

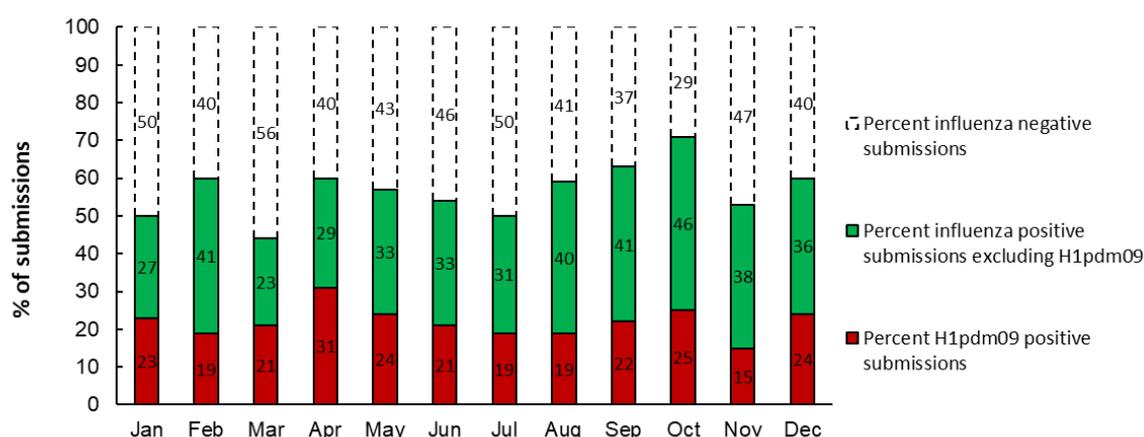
Surveillance of Influenza A virus in Danish pigs

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 | Total |
|---------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------|
| Received | | | | | | | | | | | | | |
| Samples | 60 | 151 | 124 | 148 | 67 | 110 | 93 | 123 | 172 | 230 | 176 | 200 | 1654 |
| Submissions | 22 | 52 | 43 | 42 | 21 | 33 | 26 | 37 | 46 | 59 | 53 | 58 | 492 |
| Herds | 22 | 51 | 41 | 42 | 21 | 29 | 25 | 36 | 44 | 59 | 50 | 58 | - |
| Influenza positive | | | | | | | | | | | | | |
| Samples | 28 | 69 | 42 | 60 | 27 | 39 | 25 | 50 | 72 | 115 | 71 | 85 | 683 |
| Submissions | 11 | 31 | 19 | 25 | 12 | 18 | 13 | 22 | 29 | 42 | 28 | 35 | 285 |
| Herds | 11 | 31 | 19 | 25 | 12 | 18 | 13 | 21 | 28 | 42 | 27 | 35 | - |
| H1pdm09 positive | | | | | | | | | | | | | |
| Samples | 13 | 14 | 21 | 25 | 13 | 17 | 11 | 14 | 23 | 36 | 20 | 37 | 244 |
| Submissions | 5 | 10 | 9 | 13 | 5 | 7 | 5 | 7 | 10 | 15 | 8 | 14 | 108 |
| Herds | 5 | 10 | 9 | 13 | 5 | 7 | 5 | 7 | 10 | 15 | 8 | 14 | - |

