

SURVEILLANCE OF INFECTIOUS DISEASES IN ANIMALS AND HUMANS IN SWEDEN 2019

Chapter excerpt -
Influenza



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Reporting guidelines: Reporting guidelines were introduced in 2018 for those 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, produced by authors, 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 using pandoc and R to the LaTeX typesetting language. Most figures and maps are produced using the R software for statistical computing. Development for 2019 has further improved the importing of content from Word to LaTeX. The method can now import text, tables and figure captions from Word, as well as the newly designed 'IN FOCUS' sections of some chapters. The tool is available as an R-package at GitHub (<https://github.com/SVA-SE/mill/>). This year the report was also built with a continuous integration pipeline on Microsoft's Azure DevOps platform, allowing every committed change to the content to be built and tested automatically. The report generation R-package and process was designed by Thomas Rosendal and Stefan Widgren. In 2019, figures and the final typesetting were done by Wiktor Gustafsson and Thomas Rosendal with contributions from the report authors.

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Influenza

BACKGROUND

Influenza viruses are members of the *Orthomyxoviridae* family and divided into four genera, Influenza virus type A, type B, type C and type D, which may have numerous animal species (domestic and wild) reservoirs.

Influenza type A is a viral disease affecting both birds and mammals, including humans. The causative agent is an RNA virus with a marked ability to change over time. New strains are created both through accumulation of point mutations (antigenic drift) and through genetic reassortment (antigenic shift). Influenza type 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.

There is only one serotype for influenza type B viruses with two evolutionary lineages, the B/Victoria/2/87-like and B/Yamagata/16/88-like lineages. The single serotype of influenza type C virus has six evolutionary lineages.

In 2011, a novel influenza virus was detected in pigs exhibiting influenza-like symptoms. The virus initially identified as a subtype of type C but soon was recognized as a new genus; Influenza type D virus. Although the virus was identified among pigs with respiratory illness, serological evidence indicates presence of influenza D virus in cattle populations around the globe.

AVIAN INFLUENZA

Background

Avian influenza (AI) viruses (AIV) belong to the genus influenza virus type A and can thus be divided into antigenic subtypes based on the combination haemagglutinin (H) and neuraminidase (N) (currently 18 H and 11 N). Except for the subtypes H17N10 and H18N11, which have only been found in bats, all other possible combinations can be found in the aquatic wild bird reservoir. The disease is highly contagious and is spread both directly and indirectly. Wild birds are reservoirs for low pathogenic viruses (LPAIV) including subtypes H5 and H7, which upon transmission and further adaptation to poultry may mutate and become highly pathogenic (HPAIV).

The detection of highly pathogenic avian influenza (HPAI) H5N1 in Hong Kong in the middle of 1990s, with the ability to cause disease in humans, highlighted the potential threat of AI to human and animal health.

In May 2005, an outbreak of HPAI H5N1 led to the death of over 6000 migratory waterfowl in Qinghai Lake in western China. This was the first sustained major outbreak with HPAI H5N1 viruses within wild bird populations since 1997. Subsequently, HPAI H5N1 outbreaks in wild birds or poultry were reported in Siberia (July 2005), Mongolia and Kazakhstan (August 2005), Romania, Croatia, and Turkey (October 2005). Wild bird infections with or without poultry disease were also noted in several other countries in Europe, including Sweden, in 2006. The outbreak of HPAI H5N1 in

Sweden led to deaths among several species of wild birds, one infected farmed mallard in a game bird holding and a mink.

In early 2014, HPAIV H5N8 was detected in wild birds and poultry in the Republic of Korea, China, Japan and the Russian Federation. By autumn the same year, HPAI H5N8 was detected in commercial poultry in Canada and later in December, also detected in wild birds and poultry in the United States of America (USA). By the middle of 2015, over 50 million poultry were dead or culled because of the outbreak with the estimated economy-wide losses of 3.3 billion dollars. In November 2014, almost simultaneously HPAI H5N8 viruses were also detected in The Netherlands, Germany, Italy, the United Kingdom and Northern Ireland and in Hungary. In 2014–2015, outbreaks in Europe were limited to a few commercial poultry holdings and only sporadic cases in wild birds. The last reported detection during the 2014/2015 European outbreaks was two mute swans in Sweden in February 2015.

