

SURVEILLANCE OF INFECTIOUS DISEASES IN ANIMALS AND HUMANS IN SWEDEN 2020



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Cover: Juvenile mink in hand. Photo: Elina Kähkönen

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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, 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 and the LaTeX library pgfplots. Development for 2020 has further improved the importing of content from Excel files to automatically build figures in the pgfplots LaTeX library. The tool is available as an R-package on GitHub (<https://github.com/SVA-SE/mill/>). The report generation R-package and process was designed by Thomas Rosendal, Wiktor Gustafsson and Stefan Widgren. In 2020, final typesetting was done primarily by Wiktor Gustafsson with contributions from the report authors.

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Photo: Anna Malmsten.

Introduction

Surveillance of infectious diseases in animals and humans 2020 is the annual report describing the surveillance activities carried out in Sweden during the year. The report covers surveillance for important animal diseases and zoonotic agents in humans, food, feed and animals, carried out and compiled by experts from several Swedish governmental agencies, university and the private industry with surveillance mandates along the entire food chain, from farm to fork.

This year's report refers to the disease situation and surveillance implemented during an ongoing COVID-19 pandemic which clearly has had both direct and indirect consequences on surveillance efforts and their results, in both the animal and public health sector. The report includes several chapters describing zoonotic diseases of importance to human health. Disease surveillance in humans is driven primarily by patients seeking care, *i.e.* passive surveillance, and during the pandemic fewer patients have presented to primary care with symptoms consistent with the common zoonoses. This is hypothesised to be related to both patients with these symptoms choosing to not seek care and a true reduction in disease incidence due to changes in general hygiene such as increased handwashing, physical distancing and reduced travel due to COVID-19 related recommendations. From an animal health perspective, the pandemic has resulted in extensive outbreaks of SARS-CoV-2 infections in mink, with vast consequences for the international mink fur industry and potential impact on public health. This prompted the implementation of a surveillance for the presence and dynamics of SARS-CoV-2 also in Swedish mink as well as in people associated with the mink industry, along with restrictions put in place in that industry to reduce the risk of the transmission of SARS-CoV-2 between humans and mink. With this in mind, this report includes a new chapter focused on mink-associated SARS-CoV-2 infections.

This 2020 report on disease surveillance is also written at the end of a very large outbreak of avian influenza in wild birds and domestic poultry in Europe. Sweden's poultry sector was also dramatically affected by this outbreak which began with detections of avian influenza in turkeys and wild

birds in the south of Sweden in November 2020. The chapter on influenza (page 47) is limited to what occurred during 2020 and the full details of this outbreak and its impact on Sweden will be described in later reports. Sweden also experienced its first outbreak of *Salmonella* Choleraesuis in 40 years, first detected in a breeding herd and later detected in Swedish wild boar. An intensified surveillance of *Salmonella* in wild boar and management of the affected domestic pig herd continues during 2021.

The information generated by animal disease surveillance is of key importance for the declaration of the good health and welfare status of Swedish animals. Some benefits of surveillance activities are inherent, such as the prevention of animal disease and promotion of public health. However, many surveillance activities are in place primarily to ensure safe trade and movement of animals, thereby facilitating trade and giving access to foreign markets. This is also where the major costs appear in case of outbreaks of regulated diseases; by the restrictions put in place to maintain trust between trading partners. To reinstate a favourable status, it is necessary to provide evidence in the form of high-quality surveillance data that disease is once again absent from the country, region or sector, or at least under control.

A lot of the information in this report is of key importance to demonstrate the good health and welfare of Swedish animals to the benefit of safe trade and access to foreign markets. As an EU member state, Sweden shares the implications and consequences of exotic disease introduction with many other European countries. We are part of a pan-European surveillance system, where our efforts contribute, directly and indirectly, to the understanding of risks that emerging diseases pose to other EU countries. Openness, transparency and pro-activeness are key for effective early warning and control, and it is important for trust and for joint European preparedness to which we actively contribute. In line with this, our understanding of the Swedish disease situation in 2020 is provided in this report.

Overview of active surveillance 2009–2020

BACKGROUND

Since 2009, Sweden has reported the outcome of its active surveillance programmes in an annual report on surveillance of infectious diseases in animals and humans. This yearly description of active surveillance efforts is important as it contributes to the international community's understanding of the evidence underlying Sweden's claims regarding its animal and zoonotic disease status. While passive surveillance for important diseases occurs continuously (see chapter on clinical surveillance, page 118), active surveillance for each disease does not necessarily occur on an annual basis. Surveillance activities are regularly evaluated and the

decision to conduct active surveillance for a specific disease in any given year is based on a number of factors, such as the findings of previous years' surveillance activities, changes in the disease status of other countries and the emergence of new diseases. Table 1 provides information on the years in which active surveillance was undertaken for various diseases of importance. More detailed information about the active surveillance that was conducted during a specific year between 2009 and 2020 can be found by consulting that year's annual surveillance report, which can be found at www.sva.se.

Table 1: Historical overview of active surveillance activities 2009–2020. Filled circles (●) indicate that active surveillance was carried out.

Disease	Year											
	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020
African swine fever	○	○	○	●	○	○	○	○	○	○	○	○
Atrophic rhinitis	●	●	●	●	●	●	●	●	●	●	●	●
Aujeszky's disease	●	●	●	●	●	●	●	●	●	●	●	●
Bluetongue	●	●	●	●	●	●	●	●	●	●	●	●
Bovine spongiform encephalopathy	●	●	●	●	●	●	●	●	●	●	●	●
Bovine viral diarrhoea	●	●	●	●	●	●	●	●	●	●	●	●
Brucellosis	●	●	●	●	●	●	●	●	●	●	●	●
Campylobacteriosis	●	●	●	●	●	●	●	●	●	●	●	●
Chronic wasting disease	●	●	○	○	○	○	○	●	●	●	●	●
Classical swine fever	●	●	●	●	●	●	●	●	●	○	●	●
Coccidiosis and clostridiosis	●	●	●	●	●	●	●	●	●	●	●	●
Echinococcosis	●	●	●	●	●	●	●	●	●	●	●	●
Enzootic bovine leucosis	●	●	●	●	●	●	●	●	●	●	●	●
Footrot	●	●	●	●	●	●	●	●	●	●	●	●
Infectious bovine rhinotracheitis	●	●	●	●	●	●	●	●	●	●	●	●
Avian influenza	●	●	●	●	●	●	●	●	●	●	●	●
Swine influenza	○	●	○	○	○	○	○	○	○	○	○	○
Leptospirosis	○	●	○	●	●	○	○	●	○	○	●	○
Listeriosis	○	○	○	○	○	○	○	○	○	○	○	○
Maedi-visna	●	●	●	●	●	●	●	●	●	●	●	●
Nephropathia epidemica	○	○	○	○	○	○	○	○	○	○	○	○
Paratuberculosis	●	●	●	●	●	●	●	●	●	●	●	●
Porcine reproductive and respiratory syndrome	●	●	●	●	●	●	●	●	●	●	●	●
Psittacosis	○	○	○	○	○	○	○	○	○	○	○	○
Q fever	●	●	●	○	○	○	○	○	○	○	○	○
Rabies	●	●	●	●	●	●	●	●	●	●	●	●
Salmonellosis	●	●	●	●	●	●	●	●	●	●	●	●
Swine vesicular disease	○	○	●	○	●	○	○	○	○	○	○	○
Schmallenberg virus	○	○	○	●	○	○	○	○	○	○	○	○
Scrapie	●	●	●	●	●	●	●	●	●	●	●	●
Strangles	○	○	○	○	○	○	○	○	○	○	○	○
Tick-borne encephalitis	○	○	○	○	○	○	●	○	○	○	●	○
Transmissible gastroenteritis	○	●	○	○	●	○	○	○	○	○	○	○
Trichinellosis	●	●	●	●	●	●	●	●	●	●	●	●
Tuberculosis	●	●	●	●	●	●	●	●	●	●	●	●
Tularaemia	○	○	○	○	○	○	●	○	○	○	○	○
Shigatoxin producing <i>Escherichia coli</i>	●	○	○	●	○	○	●	○	○	●	○	○
Yersiniosis	○	○	○	○	○	●	○	●	○	○	○	○

Livestock populations and trade in live animals

The Swedish agricultural industry is concentrated in the southern and central parts of the country, with the largest sectors being meat and dairy production. During the last decade the number of holdings with livestock has decreased, but the average size of those remaining has increased. Still, farms in northern Sweden tend to be smaller than those in the southern parts of the country. In the current description of the livestock industry, we define a holding as livestock production under single management.

Figures 1, 2, 3 and 4 give an overview of the livestock population in Sweden 2020.

The numbers presented reflect 2020, if not otherwise stated. Published data is from the latest available date at the time of publishing.

CATTLE

There are approximately 15 400 holdings with a total of 1.5 million cattle (dairy cows, beef cows, heifers, bulls, steers and calves younger than one year) in Sweden (Figure 2).

The number of holdings with dairy cows, as well as the number of dairy cows, has decreased consistently over a long period. There were approximately 303 000 dairy cows in 3087 holdings, with an average of 98 cows per herd in 2020. Ten percent of the holdings have 200 or more dairy cows. The number of beef cows has been increasing consistently since the 1980s, but in 2019 the trend was broken. There were almost 207 000 beef cows, with an average herd size of 21 cows.

In total, approximately 421 000 adult cattle and 13 500 calves were slaughtered. The total milk delivered increased compared to 2019 and was 2773 million kg.

PIGS

The total number of pigs was 1 367 755 (Figure 3). For many years the number was decreasing, but more recently the population size has stabilized with little differences between years. However, the number of holdings with pigs has decreased with 8% between 2016 and 2020. There were 1146 holdings in 2020, of which 919 held fattening pigs and 709 held breeding pigs.

About 2 623 000 pigs were slaughtered.

SHEEP

There were 7956 sheep holdings with a total of 263 369 ewes and rams (Figure 4). Sheep holdings in Sweden are usually small-scale enterprises with an average herd size of 33 adult sheep. Since 2016 the number of sheep has decreased with 13.3%. During this period the number of holdings with sheep decreased as well.

During 2020, approximately 240 540 sheep were slaughtered, of which 207 160 were lambs.

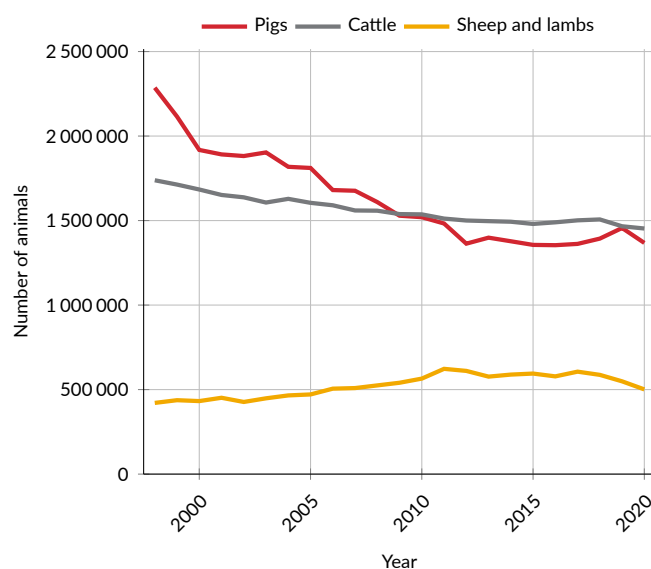


Figure 1: Number of Swedish livestock 1998–2020.

GOATS

According to an annual questionnaire there are approximately 19 000 goats (December 2020) in Sweden. In the Central Register of holdings there are about 6000 holdings registered for keeping goats, but only 2500 of them keep at least 1 goat.

The last census was carried out in 2018. In June 2018, the total number of goats was estimated to approximately 20 000, which was an increase since 2003 when the last census was carried out. 70% of the holdings had fewer than ten goats. 60% of the goats were kept as part of business activities, and one out of four farmers with goats in a business activity milked their goats. The total number of goat farmers was 2400, of which 10% milked their goats. The amount of goat milk produced was estimated to 1 471 000 kg in 2018.

The abovementioned data from the census 2018 are based on a study population including all goat holdings, even the very smallest. That is not the case for the other livestock study populations, which are based on the thresholds of the statistical farm register. As most of the goat holdings are very small, we considered these figures as the most relevant to present. The number of goats and goat farmers based on the thresholds of the statistical farm register are 11 200 and 750 respectively.

POULTRY

To provide animals for the broiler industry, grandparent stock (Ross, Kobb) and parents (other hybrids) are brought into Sweden. For the egg industry, parent stock is brought into the country. These animals are the top of the commercial breeding pyramid in Sweden.

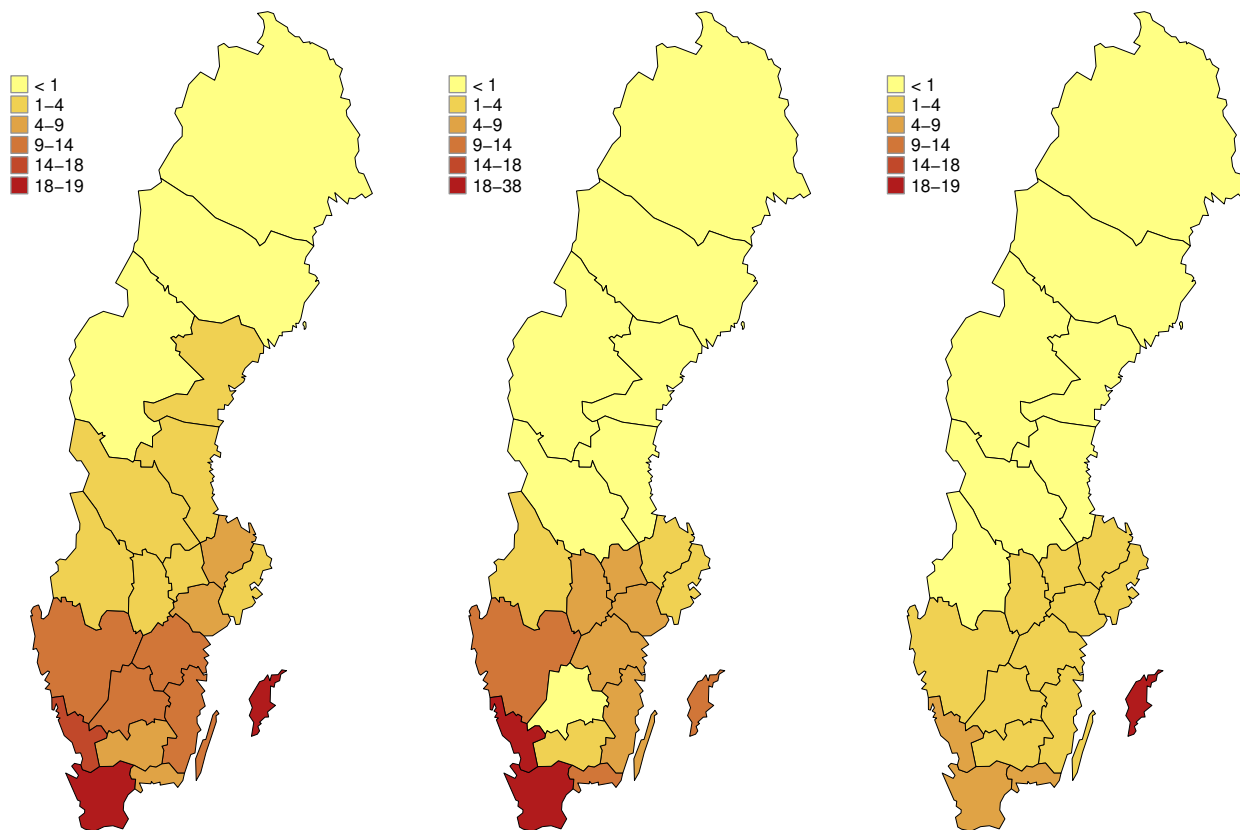


Figure 2: Number of cattle per km² in 21 Swedish counties as of June 2020. Figure 3: Number of pigs per km² in 21 Swedish counties as of June 2020. Figure 4: Number of sheep per km² in 21 Swedish counties as of June 2020.

Poultry numbers have increased continuously during the last two decades.

In 2020, there were 8.4 million hens over 20 weeks of age in 2451 commercial holdings, which represents a decrease in population size.

Eggs delivered to wholesalers amounted to 129.7 million kg.

The number of holdings with broiler production in 2020 was 186 and approximately 110 million chickens were sent for slaughter during the year. During 2020, 522 000 turkeys were sent for slaughter.

The production of other poultry is very limited. In 2020, 12 868 geese, 12 310 ducks and no guinea fowl were slaughtered.

FISH AND SHELLFISH

Rainbow trout is the most common farmed fish in Sweden, followed by trout (*S. trutta*), arctic char, eel and salmon, where salmon and trout are mainly farmed for restocking of wild populations.

Swedish shellfish production is dominated by cultivated blue mussels, of which 1986 tonnes were produced in 2018.

All mussel production and 18% of the production of rainbow trout is situated in the coastal district (marine culture) on the west and east coast respectively. The production of arctic char, eel and other food fish is freshwater based. The most common aquaculture production system is cage culture, both in fresh and saltwater.

In 2019, there were 49 holdings producing food fish, 48

holdings with fish for restocking, five with crayfish for consumption and four with crayfish for restocking. There were five holdings with production of blue mussels and one with oyster production.

In 2019, The production was 9600 metric tonnes, in fresh weight, of food fish, of which 90% was produced in northern Sweden. Production has decreased the last years due to closing of small holdings. Rainbow trout represented the largest production, with 87% of the total production of fish for consumption.

The total production of fish for restocking was estimated to be 918 tonnes. The most common species produced for restocking was rainbow trout.

REINDEER

In 2019, there were 241 013 reindeer in Sweden, including 56 164 calves, with an average of 52 reindeer per owner. During the 2019/20 season, 49 618 reindeer were slaughtered, and the average slaughter weight was 25.2 kg. There are no wild reindeer in Sweden, only semi-domesticated, and there is cross-border reindeer husbandry between Sweden and Norway. Reindeer herding is an essential part of the Sami culture.

HORSES

In 2016, when the last census was performed, there were approximately 355 500 horses in Sweden, of which 18 300 were held at riding schools and 101 000 at agricultural holdings. The number of premises with horses in 2016 was 77 800.

Approximately 1530 horses were slaughtered in Sweden in 2020.

BEES

In 2020, the number of apiaries in Sweden was 18 814 and the number of colonies was 84 543, figures approximated by bee inspectors. Over the last ten years, these numbers have increased by 67 and 29 percent respectively.

TRADE IN LIVE ANIMALS (LIVESTOCK)

The trade of livestock into and out of Sweden is very limited. In 2020, 90 pigs from Norway, one pig from Finland, 123 pigs from Denmark and two pigs from Germany were brought into Sweden, as well as one cattle from Denmark and 46 cattle from Finland. Thirteen goats, 19 sheep and three alpacas were brought from Germany and three llamas were brought from Norway. Additionally, 857 reindeer came from Finland for slaughter.

For breeding purposes approximately 335 000 grandparent and parent animals (*Gallus gallus*) entered Sweden from the Netherlands, Spain, France and Great Britain as well as 8370 turkeys (*Meleagris gallopavo*) from Great Britain. In addition, 2800 ducks (*Anas spp.*) as day-old chicks were brought from Denmark. Approximately 130 000 hatching eggs (*Phasianidae*) were brought to Sweden from Denmark, France and Poland and 60 hatching eggs (*Gallus gallus*) were brought from Germany.

In total, 40 consignments of honeybees (*Apis mellifera*) were brought to Sweden for breeding purposes, from Austria, Denmark, Estonia, Germany, Slovenia, Italy and Malta. Furthermore, 115 consignments of bumblebees (*Bombus spp.*) were brought for crop pollination to Sweden from the Netherlands and Belgium.

The number of animals that left Sweden for intra-Union trade during 2020 were: 663 cattle, 97 pigs, 56 sheep, 16 goats and 33 alpacas. In addition, 1040 reindeer were sent from Sweden, whereas 837 were sent for slaughter in Finland, 200 were sent to Norway and three to Hungary.

Approximately 4.9 million day-old chicks (*Gallus gallus*), 8200 day-old chicks (*Anas spp.*) and 1.5 million live poultry (*Gallus gallus*) left Sweden for intra-Union trade in 2020.

Approximately 9.1 million hatching eggs (*Gallus gallus*) and 176 000 hatching eggs (*Anser spp.*) were sent for intra-union trade or to Russia, the majority for breeding purposes.

A total of 6 consignments of honeybees (*Apis mellifera*) left Sweden for intra-union trade to destinations in France, Germany and Spain.

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Animal registers and other databases used in surveillance

THE CENTRAL REGISTER OF HOLDINGS

The Swedish Board of Agriculture is responsible for maintaining the Central Register of Holdings (PLATS). Each holding is assigned a unique identification number (holding number). It is required that the animal holder registers all information and all changes that occur at the holding place. It is the animal holder's responsibility to fulfil the requirements and register according to the rules. The register contains information on holdings with bovine animals, pigs, sheep, goats, laying hens and other poultry. Details on holding number, address, type of production, capacity and the geographical coordinates of the holding are included, as well as the name, address and telephone number of the keeper. All egg producers with a capacity of at least 350 laying hens and all those selling eggs for consumption must be registered. The register contains specific information about production method, capacity and the number of houses and sections on the holding. The register is regulated through European and Swedish legislation: regulation (EC) 1760/2000, regulation (EC) 911/2004, regulation (EC) 21/2004 and regulations SJVFS 2007:12, SJVFS 2007:13, SJVFS 2007:14, SJVFS 2006:11, SJVFS 2003:20; directive 2008/71/EU, directive 2005/94/EC, directive 92/66/EEC and regulations SFS 1999:1148 and SFS 2006:815.

THE CENTRAL DATABASE OF PIG, SHEEP AND GOAT MOVEMENTS

The Swedish Board of Agriculture is responsible for the Central Database of animal movements. It contains data on all holdings with pigs, sheep and goats and their movements between holdings. The database contains information from the keepers and the abattoirs, such as date of movement, address and holding number as well as name and telephone number of the keeper. It is possible to register movements in the database via the internet, or in paper form. Animals are registered in groups in the database when moved. For sheep and goats, both the keeper who dispatches the animals and the keeper who receives the animals are responsible for reporting to the database, within seven days of the movement. The establishment of the database is regulated through European and Swedish legislation: directive 2008/71/EG, SJVFS 2007:13 21/2004 and SJVFS 2007:14.

THE CENTRAL DATABASE FOR BOVINE ANIMALS

The Swedish Board of Agriculture is responsible for the Central Database for Bovine animals (CDB), to which all bovine births, deaths and movements must be reported. The keeper is responsible for reporting any changes within seven days of the occurrence. The purpose of the register is to allow swift and efficient tracing of a contagious disease, verification of the country of origin of a meat product as well as control and administration of cross compliance. For herds

enrolled in the national milk recording scheme, managed by Växa Sverige, all reporting to the Central Database for Bovine Animals is done via the Database for Dairy Herds (see below). The establishment of the database is regulated through European and Swedish legislation: regulation (EC) 1760/2000, (EC) No 911/2004 and SJVFS 2007:12.

THE SLAUGHTER REGISTER

The Slaughter Register (SLAKT) is administrated by the Swedish Board of Agriculture. The abattoirs are responsible for reporting all slaughtered animals, including wild game, but abattoirs that only process wild game do not report. The organisation number or personal identification number of the producer must be reported for all species except wild game. The holding number of the supplier is compulsory information for all species except horses and wild game. Reports must be made every week. The establishment of the register is regulated through Swedish legislation (SJVFS 2009:43).

THE DATABASE OF DAIRY HERDS

The main national coordinating organisation for dairy and beef production is Växa Sverige (approved according to SJVFS 2009:29). The organisation is responsible for the official milk recording scheme and lineage recording for dairy cows (Kodatabasen, managed according to ICAR's recommendations). The database includes milk recordings, calvings, cullings, inseminations, registrations from claw trimmings and disease recordings from the Board of Agriculture for all animals at the dairy farm. It forms the basis for the development of different management tools used by the farmers, advisers and veterinarians. It is also a valuable tool for research on topics such as feeding, animal health and genetics. Approximately 70% of all dairy herds in Sweden, covering approximately 73% of the dairy cows, are included in the official milk recording scheme.

THE ANIMAL HEALTH DATABASE

The Swedish board of Agriculture is responsible for the Animal health database (Vet@) which is used by the veterinary services for the documentation of the health situation on farms, including details about health status, treatment and vaccinations of individual animals. It is based on reports from practitioners to the Swedish Board of Agriculture. All veterinarians are obliged to continuously report activities of their veterinary practice on production animals. The purpose of the database is to monitor the animal health situation in Sweden and use it as a basis for preventive measures.



Photo: Werner Baumgarten/iStock.

CENTRAL AQUACULTURE REGISTER

All aquaculture premises authorised by the County Administrative Boards are registered in the Central Aquaculture Register. The register is administered by the Swedish Board of Agriculture. The data encompasses name and coordinates of the premise as well as type of production and species kept. It also contains results from official controls, information on the farms' water supply and discharge as well as date information on health status. The establishment of the register is regulated through European and Swedish legislation.

THE POULTRY REGISTER

The Swedish Board of Agriculture is responsible for the poultry register, which includes data on commercial holdings with ducks, pigeons, pheasants, geese, mallard ducks, chickens, turkeys, guinea fowl, partridges, ratites or quails. The purpose of the register is to allow swift and efficient tracing of contagious diseases (e.g. avian influenza and Newcastle disease). The register encompasses information about the location of the holding, contact information, type of production, species, maximum capacity, number of units on the site and more. The establishment of the register is regulated through European and Swedish legislation.

SVALA

SVALA is the Laboratory Information Management System (LIMS) used at the National Veterinary Institute to record and manage laboratory data for all samples analysed at the laboratory, covering both domestic and wild species.

The database includes information about animal owners, animals, samples, test results and geolocation. Samples analysed include samples from veterinary practices, different surveillance programs and others. There are data about approximately 400 000 samples for each year.

At SVA, a system for automated analysis of laboratory data for veterinary syndromic surveillance is in place, covering all domestic animal species nationally.

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Andrea Holmström, Växa Sverige (The Database of Dairy Herds)

Milan Miroslavljevic, Swedish Board of Agriculture (data sources at the Swedish Board of Agriculture)

Institutions, organisations and laboratories involved in surveillance

SWEDISH BOARD OF AGRICULTURE

The Swedish Board of Agriculture (SBA) is an expert authority on agricultural and food policy within the Ministry of Innovation and Enterprise, and is responsible for agriculture, aquaculture and horticulture, including animal and plant health. This includes monitoring, analysing and reporting to the Government on developments in these areas and implementing policy decisions within its designated field of activities. The aim is to fulfil the overall goals of the agro-food policy and to promote food production that is competitive, adapted to environmental and animal welfare concerns, and that benefits consumers.

SBA promotes animal health through the prevention and control of contagious animal diseases. SBA is the competent authority for official veterinary controls, for emergency measures to combat contagious diseases, disease surveillance and reporting and is the major financier of active surveillance. The national surveillance plan, which primarily involves active surveillance, is adopted by the SBA based on recommendations from the expert authority in the field, the National Veterinary Institute. SBA can also decide on surveillance outside this plan when needed, in cases of outbreaks of serious diseases.

NATIONAL VETERINARY INSTITUTE

The National Veterinary Institute (SVA) is a national expert authority with a mission to follow and communicate the infectious disease and antimicrobial resistance situation in domestic and wild animals, both nationally and internationally. SVA strives for good animal and human health, a healthy environment and sustainable food production. The authority reports to the Swedish Ministry of Enterprise and Innovation and is the nation's leading knowledge centre for infectious diseases in veterinary medicine. It has expertise in pathology, microbiology, diagnostics, risk assessment, prevention and control of contagious animal diseases and other serious transmissible hazards including zoonotic agents and antimicrobial resistance. SVA maintains 24/7 preparedness, is the National Reference Laboratory for several animal diseases including zoonoses, and is also the EU reference laboratory (EURL) for *Campylobacter*.

The SVA implements several control and monitoring programmes in cooperation with stakeholder organisations and the relevant authorities. The SVA prepares the national surveillance plan that is adopted by the SBA.

THE PUBLIC HEALTH AGENCY OF SWEDEN

The Public Health Agency of Sweden has the task of disseminating scientifically based knowledge to promote health, prevent disease and injury, and monitor the health status of the Swedish human population and the factors that affect it.

