SURVEILLANCE OF INFECTIOUS DISEASES

IN ANIMALS AND HUMANS IN SWEDEN 2022











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Cover: A cultivation of *Salmonella* at the Public Health Agency of Sweden. Photo: Nicklas Thegerström/DN/TT. Cover design by Rodrigo Ferrada Stoehrel.

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Reporting guidelines: Reporting guidelines were introduced in 2018 for those chapters related to purely animal pathogens. The guidelines build on experiences from several EU projects, and have been validated by a team of international experts in animal health surveillance. The aim is to develop these guidelines further in collaboration within the global surveillance community and they have therefore been made available in the form of a wiki on the collaborative platform GitHub (https://github.com/SVA-SE/AHSURED/wiki). Feel free to contribute!

Layout: The production of this report continues to be accomplished using a primarily open-source toolset. The method allows the source text to be edited independently of the template for the layout which can be modified and reused for future reports. Specifically, the chapter texts, tables and captions are authored in Microsoft Word and then converted to the LaTeX typesetting language using a custom package written in the R software for statistical computing. The package uses the pandoc document conversion software with a filter written in the lua language. Most figures and maps are produced using R and the LaTeX library pgfplots. Development for 2022 has focused on generalising the R package to accommodate conversion into formats other than LaTeX and PDF, with a focus on markdown files which can be published as HTML websites using the Quarto publishing system. The report generation R package and process was designed by Thomas Rosendal, Wiktor Gustafsson and Stefan Widgren.

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Avian influenza

BACKGROUND

Avian influenza virus (AIV) refers to influenza A viruses naturally circulating among wild aquatic birds worldwide, which can infect domestic poultry and other bird species and that have sporadically been found in other animal species, including marine mammals, domestic animals, and humans. The causative agent is a segmented RNA virus with a marked ability to change over time. New strains emerge through the accumulation of point mutations (antigenic drift) and genetic reassortment (antigenic shift). Influenza A viruses are classified into different subtypes based on the surface glycoproteins: haemagglutinin (H) and neuraminidase (N). Currently, there are 18 haemagglutinin (H1-H18) and eleven known neuraminidase (N1-N11) subtypes. Except for the subtypes H17N10 and H18N11, which have only been found in bats, all other possible combinations are known to circulate in the aquatic wild bird reservoir.

Avian influenza (AI) is highly contagious in poultry and is spread both directly and indirectly. Wild aquatic birds are reservoirs for low pathogenic avian influenza viruses (LPAIV) including subtypes H5 and H7, which upon transmission and further adaptation to poultry may mutate and become highly pathogenic avian influenza virus (HPAIV).

The detection of HPAIV H5N1 in Hong Kong in 1997, with the ability to cause disease in humans, highlighted the potential threat of AI to animal and human health. Since then, extensive outbreaks caused by HPAIV of the goose/Guangdong/96 (Gs/ Gd) lineage have occurred repeatedly in various regions in Asia, Africa, and Europe.

Historically, there have been four recorded HPAI outbreaks in Sweden: in 2006, 2015, 2016–2017 and 2020–2021. The 2006 and 2015 outbreaks were limited to findings among wild birds. The 2016–2017 outbreak, besides affecting the wild bird population, resulted in outbreaks in poultry and the depopulation of several thousand domestic birds (Figure 23).

The 2020–2021 outbreak of HPAI caused the largest poultry disease outbreak ever recorded in Sweden, where more than two million birds were lost to the disease itself or culled to prevent the further spread of the virus. The epidemic started in November 2020 and continued with outbreak events among wild birds and poultry all through 2022.



Figure 22: One of many guillemots (common murre) found dead on Gotland island during the summer of 2022, with the Karlsö islands in the background. Photo: Måns Hjernquist.