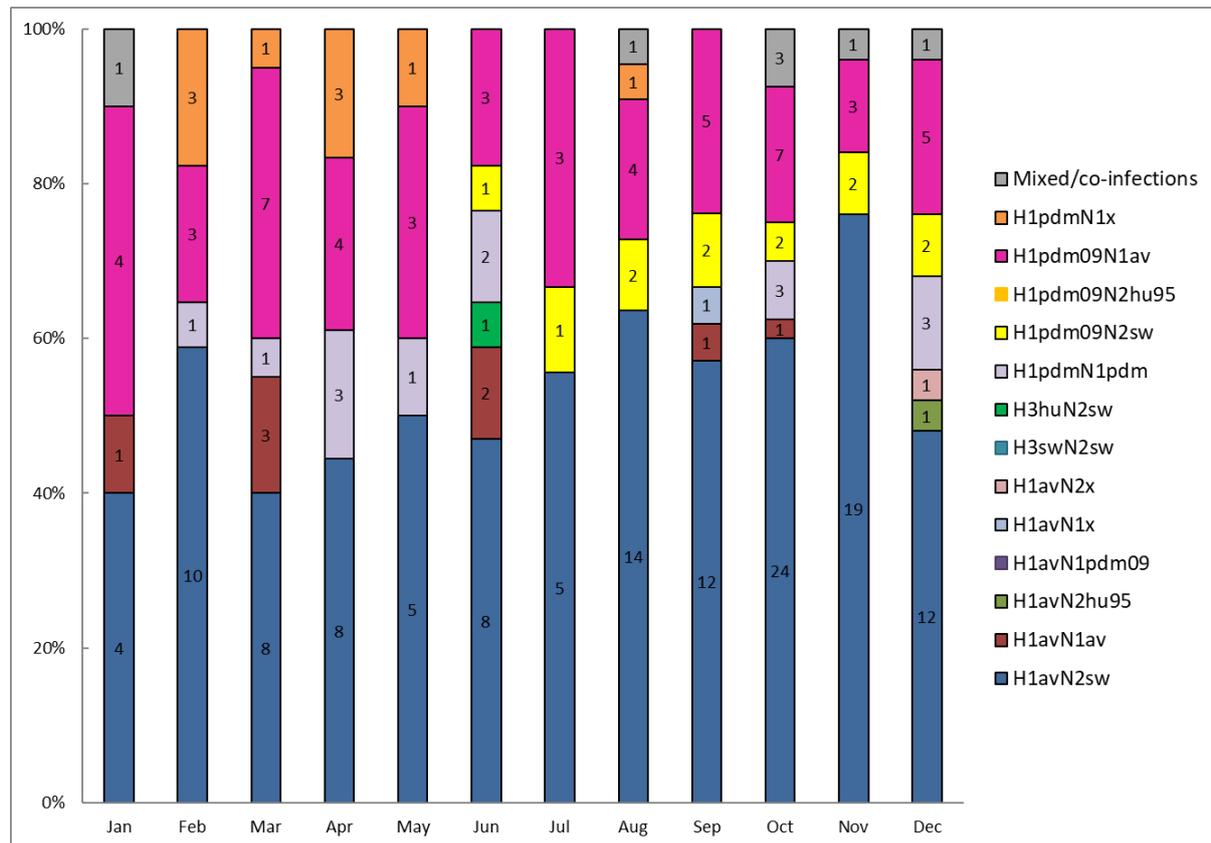
In December, 58 submissions from 58 herds registered with different CHR numbers were received. On average, each submission consisted of 3.4 samples. The percentage of influenza positive submissions was 60 % resembling the level observed in August and September. All influenza A virus-positive samples were tested for the presence of H1pdm09. Overall, 40 % 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.