Concerning communicable diseases, the agency has the

overall national responsibility and coordinates communicable disease control on a national level. Some of the agency's responsibilities include vaccination programmes, emergency preparedness for health threats and national stockpiles of communicable disease medications. In addition, it coordinates national efforts concerning antibiotic resistance, infection control and healthcare-associated infections. Another field of work is to prevent HIV and STIs (sexually transmitted infections), where the agency is also responsible for national coordination.

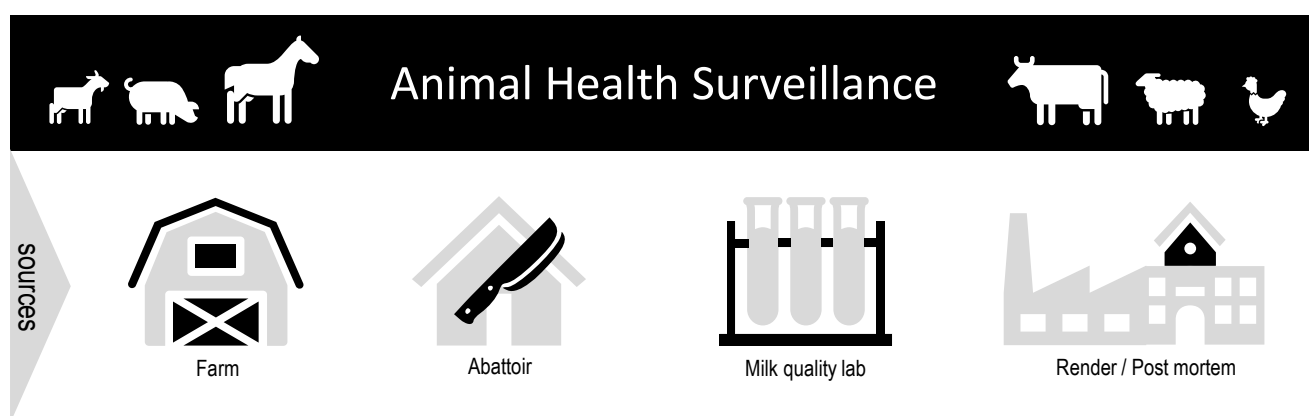
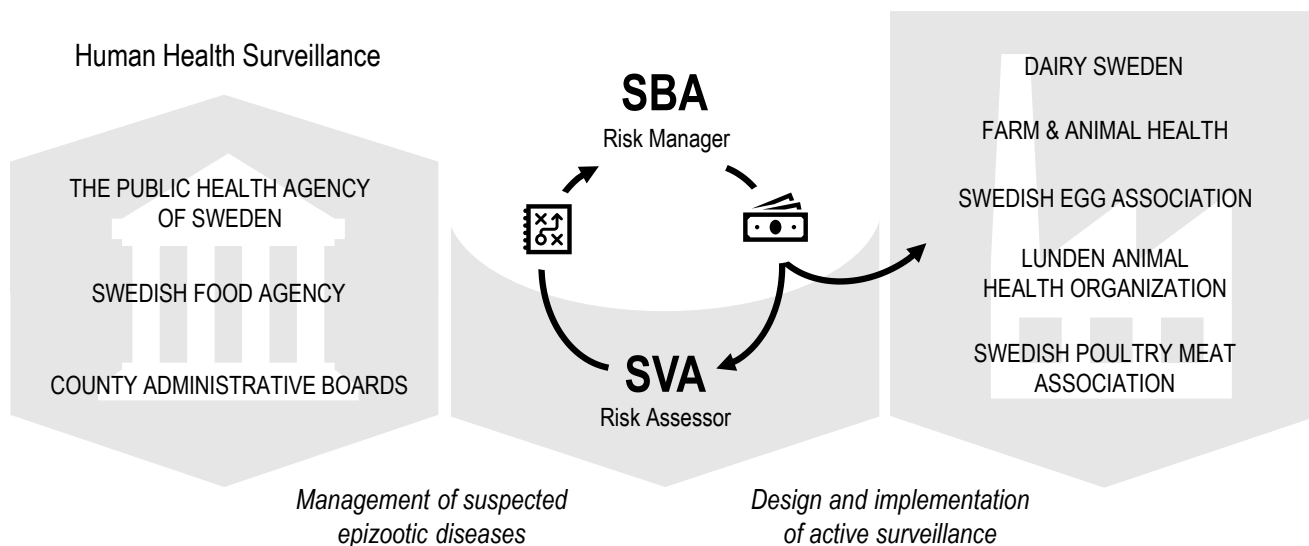
The agency also performs microbiological laboratory analyses, including diagnostics, and supports quality and method development at laboratories engaged in diagnostics of communicable disease pathogens. High containment laboratories have round-the-clock preparedness every day of the year to conduct microbiological diagnostics of high-consequence infectious agents that pose a particular danger to human health. One important task is to provide expert support to investigations of suspected or confirmed outbreaks of communicable diseases and to maintain laboratory preparedness needed for effective communicable disease control in the country.

SWEDISH FOOD AGENCY

The Swedish Food Agency is a national agency reporting to the Ministry for Enterprise and Innovation. The Swedish Food Agency works in the interest of the consumer to ensure food safety, promote fair practices in food trade and promote healthy eating habits. To accomplish this mission, the agency develops and issues regulations, advice and information as well as coordinates and carries out controls. As a basis for these activities, the agency performs risk and benefits analyses, collects data on food consumption and composition, and carries out microbiological, chemical and nutritional analyses on food and water. The Swedish Food Agency is also responsible for environmental issues, emergency preparedness, and guidance regarding official controls of drinking water. The official address to Swedish Food Agency is www.livsmedelsverket.se.

COUNTY ADMINISTRATIVE BOARDS

Sweden is divided into 21 counties, each of which has its own County Administrative Board (CAB) and County Governor. The CAB is an important link between the people and the municipal authorities on the one hand and the national government, parliament and central authorities on the other. County Veterinary Officers at the CABs have coordinating functions for prevention, surveillance and eradication of contagious animal diseases. They are supported by fisheries directors for questions relating to aquaculture. Seven CABs have a regional responsibility for bee health. They set the borders for inspection districts and are responsible for



Roles, responsibilities and relationships between organisations involved in active surveillance in domestic livestock populations (cattle, pigs, poultry, sheep and goat), and their sources of animal health information. Infographic by Arianna Comin.

appointing bee inspectors in all counties. The CABs also collaborate with County Medical Officers and veterinarians in clinical practice in issues related to zoonoses and “One Health”, and they also carry out regional supervision of animal health and welfare.

VÄXA SVERIGE

Växa Sverige is the principal organiser of the surveillance programmes for bovine leucosis and infectious bovine rhinotracheitis. Växa Sverige is also the principal organiser of the control programme for bovine viral diarrhoea virus. Starting in the autumn of 2015, the previous salmonella control programme was replaced with a more general biosecurity programme for cattle (Smittsäkrad besättning) also run by Växa Sverige. This programme is approved by the SBA and follows the plans and guidelines outlined in SJVFS 2015:17.

FARM & ANIMAL HEALTH

Farm & Animal Health is an advisory company owned by the main meat producing companies and the farmer organisations for pigs, beef cattle and sheep in Sweden. Its aim is to maintain a high level of health within efficient and profitable pig, cattle and sheep production. The company’s business idea, originating in the 1960s, is to promote healthy animals for profitable farming. Its focus is to prevent animal health

problems for pigs, beef cattle and sheep as well as to improve animal welfare.

Activities are performed with a clear national focus and the consulting services are available to all farmers. A large part of the activities and services are based on officially approved animal health programmes for pigs, cattle and sheep. In addition, Farm & Animal Health is assigned by the Swedish Board of Agriculture to implement specific disease control and surveillance programmes. Examples of such programmes are surveillance of porcine reproductive and respiratory syndrome virus in pigs, the control of Maedi-visna in sheep and paratuberculosis (Johne’s disease) in cattle, monitoring of antimicrobial resistance in disease-causing bacteria and the national postmortem programme of livestock animals.

Applied research and development are important parts of the business and projects are often performed in collaboration with the National Veterinary Institute and the Swedish University of Agricultural Sciences.

LUNDEN ANIMAL HEALTH ORGANISATION

Lunden Animal Health Organisation is a veterinary consulting company working with pig health and welfare. Its objective is to gather, develop and communicate knowledge on pig issues. The organisation is involved in national surveillance

programmes for pig diseases and is assigned by the Swedish Board of Agriculture to perform health controls as well as to implement the on-farm national biosecurity programme for pigs.

SWEDISH POULTRY MEAT ASSOCIATION

The Swedish Poultry Meat Association (SPMA) represents 99% of the chicken meat production and 95–97% of the turkey meat production in Sweden, with members from the entire production chain. Members are obligated to participate in the animal welfare and health programmes administered by SPMA, such as controls for *Salmonella*, *Campylobacter*, coccidiosis and clostridiosis, to meet high standards for food hygiene and safety.

The SPMA is multifunctional with major tasks associated with economic and political industry-related matters important to its members. SPMA is consultation body for legislative referrals from the Swedish public authorities and EU institutions. The organisation also initiates and economically supports research.

THE SWEDISH EGG ASSOCIATION

The Swedish Egg Association is the national organisation for Swedish egg producers, hatcheries, rearing companies, egg packing stations and feeding companies and represents 95% of the total Swedish egg production.

The Swedish Egg Association is responsible for the organisation of the surveillance programmes for animal health and welfare in layers and for the voluntary *Salmonella* control programme. The objective is to support profitable egg production, with a high standard of animal welfare, food hygiene and safety.

SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES

The Swedish University of Agricultural Sciences (SLU) develops the understanding, sustainable use and management of biological natural resources.

The Ecology Centre at SLU conducts research on sustainable agriculture, forest production and biological conservation. This includes both fundamental and applied research on communities and ecosystems and the influences of land use and climate on animals, plants, soil nutrient status and greenhouse gas balance. Active dissemination, outreach and frequent contacts with stakeholders are key activities.

These activities also include bee health and how this is affected by pathogens, environmental factors, pesticides and beekeeping practices. Also located in the Ecology Centre

on SLU's main campus is the National Reference Laboratory for Bee Health, whose activities are carried out in close cooperation with relevant authorities and beekeepers.

BEE INSPECTORS

Bee inspectors (bitillsynsmän) are experienced beekeepers that are specifically trained to examine honeybee colonies for disease. The main duties of the bee inspectors are to examine bee colonies and hive material for signs of disease, both when disease is suspected or with requests to move bee colonies out of designated disease protection or surveillance zones. Bee inspectors also issue transit-permits, implement or order specific control measures for certain diseases and inform beekeepers about suitable treatments for certain diseases and parasites. Seven of the Swedish CABs have a regional responsibility for bee health. They set the borders for inspection districts and are responsible for appointing bee inspectors in all counties. Sweden is divided into just over 300 bee districts and in each of these the local bee inspectors are responsible for the practical control and reporting of primarily three diseases-parasites: American foulbrood, tracheal mites and varroa mites.

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Andrea Holmström, Växa Sverige

Ebba Schwan, Farm & Animal Health

Anders Wallensten, Folkhälsomyndigheten

Maria Donis, Swedish Poultry Meat Association

Anna-Maria Erixon, The Swedish Egg Association

Erik Lindahl, Lunden animal health organisation

Ingrid Karlsson, Swedish Board of Agriculture (bee inspectors)

Eva Forsgren, Swedish University of Agricultural Sciences

Gunilla Hallgren, National Veterinary Institute

Disease Surveillance 2020

Atrophic rhinitis

BACKGROUND

Atrophic rhinitis (AR) is caused by toxin-producing strains of *Pasteurella multocida*. Since *P. multocida* is a secondary invader and not capable of penetrating an intact mucosa, it is dependent on other infections. Traditionally, *Bordetella bronchiseptica* has been considered the most important precursor, but other bacteria and viruses may also precede *P. multocida* infection. AR used to be a common disease in pig production, but improvements in rearing and disease prevention have caused the disease to gradually fade away. In Sweden, AR was successfully controlled in nucleus and multiplying herds in the early 1990s. A national control programme has been in place since 1995. It is administered by the branch organisation Farm & Animal Health and all diagnostic testing is performed at SVA.

DISEASE

When *P. multocida* penetrates the nasal mucosa, its toxins can affect the bone building process and the snout may progressively become twisted. Affected pigs will also show retarded growth. *P. multocida* toxins can also damage the nasal epithelium and cilia causing inhaled air to reach the respiratory organs without being filtered or warmed, which in turn increases the risk for other respiratory infections.

LEGISLATION

Atrophic rhinitis is a notifiable disease according to SJVFS 2013:23.

SURVEILLANCE

The purpose of the control programme is to declare herds selling breeding stock free from infection with toxigenic *P. multocida*, and thereby decrease the incidence of AR in all herds. Nucleus and multiplying herds are actively tested for the presence of toxigenic *P. multocida* at least once a year including a total of 20 animals per herd. Herds are also tested upon clinical suspicion of AR. Eradication of *P. multocida* is not realistic since it is a ubiquitous bacterium that can affect all mammals. However, when AR is suspected in a herd, tests are performed for the presence of toxigenic *P. multocida* in the nostrils of pigs. If toxigenic *P. multocida* is detected in a herd, the health declaration is withdrawn and restrictions on the sale of pigs are put in place until the herd is sanitised and declared free from the disease. Diagnostic tools developed by DAKO (Copenhagen, Denmark) and evaluated at

SVA during the late 1980s and early 1990s offered the possibility to combat AR in an effective way. Nasal swabs are cultured on a special media overnight. The entire microbial growth is harvested and diluted in water and the presence of the *P. multocida* toxin is assessed by an ELISA system.

RESULTS AND DISCUSSION

Atrophic rhinitis used to be a common disease, but the disease is now very rare thanks to efforts made in the early 1990s and the control programme that was initiated in 1995. The latest Swedish herd diagnosed with AR was in 2005 (Table 2). In 2009, *P. multocida* was detected in 10 out of 34 imported Norwegian boars in quarantine. These boars were isolated and found negative for *P. multocida* at re-sampling before moved to a boar station as intended. In 2019, all 824 samples from 42 herds tested were collected within the control programme at 42 sample occasions. One animal tested positive for toxigenic *P. multocida*, but the suspicion was later rejected based on the results from further herd investigation. In 2020, all 606 samples from 31 test occasions were negative regarding toxigenic *P. multocida*.

Table 2: The total number of samples and the outcome of nasal swabs analysed for *P. multocida* 2005–2020 at SVA. The samples have been collected in all nucleus and multiplying herds, as well as in production herds suspected for atrophic rhinitis (AR). When individual samples in a herd are positive, the herd is further scrutinised and either considered confirmed as affected, or declared free from AR.

Year	Samples	Positive samples	Diagnosed herds
2005	2413	29	2
2006	1836	2	0
2007	1878	1	0
2008	462	0	0
2009	1724	10	1
2010	1523	0	0
2011	1323	0	0
2012	1431	0	0
2013	1027	0	0
2014	1050	0	0
2015	844	0	0
2016	976	0	0
2017	1294	0	0
2018	878	0	0
2019	824	1	0
2020	606	0	0

Aujeszky's disease

BACKGROUND

Aujeszky's disease (AD) is caused by a herpes virus that has the capacity to infect many species, but pigs are the natural hosts. The disease is of importance for pig production worldwide, although it has been eradicated from the domestic pig population in many countries. AD is widespread in European wild boar populations, which may act as reservoirs, but their role in transmitting the disease is not well known. Between 2018 and 2020, several outbreaks of AD in outdoor-raised domestic pigs in France were linked to contact with wild boar. Other species, including cattle, sheep, goats, dogs and cats, develop clinical signs, but they are not considered important for transmission of the disease as they are typically dead-end hosts. A few cases of human infection have been reported but AD is not considered a zoonotic disease.

Sweden has been officially free from AD since 1996 (Commission Decision 96/725/EU with amendments). This status was achieved following a national, government-supported control programme that was introduced in 1991 and managed by the Swedish Animal Health Services (now

Farm & Animal Health). Farm & Animal Health is also responsible for the ongoing active surveillance programme financed by the Swedish Board of Agriculture.

DISEASE

The clinical presentation of AD is dependent on the age of the infected animal, with younger pigs being most severely affected but becoming more resistant as they age. Infected newborn or very young piglets develop fever, anorexia and neurological signs and mortality approaches 100%. Adult pigs show only mild respiratory signs and inappetence and, in breeding sows, reproductive failure including return to oestrus, abortion, stillbirths or weak-born piglets can occur. Species other than pigs develop neurological signs including severe itching ("mad itch") and affected animals typically die within 1–2 days.



In 2020, 2407 samples from 469 pig herds were analysed for Aujeszky's disease (AD) within the active surveillance programme. All samples were negative for antibodies to the AD virus. Photo: Marie Sjölund.

LEGISLATION

The disease is included in the Swedish Act of Epizootic diseases (SFS 1999:657 with amendments) and is thereby notifiable on clinical suspicion for all veterinarians and farmers. Sweden has been granted certain additional guarantees regarding AD by the European Commission, in order to protect the Swedish pig health status (Decision 2008/185/EC).

SURVEILLANCE

The purpose of the surveillance is to document continued freedom from the disease. The surveillance programme was designed using a between-herd prevalence of 0.5%, a within-herd prevalence of 50% and a risk of introduction of 1 in 20 years. Samples are analysed for antibodies against the AD virus using a blocking ELISA (SVANOVIR® PRV-gB-Ab ELISA, Svanova). Samples testing positive are analysed with a second ELISA (SVANOVIR® PRV-gE-AB/PRV-gE-Ak, Svanova) for confirmation. In cases of clinical suspicion of AD, samples are analysed for the presence of virus or viral genome. All analyses are performed at the National Veterinary Institute.

Passive surveillance

Farmers and veterinarians must report clinical suspicions of AD to the Swedish Board of Agriculture and all suspicions are followed up with an investigation. Investigations may include sampling of sick or dead animals, examination of the herd for the presence of clinical signs and analyses of production results.

Active surveillance

In 2020, all samples collected in the abattoir sampling component of the surveillance for porcine respiratory and reproductive syndrome (PRRS) virus, carried out by Farm & Animal Health (see chapter on PRRS for details, page 66), were also used for the active surveillance of AD. Within this programme, pigs from randomly selected production herds are sampled at slaughter throughout the year at 9 abattoirs which slaughter approximately 99.5% of Sweden's pigs. Three samples per herd are collected on each sampling occasion. For 2020, the number of samples required for the abattoir component of the PRRS surveillance programme was calculated to be 2400.

Active surveillance for AD in Swedish wild boar has also been conducted annually since 2000 (see chapter "Infectious diseases in wild boars" on page 123), with the exception of 2018 when testing was not undertaken due to a redistribution of funding.

RESULTS

Passive surveillance

In 2020, one clinical suspicion of AD was investigated. The investigation was prompted after the herd experienced a high number of late-term abortions and premature farrowings over the course of 4 days. During the investigation, tissue

samples from aborted fetuses were analysed for the presence of the virus causing AD using PCR. All samples tested were negative, and the herd was subsequently declared free from AD.

Active surveillance

In 2020, 2407 samples from pigs from 469 herds taken on 803 sampling occasions (some herds were sampled more than once during the year) were analysed for AD within the active surveillance programme (Table 3). All samples were negative for antibodies to the AD virus.

Table 3: Number of finisher pigs and herds sampled at the abattoir in the active surveillance of Aujeszky's disease each year 2010–2020.

Year	Number of pigs sampled	Number of herds sampled
2010	4371	866
2011	2308	700
2012	2152	623
2013	1548	488
2014	2028	537
2015	2383	521
2016	2418	506
2017	2625	546
2018	2706	514
2019	2548	507
2020	2407	469

DISCUSSION

The purpose of the surveillance is to document freedom from AD and to contribute to the maintenance of this situation by detecting an introduction of the disease before it is widely spread in the swine population. The design of the active surveillance for AD has changed several times since Sweden was declared officially free of the disease in 1996. Until 2008, samples collected from sows and boars at slaughter were used in the surveillance for AD. In 2009, in addition to samples from slaughtered sows and boars, samples collected from finisher pigs in the abattoir component of the PRRS surveillance programme were also analysed. Since 2011, AD surveillance has been based solely on the abattoir samples collected for the PRRS surveillance programme. Based on the surveillance undertaken in 2020, the probability of freedom from AD was calculated and found to be >99%.

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Bluetongue

BACKGROUND

Bluetongue is a vector borne disease of ruminants and camelids caused by any of 26 serotypes of bluetongue virus (BTV). The virus is transmitted by haematophagous midges (*Culicoides* spp).

Until 1998, bluetongue had not been detected in any European country, but since then, outbreaks of several different serotypes have frequently been detected in the Mediterranean countries. In August 2006, BTV-8 appeared in the Netherlands. During 2006 and 2007 this outbreak spread to a large number of countries in Northern and Western Europe. In 2008, further cases were reported, and vaccination campaigns were launched in most of EU as soon as inactivated vaccines became available. In September 2008, the first case of BTV-8 infection in Sweden was confirmed and a vaccination campaign and intensive surveillance activities were initiated nationally. In the first quarter of 2009 transplacental infection was detected in three newborn calves, all three cases originating from infections of their dams in autumn 2008. In December 2010, after extensive surveillance, Sweden was declared free from BTV-8. After that, surveillance according to Commission Regulation (EC) No 1266/2007, with amendments, has been carried out annually.

Vector surveillance was initiated in 2007 in order to document the activity of relevant *Culicoides* spp. throughout the different seasons of the year. The programme was discontinued in 2011 after Sweden was declared free from BTV-8.

DISEASE

BTV causes clinical disease in ruminants, mainly in sheep. The different serotypes appear to vary in their ability to cause clinical signs in different animal species and in the severity of clinical signs in the same species. The signs include fever, lesions in the mucous membranes of the mouth and nostrils, inflammation of the coronary band, swollen head and oedema in various body tissues.

LEGISLATION

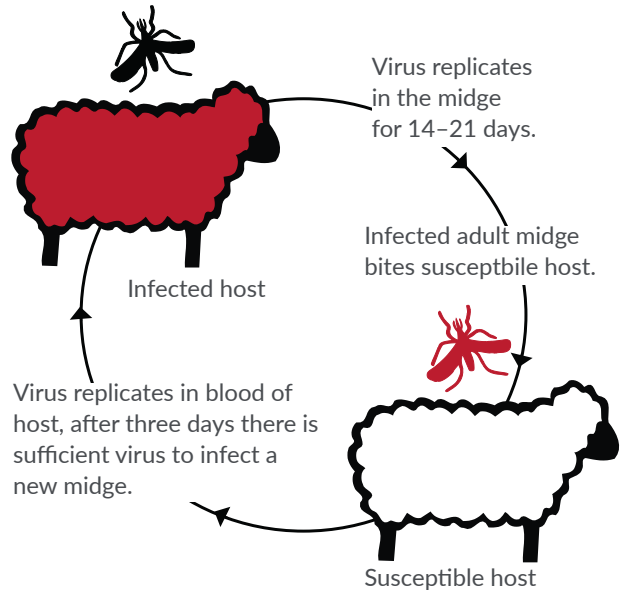
The control, monitoring, surveillance and restriction of movements of certain animals of susceptible species are governed by Regulation 1266/2007 with amendments. Bluetongue is a notifiable disease and is included in the Swedish Act of Epizootic diseases (SFS 1999:657 with amendments).

SURVEILLANCE

All diagnostic testing, as outlined below, was performed at the National Veterinary Institute with the purpose of demonstrating sustained freedom from BTV in Swedish cattle. Bulk milk samples were analysed with an indirect ELISA (ID Screen Bluetongue Milk Indirect) and serum samples were analysed with a competitive ELISA (ID Screen Bluetongue Competition ELISA). For clinical suspicions, organs or blood were analysed with real-time pan-PCR detecting 24 serotypes.

Bluetongue virus infection cycle

Uninfected adult midge bites host animal which has virus circulating in the blood.



Transmission of Bluetongue virus involves insect vectors (midges) and a ruminant host. Virus replication in the midge is highly dependent on the surrounding temperature, and is thought not to happen at all below 14°C. Infographic by Erika Chenais.

A positive case is defined as an animal giving rise to a positive PCR-product, or an unvaccinated animal without remaining maternal antibodies giving a significant antibody titre.

Passive surveillance

Suspicious based on clinical signs must be reported to the Swedish Board of Agriculture and will be subsequently investigated. The investigation includes sampling of affected animals and examination of the herd. During the investigation, the farm is placed under restrictions.

Active surveillance

In the 2020 bluetongue surveillance, 190 dairy holdings from a risk-based sampling area, comprising the nine southernmost counties of Sweden, were randomly selected for bulk milk testing. Based on the total size of the dairy cow population in the selected area, the average herd size and the test specifics, bulk milk samples from 170 holdings should be tested to detect 2% prevalence with 95% confidence. Samples were collected at the selected holdings by personnel from the milk collection service. The sampling took place after the vector season in December 2020. Samples were analysed with the milk ELISA routinely used.

In addition to the field testing, serological testing for bluetongue was performed prior to import and export and at breeding centres.

RESULTS

Bulk milk samples from 189 holdings were tested in the field surveillance, all with negative results. Four clinically suspect cases were investigated and tested during 2020 and found negative. All other testing performed prior to import and export was also negative.

DISCUSSION

In summary, no clinical suspicions of bluetongue were confirmed, nor was there any indication of viral circulation during 2020, confirming the continued sustained freedom from BTV in Sweden.

Competent vectors are present in Sweden and may spread the infection. Reintroduction of the virus to Sweden may occur by infected animals, infected vectors or other yet unidentified means.

At present, there are no indications of BTV circulation in direct neighbouring countries. However, in 2015, BTV-8, of the Northern European strain from 2007 re-emerged in France. Since 2015, several thousand cases (defined as animal found positive for BTV with real-time PCR) have been reported by France every year. Most of these cases are animals found positive within active surveillance activities; few are animals with clinical signs of disease. From December 2018 an increase in transplacental transmission of BTV-8 in cattle in France was reported. Such calves were born blind, small, and dying at a few days of age. During the vector season of 2018 and 2019 Germany, Switzerland and Belgium, and in 2020 also Luxembourg, each reported some cases of BTV-8 (using the same definition) found during routine surveillance and tests for export/import. The United Kingdom reported single cases of BTV-8 in cattle imported from France in 2018.

During 2020, as in all previous years, several BTV serotypes were circulating in sheep and cattle in the Mediterranean countries.

The detection of BTV-8 in France in 2015 after several years of silence, the numerous cases detected in France since then, as well as limited number of cases in Belgium, Germany, Luxembourg and Switzerland in 2020, again demonstrate that BTV may spread and become established in live-stock populations in northern Europe. Moreover, as the prevalence of seropositive animals due to vaccination are getting very low, the population is again becoming susceptible to BTV-8. Therefore, new introductions of this serotype, or any remaining foci in previously infected countries, could pose a threat. Likewise, new serotypes could emerge in the Mediterranean region or start circulating worldwide, underlining how the situation can rapidly change.

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Bovine spongiform encephalopathy



Classical bovine spongiform encephalopathy has never been detected in cattle in Sweden. Photo: Mia Holmberg.

BACKGROUND

Classical bovine spongiform encephalopathy (BSE) belongs to a group of diseases called transmissible spongiform encephalopathies (TSE). It was first described in cattle in the UK in 1986 and from there the disease spread to a large number of European countries as well as countries outside Europe. The current theory about the causative agent is the protein-only hypothesis. This theory assumes that prions (misfolded and aggregated proteins) induce the same misfolded structure in normal prion-proteins in the body of the host, resulting in accumulation of prions and cellular damage without involvement of any microorganism. Classical BSE primarily spread through animal feed including contaminated meat and bone meal (MBM), i.e. MBM containing parts of animals infected with BSE. However, the primary source of the epidemic was never established. The use of MBM was prohibited, first in feed to cattle and in 2001 in feed to pigs and poultry to avoid cross-contamination in the feed mills.

In 1996, the disease became a public health concern, after the detection of a new variant of Creutzfeldt-Jacob Disease in humans (vCJD), likely to be linked to classical BSE in cattle. This resulted in actions taken to prevent transmission to humans through removal of specified risk material

(such as brain and spinal cord) from cattle at slaughter, restrictions related to feed to avoid recycling of infectious material to ruminants through infected MBM and an intensified surveillance which started in 2001 after rapid diagnostic tests became available.