In May 2016, a new HPAI H5N8 virus subtype was detected in wild migratory birds in the Tyva Republic, southern Russia. This was the starting point of a new intercontinental wave of transmission by H5 viruses causing multiple outbreaks of disease in poultry and wild birds across Europe, Asia and Africa and was by far the most severe in terms of the number of countries affected.

On 27 October 2016, an infected wild swan with HPAI H5N8 was reported from Hungary. On 4 November, Hungary reported the first outbreak of H5N8 in poultry. The virus spread rapidly across central Europe with multiple notifications in wild birds, poultry and captive birds.

In November 2016, HPAI H5N8 virus was detected in a dead common goldeneye (*Bucephala clangula*) in the county of Skåne in the southern part of Sweden. Shortly after, a high-biosecurity establishment of laying hens also in Skåne became infected, and the 210 000 birds had to be culled.

During 2017 the HPAI outbreaks continued. Countries in the European Union reported a total of 874 outbreaks of HPAI in poultry or captive birds in 24 countries, and 1146 reports by 19 countries on findings in wild birds. In general, the outbreaks in the winter and spring were caused by HPAI H5N8 and by late autumn the outbreaks were sparse compared to 2016 and there was a shift towards the subtype of HPAI H5N6. Sweden had four separate introductions of HPAI H5N8 virus in poultry holdings during the winter and spring of 2017, with one layer farm and three hobby flocks affected. During the spring, 39 detections of HPAI H5N8 were made in wild birds within the Swedish passive surveillance program.

Further cases with HPAI were subsequently found in 2018, between January and June; HPAI H5N6 was confirmed in one poultry (hobby flock) holding, and 16 HPAI H5N6 wild bird events were reported in Sweden.

Table 10: Number of flocks of different poultry categories sampled in 2010–2019.

	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019
Laying hens ^A	62	61	52	44	58	68	62	68	65	73
Free range laying hens ^A	-	30	27	16	23	23	30	43	49	67
Turkeys	21	22	19	26	16	18	18	16	16	18
Ducks	4	6	3	1	3	3	4	1	2	3
Geese	11	20	20	13	9	9	7	5	6	3
Broilers ^B	24	39	34	26	12	22	33	23	33	22
Ratites	4	5	3	2	3	3	3	2	2	5
Breeding hens (parents)	34	36	36	36	32	31	34	35	30	34
Breeding turkeys (parents)	3	3	3	3	2	3	3	3	3	3
Game birds (mallards)	7	9	7	7	5	6	7	2	5	5
Game birds (pheasants)	17	15	16	16	12	13	9	13	12	8
Backyard flocks (geese, ducks)	0	0	0	0	0	0	0	0	0	0

^A Until 2011 sampling of all laying hens were reported under the same category regardless of housing system. From 2011, free-range (organic) laying hens are reported separately while the category “laying hens” includes hens in furnished cages and indoor litter-based housing systems.

^B Small-scale production.

Disease

Animals

The case fatality rate in birds infected with HPAIV may be as high as 100%, but this depends on the species affected, co-infections, 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 numbers of birds.

Humans

The reported signs and symptoms of avian influenza A virus 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.

Legislation

Animals

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 Council Directive 2005/94/EC.

The Swedish Avian Influenza surveillance programme in poultry and wild birds 2019 is based on Council directive 2005/94/EC and Commission decision 2010/367/EU.