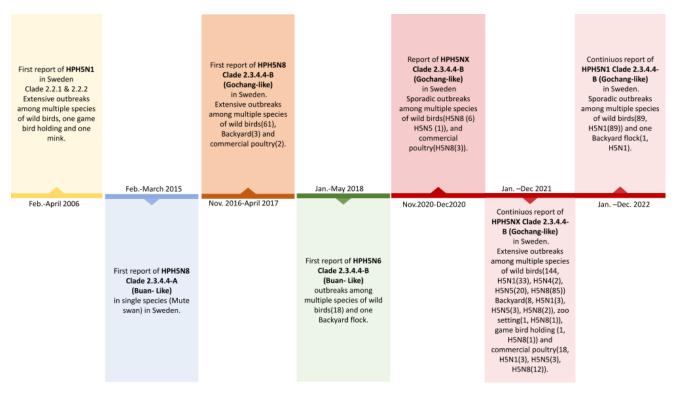


Figure 23: Timeline of HPAI outbreaks in Sweden 2006-2022. Infographic by Siamak Zohari.

Animals

The case fatality rate in birds infected with HPAIV may be as high as 100%, but this depends on the species affected, coinfections, virulence of the virus and other factors. In general, gallinaceous birds, including turkeys and chickens, suffer a more severe disease than waterfowl such as ducks and geese, which may exhibit only minor or no clinical disease. LPAIV infections most often cause asymptomatic infections or mild respiratory disease. HPAIV infections cause variable clinical signs such as cyanosis, respiratory distress, diarrhoea, nervous signs, depression, decreased food and water intake and decreased egg production with altered egg quality. Sometimes the only clinical sign is the sudden death of a large number of birds. While AIV is initially restricted to wild and domestic bird species, spillover into mammalian species, including humans may occur. Several recent reports describe the detections of HPAI H5N1 in wild terrestrial and aquatic mammals, causing morbidity and mortality.

Humans

The reported signs and symptoms of AIV infections in humans have ranged from mild to severe and included conjunctivitis, influenza-like illness (e.g., fever, cough, sore throat, muscle aches) sometimes accompanied by nausea, abdominal pain, diarrhoea and vomiting, severe respiratory illness (e.g., shortness of breath, difficulty breathing, pneumonia, acute respiratory distress, viral pneumonia, respiratory failure), neurological changes (altered mental status, seizures) and the involvement of other organ systems. In rare cases, human infections with HPAIV can lead to severe pneumonia and death.

Since 2003, 868 human cases of HPAIV H5N1 infection have been identified worldwide with a death rate of

53%. The majority of human cases of H5N1 infections have been associated with close direct or indirect contact with infected live or dead poultry. In September-October 2022, two human detections in farm workers with HPAIV H5N1 of HA Clade 2.3.4.4b were identified in Spain, associated with the confirmation of an HPAI outbreak in the poultry farm. The farm workers had been involved in cleaning tasks using personal protective equipment (PPE) and remained asymptomatic after initial positive detection and isolation. Later serology from both cases showed no specific H5-antibodies, which, together with low virus titres detected by PCR, suggest that no active infection occurred, and that rather environmental contamination explains the results obtained. Some EU/EEA countries (Spain and UK) are actively sampling personnel based on the increased occupational risk for this group. Infection with HPAIV H5N1 was also reported in one case in the United States of America associated with the handling of infected birds and in China in one human with a fatal outcome. Six human infections associated with H5N6 activity has been detected in China in 2022. In addition, one A(H5) case from a child was reported in Vietnam in November 2022. From 2014 to December 2022, 84 laboratory-confirmed cases of human infection with HPAIV H5N6 from China (83) and Laos (1), including 33 with fatal outcomes have been reported. In all cases, there was a known exposure to sick animals or a contaminated environment, and there was no link between individuals.

From 1998 to December 2022, 121 laboratory-confirmed cases of human infection with LPAIV H9N2, including two fatal cases, have been reported globally. Cases occurred in China (108), Egypt (4), Bangladesh (3), India (1), Cambodia (2), Oman (1), Pakistan (1), and Senegal (1).

Cases reported in 2022 occurred in China (17) and one in Cambodia. Most of the infections were mild and were detected in children aged 10 or younger with known exposure to poultry or contaminated environment.

