

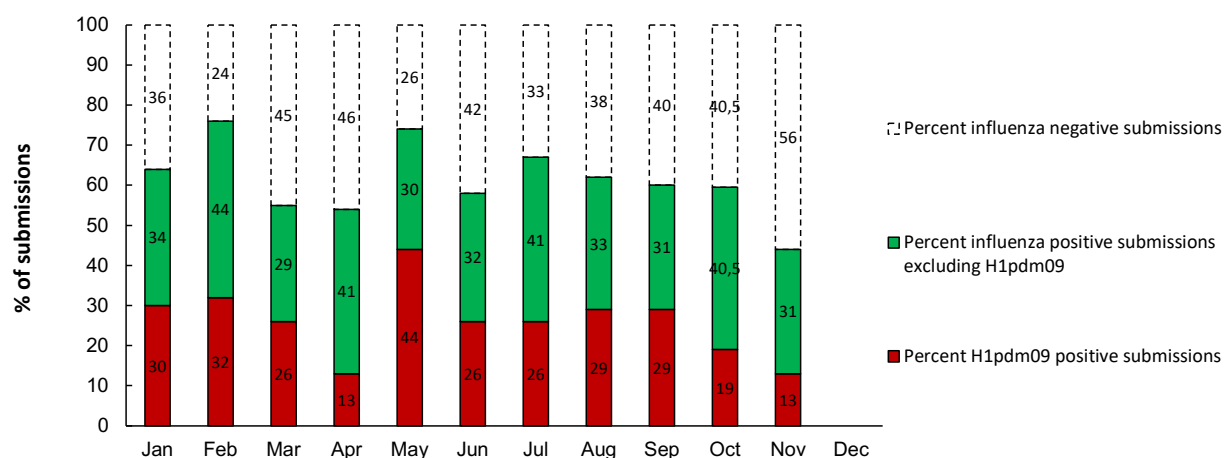
# Surveillance of Influenza A virus in Danish pigs

## Samples and results 2023

The table illustrate the number of samples, submissions and herds that contributed to the surveillance program each month. In addition, the results of the influenza A virus and H1pdm09 screening are shown.