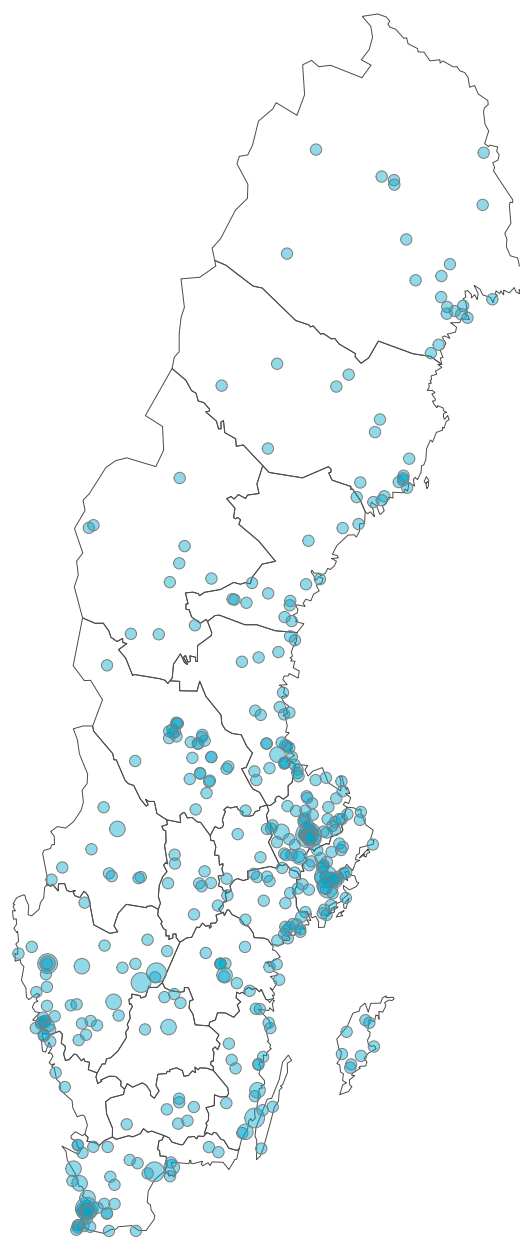


Figure 11: Geographical location of the wild birds analysed for avian influenza in 2019. Point sizes are scaled by the number of birds sampled at a given location. All 456 wild birds sampled in 2019 were found negative for avian influenza. ©EuroGeographics for the administrative boundaries.

Humans

All laboratory confirmed cases of influenza are notifiable according to SFS 2015:587, and H5N1 infection is notifiable according to the Communicable Disease Act (SFS 2004:168).

Surveillance

Surveillance programmes have been 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 in particular the subtypes H5 and H7.

Poultry

The surveillance programme in poultry for 2019 included kept game birds (mallard ducks and pheasants), layers, breeders, small-scale broiler production, turkeys, geese, ducks and ratites. Ten blood samples from each holding were collected except for holdings with geese, ducks or mallards where 20 samples from each flock were collected. In flocks 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 2019 was based on representative sampling and the serological analyses were performed at the National Veterinary Institute. All poultry samples were collected at slaughter, except breeders and game birds. Blood samples from these categories of birds were collected at their holdings. Breeders were sampled late in their production period. Samples were analysed using an ELISA (IDEXX Influenza A Ab Test). Positive results were confirmed with haemagglutination inhibition tests (for subtypes H5, H7 and H5N8) in accordance with the OIE guidelines.

Wild birds

Autumn migrations of wild birds have been implicated in the incursion of HPAIV into Europe in 2005, 2014, 2016 and in December 2019. Wild 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 surveillance in wild birds is passive and based on birds found dead or diseased and submitted for post mortem examination. The geographical distribution of wild birds examined for AI is shown in Figure 11. Swab samples (both cloacal and tracheal) taken from these birds were analysed for the detection of AIV genome by using an M-gene qRT-PCR. Samples found positive for the matrix gene were further analysed by qRT-PCR specific for the haemagglutinin gene of H5 and H7 and qRT-PCR specific for the neuraminidase gene of N1, N5, N6 and N8, and virus pathotyping by amplicon sequencing.

