

Surveillance of Influenza A virus in Danish pigs

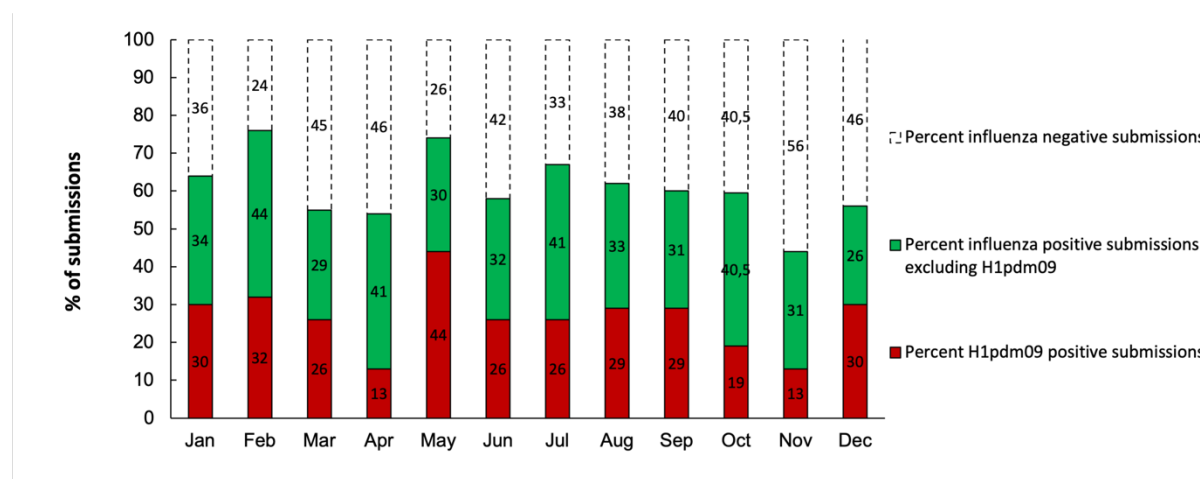
Samples and results 2023

The table illustrate the number of samples, submissions and herds that contributed to the surveillance program each month 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	169	118	163	143	89	101	97	136	144	150	263	175	1748
Submissions	50	34	49	46	27	31	27	42	42	42	70	47	507
Herds	46	34	48	45	27	31	27	41	42	42	67	46	496
Influenza positive													
Samples	84	79	67	61	54	45	44	52	76	73	85	63	783
Submissions	32	26	27	25	20	18	18	26	25	25	31	26	299
Herds	31	26	27	25	20	18	18	26	25	25	30	26	297
H1pdm09 positive													
Samples	36	32	25	12	31	21	15	16	24	15	25	32	284
Submissions	15	11	13	6	12	8	7	12	12	8	9	14	127
Herds	15	11	13	6	12	8	7	12	12	8	9	14	127