Atypical cases of BSE, which show diagnostic and epidemiological dissimilarities with classical BSE, were first described in the early 2000. These atypical BSE cases probably occur spontaneously (without known cause) and possible links to classical BSE and potential zoonotic aspects are subject to debate within the scientific community.

Sweden has historically had a low risk of introduction of classical BSE and a low risk of recirculation of the disease if it had been introduced, due to an early ban on the use of fallen stock in production of feed for livestock and limited imports. This has been assessed by the Scientific Steering Committee, by the European Food Safety Authority (EFSA) (expressed in terms of the Geographical BSE Risk (GBR)) and later by the OIE Scientific Commission. Sweden is currently recognised as having a negligible risk for classical BSE, as a result of a resolution adopted by the OIE International Committee.

One case of BSE has been detected in cattle in Sweden. This was in 2006 in a beef cow born in 1994. This case was confirmed to be atypical BSE of the H-type, i.e. not classical BSE.

DISEASE

The incubation period is long, from two years up to several years. Clinical signs of classical BSE are related to the neurological system and include altered behaviour and sensation as well as affected movement and posture. The clinical state can last for weeks or months. The disease is progressive and always fatal.

LEGISLATION

Surveillance and control of BSE is regulated through Regulation (EC) No 999/2001 of the European Parliament and of the Council of 22 May 2001. The surveillance design is in accordance with Annex III and Sweden applies derogation for remote areas with low cattle density (Commission Decision 2008/908) where there is no collection of fallen stock. The cattle population in these areas does not exceed 10% of the bovine population in Sweden. On the national level, the sampling is regulated by SJVFS 2010:9, last amended through SJVFS 2013:3. BSE is a notifiable disease under the Swedish Act of Epizootic diseases (SFS 1999:657, with amendments). Feed controls are regulated through Regulation (EC) 152/2009.

SURVEILLANCE

Feed

In order to investigate compliance with the feed bans, samples of feed and imported raw material for feed production are collected at feed mills, points of retail and at the farm level and analysed for the presence of processed animal protein (PAP) using microscopy. This is part of the official controls and the Swedish Board of Agriculture and the County Administrative Boards are responsible. Samples are chosen based on a risk assessment made by the Swedish Board of Agriculture.

Animals

The Swedish Board of Agriculture is responsible for the surveillance programme. It is carried out in cooperation with the National Veterinary Institute, which is the National Reference Laboratory (Regulation (EC) 999/2001). Samples are analysed at the National Veterinary Institute.

The risk of introduction and recirculation of BSE within the system has been controlled for many years. The purpose of the surveillance in animals is primarily to fulfil the requirements in the EU regulation and to maintain the OIE status of negligible risk for classical BSE. The OIE determines a minimum target for surveillance, which is based on a point system that needs to be reached for the preceding seven years. The points are allocated differently between different risk categories of animals, with so-called high risk animals, such as clinical suspicions, rendering the highest number of points. The relative weight of different categories is based on historical BSE data from the United Kingdom.

Passive surveillance

All suspicions of BSE (bovine animals with clinical signs that are consistent with a BSE diagnosis and not responding to treatment) must be reported to the authorities. The obligation to report applies to animal owners, veterinarians, and everyone else who is responsible for the animals. If the animal is still alive, it is examined by a veterinarian who is in close contact with disease experts and it is decided if the animal should be euthanized. Samples are analysed with Bio-Rad TeSeE short assay protocol (SAP). In case of positive or inconclusive results, the material is prepared and examined with Bio-Rad TeSeE Western Blot.

Clinical suspects are a category of animals that should be included in the surveillance, but since the control measures have been effective and the European epidemic of classical BSE has declined, it is a challenge to keep farmers and veterinarians alert and report suspected clinical cases. Substantial efforts have been made starting 2018 to find animals that display clinical signs which could be compatible with BSE and to include these in the surveillance programme.

Active surveillance

The following categories were sampled in the active surveillance (regulation 999/2001):

- Cattle of Swedish origin, above 48 months of age, that have remarks at antemortem inspection before slaughter or are emergency slaughtered.
- Cattle of other than Swedish origin above 24 months of age that have remarks at antemortem inspection before slaughter or are emergency slaughtered.
- All healthy slaughtered cattle above 30 months of age that originate in a country other than Sweden, which does not have negligible risk for BSE.
- All fallen stock (animals dead or killed on farm but not slaughtered for human consumption) above 48 months of age that originate from Sweden. For cattle that originate from a country other than Sweden which does not have a negligible risk for BSE, the age limit for sampling fallen stock is 24 months. The fallen stock are sampled by employees at the rendering plants or by veterinarians or veterinary assistants at postmortem.

The diagnostic procedures are the same as for the passive surveillance (see above).

RESULTS

Feed

In 2020, 13 feed samples were taken at feed mills; 11 of these were from feed (5 were cattle feed) and two from raw materials for feed production. All of these samples were negative for PAP, except one sample of fish meal which contained fish particles.

Animals

Passive surveillance

In 2020, 10 bovines were examined due to clinical suspicion, all with negative results.

Active surveillance

In 2020, 8998 samples were examined for BSE. All samples were negative. Of these samples 8817 were from fallen stock, 39 samples were from animals with remarks at ante-mortem inspection before slaughter and 142 samples were from emergency slaughtered animals.

DISCUSSION

No cases of BSE were detected in Sweden in 2020. The increased number of clinical suspicions in 2018, 2019 and 2020 compared to previous years is the result of substantial efforts to detect and notify animals with clinical signs compatible with BSE. There has previously been a long trend of decreasing number of clinical suspicions compared to the years during the peaks of the BSE crisis, which can be explained by a lower degree of awareness among farmers and veterinarians when there is less media reporting about the disease.

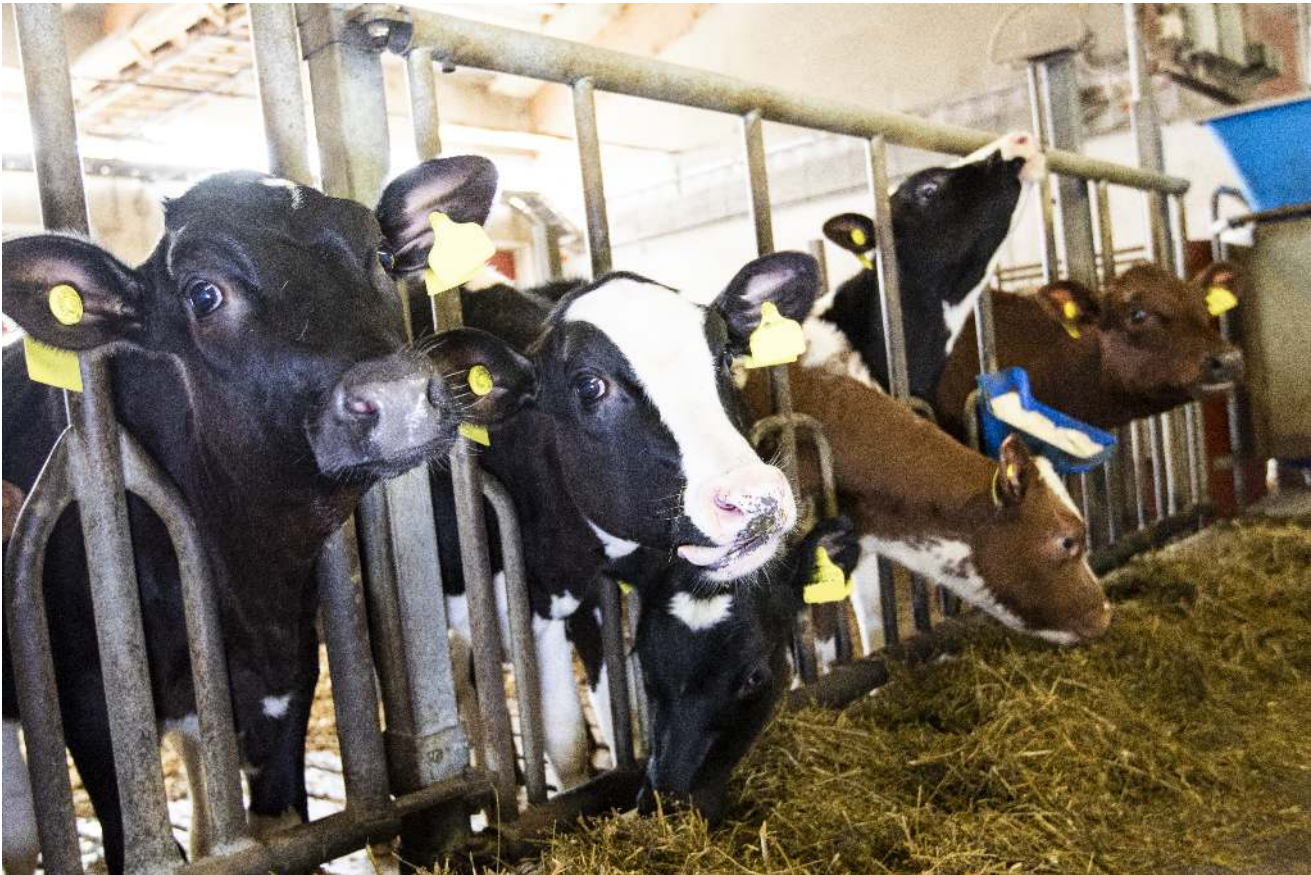
Reports of prion transmission studies, including several passages in different species, have shown that prion strains do not always remain stable through these passages. The source of the large epidemic of classical BSE has not been determined and atypical cases cannot be excluded as the source. Thus, the atypical cases could be a potential source of a new epidemic. As the number of cases of classical BSE is decreasing within the European Union, surveillance is decreasing, and suggestions have been made to once again allow the use of MBM in feed within the EU. However, strict separation and bans of these feeding practices must be kept in place to avoid any possibility of recirculation of BSE-prions, if the disease agent were to enter the system again. Sampling of feed needs to be at sufficient levels to ensure compliance with bans. However, the current number of samples is low and the ability to detect contamination in the feed system is therefore limited. Recent international reports of a few cases of classical BSE in young animals, born long after implementation of the strict feed ban, either indicates problems with the ban, or there are other causes of classical BSE that we do not yet understand.

Due to the long-term effect of preventive measures, resulting in a significant decrease of cases of classical BSE on European and global level, a revision of the current surveillance requirements on EU and OIE-level is ongoing and motivated. It is suggested to decrease the number of animals sampled as large-scale sampling is not an efficient way to prevent a new BSE crisis. However, keeping feed-bans and controls in place to avoid recirculation of prions is still relevant to avoid a new BSE crisis.

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Bovine viral diarrhoea



The fact that Sweden has been free from bovine viral diarrhoea since 2014 is very important for cattle health in the country. Photo: Therese Selén.

BACKGROUND

Bovine viral diarrhoea (BVD) is caused by bovine viral diarrhoea virus (BVDV), which is classified in the genus *Pestivirus* and the family *Flaviviridae*. Cattle are the primary host of BVDV, but most even-toed ungulates are likely to be susceptible to the disease. Cattle that are persistently infected serve as a natural reservoir for the virus. The virus may spread between animals via direct or indirect routes. A voluntary surveillance and control programme with the objective to eradicate BVD without vaccination was launched by the Swedish Dairy Association in 1993. The government and the farmers share the costs for sampling and testing. Since June 2001, there is also a compulsory control programme requiring all cattle herds to be tested for BVDV on a regular basis. Since 2014, Sweden is considered free from BVD.

DISEASE

BVDV may induce disease of varying severity, duration and clinical signs after an incubation period of 6–12 days. Fever, depression, respiratory distress, diarrhoea are typical signs of acute BVD. In pregnant cattle, infection may result in reproductive failure such as abortion, stillbirth or the birth of calves that are persistently infected with the virus. A more

uncommon form of BVD is mucosal disease, that may occur in an acute or chronic form in persistently infected animals. At the herd-level, the main impact of BVDV infection is often related to its immunosuppressive effects which commonly is expressed as problems with respiratory and gastrointestinal disease among calves and youngstock.

LEGISLATION

BVD is a notifiable disease according to SJVFS 2013:23. The voluntary control is regulated through SJVFS 2015:17 and the compulsory control in SJVFS 2011:17.

SURVEILLANCE

Surveillance of dairy herds is performed by sampling bulk milk in conjunction with milk quality testing. The laboratory gets an order from Växa Sverige (the former Swedish Dairy Association) about which herds to sample. All samples are marked using bar code labels. Surveillance of beef herds is performed by blood sampling at slaughter. Field testing can also be carried out as a backup component if herds to be tested cannot be accessed through the abattoir or through sampling of bulk milk.

Since 2018 the BVD surveillance is based on a risk-based design where herds are individually categorised based on the number of herds they have purchased from and sold

to during the preceding 12-month period (Table 4). The status of each herd is updated 1st of January each year. The system is set to order samples from high-risk herds twice a year, medium risk herds once a year and low risk herds randomly until the total number in the programme is reached. Sampling is carried out provided that the herd has sent animals to slaughter and that there is milk sent for milk quality testing. The sampling is distributed over the year.

The scheme is designed to demonstrate freedom from infection at a herd design prevalence of 0.2%, with 99% confidence. The within-herd design prevalence is set to 30%. In case of re-appearance of BVD, herds that are infected will be screened, and persistently infected virus carriers identified and removed. Details on numbers of samples and herds tested 2020 are given in Tables 5 and 6.

Diagnostic testing is performed at the National Veterinary Institute. For screening, an indirect antibody ELISA (SVANOVIR[®] BVDV-Ab ELISA, Svanova) is used on serum, milk and bulk milk samples. Presence of virus is analysed by an in-house IPX (immunoperoxidase) test or PCR tests.

RESULTS

The outcome of antibody testing of bulk milk, slaughter, and field samples tested in 2020 is given in Table 5. As shown in Table 5, four blood samples from beef-cattle herds and one bulk milk sample were antibody positive during the year. Two of the positive blood samples came from older animals that had been infected as young and had also been previously tested as antibody positive. Younger animals in these herds were tested negative. The remaining two beef and the one dairy herd were further sampled with negative results. In 2020, no newly infected herds were identified, and no virus positive animals were born.

DISCUSSION

All herds in Sweden were affiliated to the voluntary or compulsory programmes during 2020. At the end of the year, no herd was diagnosed as having an ongoing BVDV-infection. A newly infected herd has not been detected since 2011, and the last virus positive animal was born in an infected dairy herd in 2012. Since 2014, Sweden is considered free from BVDV. Continued surveillance is necessary to maintain confidence in freedom from the disease.

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Table 4: Risk-based evaluation of herds eligible for sampling of bulk milk or blood.

Livestock purchased from	Livestock sold to		
	< 2 herds	2–4 herds	> 4 herds
0–4 herds	Low	Medium	High
> 4 herds	Medium	High	High

Table 5: Total numbers of samples with different contents of bovine viral diarrhoea virus antibodies tested in 2020.

Sample type	Class/Finding	Herds	Animals
Bulk milk	0–1 ^A	2338	-
Bulk milk	2–3 ^A	1	-
Blood sample at slaughter	Negative	-	6741
Blood sample at slaughter	Positive	-	4
Field sample	Negative	-	27
Field sample	Positive	-	0

^A Class 0–1 = no or very low levels of antibodies; Class 2–3 = moderate or high levels of antibodies. (Based on Niskanen, 1993)

Table 6: Dairy and beef herd results from testing of bovine viral diarrhoea virus antibodies in bulk milk or blood samples in 2020 divided by herd level risk.

Herd level risk ^A	Herd numbers (N)	Production type	
		Dairy	Beef
<i>Low risk</i>	N of herds	2348	7655
	N of herds tested	952	1457
	N positive	1	2
<i>Medium risk</i>	N of herds	1294	2031
	N of herds tested	905	815
	N positive	0	2
<i>High risk</i>	N of herds	268	445
	N of herds tested	268	271
	N positive	0	0

^A Based on the number of herds they have purchased from and sold to during the preceding 12-month period.

Brucellosis

BACKGROUND

Brucellosis is caused by zoonotic, gram-negative bacteria belonging to the genus *Brucella*. Most human cases are caused by four species, each having a preferred animal host. *Brucella melitensis* occurs mainly in sheep and goats, *Brucella abortus* in cattle, *Brucella suis* in pigs and *Brucella canis* in dogs. The infection is transmitted by contact with placenta, foetus, foetal fluids and vaginal discharges from infected animals and may also be found in milk, urine, semen and faeces. *In utero* infections occur, but venereal transmission seems to be uncommon. Humans are usually infected through contact with infected animals or contaminated animal products, such as cheese made of unpasteurised milk. Brucellosis was eradicated from the Swedish cattle population during the first half of the last century. The last Swedish bovine case was recorded in 1957. Sweden is officially free from both *B. abortus* and *B. melitensis*. *B. suis* has never been reported from Sweden. Brucellosis in humans has been a notifiable disease in Sweden since 2004. Between 4 and 19 human cases have been reported annually and the majority of cases are travel-associated or have acquired the infection via consumption of products from countries where brucellosis is endemic. Since 2010 there has been approximately one domestic case reported annually. Predominantly these cases have, or were suspected to have, consumed unpasteurised milk products from endemic countries.

DISEASE

Animals

In animals, brucellosis mainly causes reproductive disorders such as abortion, orchitis and epididymitis. Arthritis is occasionally seen in both sexes. Systemic signs and deaths are rare, except in the foetus or newborn animal. The period between infection and abortion or other reproductive signs is variable. Infected asymptomatic females may shed the organism in milk and uterine discharges.

Humans

B. melitensis is considered to be the most severe human pathogen in the genus. Brucellosis in humans is commonly characterised by fever periods that wax and wane (undulant fever) with headache, malaise and fatigue. Untreated brucellosis can continue for months and progress to meningitis, cardiac infections, bone and joint infections. If left untreated the mortality rate is around 2%.

LEGISLATION

Animals

Brucellosis in food-producing animals is included in the Swedish Act of Epizootic diseases (SFS 1999:657 with amendments). Vaccination is prohibited and notification of suspect cases is mandatory. Sweden's bovine brucellosis free status has been officially stated in EU legislation since 1994, Decision 2003/467/EC. Ovine brucellosis is covered

by Directive 91/68/EEC. Sweden was declared officially free from brucellosis in sheep and goats in 1995, stated in Decision 2001/292/EC.

Current surveillance standards for bovine and ovine brucellosis are given in the EU legislation, Directive 64/432/EEC and Directive 91/68/EEC, respectively.

Brucellosis in non-food-producing animals is not included in the Swedish Act of Epizootic diseases but is still notifiable.

Humans

Brucellosis has been a notifiable disease since 2004 according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2013:634).

SURVEILLANCE

Animals

The purpose of the surveillance activities is to document freedom from bovine and ovine brucellosis in Sweden in accordance with the EU legislation, and also to document freedom from the disease in the Swedish pig population. The Swedish Board of Agriculture finances the surveillance, which is planned and executed by the National Veterinary Institute. Since the start of the screenings, no samples have been confirmed positive. All diagnostic testing is performed at the National Veterinary Institute. Bovine samples (serum and milk) are tested with an indirect ELISA (serum: SVANOVIR® *Brucella*-Ab Indirect ELISA or IDEXX Brucellosis serum, milk: IDEXX, Brucellosis Antibody Test Kit), and porcine, ovine and caprine samples (serum) are tested with the Rose Bengal Test (RBT). In case of positive reactions in the ELISA or RBT, serum samples are confirmed with a Complement Fixation Test (CFT). For positive bovine milk samples, serum samples are requested for re-testing with the ELISA.

Diagnostic tests for animals with clinical signs suggesting brucellosis or animals that are to be exported/imported will often be tested with the same diagnostic tests as used in the surveillance programme. Samples from animals (foetuses) included in the enhanced passive surveillance of aborted foetuses (see the chapter "Examinations of abortions in food producing animals" on page 134) are submitted to bacteriological culturing. Rapid Slide Agglutination Test (RSAT) is the most common test for dogs. A positive case is defined as an animal from which *Brucella* spp. has been isolated, or in some cases an animal with a confirmed positive serological reaction.

Humans

Diagnosis of human cases is made by real-time PCR, serology and culture. Positive colonies are investigated by MALDI-TOF and always tested for antibiotic resistance with broth microdilution.



Brucella melitensis is common in many countries in southern and eastern Europe. Photo: Erika Chenais.

Passive surveillance

Animals

Suspicious based on clinical signs in food producing animals must be reported to the Swedish Board of Agriculture and will be subsequently investigated. In addition, culture for *Brucella* spp. is included in the enhanced passive surveillance of aborted fetuses of ruminants and pigs, see the chapter “Examinations of abortions in food producing animals” (page 134).

Brucellosis in dogs is not included in the Swedish Act of Epizootic diseases and the zoonotic potential of *B. canis* is considered to be significantly smaller than that of *B. abortus*, *B. melitensis* or *B. suis*. Nevertheless, confirmed cases of infection with *B. canis* are notifiable and cases have also been investigated and put under restrictions by the Swedish Board of Agriculture.

Humans

Notification of human cases is mandatory and, surveillance is based on identification of the disease by a treating physician or by laboratory diagnosis. Both are obligated to report identified cases to the regional and national level to enable further analyses and adequate intervention measures.

Active surveillance

Animals

Screening for *B. abortus* has been conducted regularly in Sweden since 1988, for *B. melitensis* since 1995 and for *B. suis* since 1996.

Serological testing of all susceptible species prior to export, and in bulls and boars at semen collection centres, adds to the active disease surveillance of *Brucella* spp.

Surveillance for brucellosis in cattle

Since 2010 this sampling is conducted every third year and was thus not performed in 2020. From 1997 and onwards, the sampling has encompassed approximately 3000 samples (bulk milk and/or serum samples; each year 1997–2010, every third year from 2010 and onwards) for antibodies against *B. abortus*. Samples are selected by systematic random sampling of every second serum and milk sample collected in the surveillance programmes for bovine viral diarrhoea and enzootic bovine leucosis.

Sample size is calculated on a yearly basis to reach a probability of freedom of 99% at the end of the year for dairy cattle and beef cattle populations separately. To reach this target, 1000 bulk milk samples from dairy herds and 2700 serum samples from beef cattle herds are required.

Surveillance for brucellosis in sheep and goats

Serum samples are tested for antibodies against *B. melitensis*. The sheep serum samples are collected within the surveillance programme for Maedi/Visna and the goat serum samples collected within the Caprine Arthritis Encephalitis programme. The samples are selected by systematic random sample by collecting the first 5 samples submitted from each herd in these surveillance programmes.

The ovine and caprine brucellosis surveillance of 2020

was designed with a between-herd design prevalence of 0.2%, a within-herd prevalence of 40% and a risk of introduction of 1 in 25 years. Sample size is calculated on a yearly basis to reach a probability of freedom of 95% at the end of the year. To reach this target, 2000 samples (five samples per herd from 400 herds per year) is required.

Surveillance for brucellosis in pigs

From 1996 until 2008 approximately 3000 serum samples from pigs were tested for antibodies against *B. suis* each year. Beginning in 2009, serum samples are tested every second year, and thus this sampling was not performed in 2020. Serum samples are collected within the surveillance programmes for Porcine reproductive and respiratory syndrome and Aujeszky's disease. The samples are selected by systematic random sample by collecting the first sample submitted from each herd in this surveillance programme. Sample size is calculated on a yearly basis to reach a probability of freedom of 99% at the end of the year. To reach this target, 750 samples from 750 herds are required.

RESULTS

Passive surveillance

Animals

During 2020, no clinical suspicions of brucellosis were reported in any food-producing animal species.

Within the surveillance of aborted foetuses, 21 bovine, seven ovine, two caprine, and 20 porcine foetuses were examined for *Brucella* spp. All samples were negative.

Humans

In 2020, seven human cases of brucellosis were reported, which is less than the average number (n=13) during the last ten-year period. The low number can probably partly be explained by less travelling abroad due to the COVID-19 pandemic and thus less imported cases. The age and gender distributions (median age 52 years, spread 6–74 years, three female cases) were comparable with previous years. Five

cases were reported to have acquired their infections in Iraq, one in Ethiopia and for one case the country of infection was unknown. Thus, there were no domestic cases reported. For three cases unpasteurised dairy products were indicated as the probable source of infection, which has been the most common source of infection for brucellosis in recent years as well. As in previous years, *Brucella melitensis* was identified in all cases. All retrieved isolates were susceptible to relevant antibiotics for treatment.

Active surveillance

Animals

During 2020, 2072 ovine and caprine serum samples from 397 individual holdings were analysed for *B. melitensis*. All these samples were negative, assuring sustained freedom from *B. melitensis* in the ovine and caprine population. All samples from the serological testing prior to export and from bulls at semen collection centres were also negative.

DISCUSSION

In summary, *Brucella* infection was not detected in cattle, sheep, goats or pigs during 2020. The long standing and extensive serological screenings performed without finding any infection accompanied by the additional enhanced passive surveillance in aborted foetuses from food-producing animals and the very low number of human cases, only occasionally domestically acquired, confirms that *Brucella* is not present in Swedish food-producing animals.

An unknown number of stray dogs from countries where *B. canis* is endemic are brought into Sweden every year. It is important to be aware of the risk this group of dogs represents, for *Brucella* infection as well as for other diseases. Imported non-stray dogs, or dogs mated abroad are seen as a risk factor for introduction of *B. canis* into Sweden as well. During the past nine years, seven dogs have tested positive for *B. canis* using bacterial culture and/or serology. All these dogs were imported or had close contact with imported dogs.

Campylobacteriosis



Consumption and handling of chicken meat are the most important sources of campylobacteriosis in humans. Therefore, measures to decrease the prevalence in chicken and chicken meat are pivotal. Photo: Bengt Ekberg/SVA.

BACKGROUND

Thermophilic *Campylobacter* species (spp.) are the most common causes of human bacterial gastroenteritis in many countries. A majority of infections are caused by *C. jejuni*, followed by *C. coli* and a few by other *Campylobacter* spp.

Birds are considered the principal reservoir for thermophilic *Campylobacter* spp. although the intestinal tract of many other animals can be colonised by these bacteria. *Campylobacter* spp. are excreted in faeces. *Campylobacter* spp. are fragile organisms but can survive in freshwater for longer periods. The infectious dose for humans is low. Most European countries have a seasonal peak of *Campylobacter* prevalence or incidence in the summer months, both in chickens and humans. Risk factors for infection include consumption or handling of undercooked contaminated meat products (especially poultry), consuming contaminated unpasteurised milk and other dairy products, drinking from contaminated water supplies, travelling abroad, and having contact with farm animals and pets.

Since 1997, the incidence of human campylobacteriosis in Sweden has varied between 65 and 110 cases per 100 000 inhabitants (Figure 5). Most cases are infected abroad, but in 2014–2018 the proportion of domestic infections increased

due to several major outbreaks caused by domestically produced chicken meat. The COVID-19 pandemic has resulted in both a record low incidence of campylobacteriosis and a record high proportion of domestic infections in relation to infections retrieved abroad in 2020.

DISEASE

Animals

Asymptomatic carriage of thermophilic *Campylobacter* is common in several animal species, including poultry species, cattle, pigs, sheep and dogs. The prevalence is higher in younger animals.

Humans

Campylobacteriosis is an acute, usually self-limiting enteric disease that resolves within a week. In some individuals, the symptoms last longer. The symptoms are mild to severe: diarrhoea, fever, abdominal pain, nausea and malaise. The infection can be complicated by reactive arthritis, irritable bowel syndrome as well as the neurological disorder Guillain-Barré syndrome.

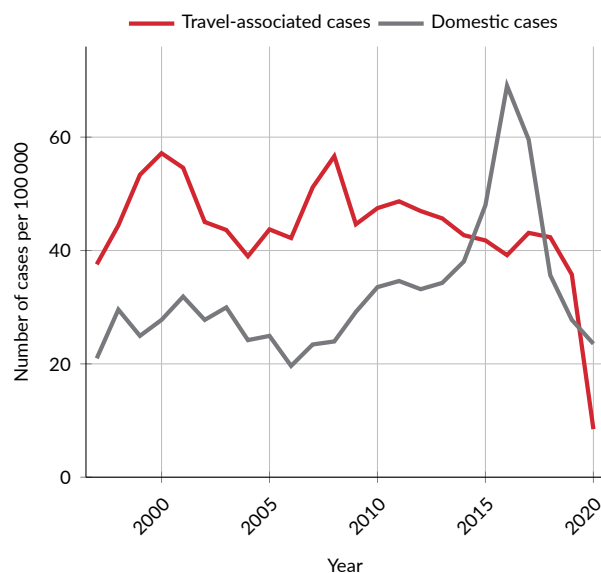


Figure 5: Incidence (per 100 000 inhabitants) of notified human cases of campylobacteriosis in Sweden, 1997–2020. Travel-associated cases are those where the patient has reported travel to another country during the incubation period prior to clinical presentation. Domestic cases are patients that have not recently travelled outside Sweden.