Humans

Every year, 1500–2000 samples are collected in Sweden from sentinel patients with influenza-like illness during the

influenza surveillance season. These samples are analysed for influenza A and B. If influenza A is detected, further subtyping is performed for A(H1N1)pdm09 and A(H3N2). If samples positive for influenza A cannot be subtyped, further characterisation is performed to rule out zoonotic influenza A. A further 200–300 of the influenza positive samples from the diagnostic laboratory are subtyped or characterised. The Public Health Agency of Sweden also performs a specific PCR for H5N1, H5N6 and H7N9, if requested.

In 2019, the influenza strains that caused zoonotic infections globally did not circulate among wild birds in Sweden.

Since 2003, 861 human cases of HPAI H5N1 infection have been identified worldwide with a death rate of 53%. The majority of human cases of H5N1 infection have been associated with direct or indirect contact with infected live or dead poultry. A decrease of cases was noted during the last years, and only one case was diagnosed globally during 2019.

Since 2014, 25 laboratory-confirmed cases of human infection with HPAI H5N6, including 15 with fatal outcome, have been reported. All cases of the cases were infected and detected in mainland China. One case was determined during 2019. It should be noted that these viruses are not related to the HPAI H5N6 viruses that circulated in wild birds in EU 2017–2018. More than 1568 laboratory-confirmed cases of human infection with H7N9 viruses, including 39% deaths, have been reported in China since 2013. In February 2017, a new H7N9 virus with mutations in the haemagglutinin gene indicating high pathogenicity in poultry was detected in three patients, as well as in environmental and poultry samples. In total 32 human cases, 13 of them fatal, have been due to infection with HPAI H7N9. During 2019, only one case of H7N9 was reported. The decrease of human cases of H7N9 is due to the introduction of control measures, including a mass vaccination programme in poultry in China.

During 2018, the first human case of H7N4 was determined in China. No further cases have been reported.

Since 1998, 50 laboratory-confirmed cases of human infection with LPAI H9N2, including one death, have been reported globally. Cases occurred in China (50), Egypt (4), Bangladesh (3), India (1), Oman (1), and Pakistan (1). During 2019, six cases of H9N2 were reported: four from China, one from Oman and one from India.

Controlling the disease in domestic animals is the first step in decreasing the risk to humans.

Results

Poultry

In 2019, all 2439 blood samples taken from 241 flocks were found serologically negative for AIV subtype H5 and H7. Table 10 gives an overview of number of poultry flocks sampled in 2010 to 2019 (Table 10).

AI was investigated following eight clinical suspicions in poultry. Clinical signs as suspicion arose included increased mortality, production losses and/or eggshell abnormalities. All eight of the suspicions were in commercial flocks (pullets (2) and layers (6)). All suspicions were investigated by

PCR on swab and/or organ samples and found negative for influenza A virus.

Wild birds

Within the passive surveillance programme in wild birds, 456 birds of 65 different species were sampled of which 236 bird of prey, 34 water or shore birds and 46 corvids. All wild birds sampled were PCR-negative for Influenza A virus.

Humans

No cases of zoonotic influenza were identified among the samples characterised during 2019 in Sweden.

Discussion

Since the first detection of HPAI H5N8 viruses at the Ubsu-Nur Lake in May 2016, closely related viruses continued affecting countries in Asia, the Middle East, Western, Eastern and Southern Africa and Europe, including Sweden.

In 2019 HPAI H5N6 was confirmed in a white-tailed eagle and a common buzzard in Denmark. These reports were the only HPAI cases reported in wild birds in Europe in 2019. These viruses showed to be closely related to the HPAI H5N6 viruses detected in wild birds in Europe during 2017–2018. In the relevant period for this report, Bulgaria was the only European country to confirmed further outbreaks of HPAI H5N8 on backyards and several commercial poultry farms. Molecular characterisation of the H5N8 viruses detected in Bulgaria revealed the similarity to viruses circulating in Europe in 2018. During the same period, no cases of AI were detected in wild birds or poultry in Sweden.