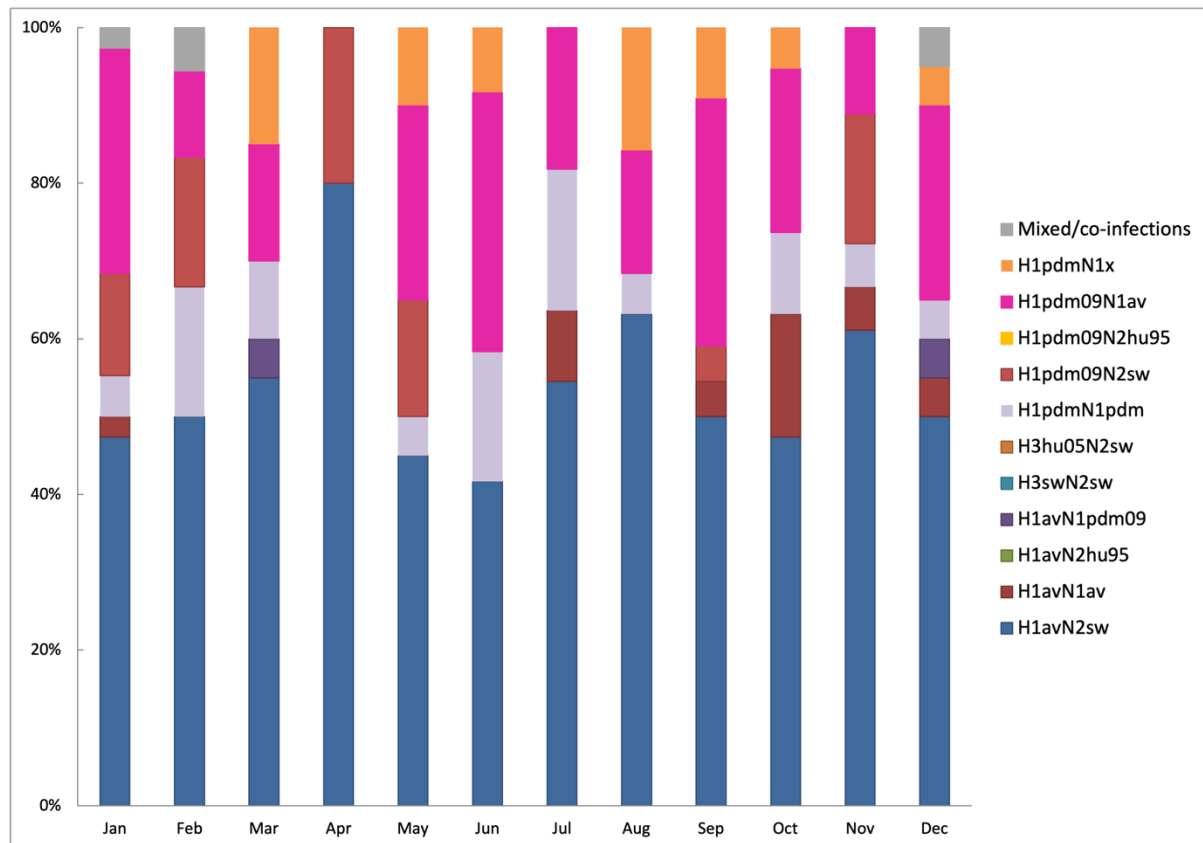
In December, 47 submissions from 46 herds registered with different CHR numbers were received. On average, each submission consisted of 3.7 samples. The percentage of the submissions that were positive for Influenza A virus in December was 54%, which is similar to previous months. All influenza A virus positive samples were tested for the presence of H1pdm09. Overall, 54% of the submissions testing positive for the influenza A virus were found to be positive for H1pdm09.

In 2023, the total number of submissions was at the same level as in 2022, but significantly lower than in 2021. The proportion of influenza A positive, and hereof H1pdm09 positive submissions, were at the same level as in 2022 and 2021.



The figure illustrates the percentage of influenza A virus negative and positive submissions including the proportion of H1pdm09 positive submissions. The proportion of influenza positive submissions and the proportion hereof of H1pdm09 was more or less constant throughout the year. This matches the general picture from previous years, where influenza A virus has been detected in submissions throughout the year.