LEGISLATION

Animals

Findings of thermophilic *Campylobacter* spp. in meat-producing poultry are notifiable in Sweden, according to SJVFS 2012:24. In addition, *Campylobacter fetus* subsp. *venerealis*, which causes bovine genital campylobacteriosis, is notifiable.

Food

Detection of *Campylobacter* spp. in food is not notifiable. From 2018 and onwards, food business operators at slaughterhouses are obliged to sample neck skins of broilers for quantitative analyses of *Campylobacter* according to regulation (EG) 2073/2005 on microbiological criteria for food-stuffs. As a minimum, the Swedish Food Agency requires that weekly samples be taken from June through September.

Humans

Infection with *Campylobacter* is notifiable according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2013:634). A laboratory confirmed case can also include cases with samples that are only positive by PCR i.e. where no isolate has been obtained.

SURVEILLANCE

Animals

The Swedish Poultry Meat Association has operated a monitoring programme for broiler chicken since 1991. The programme is mainly financed by the Swedish Board of Agriculture (SJVFS 2015:17, K152) and the goal is to achieve an overall annual *Campylobacter* prevalence of less than 10% in slaughter batches of chicken. Prior to 2017, the goal was 5%. In 2017, the guidelines for the programme were reviewed.

The programme covers more than 97% of the broilers slaughtered in Sweden. Since 2006, sampling is performed by collecting intact caeca from 10 birds per sampled slaughter batch at the major slaughterhouses. In 2020, seven slaughterhouses delivered samples. When the flock is slaughtered at more than one time point and the time interval between the slaughter batches is longer than four days, samples are taken from both batches, otherwise only from one of the batches. The caeca are pooled into one composite sample per batch and analysed according to ISO-10272 part 1.

Since 2017, all *Campylobacter* isolates collected during two periods of 2.5 weeks, starting week 8 and week 31, have been subjected to whole genome sequencing (WGS). Those periods have been selected to precede the collection of human domestic isolates.

Food

There is no official surveillance programme for *Campylobacter* spp. in food. National and local authorities may perform sampling as a part of extended official controls or targeted projects.

Since 1 January 2018, slaughterhouses are obliged to sample neck skins from poultry carcasses for *Campylobacter* analyses using a culture-based method (ISO 10272-2 or alternative methods validated against the standard method), according to regulation (EC) No. 2073/2005. A limit of 1000 CFU/g applies to a set of 50 pooled samples derived from 10 consecutive sampling sessions. In 2020, the regulation allowed up to 30% of the samples to exceed the limit.

Humans

The surveillance in humans is based on identification of the disease by a physician and/or by laboratory diagnosis (i.e. passive surveillance). Physicians and laboratories are obliged to report to the regional and national level to enable further analyses and adequate intervention measures.

Since 2017, the Public Health Agency of Sweden requests isolates from all domestic cases reported during selected periods in March (low season) and August (high season) for whole genome sequencing analysis (WGS). As a conventional nomenclature tool, the Multi Locus Sequence Typing (MLST) type, i.e. ST-type, is defined by WGS. Single nucleotide polymorphism (SNP) analysis is used to compare human isolates to identify clusters and can also be used for outbreak investigations. The aims of the typing are to assess the diversity of domestic strains and identify clusters. The long-term goal is to use the data to evaluate efforts to lower the level of domestic incidence of campylobacteriosis attributed to food borne sources.

RESULTS

Animals

In 2020, thermophilic *Campylobacter* spp. were detected in 228 (5.1%) of the 4496 broiler chicken batches tested at slaughter (Figure 6), which is at the same level as in 2019 and less than in years prior to 2019. Among the slaughter batches

at the four largest slaughterhouses, which cover 97.2% of the slaughtered chicken, *Campylobacter* spp, was detected in 4.5% of them. The monthly prevalence of *Campylobacter* in chicken slaughter batches varied between 0.0% (April) and 12.9% with the highest prevalence in August. The prevalence of *Campylobacter* in incoming batches varied between slaughterhouses. The monthly number of chickens from *Campylobacter* positive slaughter batches varied as well. Between July and October approximately 4.5 million chicken originated from *Campylobacter* positive slaughter batches (Figure 7).

In March 2020, only three isolates of *Campylobacter* were retrieved for sequencing. Typing of isolates from August to October confirmed that *Campylobacter* had been spread between chicken farms, most probably during thinning (see Outbreaks).

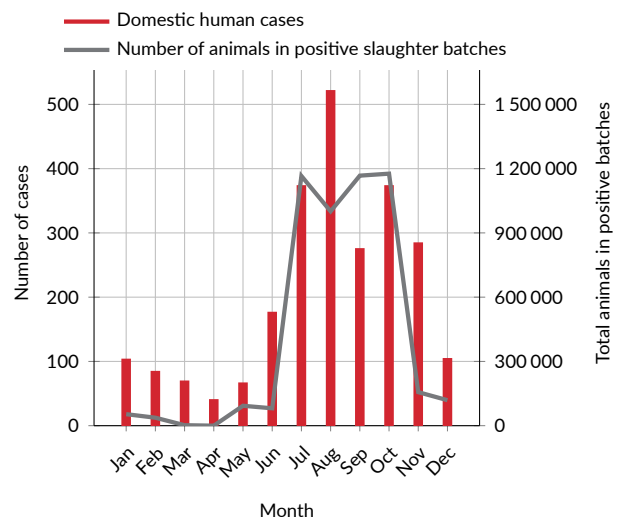


Figure 7: Number of notified domestic cases of human campylobacteriosis, along with the proportion of *Campylobacter*-positive broiler batches, broken down per month in 2020.

Food

In 2020, national and local authorities took 58 samples from different types of food. *Campylobacter* was detected in three

IN FOCUS: Occupational risk of *Campylobacter* infection

In Sweden, four abattoirs, located in four counties, dominate the chicken slaughter. These abattoirs account for over 97% of the domestic chicken meat production. As for data on human cases of campylobacteriosis, the clinical notifications always include information on the county of residence and allows for reporting details about the route of transmission and occupation, although this information is often missing. A closer examination of the clinical reports from notified cases between 2007 and 2020 from these four counties shows 168 reports of cases with an occupational connection to an abattoir. In 64% of the reports (n=108), only “work at abattoir” or other unspecific descriptions of the profession were given. In 14% of the reports (n=24), one of several occupational tasks related to the production at the abattoir was stated. However, the single most reported task was “transport of chicken” (n=20) including loading/unloading, transport and cleaning related to both live animals and of chicken meat products.

Other professions with a suspicion of the source of the infection being an abattoir were mainly related to occupations in construction and/or maintenance (n=15). For most of the cases within these occupational categories, the infection was suspected to have occurred during a temporary work at the abattoirs.

There are regulations that describe the responsibility of the employer to minimize the risk of infection. Regular risk assessments and education of employees about risks and protection are examples of tools to minimize the risk of infection at the workplace. The clinical reports show that a high awareness of the occupational risk of campylobacteriosis for different occupations all through the production chain is pivotal.

The strong association between the prevalence of *Campylobacter* in broiler flocks and infections among humans makes monitoring in broiler flocks an important tool for early warning. In addition, information on occupational infections can provide early information, considering the “time gained” between production and consumption of poultry meat. In two recent Swedish outbreaks, such information has been useful. In 2018, a regional medical officer reported that several employees at an abattoir had fallen ill, which was the prelude to an extensive outbreak caused by contamination at a large hatchery. Similarly, several illnesses among abattoir employees were noticed in summer 2020 (see “Outbreaks”) which could thus support suspicions of an outbreak on the rise despite comparatively few reports of campylobacteriosis during 2020 and especially since the start of the COVID-19 pandemic.

samples taken at retail within the framework of a control project. Two of these samples were from broiler meat and one from minced bovine meat. The sample of bovine meat and one of the samples of broiler meat were taken at a store which prepared both bovine and broiler meat, indicating a possibility for cross-contamination at retail level.

Food business operators at seven slaughterhouses collected 907 pooled neck skin samples according to regulation (EC) No. 2073/2005. Test results at all slaughterhouses were satisfactory according to the legislation, and only seven (0.8%) of the 907 samples exceeded the limit of 1000 CFU/g.

Humans

A total of 3434 cases of campylobacteriosis were reported in 2020. Of the reported cases, 71% (2444 cases) were domestic. The incidence of domestic cases decreased by 15% from the year before to 23.5 per 100,000 inhabitants. Hence, the domestic incidence was like the levels seen over a decade ago. The incidence of travel-related cases was a record low 8.5 cases per 100 000 inhabitants, a decrease of 76% from 2019, which also makes the overall incidence the lowest (33.1) since the current reporting system was introduced in 1997 (Figure 5). As many as 82% of travel-related cases in 2020 were reported during January-March, before travel restrictions were introduced due to the COVID-19 pandemic. The domestic cases were fewer for most of the year but an outbreak that lasted from the end of the summer and throughout the autumn led to a relative increase in the number of cases that during October and November were more than usually.

For the domestic cases in 2020, the median age was 47 years with a range from 0 to 96 years. The incidence was highest in the age group 1–4 years, followed by people aged

50–69 years, both of which are age groups that historically tend to have comparatively high proportions of cases. More men (58%) than women were reported with campylobacteriosis.

In the microbial surveillance programme at the Public Health Agency of Sweden, isolates from domestic cases were collected during weeks 11 and 12 and in weeks 32–35. In March, 55 isolates were characterised of which only two clustered, which indicates that most cases were sporadic. In August, 335 isolates were characterised, and 36 percent (n = 119) clustered with two or more isolates. The largest cluster belonged to ST-19 (n = 55) which was the dominant clone during an outbreak in the autumn (see the text on Outbreaks). The second largest cluster (ST-45, n = 21) was also linked to the outbreak. During the collection in August, isolates were received from people with reported occupational infections within the chicken production. These individuals carried isolates from identified outbreak clones.

Human campylobacteriosis cases versus positive chicken slaughter batches

The number of human domestic cases and the number of animals from *Campylobacter* positive chicken slaughter batches were compared during 2020. The comparison shows a clear covariation over the year with the highest numbers in the summer and autumn and the lowest in winter and spring (Figure 7).

OUTBREAKS

From having been at very low levels from the beginning of the year and especially since the start of the COVID-19 pandemic, an unexpectedly large increase in the number of people infected with campylobacter was noticed in early August. In parallel to this increase, several cases of

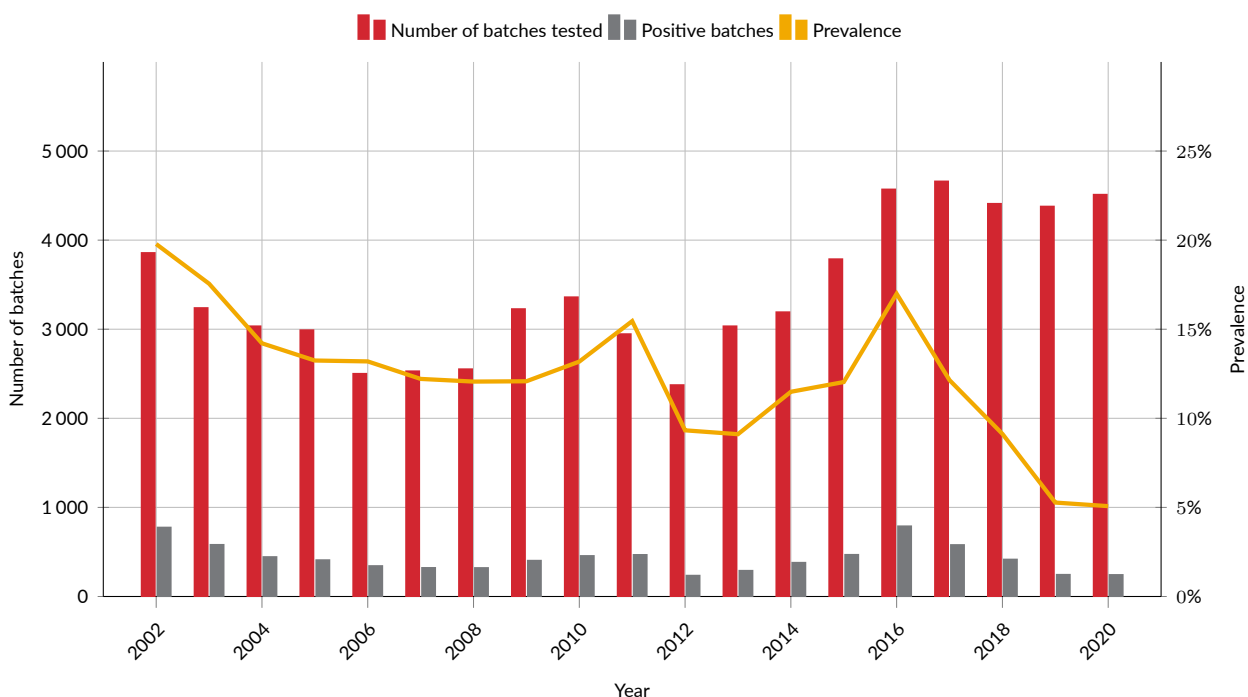


Figure 6: Prevalence of *Campylobacter* in slaughter batches of broiler chicken in 2002–2019.

infection were observed among abattoir employees at one of the large slaughterhouses. It also turned out that there had been an increase in the proportion of *Campylobacter*-positive slaughter batches of chicken from the second half of July, and this mainly among flocks delivered for slaughter to this very same slaughterhouse. The number of positive slaughter batches remained high until October and a decrease in the number of human cases occurred in mid-November. One reason for the spread of *Campylobacter* among poultry flocks was dirty transport cages that carried the bacteria between chicken farms. One factor that may have made it easier for the bacteria to gain foothold at the farms is the practice of thinning.

The signal of increased human cases in August coincided with the collection of isolates within the national microbial surveillance program, which, therefore, was extended from two to four weeks. The same sequence types (ST-19, ST-45) dominated among isolates from human cases and chicken which confirmed the source of the outbreak.

DISCUSSION

The domestic incidence of campylobacteriosis was lower in 2020 compared with previous years. Most campylobacteriosis cases have been considered sporadic, but cluster analysis of isolates typed in recent years with WGS indicates that a large part of the cases could indeed be part of outbreaks. Many of these outbreaks appear genetically linked to isolates from retail poultry meat.

In 2020, the annual prevalence of *Campylobacter* in chicken slaughter batches was at the same level as in 2019 but lower than in previous years (Figure 6). The correlation between human cases of campylobacteriosis and *Campylobacter*-positive broiler batches further underscores the need for preventive measures. *Campylobacter* prevalence varies considerably between slaughterhouses, with only a few findings at some and a higher prevalence at others. During the last ten-year period, the Swedish chicken production has increased by approximately 30% and the share of fresh chicken meat has increased compared to frozen meat. This has led to a higher amount of potentially contaminated chicken meat at the market, because *Campylobacter* are sensitive to freezing and therefore more common in fresh than in frozen meat.

Sampling of the neck skin for analysis of *Campylobacter* according to regulation (EC) No. 2073/2005 functioned well in most of the slaughterhouses concerned. The results show that no slaughterhouse in Sweden had any difficulties

in meeting the criterion in the regulation, which is set at a level that reflects the much higher prevalence of *Campylobacter* in broilers in many other EU member states.

Reducing *Campylobacter* prevalence at the farm level decreases the risk of human infection as well as the measures taken at slaughter. Over the years, applying strict biosecurity measures has decreased the number of *Campylobacter*-positive broiler slaughter batches in Sweden. The outbreaks of recent years have demonstrated that failures in the production chain may lead to an increase in human illnesses and illustrated the importance of biosecurity measures, not only at farm level but in the whole production chain.

Broiler carcasses are easily contaminated at slaughter, which necessitates that consumers apply good hygiene practices. Strict hygiene in the kitchen is essential to avoid cross-contamination between contaminated raw meat and food that is ready to eat.

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Chronic wasting disease

BACKGROUND

Chronic wasting disease (CWD) is a transmissible spongiform encephalopathy (TSE) affecting cervid species. The disease was first described in Colorado in 1967 and in 1978 identified as a TSE. The disease has spread and is now confirmed present in at least 26 states in the USA, and in three Canadian provinces (CDC, 2020). Through export of live cervids, CWD has also spread to South Korea.

Before 2016, CWD had not been reported in Europe. In spring of 2016, the first case in Europe was detected in wild reindeer (*Rangifer tarandus tarandus*) in the region of Nordfjella in Norway (Benestad et al., 2016). As a consequence of the finding, surveillance in Norway was intensified and this has so far (March 2021) resulted in the detection of the disease in 20 reindeer in two different wild reindeer areas. In addition, CWD has been found in eight old moose (*Alces alces*) and in one red deer (*Cervus elaphus*) in different locations. The cases in reindeer show similarities with the cases found in North America (e.g. several affected animals in the same flock, test positive in lymph nodes, although not identical) whilst the cases in moose and red deer have been shown to differ from the cases in reindeer (cases found in older animals only, samples test positive in brain and negative in lymph node). It is still unknown what this means in terms of differences in e.g. the disease transmission pattern, but it has been hypothesised that these “atypical” cases may be spontaneously occurring in older animals (Pirisinu et al., 2018).

Due to the detection of CWD in Norway, surveillance for CWD was mandatory in several EU member states, amongst them Sweden, in 2018–2020 (see Legislation and Surveillance).

In March 2018, the first case of CWD in Finland was reported. The case showed similarities with the cases in moose and red deer in Norway (Ruokavirasto, 2020). A similar case was reported from Finland in 2020.

The first three Swedish cases were detected in 2019. All cases were in elderly female moose, the first two (one in Arjeplog and one in Arvidsjaur) were both euthanised and sampled after displaying abnormal behaviour, both were estimated to be 16 years old. In accordance with EU legislation, an intensified sampling was carried out in the area during the following hunting (moose) and slaughter (reindeer) season and the third case, a female of at least 10 years old shot during normal hunt was detected within the intensified sampling. The cases show similar features with the cases reported from moose in Norway and Finland.

The wild cervid species in Sweden are moose, red deer, fallow deer (*Dama dama*) and roe deer (*Capreolus capreolus*), and many people are involved in hunting of these species. The farmed cervid species in Sweden are mainly fallow deer and a lower number of red deer, as well as a low number of moose. In Sweden, reindeer herding is an

essential part of the Sami culture; all reindeer are semi-domesticated and there are no wild reindeer. Wild cervid animals cross the border between Sweden and Norway. Some semi-domesticated reindeer also freely cross the border between the countries, i.e. the populations are not separated.

HISTORY

With exception of an EU regulated active surveillance in 2007–2010, and a retrospective study examining 270 frozen brains from cervids sent for postmortem between 2008 to the first part of 2016, surveillance in Sweden has historically only been passive, i.e. based on reporting of animals displaying clinical signs. However, since the disease has not been known to occur in Europe, the awareness of CWD has been low and as a consequence very few animals have been examined.

DISEASE

From what is known about strains of CWD present in North America, sometimes referred to as “classical” CWD, the incubation period is long, more than one year. The disease spreads through direct contact between animals, but also through body excretions that can contaminate and persist in the environment. The predominant clinical signs are behavioural changes, change of locomotion and loss of body condition. The disease is fatal.

Until recent years, the type of CWD described from North America was the only type known. But the strains detected in the Nordic countries differ from strains described from North America. There is accumulating support for the hypothesis that the cases in older moose may have a spontaneous rather than contagious origin, similar to what is observed in sheep (atypical scrapie/Nor98) and bovines (atypical BSE), and sporadic CJD in humans.

The currently accepted theory of TSEs, or prion diseases, is that they are transmitted through small prions (aggregated proteins with abnormal structural conformation). These prions induce a structural transformation and aggregation of normal prion proteins in the body of the recipient. The full details of these processes are not yet understood. Prions accumulate in body tissues, especially the brain where damage can be observed when studying tissue in a microscope. Within the group of prion diseases there are diseases where prions are excreted in body fluids (e.g. classical scrapie, and “classical” CWD) and are thus contagious. However, there are also prion diseases with spontaneous (without known cause) origin occurring in older individuals (e.g. atypical BSE in bovines or sporadic CJD in humans).

Due to similarities with BSE, which is linked to variant Creutzfeldt-Jakob disease in humans, and the known fact that many TSEs experimentally can be transmitted between several different species, there has been a suspicion that CWD may be a zoonotic disease. Currently, there is not

enough data to exclude that CWD could be zoonotic, however the risk is deemed to be very low (VKM 2016 and 2017, Waddell 2018). In areas where CWD is endemic, people are recommended not to consume animals displaying clinical signs consistent with CWD or animals with positive test results for CWD.

LEGISLATION

CWD is a notifiable disease under the Swedish Act of Epizootic diseases (SFS 1999:657, with amendments) and there is a scheme to compensate farmers for losses due to eradication measures. CWD is also regulated through the Regulation (EC) No 999/2001 of the European Parliament and of the Council on TSEs. The surveillance programme is regulated in the Commission Regulation (EU) 2017/1972 amending Annexes I and II to Regulation (EC) No 999/2001.

SURVEILLANCE

The EU-regulated surveillance programme, mentioned under “Legislation” above, started in January 2018. For the member states concerned, a minimum of 6000 animals are to be tested between the years 2018 and 2020. Samples shall be collected from wild, semi-domesticated and farmed/captive cervids. In Sweden, moose, red deer, roe deer and reindeer are included in the surveillance programme. Samples from wild cervids (moose, red deer, roe deer) are collected from fifty primary sampling units (PSU) covering the whole country. Samples from farmed cervids (red deer) and semi-domesticated cervids (reindeer) are collected from all red deer farms (n=130) and all Sami villages (n=51), the latter being the administrative unit for reindeer herding as well as a geographically defined area. All animals sampled must be over twelve months of age and preferably from a risk category, i.e. cervids found dead or diseased and road/train killed cervids which are assumed to have a higher probability of infection.

Brainstem and retropharyngeal lymph node samples are screened separately with Bio-Rad TeSeE short assay protocol (SAP), using the CWD addendum. Bio-Rad TeSeE Western Blot is used for confirmation of positive or inconclusive screening tests.

The CWD surveillance programme is run in collaboration between the National Veterinary Institute and the Swedish Board of Agriculture and is financed by the latter. Samples are analysed at the National Veterinary Institute, Uppsala, which is the National Reference Laboratory (Regulation (EC) 999/2001) for TSEs. Results of the testing are reported to the European Food Safety Authority by the Swedish Board of Agriculture, based on data provided by the National Veterinary Institute.

In accordance with EU legislation, an intensified sampling shall be carried out in the areas surrounding positive cases. The size of the area was determined by experts in cervid migratory patterns and experts in reindeer herding. The surveillance was designed to enable detection of a prevalence of 0.7% (detected prevalence in Nordfjella, Norway) with 99% certainty, assuming a test sensitivity of 70%, in each population in the area. In this sampling, healthy

slaughter and healthy hunted animals were included to increase the number of animals undergoing testing in the area. In 2019–2020 intensified sampling was done in around the cases detected in Arvidsjaur and Arjeplog, in 2020 Robertsfors was included.

RESULTS

The number of samples tested from 2016 to 2020 is detailed in Table 7.

In 2020, 27 cervids were sampled due to clinical suspicion of CWD (21 moose, 2 fallow deer and 4 roe deer). In total, 248 moose, 84 red deer, 71 roe deer, 4 fallow deer and 991 reindeer were examined for CWD at the National Veterinary Institute during 2020. Most of the moose and reindeer analysed were part of the intensified samplings in the county of Norrbotten, around the Arvidsjaur and Arjeplog cases, and the county of Västerbotten, around the Robertsfors case (Table 7). During 2020, 896 reindeer were sampled within the intensified sampling in Norrbotten and 98 moose were sampled within the intensified sampling in Västerbotten.

One positive case was detected in 2020 in Robertsfors municipality, it was in a female moose aged to 14 years (age estimated by counting annuli in dental cementum), shot because she had been observed limping. The moose was positive in brainstem but negative in lymph nodes, thus resembling the previous cases in old moose.

Further analyses to characterise these cases are ongoing, but so far there are diagnostic similarities between the Swedish and Norwegian cases in moose.

DISCUSSION

The number of animals examined before 2018 is limited and not well represented geographically. In January 2018, the surveillance programme (Regulation (EC) 999/2001) started. Information about the programme was sent to groups identified as suitable samplers, i.e. hunters, animal owners (reindeer and fenced red deer) and slaughterhouse personnel.

However, the number of samples received from the nationwide sampling has been relatively low. There are several reasons for this. The implementation of the programme has been complex, given several different species and categories of animals included. Also, the number of animals found dead or diseased which are preferred due to their assumed higher probability of infection, has been relatively small. The number of road-killed animals is quite high, but divergent interpretations of legislation related to work environment and taxation, related to minor compensation for sampling, has delayed the sampling of this group of cervids. It has therefore been decided to prolong the national surveillance.

Despite logistical challenges with weather-dependent slaughter in remote areas, far from postal service for sample submission, the intensified sampling which targets healthy animals have reached higher numbers of sampled animals and the proportion of hunted moose sampled during the hunt have been high.

As mentioned, the cases in moose in Norway, Finland and

Table 7: The number of animals tested for CWD per year in Sweden 2016–2020, including national surveillance and intensified sampling.

Year	Moose	Red deer	Roe deer	Fallow deer	Reindeer
2016	74	6	14	0	2
2017	191	6	13	8	21
2018	157	13	15	0	15
2019	854 ^A	31	73	5	1965 ^A
2020	248 ^B	84	71	4	991 ^C

^A The large increase in sampling in 2019 was due to the intensified sampling in the county of Norrbotten, which started that year.

^B 98 of the moose sampled in 2020 were sampled within the intensified sampling in the county of Västerbotten.

^C 896 of the reindeer sampled in 2020 were sampled within the intensified sampling in the county of Norrbotten.

Sweden differ from “classical” CWD cases; all have been detected in old female animals and prions have only been detected in the brain and not in lymph nodes. Further studies are ongoing to characterise these strains and to understand more about the epidemiology. As mentioned, it has been hypothesised that the CWD cases in older moose may not be contagious, but rather a spontaneous variant of CWD occurring in old animals (Pirisinu et al., 2018).

Consequently, the detection of three cases of CWD in moose in a limited geographical area in Sweden in 2019 (detected prevalence 0.4%) does not necessarily mean that a contagious variant of the disease is present in the region. The fact that cases were only found in relatively old animals and that prions were only detected in brain in screening tests, while not in lymph nodes, still fits the hypothesis of spontaneous cases in old animals. This region has a hunting management which leads to a relatively high proportion of old female moose in the local population. In general, most moose are harvested at a young age during hunting, and few animals reach the expected maximum life span of approximately twenty years. Fewer males reach an old age than females due to hunting practices.

The experience from North America is that “classical” CWD is very difficult to eradicate or control, and to have a chance to do this, early detection is needed while the prevalence is still low. If atype of CWD with the characteristics of “classical” CWD would be present or introduced into Sweden, it would have large negative consequences for reindeer, wild cervid populations and farmed cervids. Consequently, the disease could also have large consequences for people making their living from, or being involved in activities related to, these species. However, if the cases found in older moose in Norway, Finland and Sweden would in fact have a spontaneous origin, the disease could be expected to occur sporadically in all cervid populations, without leading to the same severe consequences as “classical” CWD. Further studies are crucial to increase the understanding of the epidemiology of the different CWD-types.

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Classical swine fever



The purpose of the surveillance programme for Classical swine fever (CSF) in Sweden is to document freedom from CSF in the pig population and to contribute to the maintenance of this situation by early detection of an introduction. In 2020, 2019 pigs were tested and found negative for the disease. Photo: Magnus Aronson.

BACKGROUND

Classical swine fever (CSF) is a disease of pigs caused by a pestivirus closely related to bovine viral diarrhoea virus and border disease virus. CSF is endemic in many parts of the world and is one of the most important diseases affecting pig production globally. The disease is endemic in parts of Asia, South America and on some Caribbean islands. In Europe, several large outbreaks of CSF occurred in the 1980s and '90s, including an extensive outbreak in the Netherlands, Germany, Belgium and Spain in 1997–1998. These outbreaks led to the implementation of highly effective control and eradication strategies. During the last 10 years there have only been sporadic reports of outbreaks of CSF in domestic pigs and cases in wild boar in the eastern parts of the EU, including Lithuania (2009, 2011) and Latvia (2012–2015). The last reported case of CSF in the EU was in 2015. Sweden, where CSF has not been diagnosed since 1944, was issued official status as a historically CSF-free country by the OIE in February 2015.