Although the number of HPAI outbreaks in poultry and cases in wild birds in Europe in 2019 have decreased compared to the previous years, the continuous global threat with HPAI viruses further signifies the need for awareness and improved biosecurity in poultry holdings to prevent the introduction of the virus from wild birds.

Influenza viruses are unpredictable and changes by mutation or reassortment occur. This might enable the virus to become more transmissible among humans. Monitoring of human infections with these viruses is also critically important to assess their pandemic potential.

SWINE INFLUENZA

Background

Swine influenza (SI), caused by several subtypes of influenza type A viruses, has a worldwide distribution and causes an acute upper respiratory disease characterised by fever, lethargy, anorexia, weight loss and laboured breathing in pigs. The most commonly occurring subtypes of swine influenza virus (SIV) worldwide are H1N1, H1N2 and H3N2. Of these, the H1N1 SIV was reported to infect pigs in North America already in 1918. In 2009, a new triple reassortant type of influenza H1N1, partly of porcine origin, began circulating among people. In a number of countries including Sweden, this virus has occasionally infected pigs by transmission from humans. This reassortant H1N1 virus became known as influenza A(H1N1)pdm09.

Animals

Influenza H1N1 was isolated from Swedish pigs for the first time in 1982. The clinical signs were severe in the previously naïve pig population but waned over time. Since 1982, H1N1 virus has been considered endemic in Sweden. Influenza H3N2 is also present in the Swedish pig population. Antibodies to H3N2 were first detected in 1999, but the clinical signs were not as evident as when H1N1 was introduced. Actually, antibodies to H3N2 were first detected in a screening of apparently healthy animals, and it is therefore less clear when this subtype was introduced. However, H3N2 has since 1999 occasionally been correlated with severe respiratory disease in pigs.

Another swine influenza A type (H1N2) that spread through Europe, was diagnosed for the first time in Sweden in a large multisite unit with respiratory disease in growers during the winter of 2009. Since the first report of the detection of pandemic influenza A(H1N1)pdm09 in early May 2009 in pigs in Canada, H1N1pdm09 has been isolated from pigs throughout the world including several European countries including Germany, Italy, Denmark, Norway, Iceland and Finland. This virus is well adapted to humans and clinical signs of disease in pigs were sparse. In 2013, a new variant of this influenza virus was identified in Swedish pigs where the HA gene revealed high nucleotide identity with contemporary human pH1 strains, suggesting that a recent human to pig transmission was the most likely route of infection in the pigs. The isolate expressed a human pandemic H1N1-pdm09 like HA gene and a H3N2 SIV-like NA gene that was closely related to avian-like H1N2 SIV NA from isolates collected in Sweden since 2009. The internal genes

Table 11: Reactors from the serological surveys performed in 2006 and 2010. This shows the prevalence of significant seroreactors to the three porcine adapted strains of influenza present in the country and the prevalences of low reaction in the HI tests. Note the difference in prevalences depending on strain used for antibody detection for H1N2 in 2010.

Seropositive samples	H1N1	H3N2	H1N2-standard	H1N2 new (9706strain)
Significant levels of antibodies ($\geq 1:64$)				
2006 (n=999)	33.0%	6.7%	0.6%	-
2010 (n=1008)	0.6%	3.7%	0.1%	0.9%
Low levels of antibodies ($\leq 1:32$)				
2006 (n=999)	15.1%	18.8%	7.0%	-
2010 (n=1008)	2.3%	9.6%	1.3%	5.1%

Table 12: Passive and active surveillance for swine influenza in Swedish pig herds from 2014 to 2019.