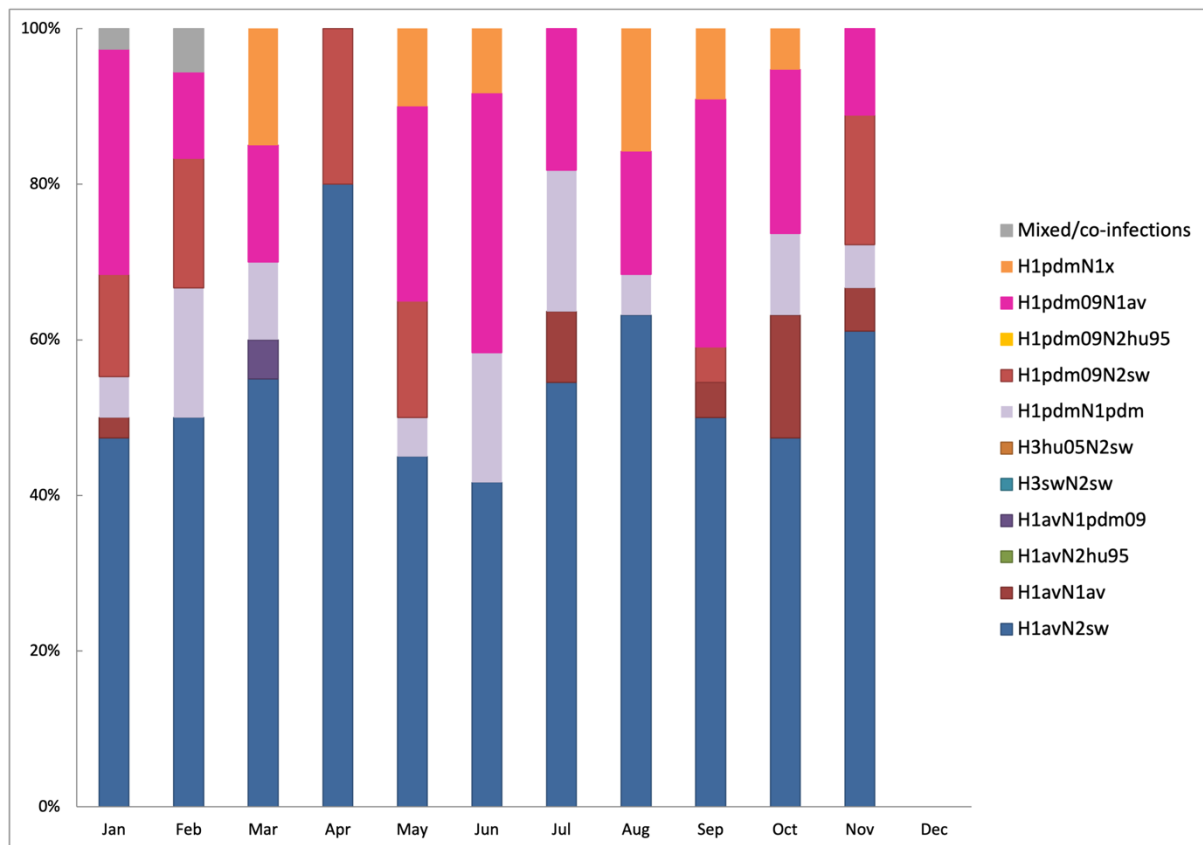
	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
<b>Received</b>												
Samples	169	118	163	143	89	101	97	136	144	150	263	
Submissions	50	34	49	46	27	31	27	42	42	42	70	
Herds	46	34	48	45	27	31	27	41	42	42	67	
<b>Influenza positive</b>												
Samples	84	79	67	61	54	45	44	52	76	73	85	
Submissions	32	26	27	25	20	18	18	26	25	25	31	
Herds	31	26	27	25	20	18	18	26	25	25	30	
<b>H1pdm09 positive</b>												
Samples	36	32	25	12	31	21	15	16	24	15	25	
Submissions	15	11	13	6	12	8	7	12	12	8	9	
Herds	15	11	13	6	12	8	7	12	12	8	9	

In November, 70 submissions from 67 herds registered with different CHR numbers were received. On average, one submission included 3.7 samples. The percentage of the submissions that were positive for Influenza A virus in November was 44 %, which is the lowest this year. All influenza A virus positive samples were tested for the presence of H1pdm09. Overall, 29% of the submissions testing positive for the influenza A virus were found to be positive for H1pdm09. This mirrors the proportion of positive observed in both October and April, during which fewer submissions were H1pdm09-positive compared to the rest of the year.



The figure illustrates the percentage of influenza A virus negative and positive submissions including the proportion of H1pdm09 positive submissions. The proportion of Influenza A virus negative submissions (56%) increased significantly compared to previous months. The reason for this is unknown, but it may be linked to the increased number of submissions facilitated by CEVA including herds with less clinical signs. While this affects the proportion of influenza A virus negative submissions in November, the absolute numbers for submissions with detected influenza A virus and H1pdm09 virus is largely unchanged (table above) compared to the previous months in 2023.