Classical swine fever virus is highly contagious and is transmitted by direct and indirect contact between animals. Wild boar can serve as a reservoir for the virus and there are several documented cases of outbreaks in domestic pigs caused by direct or indirect contact with wild boar. Feeding

pigs swill contaminated with CSFV has also resulted in the spread of the disease to new areas. Because of this, swill feeding of pigs is prohibited in the European Union.

DISEASE

CSF appears in three different clinical forms; acute, chronic and mild. The incubation period is 2–14 days and the acute form of the disease includes high fever ($<42^{\circ}\text{C}$), weakness, conjunctivitis, purple skin discolouration, diarrhoea and neurological signs. The acute form of CSF cannot be distinguished clinically from African swine fever (ASF). Chronically infected animals exhibit a more diffuse clinical picture with intermittent fever, anorexia and stunted growth. In the mild form, sow reproductive failure, including abortion, foetal mummification and stillbirths, is the main clinical sign. The mild form can also result in the birth of persistently infected piglets that initially appear healthy but shed large amounts of virus before becoming ill and dying several months later from “late onset CSF”.

LEGISLATION

CSF is included in the Swedish Act of Epizootic diseases (SFS 1999:657 with amendments) and the control of the disease is regulated in detail through Council Directive 2001/89/EC with amendments.

SURVEILLANCE

The purpose of the surveillance programme is to document freedom from CSF in the Swedish pig population and to contribute to the maintenance of this situation by early detection in case of an introduction. The National Veterinary Institute is responsible for surveillance design, sample analysis and reporting to the Swedish Board of Agriculture. Serological analyses for CSF, PCR analyses for the presence of CSF viral genome and CSFV culturing are performed at the National Veterinary Institute. CSF serology is done using a commercial kit (IDEXX® HerdChek CSFV Antibody Test Kit) and, in the case of a positive ELISA result, a serum neutralisation (SN) test for detection of antibodies against CSFV is performed for confirmation.

Passive surveillance

Because CSF is notifiable on clinical suspicion for both veterinarians and farmers, cases with clinical signs consistent with CSF are investigated following notification to the Swedish Board of Agriculture. The investigation may include sampling of sick or dead animals, examination of the herd for the presence of clinical signs and analyses of production results. Due to the similarity in clinical signs, samples are analysed for both CSF and ASF, which is a strategy that is strongly recommended by the EU.

In addition, PCR analysis for the presence of CSFV genome is included in the enhanced passive surveillance of aborted foetuses (see chapter “Examinations of abortions in food producing animals” on page 134).

Active surveillance

The surveillance was designed using a between-herd design prevalence of 0.5%, a within-herd design prevalence of 40% and a risk of introduction of 1 in 25 years. The number of samples needed to achieve a probability of freedom of 99% is calculated yearly, taking the surveillance results of previous years into account. For 2020, the calculated number of samples needed was 2000. Blood samples collected within the abattoir sampling component of the surveillance for porcine reproductive and respiratory syndrome (PRRS), carried out by Farm and Animal Health (see chapter “Porcine reproductive and respiratory syndrome” on page 66), were used for the active surveillance of CSF in domestic pigs. Two to three samples per herd tested for PRRS were also analysed for CSF.

In addition to the active surveillance of CSF in domestic pigs, active surveillance of CSF in hunted Swedish wild boar has been undertaken yearly since 2000 (see chapter “Infectious diseases in wild boars” on page 123).

RESULTS

Passive surveillance

Eight herd investigations following clinical suspicions of CSF in domestic pigs were carried out during 2020. In three herds, the primary clinical sign was the sudden, unexplained death of multiple animals within a short period of time. In four herds, findings during post-mortem examinations, including enlarged spleens and organ haemorrhages, prompted the herd investigations. In one herd, unexplained, bluish skin discolouration in otherwise healthy sows initiated the CSF investigation. During one herd investigation, post-mortem examination of pigs that died suddenly revealed a clear cause of death, unrelated to CSF, so further sampling and testing for CSF was not carried out. During the investigations in the other seven herds, samples were collected and analysed for CSF (and ASF). All samples were negative and all investigated herds were subsequently declared free from CSF.

Within the programme for enhanced passive surveillance of aborted foetuses, 21 foetuses from 11 herds were examined for the presence of CSF virus genome and all samples were negative.

Active surveillance

Serum samples from 2019 domestic pigs were analysed for the presence of antibodies for CSF in 2020. All samples were negative. Taking the surveillance outcome from previous years into account, the probability of freedom from CSF during 2020 was >99%.

DISCUSSION

The results from the active and passive surveillance for CSF in Sweden in 2020 add to the documentation of freedom from this infection in the Swedish commercial pig population. In recent years, the Swedish pig industry has undergone significant structural changes, leading to a rapidly declining number of herds and extensive changes in the market and in the habits of farmers. The active surveillance, in terms of planning design and number of samples, is therefore evaluated yearly and adjusted accordingly if needed. Although the EU is now free from CSF, occasional outbreaks in domestic pigs in countries close to Sweden and the extensive movement of products and people, including labour in the animal production sector, emphasise the continued need for both passive and active surveillance for CSF.

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Cryptosporidiosis

BACKGROUND

The unicellular parasites *Cryptosporidium* spp. belongs to the phylum Apicomplexa and can be either host specific or have a broad host range. Several *Cryptosporidium* species are clearly zoonotic, for example *Cryptosporidium parvum*, while the zoonotic potential is lower in other species.

The infective life stage, the oocysts, are transmitted between hosts via the faecal-oral route, sometimes involving vehicles such as food and drinking water. Oocysts are infectious immediately upon excretion with the host faeces, have the capacity to persist long periods in the environment and can withstand standard water treatment such as chlorination.

Cryptosporidium was first described in animals and was not officially recognised as a significant human pathogen until the early 1980s. Its global significance as a pathogen of infants and young children became clearer after the Global Enteric Multicenter Study (GEMS) in which it was determined to be the second leading cause of moderate to severe diarrhoea in infants and toddlers, only behind rotavirus. However, in Sweden reported cases of cryptosporidiosis are mainly adults 20–50 years and only approximately 10% are in the age group 0–4 years. *Cryptosporidium* spp. have been ranked as the fifth most important foodborne parasite globally, as well as in Europe.

DISEASE

Animals

Cryptosporidiosis in animals is of veterinary importance and may result in clinical morbidity, mortality, and associated production losses. However, different *Cryptosporidium* species infect different host species of animals and may or may not be of clinical relevance. The *Cryptosporidium* species can have a broad host range or be host specific, including having zoonotic potential. The zoonotic nature of various *Cryptosporidium* species means they may be of public health relevance, as humans can acquire the infection from animals, also when the animals have an asymptomatic infection. *C. parvum*, an important zoonotic *Cryptosporidium* species and the major species of clinical importance in Swedish cattle causes diarrhoea in young calves. The symptoms are pasty to watery diarrhoea, sometimes accompanied by inappetence, fever and dehydration. The animals most often recover spontaneously within 1–2 weeks. In some cases, the infection is fatal.

Humans

The disease in humans can range from asymptomatic to severe infection. The infectious dose is low, and the incubation period varies from 2–12 days. Symptoms, which normally last for up to 2 weeks, include moderate to severe watery diarrhoea, low-grade fever, cramping abdominal pain, nausea and vomiting.

IN FOCUS: *Cryptosporidium* chipmunk genotype I

Since 2018 the Public Health Agency of Sweden initiated a microbiological surveillance program for *Cryptosporidium* totally 43 cases of *Cryptosporidium* chipmunk genotype I have been identified in domestically acquired cryptosporidiosis. During 2020 totally 23 human cases were found, making *Cryptosporidium* chipmunk genotype I the second most common *Cryptosporidium* variant found in Sweden, although the vast majority of cases are still caused by *C. parvum*. *Cryptosporidium* chipmunk genotype I whose natural hosts are mainly chipmunks, squirrels and deer mice has also been identified earlier in humans in Sweden; eight sporadic cases between 2006 and 2017.

A small outbreak of cryptosporidiosis caused by *Cryptosporidium* chipmunk genotype I and a first confirmed case of zoonotic transmission of *Cryptosporidium* chipmunk genotype I from a red squirrel to a human has been identified within the surveillance program.

All samples included in the surveillance program for *Cryptosporidium* were investigated at the small subunit rRNA, the genetic marker used to determine species and genotypes of *Cryptosporidium*. When possible, further analysis was performed with sequencing of the polymorphic 60 kDa glycoprotein (*gp60*) gene to determine subtype. On all cases identified as *Cryptosporidium* chipmunk genotype I the same *gp60* subtype, XIVaA20G2T1 was identified. This subtype has only been reported from Sweden and has been found in both humans and in *Cryptosporidium* positive red squirrels, the natural host in Sweden.

In Europe only one human case of *Cryptosporidium* chipmunk genotype I, from France, has been reported outside Sweden, but the organism has been identified in red and grey squirrels as well as Pallas's squirrels from Italy. There are only red squirrels in Sweden and as all the isolates (humans and squirrels) harboured the same subtype, it is likely that the human cases were infected by this host. The prevalence of *Cryptosporidium* chipmunk genotype I among squirrels in Sweden is still under investigation.

SURVEILLANCE

Animals

The surveillance of *Cryptosporidium* spp. in animals is passive. Most knowledge about the prevalence in different animal host species, both domestic and wild, comes from project-based investigations and studies.

Humans

Notification of human cases is mandatory and surveillance is based on identification of the disease by treating physician and/or by laboratory diagnosis. Both are obliged to report to the regional and national level to enable further analyses and adequate intervention measures.

In 2018, the Public Health Agency of Sweden initiated an annual microbiological surveillance programme with the aim of determining species and subtypes of all domestic cryptosporidiosis cases in order to better understand the national epidemiology. Starting in 2020, the programme was changed from annual collection to a four-month period (1 Aug – 30 Nov) when most human cases are reported.

LEGISLATION

Animals

Detection of *Cryptosporidium* spp. in animals is not notifiable.

Humans

Cryptosporidiosis is notifiable according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2004:255).

RESULTS

Humans

In 2020, a total of 641 cases of cryptosporidiosis were reported corresponding to an incidence of 6.2 cases per 100 000 inhabitants. (Figure 8). Among reported cases the median age was 37 years (1–97 years) and 57 percent were women (n=366/641). In 2020, the majority of cases were reported infected in Sweden (n=553), 72 cases were infected abroad and for 16 cases information was missing. Nearly half of the reported domestic cases (48%) were reported during January (n=86), July (n=68) and August (n=114). A summer peak is usually seen especially in late summer. Many reported cases in January were a continuation of a national increase of reported cases late 2019 where different sources of vegetables as sources of infections were investigated. Of 72 travel-related cases, 79% (n=57) were reported January-March with Thailand (n=8) and Portugal (n=7) as the most common destinations. Due to COVID-19 restrictions travel related cases decreased sharply after March.

274 positive samples were further analysed and the *Cryptosporidium* spp. were genotyped as part of the microbiological surveillance program. The majority of samples were *C. parvum* (83%; n=228). Of note is that no *C. hominis* samples were detected in 2020.

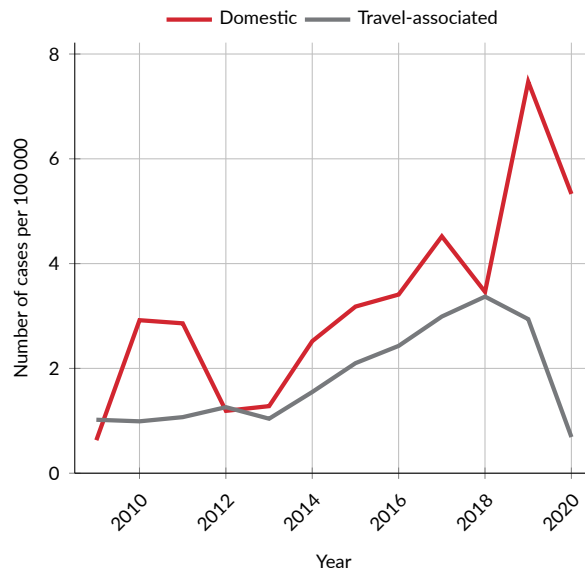


Figure 8: Number of notified human cases of cryptosporidiosis per 100 000 inhabitants from 2009 to 2020.

Instead, the second most common cause of cryptosporidiosis in 2020 was *Cryptosporidium* chipmunk genotype I (8%; n=23). The most common *C. parvum* subtypes were IIdA24G1 (n=34), IIaA16G1R1b (n=33) and IIaA17G1R1c (n=27).

In August, several cases (n=7) of cryptosporidiosis were detected in the same geographical area in Gävleborg county. All cases were positive for *C. parvum* subtype IIaA17G1R1c. Several of the cases had eaten at two local pizzerias. Analysis of the drinking water showed no faecal contamination. Lettuce and/or garden rocket from the local pizzerias was suspected as the probable cause of infection.

Three samples of *Cryptosporidium erinacei*, main host is hedgehogs, were also detected in 2020.

DISCUSSION

Most domestic human cases are reported during the end of summer and this was also the case 2020. This seasonal pattern was the reason the annual national surveillance program for *Cryptosporidium* was changed from annual collection to a four-month period (1 Aug – 30 Nov). Due to COVID-19 pandemic restrictions the travel related cases dropped from March and for the rest of the year.

The increase of reported cases of cryptosporidiosis over time is primarily the result of altered laboratory methods and increased awareness of the disease in primary care. Also contributing to the number of cases are outbreaks caused by “new” types of exposures, e.g. “open farm” which in recent years have become increasingly popular and well visited events.

Vegetables as vehicles for *Cryptosporidium* spp. warrants further investigation. This route of transmission is complex as it may involve animals, irrigation water, contaminated water and natural fertilizers. Not seldom are these outbreaks widespread, as the distribution of vegetables can be nationwide and require national coordination and collaboration between various agencies and regional disease prevention offices.

Echinococcosis

BACKGROUND

Echinococcosis is a common name for different diseases in humans caused by tapeworms belonging to the genus *Echinococcus*. The genus contains several species, of which *E. multilocularis* is the causative agent of alveolar echinococcosis, while cystic echinococcosis (hydatid disease) is caused by species within the *E. granulosus* sensu lato (s.l.) complex, mainly *E. granulosus* sensu stricto (s.s.), but also other species such as *E. canadensis* and *E. ortleppi*.

The life cycles of these parasites are similar with carnivorous definitive hosts and intermediate herbivorous/omnivorous intermediate hosts. However, host ranges vary between the different *Echinococcus* species. Humans are dead-end hosts and may become infected by accidental ingestion of eggs shed by the definitive host.

ALVEOLAR ECHINOCOCCOSIS

Background

Echinococcus multilocularis is endemic in large parts of Europe and has a reported increasing geographical range. Although a rare disease in humans, alveolar echinococcosis is of considerable public health concern due to its high mortality if untreated as well as high treatment costs.

The definitive hosts of this parasite are mainly foxes, but raccoon dogs, dogs, coyotes and wolves can also act as definitive hosts. Rodents, mainly voles, serve as intermediate hosts. Foxes contract *E. multilocularis* by eating infected rodents.

History

Prior to 2010, *E. multilocularis* had not been detected in any definitive host, and no case of alveolar echinococcosis had been reported in Sweden. As a response to the finding of *E. multilocularis* in foxes in Denmark, an active monitoring programme of red foxes (*Vulpes vulpes*) was implemented in Sweden in 2000. From 2000 to 2009, a total of 2962 red foxes, 68 raccoon dogs (*Nyctereutes procyonoides*) and 35 wolves (*Canis lupus*) were examined for *E. multilocularis*, all with negative results. Samples from the majority of foxes ($n=2675$) were examined by ELISA (CoproAntigen ELISA) at the Institute for Parasitology, Zurich University, for the presence of the *E. multilocularis* coproantigen. The remaining samples and those that were ELISA positive, were examined using the sedimentation and counting technique (SCT) ($n=726$). All samples from raccoon dogs and wolves were examined by SCT.



During 2020, fox scats were collected from three areas in Sweden where *Echinococcus multilocularis* previously has been found. The results show that the parasite is still present in two of the areas. Photo: SVA.

During 2010, 304 foxes were examined for *E. multilocularis*. A total of 103 were tested by SCT and 201 by egg PCR. One fox shot in south-west Sweden (county of Västra Götaland) and analysed in 2011 was found to be positive.

During the spring of 2011, a national surveillance programme was implemented where 2985 hunter-shot foxes were analysed with the segmental sedimentation and counting technique (SSCT). Three foxes were found positive: one in Västra Götaland, one in Södermanland and one in the county of Dalarna. In addition, 119 faecal samples from hunting dogs collected in the region of the first positive finding were analysed with egg PCR and all were negative. In the same area 236 rodents were necropsied and all potential lesions examined by an in-house PCR without any positive finding.

To obtain a better prevalence estimate in a known infected area, fox scats were collected, by a systematic sampling procedure, from a circular area with a diameter of 25 km surrounding a positive finding in the county of Södermanland. The samples were collected in 2011 and analysed in 2012, using semi-automated magnetic capture probe-based DNA extraction and real-time PCR method (MC-PCR). Six out of 790 (0.8%) faecal samples were positive.

A second national screening was initiated in 2012 and continued in 2013 and 2014. In all, a total of 2779 fox scat samples were analysed, and three positive fox scats were identified, one from Gnesta, one from Katrineholm (both in the county of Södermanland) and one from the county of Västra Götaland.

From the five known infected areas (including one area in the county of Kronoberg which was identified as infected in 2014, see below), hunters were asked to submit 30 foxes from each circular area with a diameter of 40 km. The aim was to follow up the positive findings, and to collect parasites from any positive cases, for further subtyping. Sampling was initiated in 2012 and finalized in 2016. In Västra Götaland two foxes were positive, in Södermanland three foxes from Katrineholm and one from Gnesta were positive, whereas no fox from Dalarna or Kronoberg was positive. In 2018, on one single occasion, fox scats were collected in Gnesta and 6 of 13 samples tested positive. This showed that the parasite was still present in this location.

Within the Emiro research project (finalized in 2016) and the FoMA Zoonosis monitoring programme (www.slu.se/en/environment) at the Swedish University of Agricultural Sciences (SLU), the parasite was found for the first time in intermediate hosts; voles caught in the county of Södermanland in 2013 (Gnesta/Nyköping). One out of 187 field voles (*Microtus agrestis*) and eight out of 439 water voles (*Arvicola amphibius*) had metacystode lesions confirmed by PCR and sequencing. Protoscoleces were demonstrated in the *Microtus agrestis* and in three out of eight *Arvicola amphibius*. No lesions were found in bank voles (*Myodes glareolus*; $n=655$) or mice (*Apodemus* spp.; $n=285$). Within this project, a new infected area was identified in 2014 near the town Växjö in the county of Kronoberg.

In 2012, alveolar echinococcosis was diagnosed in humans in Sweden for the first time. There were two human

cases with clinical symptoms, and both were considered to have been infected abroad. No human cases were diagnosed in 2013 to 2015. From 2016 and onwards, there have been one to four cases reported yearly.

Disease

Animals

In the definitive animal host, the infection is asymptomatic. The main intermediate hosts, rodents, will usually die from the infection if not captured by a predator.

Humans

In humans, alveolar echinococcosis may develop into a serious, potentially fatal disease characterised by infiltrative tumour-like lesions in the affected organ. The incubation period for developing alveolar echinococcosis in humans is assumed to be between 5 and 15 years. Because of the long incubation period, the disease is most frequently seen in adults. The most common site of localisation is the liver but other organs can also be affected. Symptoms depend on the site and size of the lesion.

Legislation

Animals

Detection of the parasite is notifiable according to Swedish legislation (SJVFS 2013:23). Before 2012, all imported dogs and cats (except from certain countries) were required to be de-wormed with praziquantel before entering Sweden as a preventive measure. Because *E. multilocularis* has been detected in Sweden, there is presently no legal requirement to deworm pets entering the country. However, as the prevalence of the parasite in foxes is very low in Sweden compared to many European countries, dog owners are still encouraged to deworm their dogs prior to entry to Sweden.

Humans

Infection with *Echinococcus* spp. has been notifiable since 2004 according to the Communicable Disease Act (SFS 2004:168) with the amendments of SFS 2013:634. However, notification at the species level is not required. If cases of *E. multilocularis* occur in humans, the data will be presented in the annual report at the website of the Public Health Agency of Sweden (www.folkhalsomyndigheten.se). Before 2004, *Echinococcus* spp. was reported on a voluntary basis by the laboratories.

Surveillance

Animals

As *E. multilocularis* does not cause clinical signs in the definitive host, surveillance in these species must either be active or enhanced passive for example by collection of materials from animals submitted for other reasons. In 2020, all free-living wolves submitted to necropsy at the National Veterinary Institute were tested with MC-PCR. In addition, fox scats were collected from the areas in Uddevalla, Gnesta, and Katrineholm/Finspång where the parasite has been previously found.

Humans

Surveillance is passive and based on identification of the disease by a treating physician or by laboratory diagnosis. Both the physician and the laboratory are obligated to report identified cases to the regional and national level to enable further analyses and adequate intervention measures.

Results

Animals

During 2020, 29 wolves (*Canis lupus lupus*), four red foxes, three dogs and one cat were tested with the MC-PCR and all were negative. However, analysis of fox scats collected from areas where the parasite has previously been found revealed that it was still present in two of the three areas (12 of 109 fox scats from Uddevalla, Västra Götaland and 7 of 18 from Gnesta, Sörmland were positive), while none of 108 samples from the area in Katrineholm, Sörmland/Finspång, Östergötland tested positive.

Humans

In 2020, there were three cases of alveolar echinococcosis reported. One person had probably acquired the infection in his country of origin in Eastern Europe, while it cannot be ruled out for the remaining two cases that they had been infected in Sweden, but they could also have acquired the infection while travelling abroad.

Discussion

E. multilocularis occurs sporadically in Sweden. It is not known how and when the parasite was introduced into the country. The national screening finalised in 2014 can be used as a baseline estimate of the national prevalence, against which the future trend can be assessed. It is well known from other countries that the prevalence of this parasite varies geographically. Regional screenings have previously shown a prevalence of more than 1% in a part of the county of Södermanland, and within the Emiro research project and FoMA Zoonosis monitoring programme 18 of 80 (20%) fox scats were found to be positive in one of four investigated small areas. However, the true geographical distribution is unknown but so far no positive cases have been found north of Dalarna county. Until now, the infection has been detected in five different areas. The recent finding of positive fox scats in two of these areas shows that the parasite is still present in these locations. In 2021 a new national screening to assess the present prevalence in foxes will be initiated, which is expected to run for three years.

E. multilocularis has also been found in intermediate hosts, for the first time in 2014 within the Emiro research project. This finding increases our knowledge about in which biotypes the life cycle of the parasite can be completed. It has been suggested that the absence of *Microtus arvalis* in Sweden may be a contributing factor to the low prevalence of the parasite. However, in some small areas, prevalence has been reported to be higher and more research is needed to clarify which intermediate host(s) are most important.

Based on the knowledge available today, there is a risk for occasional cases of alveolar echinococcosis acquired in Sweden in the future, but the infection will most likely continue to be very rare in humans.

CYSTIC ECHINOCOCCOSIS

Background

Cystic echinococcosis is caused by *Echinococcus granulosus* s.l. and domestic dogs and wolves are the most frequent definitive hosts. Eggs of the parasite are excreted in faeces into the environment where they can infect intermediate hosts such as sheep, pigs, cattle, horses and wild ruminants. The eggs develop into the larval stage (hydatid cyst) mainly in the liver but also in other organs of the intermediate host. The definitive hosts get the infection when consuming organs containing hydatid cysts.

History

Echinococcosis was quite common in reindeer in the northern parts of Scandinavia in the first half of the 20th century. In the 1990s, single cases of *E. granulosus* s.l. were detected in moose and reindeer in Sweden. Since then, the parasite has not been detected in any intermediate host. However, in a retrospective study of biobank material from 116 wolves submitted to the National Veterinary Institute during 2012–2020, two wolves shot in 2012 tested positive with a MC-PCR detecting *E. canadensis* genotype 8/10 as well as *E. ortleppi*.

Disease

Animals

In animals, the infection is usually asymptomatic.

Humans

In humans, the main site for cystic echinococcosis is the liver. However, it may also be located in the lungs, brain or other tissues. Infected patients may remain asymptomatic for years or permanently. Clinical signs of disease depend on the number of cysts, their size, localisation and pressure exerted on surrounding organs or tissues. The incubation period for developing cystic echinococcosis ranges from one to several years.

Legislation

Animals

Detection of the parasite is notifiable in all animals according to (SJVFS 2013:23).

Humans

Echinococcosis has been notifiable according to the Communicable Disease Act since 2004 (SFS 2004:168) with the amendments of SFS 2013:634. However, notification on species level is not required. If cases of *E. granulosus* occur in humans, the data will be presented in the annual report at the website of the Public Health Agency of Sweden (www.folkhalsomyndigheten.se). Before 2004 Echinococcus spp. was voluntarily reported by the laboratories.

Surveillance

Animals

At slaughter, all livestock are inspected for cysts during routine meat inspection. Semi-domesticated reindeer are inspected at slaughter, but not all free-ranging hunted cervids are inspected. If cysts, that could be hydatid cysts, are found in the liver or lung they should be sent to the National Veterinary Institute for diagnosis.

Humans

Surveillance is passive and based on identification of the disease by a treating physician or by laboratory diagnosis. Both the physician and the laboratory are obligated to report identified cases to the regional and national level to enable further analyses and adequate intervention measures.

Results

Animals

E. granulosus s.l. was not detected in any animal sampled in 2020. In addition to the routine inspection at slaughter, 5 wolves and 2 dogs were tested by MC-PCR detecting *E. canadensis* genotype G8 and G10 as well as *E. ortleppi*.

Humans

In 2020, 20 cases of cystic echinococcosis were reported. For eleven of these cases, it was not possible with available laboratory methods to determine which species they were infected with, but the epidemiology suggested that they also had cystic echinococcosis. Annually around 15–30 cases are reported in Sweden. In 2020, the reported cases ranged in age from 8 to 68 years (median 34 years). Eight cases were women and 12 were men. They were all considered to have been infected abroad in areas where the parasite is endemic. The most frequently specified countries of infection were Syria (6 cases) and Iraq (4 cases).

Discussion

E. granulosus s.l. has not been detected in animal intermediate hosts in Sweden since the late 1990s, when it was reported in three reindeer in the northernmost regions of Sweden, bordering to Norway and Finland. However, retrospective analysis of biobank samples from 2012–2020 has revealed that two wolves shot in 2012 were infected with genotype G8/10 (or possibly G5). In Finland, the parasite is present at a low prevalence in wildlife (wolves, moose and reindeer) and has been genotyped as *E. canadensis*.

This species is considered as less pathogenic, and possibly with a lower zoonotic potential, than *E. granulosus* sensu stricto that is prevalent in other parts of Europe and identified mainly in a cycle between dogs and farm animals.

In humans, cystic echinococcosis is a rare disease seen in immigrants or other people who have resided in endemic countries. In Sweden, no domestically acquired human cases have been reported since the infection became notifiable. In Finland, on the other hand, pulmonary cystic echinococcosis (*E. canadensis*) was confirmed in 2015 in a patient with no history of travelling abroad. The infection was presumably transmitted by hunting dogs.

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Enzootic bovine leucosis

BACKGROUND

Enzootic bovine leucosis (EBL) is caused by bovine leukaemia virus (BLV), which is an oncovirus in the family *Retroviridae*. The viral infection is transmitted by infected lymphocytes via contact with contaminated biological material from an infected animal. Sweden was declared officially free from EBL by the European Union (EU) in January 2001 (former Decision 2001/28/EC, currently Decision 2003/467/EC last amended by Decision 2005/764/EC). Before this, a voluntary control programme had started in 1990 and a mandatory eradication programme had been running since the autumn of 1995.

DISEASE

EBL is characterised by multiple cases of multicentric lymphosarcoma in adult cattle within a herd after an incubation period of 4–5 years. The tumours can develop rapidly in many sites, which may cause variable clinical signs depending on the site. Persistent lymphocytosis, without clinical signs, develops earlier but rarely before two years of age. The infection can also result in immunological dysfunction with a greater susceptibility to other infectious diseases, a decrease in milk production and lower conception rate.