One human case of infection with AIV H10N3 was reported from China in 2021. A second case was detected in Zhejiang, China in June 2022. The H10N3 has been detected in poultry and may be detected in humans exposed to infected birds.

Two laboratory-confirmed cases of LPAIV H3N8 in humans (both children) have been reported to WHO in China (Western Pacific Region), one of the cases was fatal.

LEGISLATION

Animals

HPAI and infection with LPAIV are listed diseases (category A, D and E for HPAI, and D and E for LPAIV) in the Animal Health Law, (EU) 2016/429. Moreover, HPAI of all subtypes, as well as LPAI of H5 and H7 subtypes, are included in the Swedish Act of Epizootic diseases (SFS 1999:657 with amendments) and cases are notifiable upon suspicion. If AI is suspected or confirmed on a farm, measures will be taken to combat the disease and to prevent further spread according to Delegated regulation 2020/687 supplementing Regulation (EU) 2016/429 as regards rules for the prevention and control of certain listed diseases that came into force on April 21, 2021.

The Swedish avian influenza surveillance programme in poultry and wild birds 2022 is based on the delegated regulation 2020/689 supplementing Regulation (EU) 2016/429 as regards rules for surveillance, eradication programmes, and disease-free status for certain listed and emerging diseases started in 2022.

Humans

All laboratory-confirmed cases of influenza are notifiable, and HPAIV H5N1 is classified as a high consequence pathogen according to the Communicable Disease Act (SFS 2004:168 with amendments). All human infections caused by a new influenza subtype are required to be reported

immediately to the European Centre for Disease Prevention and Control, ECDC, the Early Warning and Response System of the European Union (EWRS) under the International Health Regulations (IHR, 2005). Specimens should be shared with WHO Collaborating Centres.

SURVEILLANCE

Surveillance programmes are carried out annually in all EU member states since 2002 to monitor the AIV situation in poultry and wild birds, with a focus on early detection/early warning of the subtypes H5 and H7 in particular. The molecular and serological assays for testing the samples collected within the surveillance programmes were recommended by the European Reference Laboratory for Avian Influenza, Padua, Italy (EURL, ISZVE).

Poultry

The surveillance programme in poultry is based on both serological and virological active surveillance in addition to the passive clinical surveillance. The aim of the serological surveillance is mainly to detect exposure to LPAIV. Virological testing is carried out in Anseriformes birds (mallards, ducks and geese) mainly to detect HPAIV as these species may not display clear clinical signs of disease. Twenty birds per flock was sampled with oropharyngeal and cloacal swabs that were analysed with PCR. Serological surveillance for 2022 included kept game birds (mallards), layers, breeders, turkeys, geese and ducks. Ten blood samples from each holding were collected except for holdings with geese, ducks or mallards where 20 samples from each holding were collected. In holdings with fewer individuals than the abovementioned sample size, all individuals were sampled. In addition to the surveillance programme, samples were taken on clinical suspicion. On clinical suspicion of AI or Newcastle disease, laboratory analyses for both diseases are generally performed.

The surveillance programme for 2022 was based on partly risk-based and partly representative sampling and the laboratory analyses were performed at the National Veterinary Institute (SVA). All poultry samples were collected at slaughter, except breeders and game birds. Samples from

Table 9: Number of holdings of different poultry categories sampled in the surveillance for avian influenza 2013-2022.

Category	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022
Laying hens kept indoors	44	58	68	62	68	65	73	63	57	50
Free range laying hens	16	23	23	30	43	49	67	52	47	47
Turkeys	26	16	18	18	16	16	18	18	14	15
Ducks	1	3	3	4	1	2	3	1	5	0
Geese	13	9	9	7	5	6	3	1	2	2
Broilers ^{A B}	26	12	22	33	23	33	22	14	3	0
Ratites ^B	2	3	3	3	2	2	5	3	7	0
Breeding hens (parents)	36	32	31	34	35	30	34	35	28	31
Breeding turkeys (parents)	3	2	3	3	3	3	3	3	3	3
Game birds (mallards)	7	5	6	7	2	5	5	6	10	9
Game birds (pheasants) ^B	16	12	13	9	13	12	8	10	8	1
Total	190	175	199	210	211	223	241	206	184	158

^ASmall-scale production.