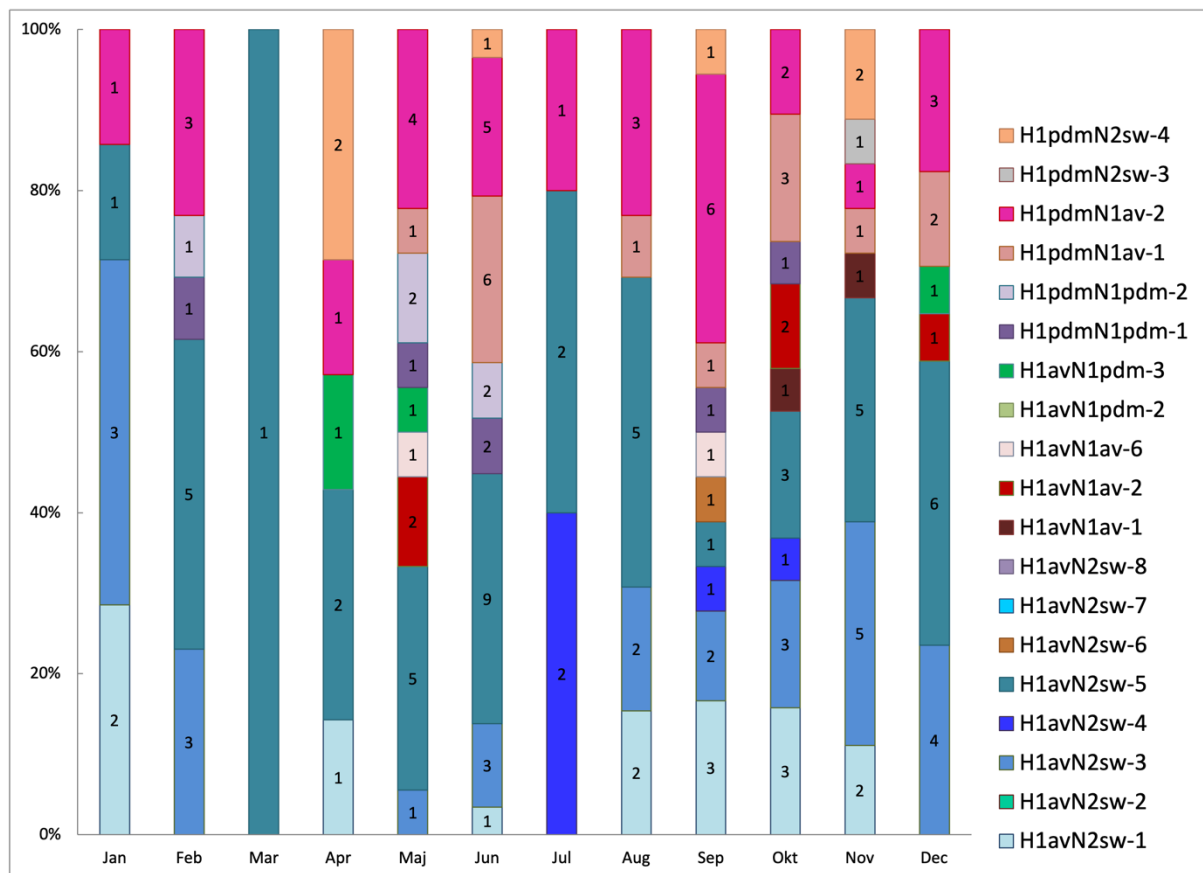
Distribution of swine influenza A virus subtypes



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 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 determined for 20 submissions. The H1avNx viruses were slightly dominating over H1pdm09 subtype, with H1avN2sw (n=10 submissions) being the most prevalent. The determined H1pdm09 subtypes were H1pdmN1av (n=5 submissions), H1pdmN1pdm (n=1) and H1pdmNx (n=1). One submission was identified as having mixed/co-infection with H1av, H1pdm, N1pdm and N2sw segments.

Distribution of swine influenza A virus genotypes



For December, 17 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. Additionally, two submissions were genotyped H1avN1av-2, which contained mainly gene segments of avian-like swine origin and the MP segment from pandemic origin, and H1avN1pdm09-2, which contained all pandemic origin segments with the NS of avian-like swine origin. For the H1pdmNx viruses, we genotyped three submissions with H1pdmN1av-2 and two with H1pdmN1av-1.

Phylogenetic analysis

Epidemiology and Infection (2017), 145, e107. doi:10.1017/S0950268817000000

© 2017 Cambridge University Press
This is an Open Access article, distributed under the terms of the Creative Commons Attribution licence (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted re-use, distribution and reproduction in any medium, provided the original work is properly cited.

