was identified for 21 submissions. The majority were of the H1avN2sw subtype (n=12) while the H1pdm09N1av was observed in five submissions. In addition, H1pdm09N2sw was observed in two submissions and H1avN1av and H1pdmH1pdm in single submissions.

Distribution of swine influenza A virus genotypes



For September, 21 submissions were genotyped and included twelve different genotypes including one novel genotype “H1pdmN1av-4” carrying a PB1 gene of Eurasian avian-like origin and the remaining internal genes of H1N1pdm09 origin. H1avN2sw-5 was like the two previous months, the most observed genotype represented in five submissions. H1avN2sw-3 and H1pdmN1av-2 were both detected in three submissions, whereas the remaining genotypes were only detected in single submissions.

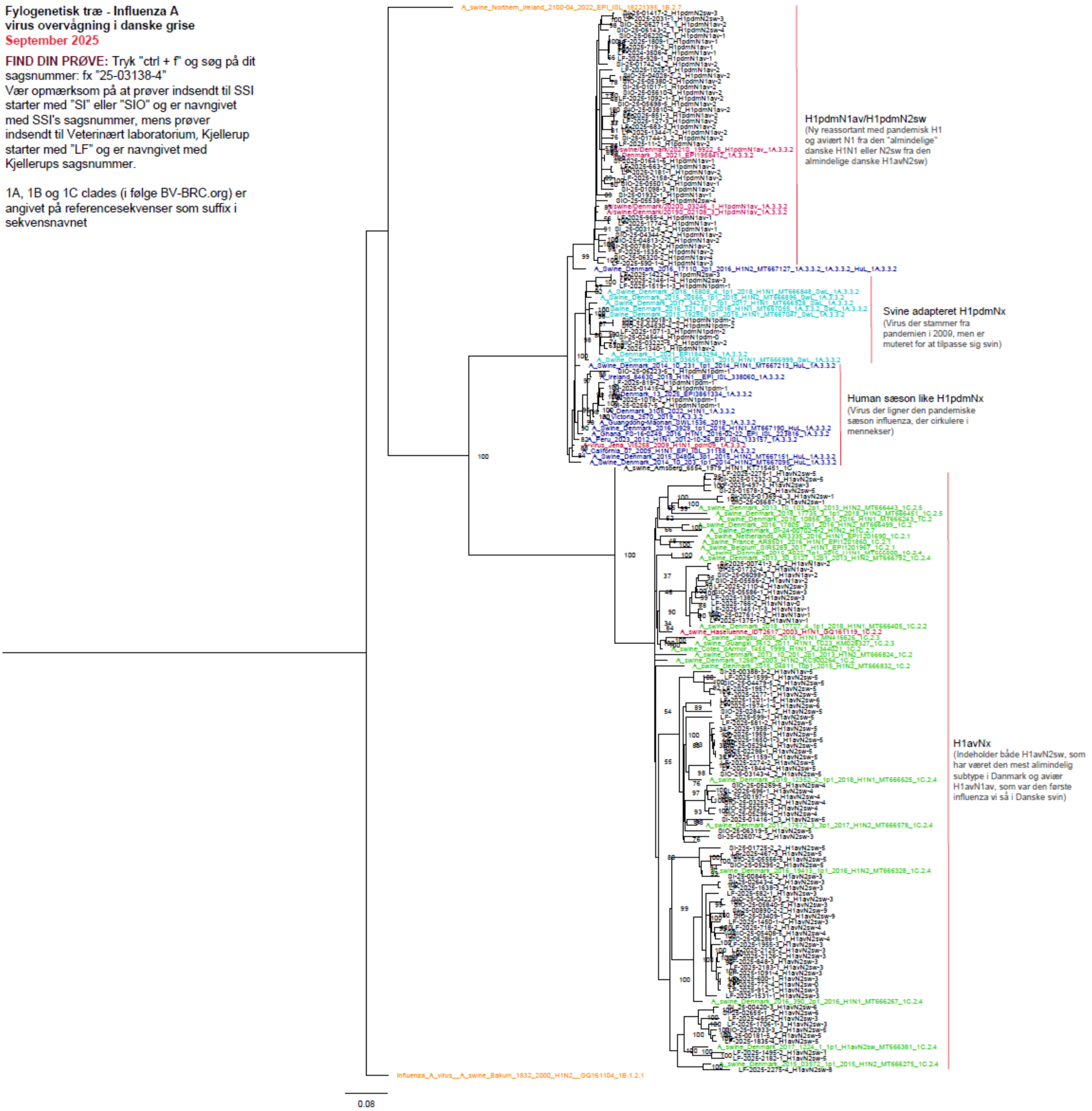
Phylogenetic analysis

Fylogenetisk træ - Influenza A virus overvågning i danske grise

September 2025

FIND DIN PRØVE: Tryk "ctrl + f" og søg på dit sagsnummer: fx "25-03138-4"
Vær opmærksom på at prøver indsendt til SSI starter med "SI" eller "SIO" og er navngivet med SSI's sagsnummer, mens prøver indsendt til Veterinært laboratorium, Kjellerup starter med "LF" og er navngivet med Kjellerups sagsnummer.

1A, 1B og 1C clades (i følge BV-BRC.org) er angivet på referencesekvenser som suffix i sekvensnavnet



H1pdmN1av/H1pdmN2sw
(Ny reassortant med pandemisk H1 og aviært 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 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)