LEGISLATION

EBL is included in the Swedish legislation for notifiable diseases (SJVFS 2013:23). EBL is also on the OIE list of infectious diseases and current surveillance standards are given in EU legislation, Directive 64/432/EEC.

SURVEILLANCE

The purpose of the active surveillance is to document freedom from EBL in accordance with Directive 64/432/EEC. Växa Sverige (former Swedish Dairy Association) is responsible for this surveillance, which is financed by the Swedish Board of Agriculture.

From 2010 onwards, surveillance in dairy herds has been performed by random sampling. The between-herd design prevalence is 0.2% and the within-herd design prevalence 15%, with a 99% confidence, given known freedom of infection the previous year. To achieve this, approximately 1500 herds need to be randomly sampled per year. Bulk milk samples are collected within the quality control programmes of the dairies. The surveillance in beef herds is performed with an aim to randomly sample 1–3 animals per herd in 2000 herds every year. Serum is collected from slaughtered cattle above 2 years of age originating from sampled herds. Details on numbers of herds and animals tested in 2020 are given in Table 8.

Diagnostic testing is performed at the National Veterinary Institute. Milk is analysed using Enzootic Bovine Leukosis Virus (BLV) Antibody Test Kit (IDEXX Leukosis Milk Screening) and serum is analysed using Bovine Leukosis Virus (BLV) Antibody Test Kit (IDEXX Leukosis Serum X2 Ab Test).

Table 8: Total numbers of herds and animals tested for bovine leukaemia virus antibodies in 2020.

Herd type (sample type)	Herds	Animals
Dairy herds (one bulk milk sample per herd)	2053	-
Beef herds (blood from 1–3 animals per herd)	2264	5649
Beef herds with at least three animals tested	567	-
Beef herds with two tested animals	1239	-
Beef herds with one tested animal	458	-

In addition to the active surveillance, pathological findings indicating lymphoma are investigated for EBL using PCR (Ballagi-Pordány & Belák 1996) as a part of passive surveillance.

RESULTS

Five bulk milk samples were tested antibody positive in 2020. After investigation and field sampling of the herds the conclusion was that these were false positive results.

Samples from five cases of tumours in lymph nodes were analysed for EBL at SVA using PCR in 2020 and all cases were negative.

DISCUSSION

Sweden was declared free from EBL in 2001 (Commission Decision 2001/28 EC), and has had a very stable disease-free situation since then. In 2012, one slaughtered animal above two years of age was positive for EBL. All animals over six months in the herd from which the positive animal originated were tested for EBL in spring 2013, and all samples were negative. The herd was thereafter cleared from suspicions of EBL infection. The number of milk samples being falsely positive has increased somewhat most likely due to the introduction of a new test kit for milk samples.

EBL is present in many countries in the world, but several countries, especially in Western Europe, are officially free from this infection. However, the infection is present in several countries close to Sweden such as Poland, Latvia, Lithuania, Russia and Ukraine. This may pose a risk for new introduction of the disease into the country.

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Footrot



Lameness is a common sign of footrot. Photo: Bengt Ekberg/SVA.

BACKGROUND

Footrot is a globally distributed contagious disease in sheep and goats. The causative agent is *Dichelobacter nodosus* (*D. nodosus*). The disease is characterised by interdigital necrotising inflammation with underrunning of part or all the soft horn of the heel and the sole. Predisposing factors are humid and warm weather conditions. The severity of footrot can vary by the strain of *D. nodosus* and the environmental conditions.

The first case of footrot in Swedish sheep was identified in 2004. Data on all affected flocks have been recorded since 2004. A voluntary control programme for footrot (“Klövkontrollen”) was established by Farm & Animal Health in 2009. Within the programme, the definition of footrot is when virulent strains of *D. nodosus* are detected with or without clinical lesions or when benign strains are detected together with clinical lesions.

DISEASE

The clinical signs of the disease are typically foot lesions, and lameness due to the painful lesions. However, lameness is not a consistent clinical sign in affected sheep. Footrot varies greatly in severity from inflammation of the interdigital skin to complete underrunning of hoof horn.

LEGISLATION

Footrot is a notifiable disease in Sweden (SJVFS 2013:23).

SURVEILLANCE

The aim of the control programme is to eliminate footrot from affected sheep flocks and to provide certification of freedom from footrot for the sheep trade. Another important part of the programme is training of veterinarians and non-veterinary staff to perform clinical inspection and footrot scoring. The feet of sheep are inspected by veterinarians and farmers on an annual basis. The inspections are performed from August 15 to October 15, when the risk of footrot is highest due to the weather conditions. For all newly affiliated flocks and for all affiliated flocks with clinical signs suspecting footrot, a real-time PCR is used for detecting *D. nodosus* and determining strain virulence.

Flocks in which no clinical signs of footrot or virulent strains of *D. nodosus* are detected in any of the adult sheep are certified as free (F-status). If signs of footrot (virulent strains with or without clinical lesions or benign strains with clinical lesions) are detected, measures to eliminate footrot are undertaken, including foot baths in zinc sulphate and if necessary antibiotic treatment, moving of animals to clean pasture and culling of chronically infected sheep. Flocks

with a history of footrot can be certified as free at the earliest ten months after the last signs of infection.

328 (out of a total of 7900) sheep flocks are affiliated to the control programme. Most of the pedigree flocks in Sweden are affiliated to the programme.

RESULTS

In 2020, footrot was confirmed in 5 new flocks; 2 within the control programme and 3 outside the programme (Figure 9). In 3 of the 5 flocks, virulent strains of *D. nodosus* were detected. In the programme, 326 flocks were certified free from footrot (F-status). Actions for elimination were taken in two flocks with footrot. Actions for elimination are voluntary, hence why not all positive flocks undergo elimination procedures. Prevalence studies in slaughter lambs were performed in 2009 and 2020. In the period between these screenings the prevalence had decreased from 5.8% to 1.8%.

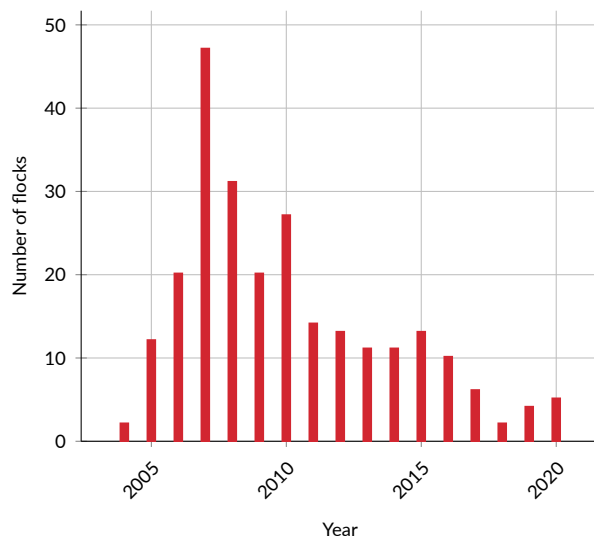


Figure 9: Number of sheep flocks detected with footrot within the programme, 2004–2020.

DISCUSSION

The control programme demands quarantine before new animals can enter the flock, and hence the awareness of biosecurity and disease control in general has been enhanced in the sheep farming community. Since most of the pedigree flocks are affiliated, the impact of the programme is significant although they represent a minority of sheep flocks in Sweden. The sheep farmers association's agreement on a trade ban from infected flocks has been essential to the programme's success. Good collaboration between authorities, the sheep farming community and individual sheep farmers

has resulted in a cost-effective control programme. The new real-time PCR can discriminate between benign and virulent strains. This typing might make it possible to limit mandatory notification to virulent strains of footrot.

TWO CASES OF CONTAGIOUS OVINE DIGITAL DERMATITIS

Contagious ovine digital dermatitis (CODD) is a severe infectious foot disease of sheep. In United Kingdom this condition is an important cause of severe lameness in sheep, typically affecting one digit of one foot. The etiology is not fully established, but *Treponema* spp. resembling those involved in digital dermatitis in cattle, are probably involved. There is no effective treatment of CODD, and it has a substantial impact on animal welfare. Outside UK, CODD has only been reported from a few countries, and in 2019 and 2020 the first two cases of CODD were diagnosed in Sweden. No connection between the two farms has been found. Both flocks were slaughtered. Through an intensive communication campaign from authorities and farm organizations, Swedish sheep farmers and veterinarians have been encouraged to increase their preparedness for symptoms related to CODD.

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Infectious bovine rhinotracheitis

BACKGROUND

Infectious bovine rhinotracheitis (IBR) is caused by Bovine herpes virus 1. The same virus can affect different organ systems causing respiratory, abortive, genital or conjunctival disease. Transmission is mainly by aerosol for the respiratory form and by venereal transmission for the genital form.

Examination of Swedish bulk milk samples during the early 1990s showed the presence of a small number of seropositive herds. No signs of clinical disease were present in these herds. An eradication programme was initiated in 1994 and the last seropositive animal was found in 1996.

DISEASE

The incubation period of IBR is 3–21 days, but the virus can be silently present in the host animal and be reactivated by stress or immunosuppression. The clinical picture varies by subtype of the virus but also with the environmental and management factors. Several manifestations of the disease can be present during the same outbreak in the same herd. However, the clinical signs are typically concentrated either to the respiratory tract, reproductive organs or the eyes.

LEGISLATION

The Swedish IBR eradication programme was approved in 1994 (Decision 73/94/ COL and Decision 95/71/EC). Sweden was allowed additional guarantees by the EU to reduce the chance of IBR introduction in 1995 (Decision 95/109/EC) and was officially declared free from IBR in 1998 (former Decision 98/362/ EC, current Decision 2004/558/ EC). Since 2004, all neighbouring Nordic countries have additional guarantees from the EU relating to this disease (Decision 74/94/ COL and Decision 95/71/EC). IBR is included in the Swedish Act of Epizootic diseases (SFS 1999:657 with amendments). Vaccination is prohibited and notification of clinical suspicion is mandatory.

SURVEILLANCE

During 2020 all diagnostic testing was performed at the National Veterinary Institute. Milk samples were analysed for the presence of antibodies using an indirect ELISA (ID screen IBR Milk indirect, IDvet), and serum samples were analysed with a blocking ELISA (IDEXX BHV1 gB AB test kit x3, IDEXX). Positive milk samples were confirmed with a blocking ELISA (IDEXX BHV1 gB AB test kit x3, IDEXX), and serum samples with virus neutralisation test (in accordance with the OIE manual). Semen and organ samples were tested with a real-time PCR (Wang et al., 2007). A positive case is defined as an animal with a positive PCR result or a confirmed positive serological reaction for IBR.

Passive surveillance

Suspicious based on clinical signs must be reported to the Swedish Board of Agriculture and will be subsequently investigated.

Active surveillance

The purpose of the surveillance is to document freedom from IBR. The Swedish Board of Agriculture is responsible for the surveillance, which is implemented by Växa Sverige through their milk quality control programme and is synchronised with the programmes for bovine viral diarrhoea and enzootic bovine leucosis. The surveillance also includes serum samples from beef cattle, collected at abattoirs. The sample size for dairy herds is calculated based on a herd design prevalence of 0.2% and a confidence level of 99%, and for beef cattle on a herd design prevalence of 0.2%, an animal design prevalence of 10% (beef cattle) and a confidence level of 99%.

In addition to the official active surveillance programme, bulls are tested within health schemes at semen collection centres and all cattle (and other potentially susceptible ruminants) are tested before export and import.

RESULTS

Within the active surveillance in 2020, 3093 bulk milk samples and 6618 serum samples from beef cattle were examined. Of these, 19 serum samples tested positive in the screening test but negative in the confirmatory test. In addition, 191 cattle, 11 alpaca, 9 fallow deer and 1 moose were tested as part of health schemes or prior to export. All samples were negative.

Three herds were investigated due to clinical suspicion of IBR, with negative results.

DISCUSSION

In summary, no herd or individual animal was diagnosed with IBR infection during 2020. This supports Sweden's IBR-free status.

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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



Seven wild birds were found positive for highly pathogenic avian influenza (HPAI) in 2020, of which five were barnacle geese. Photo: Bengt Ekberg/SVA.

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. 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.

In early 2020 several outbreaks in poultry and wild birds caused by a novel reassortant of the HPAI H5N8 clade 2.3.4.4b virus were reported in multiple European countries. The H5N8 viruses carrying six gene segments derived from sub-Saharan African HPAI viruses, and two gene segments

from Eurasian LPAI viruses were reported from Poland, the Czech Republic, Hungary, and Germany up to April 2020.

Later in October 2020, another novel HPAI H5N8 virus was detected first in a dead mute swan in the Netherlands. The genome constellation of the virus detected in the Netherlands was distinct from the H5N8 viruses causing outbreaks in Europe in the first half year of 2020. Prior to the detection of these viruses in poultry and wild birds in the fall 2020 in Europe, H5N8 outbreaks with genetically similar viruses had been reported in central Russia in early summer and in September in Kazakhstan.

In Sweden, HPAI virus had not been detected between June 2018 until November 2020. From mid November 2020 and onwards, H5Nx clade 2.3.4.4b HPAI viruses were detected in poultry and wild birds in Sweden.

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.

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 2020 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 2020 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, 2019 and 2020. 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 10.

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.

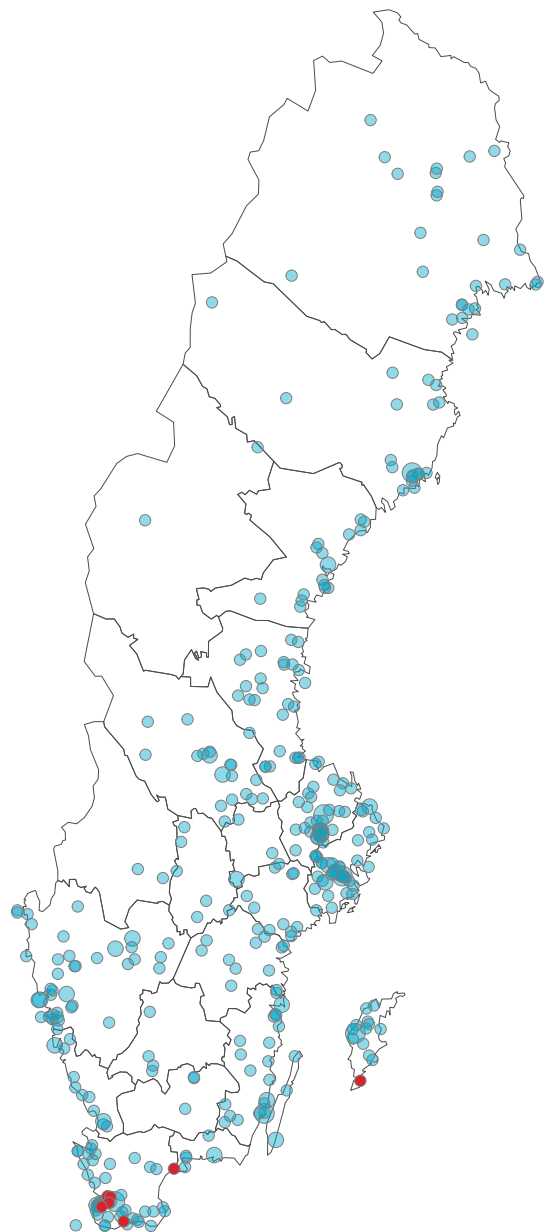


Figure 10: Geographical location of the wild birds analysed for avian influenza in 2020. Point sizes are scaled by the number of birds sampled at a given location. Seven out of 412 wild birds sampled in 2020 were found positive for HPAI.

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, H5N8 and H7N9, if requested.

Seven human cases in December 2020, were reported 2021 in Russia with A(H5N8), all with mild or no symptoms.

Since 2003, 862 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 2020.

Since 2014, 26 laboratory-confirmed cases of human infection with HPAI H5N6, including 16 with fatal outcome, have been reported. All cases of the cases were infected and detected in mainland China. One case was determined during 2020. 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 2020, no 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, 68 laboratory-confirmed cases of human infection with LPAI H9N2, including one death, have been reported globally. Cases occurred in China (57), Egypt (4), Bangladesh (3), India (1), Oman (1), Pakistan (1), and Senegal (1). During 2020, eight cases of H9N2 were reported: seven from China and one from Senegal.

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

Diagnostics

Samples including swab (both cloacal and tracheal) or/and different organs taken from birds were analysed for the presence of the 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.

Results

Poultry

In 2020, 2110 blood samples were collected from 206 flocks. Three flocks with game birds (mallards) had single serologically positive H5 results with haemagglutination inhibition tests. These establishments were investigated with oropharyngeal and cloacal swabs with PCR and found negative for Influenza A H5 and H7. One sample was positive for Influenza A. All other samples were found negative for AIV subtype H5 and H7. Table 9 gives an overview of number of poultry flocks sampled in 2011 to 2020 (Table 9).

HPAI was detected in two flocks during 2020, one farm with fattening turkeys and one backyard flock, both in Skåne region. Both infected flocks were investigated following that high mortality was noted. In total AI was investigated in 13 poultry flocks during 2020 of which eight were clinical suspicions, three were follow up from serological surveillance, one following post mortem findings and one was contact tracing. Investigations were done in two layer flocks,

two flocks with fattening turkeys, one flock with broiler parents, one flock with broiler grandparents, one flock with pigeons, three flocks with mallards and two backyard flocks. The clinical suspicions aroused from increased mortality in the flock and some also had birds that displayed symptoms such as neurological signs.

Wild birds

Within the passive surveillance programme seven wild birds were found positive for HPAIV of which six was H5N8 and one was HPAIV H5N5. In total 412 birds of 69 different species were sampled of which 199 bird of prey, 66 water or shore birds and 46 corvids. The first HPAIV positive birds were one Barnacle goose and one Peregrine falcon found positive on 25th November 2020 in Skåne region. Subsequently another four Barnacle geese (3 HPAIV-H5N8 and 1 HPAIV H5N5) and one Eurasian eagle-owl and one common buzzard were found positive for HPAI during the year. Geographical location of sampled and wild birds including positive findings are available in Figure 10.

Humans

No cases of zoonotic influenza were identified among the samples characterised during 2020 in Sweden.

Discussion

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

In 2020, Sweden reported one outbreak of HPAI H5N8 in commercial poultry, one incident in captive birds and seven cases of HPAI in wild birds. During the same period, outbreaks with HPAI in poultry and cases in wild birds were reported from several European countries. The detection of HPAI in Europe was not unexpected given the early reports on the situation with massive HPAI outbreaks among wild birds and domestic poultry in central Russia in the summer of 2020. In December 2020, seven human cases in Russia with A(H5N8), all with mild or no symptoms were observed and reported 2021.

The location of the epidemics in central Russia coincided with the major migratory route for several wild bird species, connecting the breeding sites in northern Russia to the wintering habitat in western Europe. Compared to 2016–2018 epizootic, the newly introduced H5Nx viruses in Europe shows high viral genetic diversity and has a more diverse gene segment composition. 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.

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

Table 9: Number of flocks of different poultry categories sampled in the surveillance for avian influenza 2011–2020.

	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020
Laying hens	61	52	44	58	68	62	68	65	73	63
Free range laying hens	30	27	16	23	23	30	43	49	67	52
Turkeys	22	19	26	16	18	18	16	16	18	18
Ducks	6	3	1	3	3	4	1	2	3	1
Geese	20	20	13	9	9	7	5	6	3	1
Broilers ^A	39	34	26	12	22	33	23	33	22	14
Ratites	5	3	2	3	3	3	2	2	5	3
Breeding hens (parents)	36	36	36	32	31	34	35	30	34	35
Breeding turkeys (parents)	3	3	3	2	3	3	3	3	3	3
Game birds (mallards)	9	7	7	5	6	7	2	5	5	6
Game birds (pheasants)	15	16	16	12	13	9	13	12	8	10
Backyard flocks (geese, ducks)	0	0	0	0	0	0	0	0	0	0

^A Small-scale production.

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 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 10).

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 2020, 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, 436 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 2020, three cases of A(H1N1)v were reported from three different countries (China, Netherlands and Germany). Two cases of A(H1N2)v were reported during 2020, one case in Brazil and one case in Canada. Human infection with swine influenza has been associated with agricultural fairs, where people are in close contact with potentially infected swine

Table 10: 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%

populations. The US Center 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 cases of infection with influenza A viruses are notifiable according to SFS 2015:587.

Surveillance

Animals

Passive surveillance

During the period from 2009 to 2020, 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 11).

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 sequencing method.

No active surveillance was performed in 2020.

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

A total of 138 samples from 64 herds with respiratory signs were analysed for swine influenza virus in 2020. Fourteen influenza infected herds were identified.

Table 11: Passive and active surveillance for swine influenza in Swedish pig herds from 2014 to 2020.

Period	Number of herds investigated	Number of Influenza A positive cases	Frequency of positive cases	H1N1pdm (2009)	Av-likeH1N2 (H1avN2)	reass. H1pdmN2 (H1pdmN2)
2014-passive	18	7 herds (40 animals)	38% herds / 27% animal level	19	14	7
2014-active ^A	10	5 herds (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	20	3 herds	single animal per herd	2	1	-
2018-passive	31	0	-	-	-	-
2019-passive	46	5 herds	single animal per herd	-	1	-
2020-passive	64	14 herds	single animal per herd	2	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.

Active surveillance

No active surveillance was performed in 2020.

Humans

No cases of zoonotic influenza were identified among the characterised samples during 2020 in Sweden.

Discussion

The results of the passive surveillance indicate presence, but no large impact, of swine influenza in the Swedish pig population. In the 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. It would be of value to perform an active surveillance effort within the next few years. Monitoring of human infections caused by these viruses is critically important to assess their pandemic potential.

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Leptospirosis

BACKGROUND

Several species of the spirochaetal bacterium *Leptospira* can cause leptospirosis. All mammals including humans are susceptible to one or several *Leptospira* serovars.

Leptospirosis occurs worldwide but the dominant serovars vary by region. Cattle and pigs are considered to be reservoirs for *L. Hardjo* and *L. Pomona*, respectively. Serovars known to infect and cause clinical disease in dogs include *L. icterohaemorrhagiae*, *L. Canicola*, *L. Grippotyphosa*, *L. Pomona*, *L. Sejroe* and *L. Australis*. These are all serovars also known to infect and cause disease in humans.

Serovars that can cause disease in horses include *L. icterohaemorrhagiae*, *L. Grippotyphosa*, *L. Pomona* and *L. Bratislava*.

Seropositivity to *Leptospira* spp other than *L. Pomona* are occasionally confirmed in Swedish pigs, mostly to an indigenous serovar of *L. Sejroe*, *L. Bratislava* and *L. icterohaemorrhagiae*.

Sporadic cases of seropositivity towards the indigenous strain of *L. Sejroe* in cattle have also been recorded.

Between 1994 and 2006 sampling and testing for antibodies to *L. Hardjo* and *L. Pomona* in cattle and pigs respectively, was performed each year and after 2006 every third year. The commercial cattle and pig populations in Sweden are considered free from *L. Hardjo* and *L. Pomona* based on only negative results from this surveillance system.

Surveillance in other animal species including dogs and horses is passive only.

DISEASE

Animals

L. Hardjo is one of several pathogenic serovars and is associated with disease in cattle, sheep, goats and horses. In cattle, infections may be acute or chronic; asymptomatic, mild or severe. Acute disease is more often seen in calves. Disease in adults may go unnoticed, because the early clinical signs of fever and depression are often transient and mild. Infected herds may have problems with abortions, decreased fertility and decreased milk yield as well as increased mortality in calves.

The clinical signs in sheep and goats are similar to those in cattle. Both sheep and cattle can act as asymptomatic reservoir hosts.

Leptospira infections in pigs may also be asymptomatic or may give rise to reproductive failure. In piglets, fever, gastrointestinal disorders and jaundice may be present.

The clinical presentations in dogs infected with *Leptospira* range from subclinical to severe clinical illness and death; liver and/or kidney affection as well as varying degrees of vasculitis is typical. A peracute pulmonary form with high mortality rate is not uncommon.

In horses, most infections are subclinical and when clinical signs are present, they resemble those seen in dogs. Late abortions and recurrent uveitis have also been described.

Humans

Leptospirosis in humans ranges from asymptomatic or mild influenza-like illness to a severe infection with renal and hepatic failure, pulmonary distress and death.

LEGISLATION

Animals

Since 2004, leptospirosis is a notifiable disease on laboratory confirmation in Sweden (SJVFS 2013:23), in all animal species concerned. Single serologically positive samples are reported. Reporting is not serovar specific *i.e.*, to which serovar or serovars antibodies are detected is not reported.

Based on the legislation on testing of animals (SFS 2006:806), the Swedish Board of Agriculture can decide to initiate an epidemiological investigation in case of clinical disease consistent with leptospirosis in animals.

Humans

Leptospirosis in humans is notifiable according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2013:634).

SURVEILLANCE

Animals

Active surveillance in cattle and pigs is at present performed every third year. The aim is to demonstrate freedom from *L. Hardjo* in cattle and *L. Pomona* in pigs. Animals sampled for export and in breeding centres adds to the active surveillance.

All serological analyses included in the active surveillance are performed at the National Veterinary Institute. The diagnostic test used for *L. Hardjo* is an indirect ELISA (PriO-CHECK® *L. Hardjo*, Antibody detection ELISA, Lelystad, Holland) for both serum and bulk milk samples. Positive serum samples are further tested with MAT (Microscopic agglutination test) with results reported as positive at 1:100 or above. For positive or doubtful ELISA results on bulk milk samples, an investigation is carried out in the herd and additional individual samples are taken. Antibodies against *L. Pomona* are analysed using the microscopic agglutination test (MAT) with results reported as positive at 1:100 or above.

The surveillance in cattle is based on serum and bulk milk samples selected by systematic random sampling from the surveillance programme for bovine viral diarrhoea virus (BVDV) and evenly distributed throughout the sampling period. See chapter on BVDV (page 22) for details on sampling and population. The surveillance was designed using a between-herd design prevalence of 0.2%, a within-herd design prevalence of 40% (based on anticipated prevalence in naïve herds) and a risk of introduction of 1 in 50 years. In domestic pigs, the active surveillance is based on samples collected for the abattoir sampling part of the surveillance



As for other animal species, most *Leptospira* infections in horses are subclinical. Recurrent uveitis has been described as one of several clinical manifestations, and in 2020, three of four reported seropositive Swedish horses were sampled as part of investigations of chronic uveitis. The fourth horse was asymptomatic. Photo: Bengt Ekberg/SVA.

carried out by Farm & Animal Health for porcine reproductive and respiratory syndrome (PRRS). See chapter on PRRS (page 66) for details on sampling and population. The surveillance was designed using a between-herd design prevalence of 0.5%, a within-herd design prevalence of 40% and a risk of introduction of 1 in 25 years.

The surveillance in other animals including dogs and horses is passive and consists of mandatory reporting of positive results from onsite tests detecting antibodies used at veterinary clinics, PCR-positive samples, and seropositivity confirmed at laboratories, including titers as low as 1:100 regardless of serovar. Furthermore, all positive results are reported regardless of whether clinical suspicion of disease is present or if previous vaccination might be the cause of the detected antibodies. Serum samples submitted to the National Veterinary Institute for MAT-testing are currently routinely tested for *L. icterohaemorrhagiae*, *L. Canicola*, *L. Grippotyphosa*, *L. Bratislava*, *L. Saxkoebing*, *L. Sejroe*, *L. Automnalis*.

Humans

Notification of human cases is mandatory, and surveillance is based on identification of the disease by a treating physician or by laboratory diagnosis. Both are obligated to report identified cases to the regional and national level to enable further analyses and adequate intervention measures.

RESULTS

Animals

No active surveillance was performed in cattle and pigs during 2020. See previous reports for surveillance results from 2019 and earlier.

In dogs, 48 *Leptospira*-positive laboratory analyses were reported, of which 41 (85%) were from the National Veterinary Institute. In 16 individual cases blood and/or urine samples submitted for PCR-analyses were positive, and seven of these also had positive serological results. In comparison, 30 *leptospira*-positive laboratory analyses were reported in 2019, of which 20 (60%) from the National Veterinary Institute.

The reasons for samples being submitted to the National Veterinary institute include clinical suspicion of acute disease as well as sampling of clinically healthy dogs and horses due to export requirements or suspected leptospirosis in other animals in the household.

Leptospira infection was suspected in aborting sows in one pig herd. The sows were serologically negative when sampled two weeks after abortion and it was concluded that the abortions were not caused by infection with *Leptospira*.

