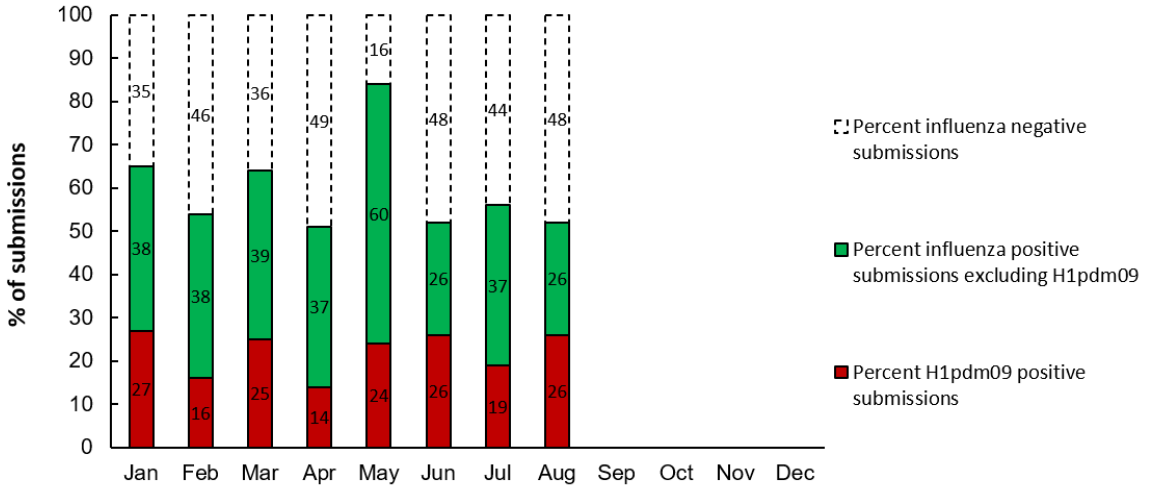
# Surveillance of Influenza A virus in Danish pigs

# Samples and results 2026

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 | 161 | 189 | 193 | 105 | 101 | 134 | 63 | 97 | | | | |
| Submissions | 48 | 57 | 56 | 35 | 25 | 36 | 16 | 31 | | | | |
| Herds | 45 | 53 | 54 | 35 | 25 | 35 | 16 | 30 | | | | |
| **Influenza positive** | | | | | | | | | | | | |
| Samples | 92 | 79 | 89 | 41 | 55 | 60 | 28 | 31 | | | | |
| Submissions | 31 | 31 | 36 | 18 | 21 | 26 | 9 | 16 | | | | |
| Herds | 31 | 29 | 36 | 18 | 21 | 26 | 9 | 16 | | | | |
| **H1pdm09 positive** | | | | | | | | | | | | |
| Samples | 43 | 16 | 33 | 12 | 12 | 9 | 9 | 11 | | | | |
| Submissions | 13 | 9 | 14 | 5 | 6 | 5 | 3 | 8 | | | | |
| Herds | 13 | 9 | 14 | 5 | 6 | 5 | 3 | 8 | | | | |

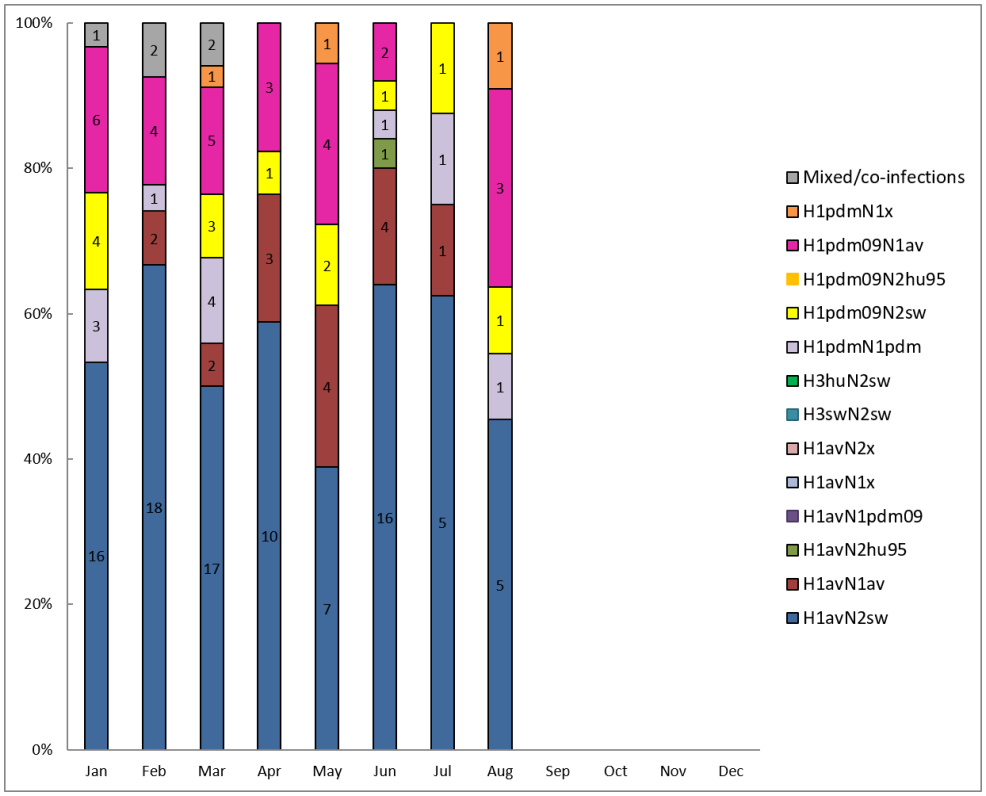
In August, 31 submissions from 30 herds registered with different CHR numbers were received. On average, each submission consisted of 3.1 samples. The percentage of influenza positive submissions was 52 %, corresponding to the levels observed in the two previous months. All influenza A virus-positive samples were tested for the presence of H1pdm09. Overall, 50 % of the submissions testing positive for the influenza A virus were positive for H1pdm09, comparable to the proportion observed in June.