Period	Number of herds investigated	Number of Influenza A positive cases	Frequency of positive cases	H1N1pdm (2009)	Av-likeH1N2 (H1 _{av} N2)	reass. H1pdmN2 (H1 _{pdm} N2)
2014-passive	18	7 herds (40 animals)	38% herds (27% animal level)	19	14	7
2014-active ^A	10	5 herd (79 animals)	50% herds (9% animal level)	60	5	14
2015-passive	8	2 herds (6 animals)	25% herds (22% animal level)	3	3	-
2015-active ^A	10	4 herds (20 animals)	40% herds (2% animal level)	12	6	2
2016-passive	7	2 herds	single animal per herd	1	1	-
2017-passive	9	3 herds	single animal per herd	2	1	-
2018-passive	9	0	-	-	-	-
2019-passive	9	5 herds	single animal per herd	-	1	-

^A In collaboration with farmer's association, ten field veterinarians who agreed to participate in the study were asked to select ten pig farms that were representative of the pig production systems in Sweden and that were owned by producers interested in participating in the study. The participating farms were visited every second week for 6 consecutive visits by the field veterinarian. A total of 15 nasal swab samples were collected at each farm during each visit.

were entirely of pandemic H1N1-pdm09 origin which is well adopted to humans. Although the pH1N2 subtype influenza A virus was exclusively prevalent in the Swedish pig population in 2014, the clinical signs of the disease were minor, as later also seen in other countries.

There has not been a regular monitoring of influenza in pigs in Sweden, but serological screenings were performed in 1999, 2002, 2006 and 2010. On each occasion, 1000 porcine sera were analysed for H1N1, H3N2 and H1N2. The screening in 2006 also included analyses for antibodies to H5 and H7. During the past five years, 10–15 herds have been sampled annually with special focus on influenza; in these herds influenza virus has been demonstrated in 3–5 herds per year (Table 11).

Infection with influenza virus can produce clinical respiratory disease including dyspnoea, sometimes with nasal discharge and coughing, accompanied by fever, inappetence and lethargy. The disease can affect pigs of varying ages and the severity of clinical signs varies from severe respiratory disease to subclinical infection. The morbidity of affected herds is generally high, but mortality is low.

Humans

Globally, 1–10 human cases of influenza virus infections with influenza from swine are reported yearly. In 2019, the influenza strains that caused zoonotic infections globally did not circulate in Sweden. People who have been infected with influenza virus from pigs have had symptoms similar to the symptoms of regular human seasonal influenza. These include fever, lethargy, lack of appetite and coughing. Some people also have reported runny nose, sore throat, eye irritation, nausea, vomiting and diarrhoea.

Since 2005, 435 human cases of A(H3N2)v have been detected in the USA and Canada. Since 2005, 25 human cases of A(H1N2)v and 22 human cases of A(H1N1)v have been detected in the USA. During 2019, only one case of A(H1N1)v was reported from the USA. Human infection

with swine influenza has been associated with agricultural fairs, where people are in close contact with potentially infected swine populations. The US Centers for Disease Control and Prevention has given recommendations on how to avoid swine influenza infections at agricultural fairs. The number of human cases infected with swine influenza have decreased over the last few years in the USA.

Legislation

All laboratory confirmed influenza A is notifiable according to SFS 2015:587.

Surveillance

Animals

Enhanced passive surveillance

During the period from 2009 to 2019, samples from pig herds with respiratory signs consistent with influenza were collected and analysed for presence of the pandemic influenza A (H1N1)pdm09 virus using a polymerase chain reaction (PCR) method. From each affected herd, 5–10 nasal swab samples were collected and analysed first for swine influenza A and if positive, samples were further analysed for pandemic influenza A(H1N1)pdm09. These samples were also investigated for other influenza A types (Table 12).

Active surveillance

The serological surveillance in 2010 included 1008 pig sera collected at slaughter. These sera were randomly selected from the porcine reproductive and respiratory syndrome control programme and included a maximum of 4 sera per herd and sampling occasion. The samples were tested for antibodies to swine influenza types H1N1, H1N2 and H3N2 using haemagglutination inhibition tests (HI). Titres of $\geq 1:64$ were interpreted as significant levels of serum antibodies. For the recently demonstrated influenza H1N2 virus, two HI-tests were carried out, one using a traditional strain and one based on the strain isolated in Sweden (the 9706-strain).