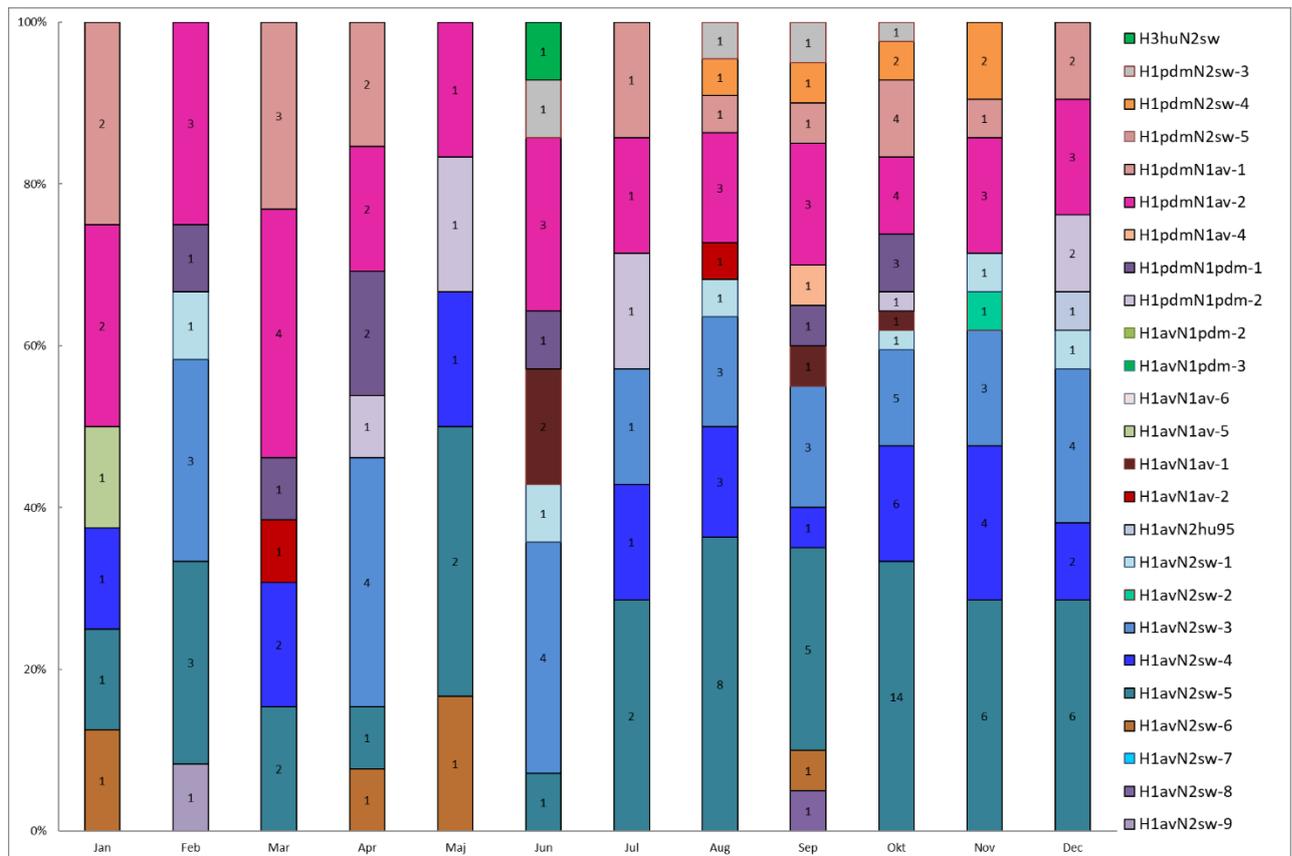
Distribution of swine influenza A virus subtypes

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 December, the full subtype (both HA and NA gene segments) was identified for 25 submissions. The majority were of the H1avN2sw subtype (n=12) while the H1pdm09N1av was observed in five submissions. In addition, H1pdmN1pdm and H1pdmN2sw were observed in three and two submissions, respectively. H1avN2hu95 was observed in a single submission for the first time since 2022. In addition, a submission was positive for H1avN2x carrying a novel N2 gene, that remains to be fully classified. This month one submission showed signs of co-infections with several swIAV strains.

Distribution of swine influenza A virus genotypes



For December, 22 submissions were genotyped. In total eight different genotypes were observed, with H1avN2sw-5 being most often detected (n=6). In addition, the H1avN2sw-3 and H1pdmN1av-2 genotypes were also observed in four and three submissions respectively, both carrying an NS segment of Eurasian avian-like origin, whereas the remaining internal genes are of H1N1pdm09 origin.

Phylogenetic analysis

Fylogenetisk træ - influenza A virus overvågning i danske grise
December 2009
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