^BNot included form 2022 onwards.

these categories of birds were collected at their holdings. Breeders were sampled late in their production period. Samples were analysed using an ELISA (ID Screen Influenza A antibody competition ELISA kit, Innovative Diagnostics, Grabels, France). Positive results were confirmed with haemagglutination inhibition tests (for subtypes H5 and H7) in accordance with the EURL guidelines.

Wild birds

Annual migrations of wild birds have been implicated in the incursion of HPAIV into Sweden in 2006, 2015, 2016, 2018, 2020 and 2021. Wild migratory birds play a key role in the long-distance spread, introduction into new areas or countries and further local amplification and spread of HPAIV.

The AI surveillance in wild birds is passive and based on birds found sick or dead and reported to SVA's web application rapporteravilt.sva.se. A selection of birds is submitted for postmortem examination and sampling for AIV. Species not previously confirmed positive in a given municipality during the preceding 30 days are eligible for sampling. The wild bird surveillance in Sweden includes a wider list of species compared to the list of target species for avian influenza surveillance published by the European Food Safety Authority (EFSA), (EFSA, Avian influenza overview September–November 2017) and only small passerine birds are excluded from sampling. Vulnerable and protected species that are considered as state wildlife species are mandatory to submit post-mortem and these birds are then also sampled for AIV.

Humans

Every year, samples are collected in Sweden from sentinel patients with influenza-like illnesses during the influenza surveillance season. Samples are analysed for influenza A and B and since spring 2020 also for SARS-CoV-2. If influenza A is detected, further subtyping is performed by rRT-PCR for H1 (A(H1N1)pdm09) and H3 (A(H3N2)). If samples positive for influenza A virus (IAV)cannot be subtyped, sequencing is performed to rule out zoonotic IAV. Assessment of susceptibility to antivirals is achieved by screening genotypic markers. A further 200–300 of the IAV positive samples from the diagnostic laboratories are subtyped or characterised at The Public Health Agency of Sweden who performs acute rRT-PCR of human samples including a subtype-specific rRT-PCR for H5 and H7 when AIV is suspected. Current guidelines recommend professionals

working in culling activities upon HPAIV outbreaks to contact health care and to be tested if they developed influenzalike symptoms. ECDC published in autumn 2022 a Guidance document for public health to early identify human infections with influenza viruses of zoonotic origin. The document describes the groups that are at risk of being in contact with avian or swine viruses due to occupational (farmers, veterinarian or health care workers amongst others) or recreational (hunters, bird ringers, general public handling sick birds) exposure. Occupational safety is regulated and it is the responsibility of the employer to ensure that preventive measures are followed and to provide personal with adequate protective equipment (PPE) to minimise the exposure risk.

RESULTS

Poultry

In 2022, 1611 blood samples were collected from 158 holdings and swab samples were collected from 140 birds on 7 holdings. LPAIV subtype H5N3 was detected in a flock of mallards in the county of Skåne in August 2022. Table 9 gives an overview of the number of poultry holdings sampled from 2013 to 2022 (Table 9).

HPAIV was detected in one holding through passive surveillance during 2022 (Table 10). In total suspected cases of AI were investigated using diagnostic sampling in 31 poultry holdings during 2022, of which 28 were clinical suspicions, two were positive in active surveillance and one suspicion was raised due to post mortem findings. An additional two clinical suspicions of HPAIV could be ruled out based on post mortem investigation. The clinical suspicions were raised because of increased mortality and in some cases combined with other clinical signs.

Wild birds

Within the passive surveillance programme, 89 wild birds were found positive for HPAIV of which all were H5N1 subtype. In total 610 birds of 81 different species were sampled of which 231 were birds of prey, 248 water- or shorebirds, 51 columbiform birds and 36 corvids. The geographical location of sampled and wild birds including positive findings are available in Figure 24.