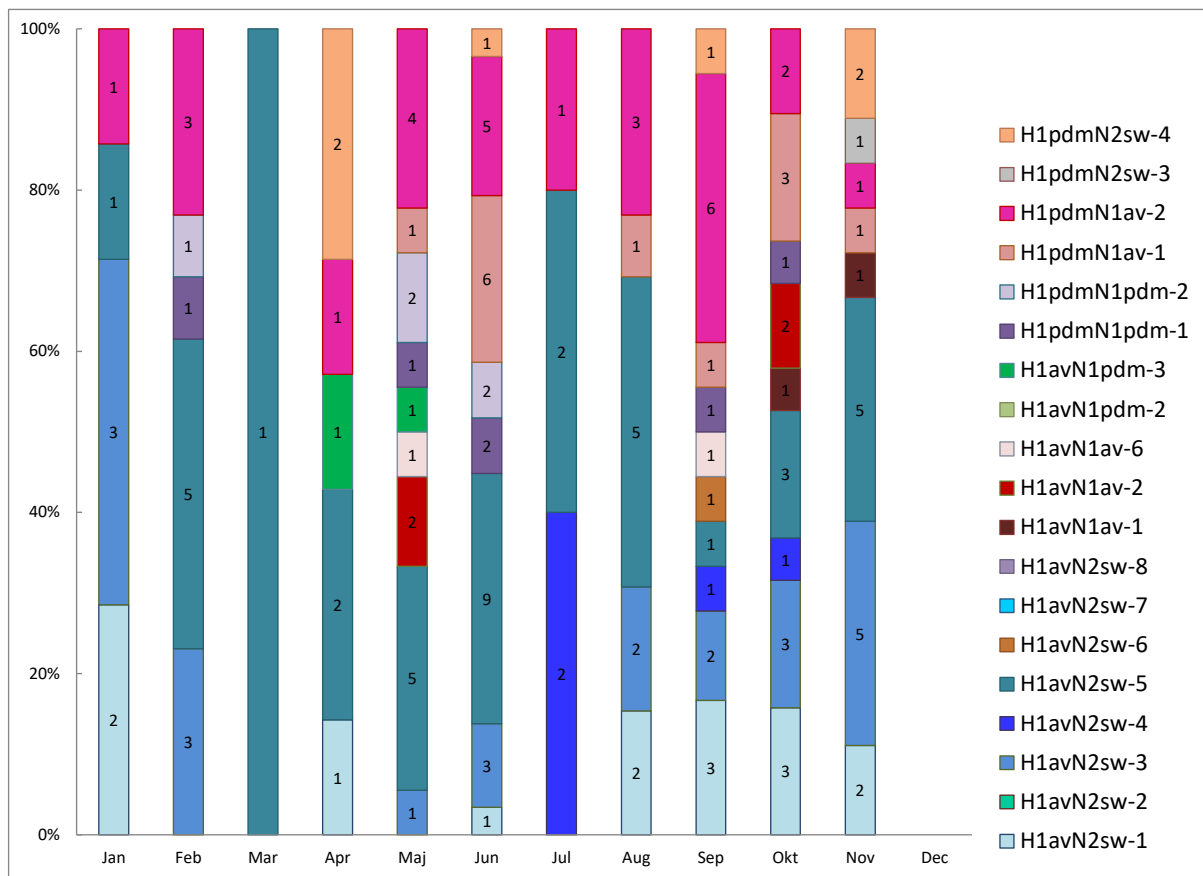
## Distribution of swine influenza A virus subtypes



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 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 November, the subtype (HA and NA gene segments) was determined for 18 submissions. The H1avNx viruses were dominating, with H1avN2sw being the most prevalent. In addition, 30% of the submissions were subtyped as H1pdmNx, which included three H1pdmN2sw, one H1pdmN1pdm and two H1pdmN1av.

## Distribution of swine influenza A virus genotypes



For November, 18 submissions were genotyped. For the H1avN2sw viruses, the dominating genotypes were H1avN2sw-3 and H1avN2sw-5 with a mix of avian-like swine and H1pdm origin internal genes, followed by H1avN2sw-1, which contained all gene segments of avian-like swine origin. For the H1pdmNx viruses, we detected H1pdmN2sw-4 in 2 submissions, while H1pdmN2sw-3 was detected for the first time since 2022 in a single submission this month. H1pdmN1av-1 and H1pdmN1av-2 were each detected in a single submission.

# Phylogenetic analysis

**Fylogenetisk træ - Influenza A virus overvågning i Danske svin Nov 2023**

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