Four premises with horses seropositive to *Leptospira* spp (*L. icterohaemorrhagiae*, n=3; *L. grippotyphosa*, n=1) were reported during 2020. Three concerned singles cases of imported horses from Germany or Spain that were sampled as part of investigations of chronic uveitis. In one instance seropositivity was confirmed at a health check of asymptomatic Swedish horses.

Humans

In 2020, no cases of leptospirosis were reported. In previous years, the majority of cases reported have been acquired abroad. The absence of travel-associated cases in 2020 might at least partly be explained by less travelling due to the COVID-19 pandemic.

DISCUSSION

Leptospirosis occurs worldwide, but the predominant serovars vary by geographic region. The disease is an important zoonosis as well as being associated with reproductive losses in livestock causing significant economic costs worldwide.

The commercial cattle and pig populations in Sweden are considered free from *L. Hardjo* and *L. Pomona* based on only negative results from the surveillance system since 1994. Seropositivity to *Leptospira* spp other than *L. Pomona* are occasionally confirmed in Swedish pigs, mostly to an indigenous serovar of *L. Sejroe*, *L. Bratislava* and *L. icterohaemorrhagiae*, and sporadic seropositive cases of the indigenous strain of *L. Sejroe* in cattle have also been recorded.

Several *Leptospira* serovars have been shown to be present in Swedish dogs by detection of seropositivity to *L. icterohaemorrhagiae*, *L. Canicola*, *L. Grippotyphosa*, *L. Bratislava*, *L. Saxkoebing*, *L. Sejroe* and *L. Autumnalis*. Serovars including e.g. *L. Bratislava* and *L. Grippotyphosa* have also been detected in wild rats caught in Swedish cities in research studies, a further indication of presence of leptospiral serovars in Sweden.

Currently, all positive MAT results in dogs are reported without knowledge of vaccination status, travel history and whether clinical disease is suspected or not. Furthermore, in clinical cases, paired samples (sometimes three samples) are needed for diagnosis as the immune response providing specific antibodies to the causing serovar often is delayed. A negative result is common during the acute phase of illness, as is cross reactions leaving the causative serovar unidentified. As all laboratory diagnostics must be paid for by the dog owner there is a lack of such paired samples. In addition, not all dogs survive the infection and autopsies are rare due to the cost to the owner as well as the emotional aspect.

The number of samples sent to laboratories abroad, and to what extent possible positive results are being reported or not by the referring veterinarians, is currently unknown. Furthermore, an onsite ELISA test not distinguishing between different serovars is available and is currently used in several small-animal hospitals and clinics. Positive onsite test results are mentioned during phone calls to the National Veterinary Institute from clinically active small animal veterinarians, including during 2020. However, no such cases

were reported during 2020, indicating underreporting. Reliable data on underreporting is however lacking.

In short, seropositivity to leptospiral serovars in Swedish dogs is currently probably underreported and data on seropositivity can neither be compared to or between previous years. Furthermore, prevalence of clinical disease in Swedish dogs due to leptospiral infection is currently not reflected in the surveillance data and not readily available.

Further studies are however warranted, as the number of suspected clinical cases according to regular out-reach contacts from the National Veterinary Institute to veterinary small animal hospitals and clinics continue to rise, indicating a possible increase in exposure- but confirmatory data is lacking. There is currently no available system to aid in reporting and evaluating suspicion of Leptospiral infection as the true cause of disease in clinical cases. Information on presence or absence of clinical disease or results from any confirmatory laboratory investigations carried out is currently not included in the data reported.

The reporting procedures and challenges in horses are largely the same as in dogs.

Few cases of human infections are reported each year and the majority are travel-associated.

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Listeriosis



Gravad and cold-smoked fish products are well-known vehicles for food-borne listeriosis. Photo: istetiana/iStock.

BACKGROUND

The genus *Listeria* contains several species, but *Listeria monocytogenes* is the only zoonotic species and was first described in 1926. Previously, sporadic cases of listeriosis were reported, often in employees in contact with diseased animals but since the 1980s outbreaks and cases of listeriosis have been traced to food products.

Listeria bacteria are widely distributed in the environment, such as in soil, silage and water. They can survive for long periods in the environment and tolerate disinfection and also grow at refrigerator temperatures, in vacuum packed food and in modified atmospheres. These properties make elimination of *L. monocytogenes* difficult. *L. monocytogenes* and other *Listeria* species are often found as environmental contaminants in food producing establishments. However, it is only *L. monocytogenes* that is relevant regarding human health. The main sources of human listeriosis are contaminated food products, such as cold-smoked or gravad vacuum-packaged fish products, meat products and soft cheeses or other ready-to-eat foods with a long shelf-life. *L. monocytogenes* is destroyed by heating (pasteurisation or cooking).

The main sources of listeriosis for animals are feed or environment. To prevent listeriosis in ruminants it is essential to

feed animals with a silage of good quality (low pH and without contamination with soil) as the less acidic pH enhances multiplication of *L. monocytogenes*.

In Sweden, during the last ten years approximately 50–120 human cases have been reported annually. Outbreaks have been associated with vacuum-packaged fish, with cheese made of unpasteurised milk, cold cuts, frozen corn and with convenience meals.

DISEASE

Animals

L. monocytogenes can infect a wide range of animal species, both domestic and wild. The clinical picture of the infection in animals varies from an asymptomatic infection to severe. Especially in sheep and goats, listeriosis manifests as an encephalitis, abortion, mastitis or septicaemia.

Humans

Listeriosis can be manifested either as a milder non-invasive form or as a severe invasive disease. The non-invasive form is generally presented as a febrile gastroenteritis. The severe form most often occurs in immunocompromised persons, newborns, pregnant women and the elderly. Symptoms of invasive listeriosis are septicaemia, meningitis and meningoencephalitis. For those with severe infection, the

case fatality rate is high (20–40%). The infection can lead to miscarriage, premature delivery or neonatal death.

LEGISLATION

Animals

Listeriosis is a notifiable disease in animals according to SJVFS 2013:23.

Food

Food safety criteria for *L. monocytogenes* are specified in the Commission Regulation (EC) No 2073/2005 on microbiological criteria for foodstuffs. Food business operators shall ensure that foodstuffs are in compliance with the regulation. Different criteria apply to ready-to-eat (RTE) foods in which growth of *L. monocytogenes* can occur and in RTE foods in which growth of *L. monocytogenes* will not occur during their shelf-life (see criteria 1.1 - 1.3 in Annex I to the regulation).

Humans

The invasive form of listeriosis has been a notifiable disease in Sweden since 1960. It is notifiable according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2014:1549).

SURVEILLANCE

Animals

Surveillance in animals is passive. Suspicions on listeriosis can be raised on clinical signs and/or laboratory analyses. The diagnosis is based on histological findings at post-mortem or by detection of the organism by cultivation methods using enrichment in selective broth followed by culture on selective and non-selective agar or by direct plating.

Identification is made by mass spectrometry (MALDI-TOF). The Swedish Board of Agriculture can decide on epidemiological investigations if needed.

Food

No official control programme exists for *L. monocytogenes*. National and local authorities may perform sampling as part of extended official controls or targeted projects. Producers of ready-to-eat foods are obliged to take samples for analysis of *L. monocytogenes* as part of their self-controls, but the results are not normally reported to the authorities.

Humans

Notification of human cases is mandatory and surveillance is based on identification of the disease by treating physician and/or by laboratory diagnosis; both are obliged to report to the regional and national level to enable further analyses and adequate intervention measures. Isolates from human cases are sent to the Public Health Agency of Sweden for typing using whole genome sequencing (WGS) to determine molecular serotype and for cluster detection. As a conventional nomenclature tool, not only the serotype but also the Multi Locus Sequence Typing (MLST) type, i.e. ST-type, is defined by WGS.

RESULTS

Animals

In 2020, listeriosis was reported in 12 sheep, ten cattle, four horses, three goats, and in one cat.

Food

In 2020, 245 samples from different types of food taken by national and local authorities were analysed for presence

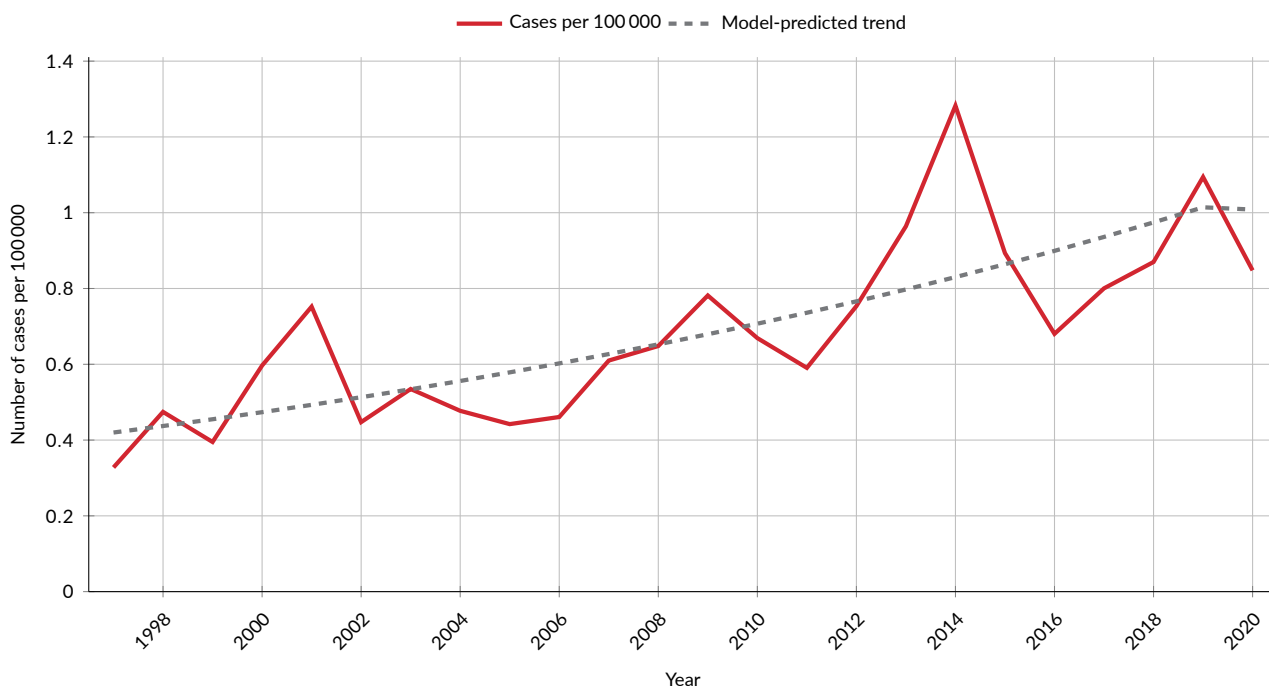


Figure 11: Notified incidence per 100 000 inhabitants of human cases of listeriosis in Sweden 1997–2020 and a model-predicted trend (negative binomial regression). The higher incidence in 2013–2014 is due to two larger outbreaks with in total 49 and 28 cases, respectively.

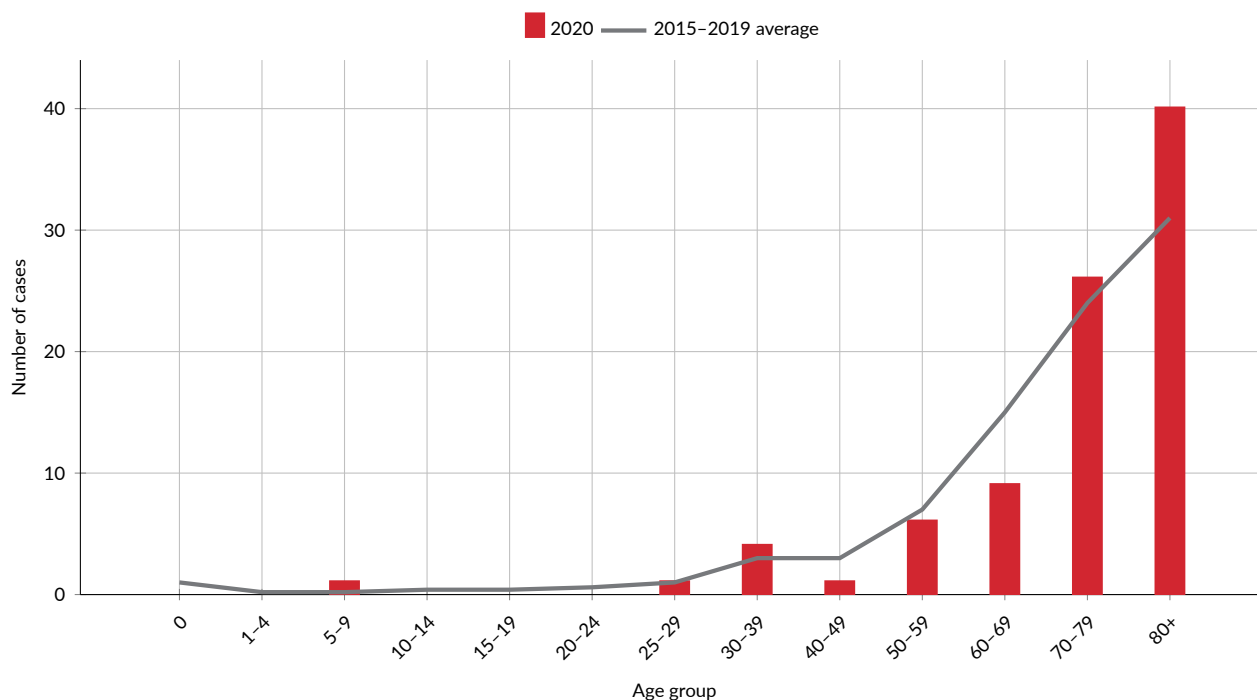


Figure 12: Number of notified human cases of listeriosis per age group in 2020 and annual average for 2015–2019.

of *L. monocytogenes* in qualitative analysis (presence or no presence). *L. monocytogenes* was detected in eight samples (Table 12). In addition, 14 samples were analysed in quantitative analysis (number of colony forming units per gram). The levels of *L. monocytogenes* in these samples were <10 cfu/g, except for two samples (a ready meal and a cheese) in which the levels were 260 cfu/g and >1000 cfu/g, respectively. Sequence types from most isolates from samples taken by competent authorities were identified by WGS. In addition, isolates from 14 samples taken by food business operators were sent to the Swedish Food Agency for typing on a voluntary basis.

Humans

During 2020 the incidence of listeriosis decreased slightly compared to 2019 but the overall picture shows an increasing trend of cases of listeriosis in Sweden (Figure 11). In total, 88 cases were reported compared to 113 cases in 2019 (incidence 0.8 cases per 100 000 inhabitants) (Figure 11). The majority of the cases reported with listeriosis belong to the older age groups. The median age was 79 years and as in previous years, most cases were reported in the age group over 80 years (Figure 12). Forty-eight cases were males and 40 were females. In total, 23 cases (26 percent of reported cases) died within one month from diagnosis. Listeriosis is most often a domestic infection and for 96 percent of the reported cases in 2020 Sweden was noted as the country of infection. In 2020 all but one (99 percent) of the human isolates were sent to the Public Health Agency of Sweden for typing. The most common molecular serotypes were as in previous years IIa (n=69) and IVb (n=16) while only one case each of IIb and IIc was reported. In addition to serotypes, sequence types (ST) are also identified by WGS. During 2020 the most common STs were ST8 and ST1. Two

cases with ST1 had the same outbreak strain which caused an outbreak in 2018 linked to ready-to-eat meals. A more in-depth cluster analysis showed that the proportion of the isolates belonging to a cluster decreased compared to the years before (36 percent compared to an average of 52 percent in 2017–2019). In total, 14 different clusters were identified of which 13 contained identical or closely related isolates identified already before 2020.

Investigations of outbreaks and single cases of listeriosis

Two investigations involving a national cross-sectoral approach were conducted in 2020. The two persistent clusters of *L. monocytogenes* (ST155 and ST14) with in total 12 isolates during 2020, included isolates identified during a time period of up to ten years. This indicates that such strains may be established in production facilities and occasionally contaminate food products causing illness in patients during long time periods (Figure 13).

The cluster of ST14 includes 19 cases with identical or nearly identical isolates identified since 2014 of which eight cases were identified in 2020. The majority of cases (84 percent) are from two counties in the northern parts of Sweden which indicates that the source of transmission is a locally produced food product. Due to epidemiological information and earlier notification of positive sampling results from the producers, the Swedish Food Agency performed additional control and sampling measures at several producers in one of the northern regions. The outbreak strain could not be found in any sample. Additional communication efforts to the regional authorities have also been performed.

The cluster of ST155 includes 26 cases with identical or nearly identical isolates identified since 2011 of which four cases were identified in 2020. The outbreak strain was

Table 12: Results of analyses in 2020 for presence of *L. monocytogenes* in food samples taken by authorities.

Reason for sampling	No. of samples	No. of positive samples	Food in which <i>L. monocytogenes</i> was detected
Survey	7	0	-
Routine control	148	2	Ready meal
Suspected food poisoning or complaint	31	4	2 Cheese 2 Meat from pig (ham)
Other or not reported	59	2	2 Cheese
Total	245	8	

found in blue cheese and ham sampled from refrigerators of two cases in 2020, but the source of the outbreak is still unknown. The whole genome sequence of the outbreak strain was shared with other European countries within the ECDC network. No close match could be identified, which indicates that the source of transmission is a Swedish food product.

In addition, a rare strain of *L. monocytogenes* in Sweden, ST91, caused one case of listeriosis linked to a locally produced cheese. A sample of washed rind cheese was collected from the refrigerator of the case and found positive for the outbreak strain in microbiological analysis. The cheese was made from pasteurised milk, but analysis of environmental samples from the dairy showed that premises and equipment were contaminated by the outbreak strain.

DISCUSSION

During 2020 the incidence of listeriosis decreased compared to the year before but the overall picture shows an increasing trend of listeriosis. (Figure 11). The same trend has been observed in other European countries. The reasons for the increase remain unclear but are most likely related to the increased population size of the elderly and an increased proportion of susceptible persons within different age groups, possibly in combination with other factors such as preference changes to more ready-to-eat foods. The ECDC collaborates with the member states to strengthen the molecular surveillance and thereby facilitate detection of cross-border clusters and outbreaks of *L. monocytogenes*. This collaboration includes the EFSA and is essential for investigation of foodborne cross-border outbreaks in Europe.

In 2020 as in previous years, typing using WGS indicated that many of the linked cases were geographically dispersed and that the sources of infection had persisted for many years. Continued surveillance of *L. monocytogenes* in humans and in food and food processing environments is essential for understanding the sources for human infection and providing tools for prevention. For identification of possible links between human cases and food products, subtyping of isolates is essential.

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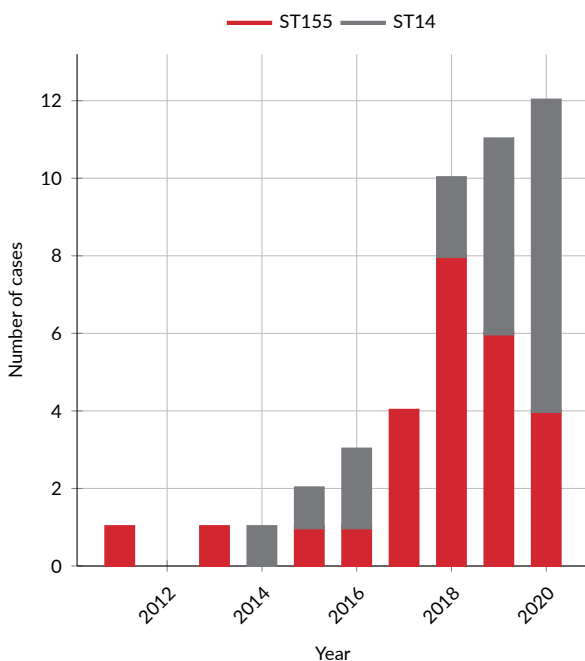


Figure 13: Number of human cases of listeriosis with isolates belonging to two persistent clusters of *L. monocytogenes* (serotype IIa) of sequence type (ST) 155 and 14 during 2011-2020.

Nephropathia epidemica



Humans may be exposed to Puumala virus during occupational or recreational activities, such as working with hay, cleaning barns or summer cottages, cutting wood and entering buildings contaminated with rodent excretions. Photo: Cleardesign1/iStock.

BACKGROUND

Nephropathia epidemica (NE) is caused by Puumala virus, a member of the Hantavirus genus in the *Bunyaviridae* family. Hantaviruses are the cause of rodent-borne haemorrhagic fevers with renal syndrome (HFRS) and hantavirus pulmonary syndrome (HPS). Puumala virus is likely to be the most prevalent hantavirus in Europe. The virus is excreted in saliva, urine and faeces from its natural reservoir, the bank vole. Puumala virus can remain infectious in bank vole cage bedding for two weeks. Transmission to humans often occurs in an aerosolised form. Humans may be exposed to virus aerosols during occupational or recreational activities, such as working with hay, cleaning barns or summer cottages, cutting wood and entering buildings contaminated with rodent excretions.

Nephropathia epidemica was first described by two Swedish physicians, independently, in 1934. The linkage to the bank vole was suggested many years later. The virus was first isolated in 1982 in Puumala, a municipality in south-eastern Finland.

In Sweden, between 50 and 600 cases are reported each season with a considerable interannual variation coupled to the 3–4-year population cycle of the bank vole. During the winter seasons 2006–2007 and 2007–2008 the number of

notified cases rose to 1400, where most of the cases occurred in 2007 (Figure 14). It is hypothesised that a parallel occurrence of a peak in the bank vole population and lack of snow cover in December 2006 caused bank voles to seek refuge in buildings and barns, hence increasing their contact with humans.

DISEASE

Animals

In the bank vole, the infection is understood to be subclinical.

Humans

The clinical picture is characterised by a sudden onset of high fever, headache, backache and abdominal pain. The symptoms range from sub-clinical to renal failure requiring intensive care and dialysis, but fatal cases are rare. The incubation period varies from 2 to 6 weeks.

LEGISLATION

Animals

Hantaviruses are not notifiable in animals.

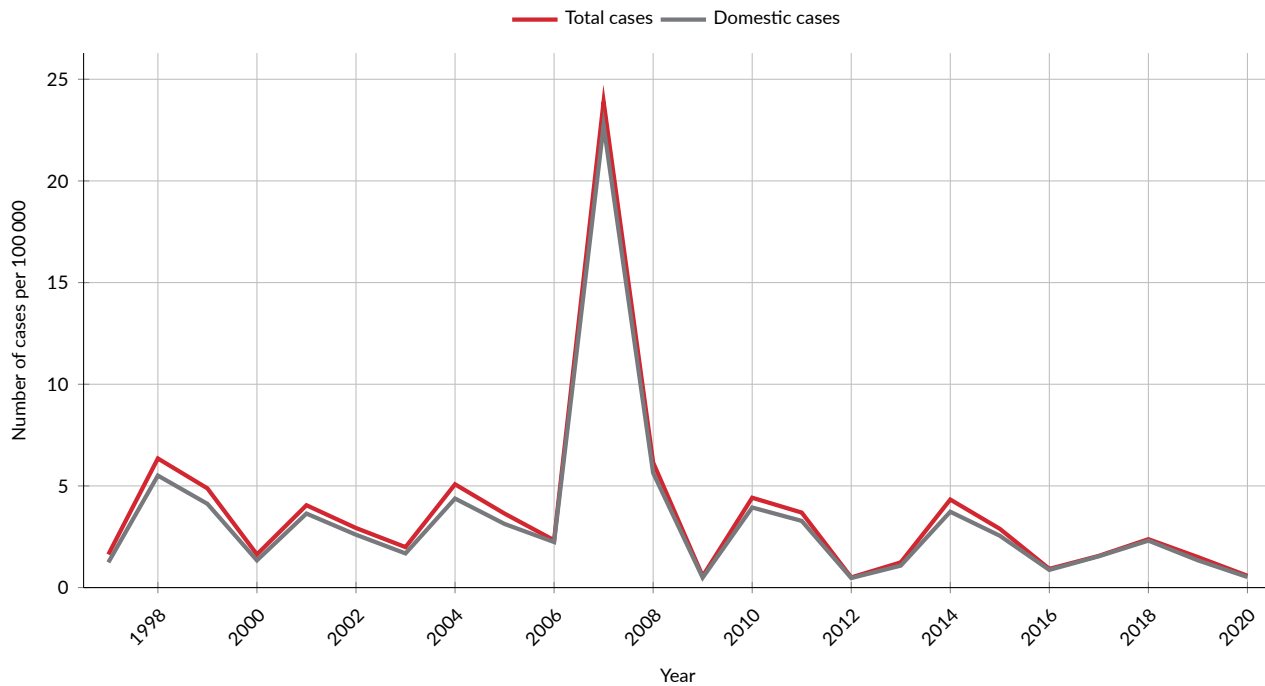


Figure 14: Notified incidence per 100 000 inhabitants of human Nephropathia epidemica in Sweden 1997–2020.

Humans

Nephropathia epidemica has been notifiable since 1989 according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2013:634).

SURVEILLANCE

Animals

There is no surveillance in animals.

Humans

The surveillance in humans is mandatory and based on identification of the disease by a treating physician or by laboratory diagnosis. Both are obligated to report identified cases to the regional and national level to enable further analyses and adequate intervention measures.

RESULTS

Humans

In 2020, 61 cases of NE were reported, which was a decrease in comparison to the previous year and the lowest number of reported cases since 2012 (Figure 14). The median age among all cases was 52 and most reported cases were males in the age category 30 years and older. There were very few cases below the age of 20 years reported, both among men and women. Consistent with previous years, more cases were reported in men (62%) than in women. The reason for this difference in incidence between age groups and sexes is not completely understood, but behaviour is most likely an

important factor.

Most of the reported NE cases acquire their infections in Sweden. In 2020, all cases, for whom the country of infection had been stated, had been infected in Sweden. For eight cases the countries of infection were unknown.

A majority of the cases were reported to have been infected in Norrland and the northern parts of Svealand. The incidence was highest in the Region of Norrbotten (8.4 cases per 100 000 inhabitants) followed by the Region of Västerbotten (5.1 cases per 100 000 inhabitants). All cases reported from the southern parts of Sweden, except one, were infected further north, i.e. in areas where NE is already known to occur. This regional pattern is consistent with patterns observed during previous years. But, rare enough, one case was suspected to have been infected in Skåne, in the same part of the region as a case who was notified in 2018.

DISCUSSION

During recent years, fluctuations in the bank vole population have coincided with increases and decreases in the number of human cases of Puumala virus infections. The 3–4-year natural population cycle and variations in the climatic conditions impact the rodent populations.

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Paratuberculosis



The voluntary surveillance programme for paratuberculosis includes all main beef breeding herds in Sweden. Photo: Bengt Ekberg/SVA.

BACKGROUND

Paratuberculosis, caused by *Mycobacterium avium* subsp. *paratuberculosis* (MAP), is a common disease of ruminants in most parts of the world. Throughout the 20th and 21st century, detection of cases in Sweden has been followed by whole herd stamping-out, tracing and sanitation measures, with the goal of eradicating the disease and to prevent spread of infection, should it be introduced.

Previous cases of MAP in Sweden have all been directly or indirectly linked to imported beef cattle. The latest case of MAP was detected in 2005, in an imported beef bull. Paratuberculosis has never been detected in dairy cattle, other ruminant species or wildlife in Sweden.

Previous active surveillance

Several screenings in cattle were initiated after detection of a positive beef cow in 1993:

- Screening of 200 dairy herds in the years of 2000, 2003 and 2005.
- Screening of sheep herds during the years 1993–2011, first with serology, then with faecal culture.
- In 2007–2009 faecal culture screening of beef herds with animals imported during 1990–2005. In 2012,

another screening of beef herds with animals imported during 2005–2011 was conducted.

- Risk-based screening of older cows at abattoirs in 2009–2010, including cows older than six years with signs of weight loss, resulted in 1211 sampled cows.
- In 2012–2013, bovine practitioners were encouraged to look for and sample cows with low bodyweight, with or without diarrhoea and 258 samples were analysed by faecal PCR.

DISEASE

Paratuberculosis, also known as Johne's disease, causes chronic diarrhoea and emaciation, resulting in suffering and death. If present, the disease causes great economic losses due to reduced milk production, reproductive losses and increased replacements of affected animals.

The incubation period ranges from months to several years. In areas with endemic infection, clinical disease is most commonly seen at the age of 2–5 years. The bacteria are excreted in the faeces of an infected animal and the normal transmission route is faecal to oral. There is no reliable method to detect the infection in the individual animal during the incubation period.