In 2015, the National Veterinary Institute (SVA) and the Public Health Agency of Sweden carried out a study on the transmission of human and swine influenza among farmers, veterinarians and pigs. In collaboration with the industry, ten field veterinarians were asked to select pig farms that were representative of the pig production systems in Sweden and that were owned by producers interested in participating in the study. All workers on the pig farms with a daily contact with pigs, pig farmers and their families were asked to collect nasal swabs from themselves every third week and whenever they had influenza-like symptoms. Concurrently, samples were collected from the pigs at these farms. Participants were asked to complete a health questionnaire about the type of symptoms, duration of illness, and possible exposures to infected pigs. The participants were also asked if they had been vaccinated against seasonal influenza A viruses.

Starting from the last week of January 2015, participating farms were visited every third week for 6 consecutive visits by the field veterinarian. A total of 15 nasal swab samples from pigs were collected at each farm during each visit. During the visit, the age of the pigs and any respiratory clinical signs (absence or presence of sneezing, coughing and nasal secretion) among the sampled individuals was recorded.

The nasal swabs and submission sheets from animals and humans were shipped overnight to SVA or the Public Health Agency, respectively.

Nasal swab samples were initially screened for influenza A virus by real-time reverse transcription PCR (rRT-PCR) selective for the matrix gene. Samples positive by rRT-PCR were further analysed for determination of subtype, including the influenza A(H1N1)pdm09 virus using rRT-PCR specific for haemagglutinin gene of influenza A(H1N1)pdm09 virus. The haemagglutinin and neuraminidase fragments from all positive pig and human isolates were sequenced by the Sanger sequencing method.

No active surveillance was performed in 2019.

Humans

Every year 1500–2000 samples are collected in Sweden from sentinel patients with influenza-like illness during the influenza surveillance season. These samples are analysed for influenza A and B. If influenza A is detected, further subtyping is performed for A(H1N1)pdm09 and A(H3N2). If influenza A positive samples cannot be subtyped, further characterisation is performed to rule out zoonotic influenza A. A further 200–300 of the influenza positive samples from the diagnostic laboratory are subtyped or characterised.

Results

Animals

Passive surveillance

Samples from 9 herds with respiratory signs were analysed for swine influenza virus in 2019. Five influenza infected herds were identified.

Active surveillance

No active surveillance was performed in 2019.

Humans

No cases of zoonotic influenza were identified among the characterised samples during 2019 in Sweden.

Discussion

The surveillance in 2010 revealed low frequencies of pigs with significant levels of antibodies to swine influenza types H1N1, H1N2 and H3N2 using HI tests (Table 11). The prevalence of pigs with significant levels of serum antibodies was lower during 2010 than 2006. It is, however, notable that the prevalence of pigs with significant levels of antibodies to H1N2 increased somewhat when the analysis was based on the recent Swedish isolate of the strain.

During the active surveillance in 2014 and 2015, no pigs with clinical disease were observed during the 6 visits to 10 farms as part of the study on the transmission of human and swine influenza among farmers, veterinarians and pigs. Out of ten participating farms, four farms had at least one positive result during this period and two farms were tested positive on at least two occasions. In total, 825 swabs collected from pigs and 330 swabs collected from humans were analysed for the presence of influenza A viruses. Of these, 19 samples (2%) were positive for influenza A viruses with rRT-PCR.

The results indicate presence, but no large impact, of swine influenza in the Swedish pig population. In last five years two new influenza A viruses were detected in the Swedish pig population. Both of these viruses were the result of multiple reassortments between avian or/and human and swine influenza A viruses. Influenza A viruses are unpredictable and changes (mutations or reassortment) might be induced. This could enable the virus to be more transmissible among humans. The veterinary importance and the public health significance of influenza A virus in pigs should not be underestimated. Monitoring of human infections caused by these viruses is critically important to assess their pandemic potential.

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