Humans

No cases of zoonotic avian influenza were identified among the two samples tested in 2022 (negative) at the Public Health Agency of Sweden preparedness laboratory.

Table 10: Confirmed HPAI in poultry and other captive birds during 2022.

Date of confirmation	Virus subtype	County	Type of establishment	Number of susceptible animals
2022-03-01	H5N1	Skåne	Hobby	35

DISCUSSION

During the period covered by this report, the global spread of HPAI has increased significantly, and it has affected countries in Asia, Africa, Europe, North- and Central America. The global spread of the virus is threatening not only animal and human health and welfare but also the economic stability and food security in the affected countries. Extensive cocirculation of HPAIV and LPAIV in the period covered by this report, among wild and domestic birds in Europe has resulted in an exceptional genetic variation among detected viruses.

In 2022, Sweden reported one outbreak of HPAI H5N1 in domestic backyard poultry and 89 cases of HPAI in wild birds. These outbreaks were all caused by HPAIV H5N1 clade 2.3.4.4b viruses of the Gs/Gd lineage. Several distinct genotypes from this clade were involved in these outbreaks. During the summer of 2022, mass mortality was observed in various colonies of seabirds, affecting sandwich terns (*Thalasseus sandvicensis*), common murre (*Uria aalge*) and northern gannet (*Morus bassanus*) colonies. While the virus was detected in common murre (*Uria aalge*) mainly on the Island of Gotland on the Baltic Sea, outbreaks among Sandwich terns and northern gannet were reported from several colonies along the Southern East and West coast of Sweden.

In June 2022, an immature male harbour porpoise presenting clinical signs suggestive of neurological disease was observed in shallow waters off the Swedish west coast and drowned shortly thereafter. Necropsy was performed at SVA, Uppsala, Sweden, within the marine mammal disease surveillance programme. No significant macroscopic lesions were found. Stranded porpoises in Sweden are screened routinely (PCR) for cetacean morbilliviruses (CeMV) and IAV. HPAIV H5N1 clade 2.3.4.4b was found in several organs, with the highest viral loads in the brain. The virus contained no genetic motif of mammalian adaptation besides those already described for the H5 clade 2.3.4.4b. It was closely related to strains recovered from wild birds from the same area, supporting spill over from wild birds.

The continuous global threat of HPAIV further emphasises the need for awareness and improved biosecurity in poultry holdings to prevent the introduction of the virus from wild birds.

Repeated detections of H5 and H9 in humans may reflect infections in poultry, considering that H5 and H9N2 viruses are enzootic in Asia. Infections in Humans infected by other LPAIV, such as H3N8 and H10N3, with close contact with poultry have been reported. It may also reflect the increase in testing efforts for respiratory infections and diagnostic capacity as a consequence of the COVID-19 pandemic. Controlling the disease in domestic animals is the first step in decreasing the risk to humans. In EU/EAE the risk of zoonotic influenza transmission for the general population is low, for specific occupational groups exposed to the virus (in culling activities) the risk may be low to moderate.

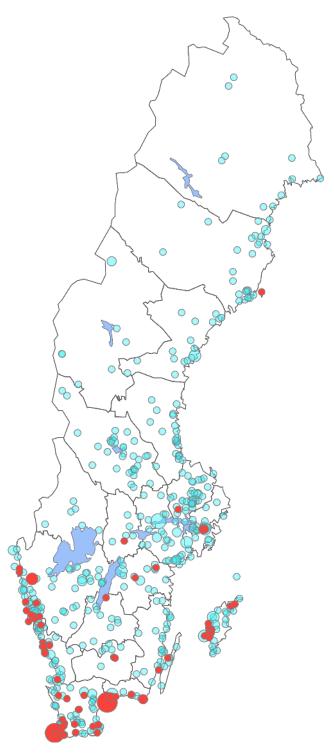


Figure 24: Geographical location of the wild birds analysed for avian influenza in 2022. Point sizes are scaled by the number of birds sampled at a given location. In total, 89 out of 610 wild birds sampled in 2022 were found positive for HPAI.

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