The figure illustrates the percentage of influenza A virus negative and positive submissions including the proportion of H1pdm09 positive submissions.

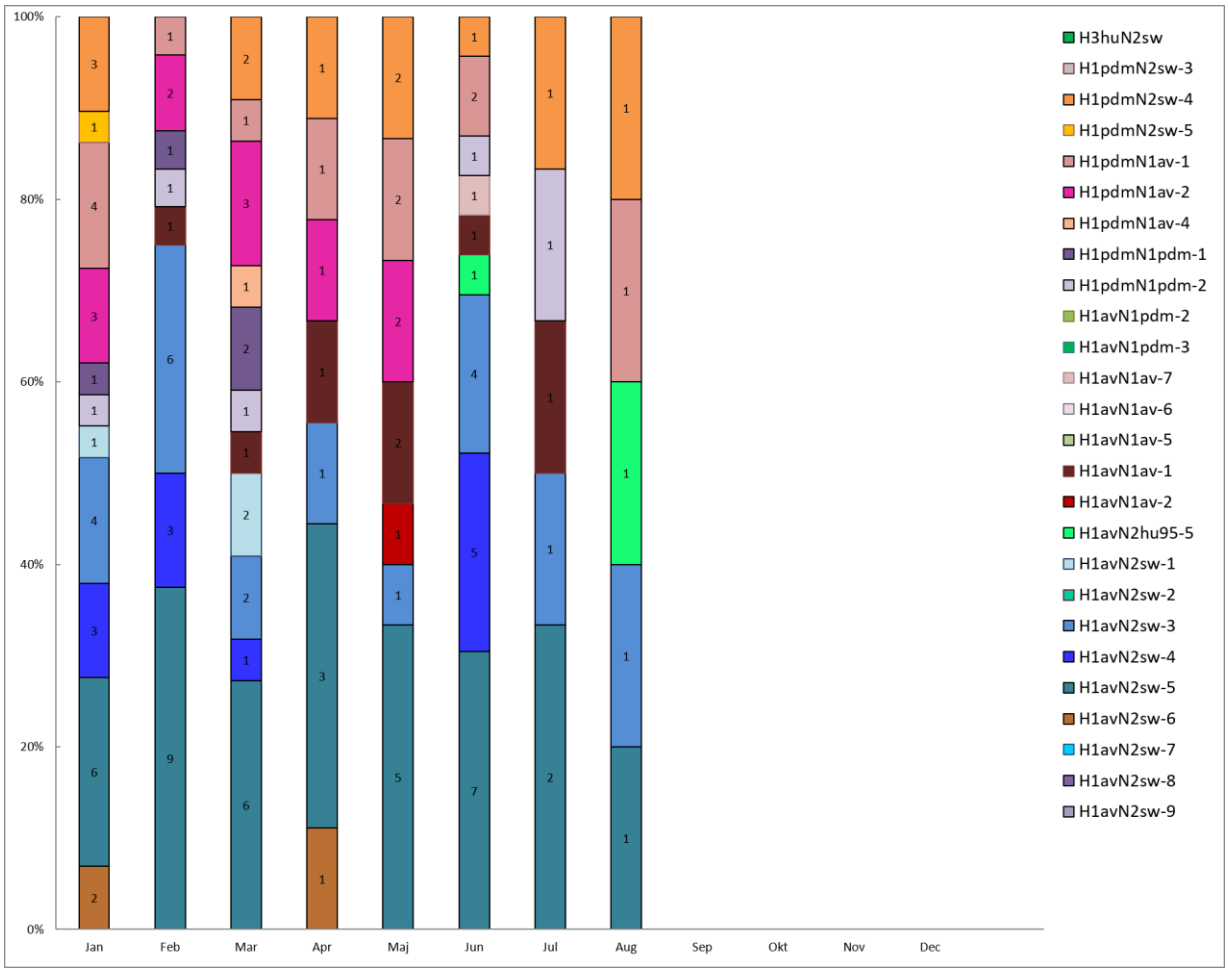
# Distribution of swine influenza A virus subtypes

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 11 submissions. The majority were of the H1avN2sw subtype (n=5) while the H1pdm09N1av was observed in three submissions. H1pdmN1pdm, H1pdmN2sw and H1pdmN1x were observed in single submissions.

# Distribution of swine influenza A virus genotypes




For August, five submissions were genotyped. In total five different genotypes were observed including H1avN2sw-3, H1avN2sw-5, H1avN2hu95-5, H1pdmN1av-1 og H1pdmN2sw-4.

# Phylogenetic analysis

**Fylogenetisk træ - Influenza A virus overvågning i danske grise**
August 2026

**FIND DIN PRØVE:** Tryk "ctrl + f" og søg på dit sagsnummer: fx "26-00445-3"
Vær opmærksom på at prøver indsendt til SSI starter med "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