The zoonotic potential of MAP is a recurring question and there are ongoing discussions about MAP as a possible contributing factor to the development of Crohn's disease in humans.

LEGISLATION

Paratuberculosis has been included in the Swedish Act of Epizootic diseases since 1952 (SFS 1999:657 with amendments). Vaccination is prohibited by law and notification of the infection is mandatory on clinical suspicion. The Swedish Board of Agriculture decides on actions when MAP is detected in a herd. Quarantine and testing at trade and import is mandatory as regulated in SJVFS 1998:70 (amended by SJVFS 2018:29).

SURVEILLANCE

The overall purpose of the surveillance is to document freedom from bovine paratuberculosis and to allow for early detection of the infection and prevent possible spread by early detection of the infection.

Passive surveillance

Notification, sampling and diagnostic testing are mandatory in animals of any ruminant species exhibiting clinical signs that lead to suspicion of paratuberculosis. Sampling includes faecal samples from live animals and post mortem samples from dead or culled animals. The latter consists of samples from the ileal wall, ileal contents and ileocaecal lymph nodes as well as any macroscopic lesions in the intestines. Wildlife is sampled when paratuberculosis is suspected at postmortem.

Post mortem examinations

Since 2004 sampling is performed on all ruminants above one year of age submitted for post mortem examinations as part of the enhanced passive surveillance for MAP. Samples are taken from the ileal wall, ileal contents and ileocaecal lymph nodes and submitted to the National Veterinary Institute. The average number of animals examined per year has been around 370, most of them being cattle, the others being predominantly sheep but also a few goats and exotic ruminants like bison and camelids.

Active surveillance

Programme for targeted surveillance in beef cattle

In the voluntary programme, the target population is beef herds that sell animals for breeding. The programme is managed by Farm & Animal Health and financed by the Swedish Board of Agriculture. In total, at the end of 2020, the voluntary programme for bovine paratuberculosis encompassed 451 herds, of which 426 were of the highest status within the programme. The voluntary targeted surveillance programme includes all main beef breeding herds and a smaller number of dairy herds selling calves to beef herds within the programme.

In affiliated herds, individual faecal samples are collected annually for three consecutive years from all cattle

over two years of age. While most of these samples are analysed individually, pooling of samples three and three or five, is occasionally done at the lab. Herds affiliated with the programme are only allowed to trade with herds of the same status or higher to maintain their level within the programme. After three years of negative test results, the faecal sampling is replaced by postmortem of all deceased or euthanised cattle on the premises where paratuberculosis cannot be excluded as a cause of culling. In the case affiliated beef herds have sheep in contact with the cattle, the sheep are sampled as well.

Bulk milk testing

To improve the surveillance in the dairy cattle population, bulk milk testing was recently added. The aim was to sample all dairy herds in Sweden and milk samples were originally collected during 2019 and analysed during 2020.

Abattoir testing

To increase the surveillance in beef cattle herds not affiliated to the voluntary surveillance programme, testing of slaughterhouse serum samples from non-dairy cattle was implemented in 2020.

Health controls for export reasons

Testing for MAP is performed for export reasons when requested. The choice of analysis depends on the recipient country.

Diagnostic tests

Samples collected from clinical suspicions and individual faecal samples from the voluntary beef herd control programme are analysed with direct PCR. Samples are pre-treated by homogenization in lysis buffer and subsequently DNA is recovered by a robotic extraction system. Real-time PCR is performed using a commercial kit.

Blood and bulk milk samples are analysed with the commercial indirect ELISA kit *ID Screen Paratuberculosis Indirect* on an automated ELISA system (Tecan). Positive reactions in the screening test are manually confirmed using the *IDEXX Paratuberculosis Verification Ab Test*, also an indirect commercial ELISA kit but with improved specificity by using individual negative control samples. Any positive serological reactions are always followed up with stool samples for antigen detection and/or extensive serological re-testing in the herd.

Cultures are pre-treated with HPC (an antibiotic to inactivate other bacteria but mycobacteria) and double incubation. Samples are subsequently cultured on modified Löwenstein-Jensen medium supplemented with mycobactin and on Herrolds Egg Yolk medium for up to 4 months. Faecal samples from sheep are cultured for up to 6 months on modified L-J with mycobactin. Direct PCR on a new preparation from the stored samples are performed on cultures with mould overgrowth.

All diagnostic analyses are performed at the National Veterinary Institute.

RESULTS

In 2020, two suspicions of paratuberculosis in cattle, one in moose (*Alces alces*) and one in addax antelopes (*Addax nasomaculatus*) (all wild species from a Swedish zoo) were raised due to clinical signs of the disease. All suspected cases tested negative for MAP with PCR and the suspicions were ruled out.

Bulk milk samples from 3303 dairy herds have been tested, all with negative results except one herd. The test positive herd was followed up by additional bulk milk testing and serological testing of all cows in the herd. All follow-up samples were test negative and MAP was excluded.

In the abattoir serum sampling, 4252 analyses of samples from 2250 herds have been conducted. Three samples had a positive test result, and the source herds are currently under investigation to rule out paratuberculosis.

Moreover, 1170 samples, corresponding to approximately 1377 cattle (there is an uncertainty of 10 animals due to the pooling of samples) from 38 herds, and 25 sampled sheep from 4 herds, were analysed and tested negative within the programme in beef herds. For export reasons, four cattle were tested with serology. Two hundred and seventy-one animals were sampled at post mortem examination; 188 cattle, 69 sheep, 10 goats, 1 bison (*Bison bison*), 2 alpaca and 1 camel (*Camelus bactrianus*). No cases of MAP were detected in the examinations completed in 2020 (Tables 13, 14 and 15).

Table 13: Cattle sampled for paratuberculosis in 2020.

Surveillance in cattle	No. of sampled animals	No. of herds
Beef herd surveillance programme	1377	38
Cattle sampled at post mortem examinations	188	138
Cattle sampled for export	4	2

Table 14: Exotic ruminants sampled for paratuberculosis in 2020.

Surveillance in exotic ruminants	No. of sampled animals	No. of herds
Exotic and wild kept ruminants sampled at post mortem examination ^A	4	4
Exotic and wild kept ruminants sampled for export	0	0

^A 1 bison, 2 alpaca, 1 camel.

Table 15: Sheep and goats sampled for paratuberculosis in 2020.

Surveillance in sheep and goats	No. of sampled animals	No. of herds
Sheep sampled in cattle herds within the beef herd surveillance programme	25	4
Sheep sampled at post mortem examinations	69	56
Goats sampled at post mortem examinations	10	7

DISCUSSION

If present at all, the prevalence of MAP in Swedish ruminants remains at a very low level. The risk of introduction of paratuberculosis to Swedish herds is assessed to be very low, due to the existing legislation and the low number of animals brought in from other countries.

The screenings of beef herds with cattle imported from 1990–2011 was targeting the highest risk group of animals for MAP in Sweden; MAP has never been detected in any other breeds or species than beef cattle and all cases have been traced back to imported animals with the latest case in 2005.

Fallen stock is considered a risk category for paratuberculosis and therefore all ruminants older than one year of age, submitted for post mortem examination, are sampled for MAP and examined by culture. All herds affiliated to the voluntary programme must send fallen stock for post mortem examination if paratuberculosis cannot be ruled out as a cause for death or culling. The post mortem sampling also includes other susceptible species, like sheep, goats and exotic ruminants. The exotic ruminants are sometimes imported or kept in herds with other exotic ruminants imported from countries where MAP is prevalent.

A previous update of the evaluation of the paratuberculosis surveillance programme indicated that the surveillance sensitivity in the last years has decreased. Testing of bulk milk samples and slaughterhouse serum samples to increase the surveillance in the dairy cattle population and beef cattle herds not affiliated to the voluntary programme is currently being done, to improve the surveillance sensitivity.

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Porcine reproductive and respiratory syndrome



After the successful eradication of Porcine Reproductive and Respiratory Syndrome virus (PRRSV) following an outbreak in 2007, annual surveillance shows that Sweden has remained free from the PRRSV since 2008. Photo: Marie Sjölund.

BACKGROUND

Porcine reproductive and respiratory syndrome (PRRS) is a disease of domestic pigs caused by an enveloped RNA-virus belonging to the family Arteriviridae. The disease was first described in the USA in 1987 and the virus (PRRSV) was subsequently identified in 1991. PRRSV has since become endemic in most pig populations of the world and is considered one of the most economically important viral diseases affecting pig production globally. PRRS is highly contagious and is transmitted between pigs through both direct and indirect contact. Sero- and virus-positive feral pigs and wild boars have been described but there is no evidence that they serve as a reservoir for PRRSV.

Sweden has had an active PRRSV surveillance programme since 1998, with Farm & Animal Health collecting samples that are analysed by the National Veterinary Institute. In July 2007, the first case of PRRS in Sweden was detected through this active surveillance programme. Until

then, Sweden had been one of only a few countries to declare itself free from PRRSV. At the time of detection, the disease was not widespread, so a decision was made to control the outbreak through a modified stamping out procedure. The actions taken to eradicate the disease proved to be effective as, following extensive surveillance during the fall of 2007, Sweden was once again declared free from PRRSV with a high probability by the beginning of 2008. Despite extensive investigation, the source of the outbreak could not be established.

After the outbreak in 2007, the surveillance programme was revised in order to enable even earlier detection of an introduction of PRRSV. The programme underwent revision again in 2012 following extensive changes in the pig production system in Sweden.

DISEASE

Infection with PRRSV causes varying clinical signs depending on the age of the infected animals. The incubation period

is 2–7 days and, in adult pigs, the clinical signs are typically mild, consisting of fever, lethargy and inappetence. The devastating effect of PRRSV infection in this category of animals is that it causes reproductive failure including abortions, mummified foetuses, small litters, weak-born piglets and increased incidence of non-pregnant sows. The primary clinical signs in weaned and fattening pigs are fever, respiratory signs, reduced growth and increased mortality.

In 2006, an atypical variant of PRRSV was reported from Asia. This variant causes more severe clinical signs and higher mortality than previously described genotypes of the virus. This atypical variant may cause high fever, discolouration of the skin and high mortality rates in all age groups.

LEGISLATION

PRRS was included in the Swedish Act of Epizootic diseases in 1999 (SFS 1999:657 with amendments) and is consequently notifiable on suspicion. Notification leads to further investigation.

SURVEILLANCE

The purpose of the surveillance is to document freedom from PRRSV and to detect introduction of the virus before it becomes widespread in the population. Tests to detect both viral genome and antibodies against PRRSV are used in the surveillance. All samples are analysed at the National Veterinary Institute. To detect antibodies against PRRSV, a commercial ELISA method (IDEXX PRRS X3 Ab Test, Idexx Laboratories) is used. Samples testing positive for PRRSV antibodies by ELISA are sent to the Danish Technical University for confirmation testing using an immunoperoxidase monolayer assay (IPMA). Analysis for the presence of PRRS viral genome is done using an in-house PCR method (modified from Kleiboeker *et al*, 2005).

Passive surveillance

PRRS is notifiable on clinical suspicion by both veterinarians and farmers and cases with suspect clinical signs are investigated following notification to the Swedish Board of Agriculture. The investigation may include sampling of sick or dead animals, examination of the herd for the presence of clinical signs and analyses of production results. During the investigation the farm is placed under restrictions.

In addition, PCR analysis for the presence of PRRSV genome is included in the enhanced passive surveillance of aborted foetuses (see chapter on “Examinations of abortions in food producing animals” on page 134).

Active surveillance

Within the active surveillance programme, which has been running in its current, revised form since 2013, all Swedish nucleus herds, multiplying herds and sow pools are sampled twice a year, with the aim to collect eight samples per herd on each sampling occasion. In addition, pigs from randomly selected production herds are sampled at slaughter throughout the year at the 9 largest Swedish abattoirs which slaughter approximately 99.5% of Sweden’s pigs. Three samples

per herd are collected on each of these sampling occasions.

The revised programme was designed to take into consideration an increased risk of PRRSV introduction and changes in the structure of Swedish pig production, as well as to keep the probability of freedom from PRRS at the same level as it was after demonstration of freedom following the outbreak in 2007. To achieve this, the programme was designed using a between-herd design prevalence of 0.5%, a within-herd design prevalence of 40% and a risk of introduction of 1 in 5 years. The number of samples needed is calculated yearly taking the outcome of the surveillance in previous years into account. For 2020, the calculated number of samples required was 2400 from the abattoir sampling in addition to the field sampling described above.

RESULTS

Passive surveillance

Five investigations following clinical suspicions of PRRS were conducted in 2020. In all of these herds, reproductive problems such as abortion, weak-born piglets, high piglet mortality and increased numbers of open sows were the primary clinical signs. The number of animals sampled and the methods used during the investigations varied and were dependent on factors such as the nature of the suspicion, the clinical manifestation and how widespread the clinical signs were in the herd. All samples taken during the course of the investigations were negative and all herds were subsequently declared negative for PRRSV.

Within the programme for enhanced passive surveillance of aborted foetuses, 21 foetuses from 11 herds were examined for the presence of PRRSV genome and all samples were negative.

Active surveillance

In 2020, 601 samples from 43 nucleus herds, multiplying herds and sow pools were analysed. In the abattoir sampling, 2410 samples originating from 468 herds on 806 sampling occasions (some herds were sampled more than once during the year) were analysed. For comparison, the number of samples tested per year since 2009 is given in Table 16. Of all samples collected during 2020’s active surveillance, 4 samples from 4 different herds were serologically positive by both ELISA and IPMA testing. Three of these positive samples were collected in sow herds and one sample was collected at an abattoir. Herd investigations were conducted in all 4 herds. Clinical examination of the herds found that none of the herds displayed clinical signs consistent with PRRS. Additional serum samples were also collected in each of these herds and analysed for the presence of PRRS antibodies. All additional samples were negative, and it was concluded that the positive samples were singleton reactors and not due to infection with PRRSV.

Taking the surveillance outcome from previous years into account, the probability of freedom based on the surveillance during 2020 was >99%.

Also in 2020, one herd investigation was initiated after a serum sample taken from an imported boar in a quarantine

Table 16: Number of samples and herds tested in the active surveillance for porcine reproductive and respiratory syndrome 2009–2020 in relation to the number of registered swine herds.

Year	Field sampling		Abattoir sampling			Total number of samples	Number of registered swine herds in Sweden ^A
	Number of samples	Number of sampled herds	Number of samples	Number of sampling occasions	Number of sampled herds ^B		
2009	1106	69	2712	904	841	3818	2027
2010	2012	126	4424	1475	931	6436	1695
2011	1240	78	2308	770	700	3548	1297
2012	1055	66	2145	717	623	3200	1113
2013	1024	64	1548	516	488	2572	1281
2014	912	57	2028	676	537	2940	1282
2015	824	52	2382	780	521	3206	1228
2016	875	60	2446	815	506	3321	1252
2017	826	54	2625	875	546	3451	1272
2018	784	54	2707	903	514	3491	1346
2019	647	42	2550	851	506	3197	1089
2020	601	43	2410	806	468	3011	1146

^A Jordbruksverket statistikdatabas (statistik.sjv.se/pxweb).

^B Some herds were sampled more than once.

unit tested positive for PRRS by both ELISA and IPMA analysis. No clinical signs indicative of PRRS were observed in the herd and follow-up samples taken from animals in the quarantine unit were negative so the herd was subsequently declared PRRS negative.

DISCUSSION

Before the outbreak of PRRS in 2007, the active surveillance programme was based on field sampling in all nucleus herds, multiplying herds, sow pools and 50 production herds once a year, usually clustered in time. This surveillance design had the drawback of being expensive, having a low sensitivity and a risk of poor timeliness. After the outbreak, the surveillance was further developed by employing continuous abattoir sampling and more effective field sampling in nucleus herds, multiplying herds and sow pools to improve early detection of a PRRSV introduction and to increase the sensitivity of the surveillance. The evaluation of the programme in 2012 indicated that the probability of freedom and the sensitivity of surveillance were declining over time and the changes that were suggested aimed at breaking this trend. The main reason for the declining probability of freedom was a decreasing number of samples tested. During recent years, the Swedish pig industry has undergone substantial structural changes leading to a rapidly declining number of herds and extensive changes in the market and in the habits of farmers. These changes emphasise the need for continuous monitoring of surveillance performance over the year and a yearly evaluation of performance and design. The present design, with continuous sampling and testing over the year

in combination with the clinical surveillance, increases the probability of early detection compared to the strategy used before the outbreak.

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Psittacosis

BACKGROUND

Psittacosis is caused by *Chlamydia psittaci*, an intracellular bacterium. In 1879, psittacosis was described for the first time when an outbreak of pneumonia associated with exposure to tropical pet birds was detected among Swiss patients. The organism was identified in the 1930s. Since then, outbreaks have been described worldwide.

The main reservoir is the bird population, and the organism is excreted in faeces and nasal discharges. Birds may become carriers of the organism and shed it intermittently for years without any clinical signs. People acquire the infection mainly via inhalation of contaminated dust or through contact with infected birds. In birds, the infection is transmitted via contact, by ectoparasites or contaminated equipment. *C. psittaci* may persist in dry faecal material for months.

Control of psittacosis in animals is very difficult since the organism exists in both domestic and wild birds.

DISEASE

Animals

Birds commonly develop clinical signs when stressed or when their immune system is suppressed. Clinical signs in birds range from an asymptomatic infection to conjunctivitis, sneezing, pneumonia, and generalised infection. Adult birds recover from the infection, but mortality can be up to 90% among young birds.

Humans

In humans, the symptoms often include fever, headache, rash, myalgia, chills and upper or lower respiratory tract infection. The disease is usually mild or moderate but can be severe especially in untreated elderly persons. Most human cases are considered sporadic and many mild infections are likely not diagnosed. The incubation period is usually around 10 days but can vary from 1 to 4 weeks.

LEGISLATION

Animals

Psittacosis is notifiable in animals according to SJVFS 2013:23.

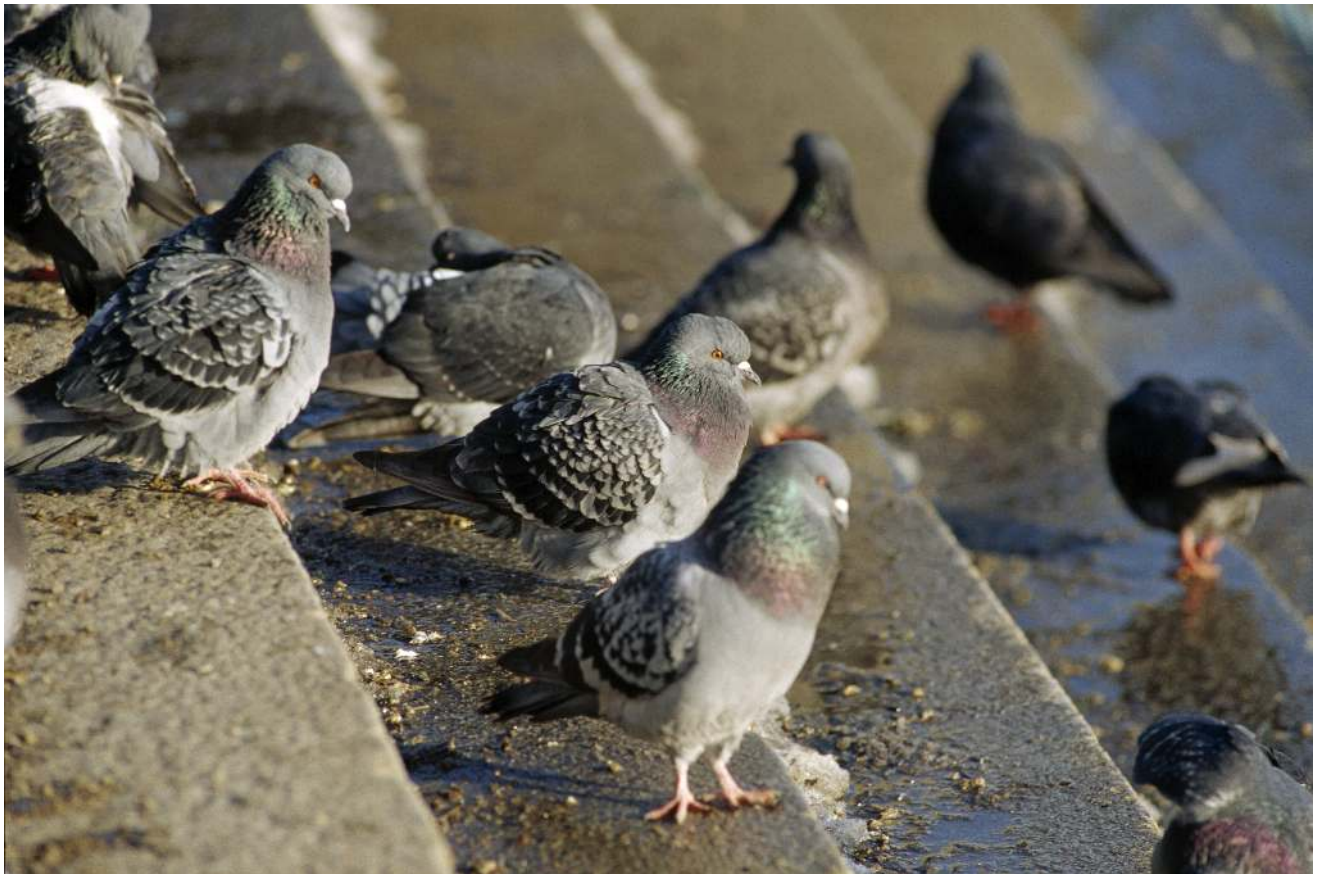
Humans

Psittacosis in humans has been a notifiable disease since 1969 according to the Communicable Disease Act (SFS 2004:168) with the amendments of SFS 2013:634.

SURVEILLANCE

Animals

Surveillance in animals is passive. Notification is based on detection of the organism. At SVA, since 2020, detection is performed by a real-time PCR targeting *Chlamydia psittaci*.



Many domestic and wild bird species may harbour *Chlamydia psittaci*. Photo: SVA.

Humans

Notification of human cases is mandatory and surveillance is based on identification of the disease by a treating physician or by laboratory diagnosis. Both are obligated to report identified cases to the regional and national level to enable further analyses and adequate intervention measures. For laboratory verification of the infection, serology and, especially, PCR are the methods predominantly used.

RESULTS

Animals

In 2020, one pet bird and one pigeon were tested at SVA for *C. psittaci* with negative results.

Humans

In 2020, 51 cases of psittacosis were reported which is more than during the entire 2000s so far except for 2019 when 77 cases were reported (Figure 15). In Sweden, psittacosis is mainly a domestic infection and only five of the cases were suspected to have been infected abroad. Of the cases 42 (82%) were male and 37 (73%) over 60 years old. Contact with birds and bird droppings were considered an important route of transmission. For nearly half (n=24) of the cases, handling of poultry, cage birds or bird feeders were reported as likely vehicles for infection. Psittacosis exhibits a strong seasonal pattern with most reported illnesses during the winter months. In 2020, 31 (61%) of the cases were reported in January-March and December.

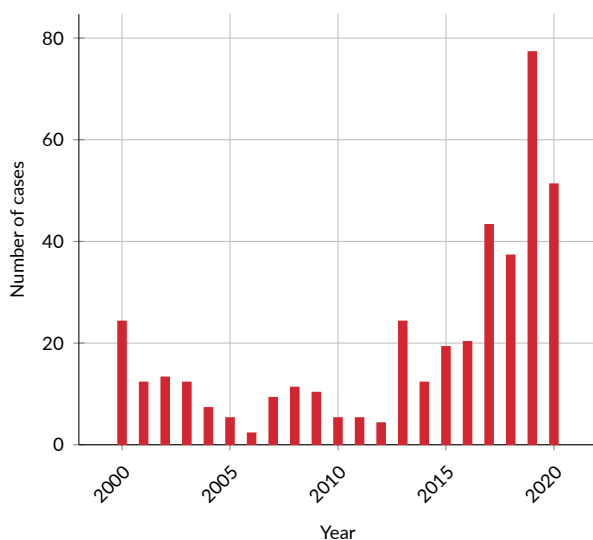


Figure 15: Number of notified human cases of psittacosis in Sweden 2000–2020.

DISCUSSION

During the last four years, there has been a marked increase in the number of notified cases of psittacosis. The reasons for this increase are not known. One explanation could be the recently introduced PCR panels for screening of respiratory tract infections where *C. psittaci* is one of the target organisms. Without such screening, a clear suspicion from the physician is required which demands awareness of the illness. In 2019, a pilot questionnaire study aimed at clinical microbiological laboratories across Sweden showed a clear regional overlap between a larger number of notified cases and usage of a PCR screening approach that includes *C. psittaci*.

In Sweden, like in many other countries, human psittacosis is considered underdiagnosed and underreported. In published reports of psittacosis from other countries, the source has most often been associated with poultry, especially turkeys, or pet birds. In Sweden, however, contact with faeces from wild birds, for example when cleaning wild bird feeders, is considered a major source of infection although pet birds and hobby poultry are also well documented risk factors for psittacosis.

C. psittaci has been detected in a variety of wild bird species, most often in water birds, doves, and pigeons. At present, knowledge on the epidemiology of *C. psittaci* in domestic and wild birds in Sweden is scarce. In a survey performed 2019 of wild garden birds collected during a ten-year period, *C. psittaci* was detected in 2.2% of the birds tested.

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Q fever

BACKGROUND

Q fever is a zoonotic disease caused by the bacterium *Coxiella burnetii*. Because of its tolerance to heat, dryness and many disinfectants, the organism is difficult to eradicate. Cattle, sheep and goats are considered to be the main reservoirs of the organism, but pets such as dogs and cats may also become infected. The agent is shed through several routes, such as milk, foetal and vaginal fluids, faeces, urine and semen. *C. burnetii* has also been isolated from ticks.

Transmission to humans is mainly considered to be through inhalation of contaminated aerosols and dust. Therefore, contact with dusty animal products and environments, such as wool, hay and bedding material may pose a risk. Also, consumption of unpasteurised milk may be a risk to susceptible individuals. In humans, immunosuppression, predisposing valvular heart disease and pregnancy may increase susceptibility to Q fever.

Larger outbreaks of Q fever, when reported, are principally associated with small ruminants, whereas cattle can be a source of sporadic cases. In many countries, Q fever is seen as an occupational hazard for professionals in contact with domestic ruminants and their environments, such as farmers, veterinarians and abattoir workers.

The presence of *C. burnetii* in domestic animal populations in Sweden has been known since the early 1990s. In Sweden the bacterium was first isolated from a sheep placenta in a herd on the isle of Gotland. In 2008/2009, a national survey of dairy cattle herds showed that 8% of the herds were antibody positive in bulk milk. There were large regional differences with the highest prevalence on the isles of Gotland and Öland (59% and 35%, respectively). In 2010, national surveys of sheep and dairy goat herds showed a very low prevalence of antibodies: 0.6% (three out of 518 investigated herds) and 1.7% (one out of 58 investigated herds), respectively. In addition, goat bulk-milk was analysed for the agent; *C. burnetii* was not detected. In 2011, 80 sheep farms were investigated by analysing vaginal swab samples from sheep taken in conjunction with lambing without detecting the agent in any of the samples. These results suggest that *C. burnetii* is a rare pathogen in the Swedish sheep and goat populations. In a survey of 99 Swedish moose during 2008–2010 no antibody positive samples were found, indicating that exposure to *C. burnetii* is rare also in this wild species.

In humans, only two domestic cases were reported in the 1980s and 1990s. During the same period, a serological survey in humans identified 28% of sheep farmers and 13% of veterinarians to be antibody positive, indicating a larger extent of the exposure. However, a prospective study on cases of endocarditis showed that only one of 329 patients had antibodies to *C. burnetii* indicating that chronic Q fever endocarditis is rare.



Surveillance for Q fever in animals is passive in Sweden. Cattle, sheep and goats are considered to be the main reservoirs of the causing bacterium *Coxiella burnetii*. Photo: Ylva Persson.

Since Q fever became notifiable in humans in 2004, one to three cases have been reported annually until 2008, when an increase was observed. Only one case was classified as domestic during the period from 2004–2009. In 2010, the situation changed as eight of the totally 11 reported cases claimed to have been infected in Sweden. All these domestic cases were identified as a result of contact tracing when investigating a farm in southern Sweden, which was included in a national survey on dairy herds and where the bulk milk from the cows was shown to be antibody positive for *C. burnetii*. During the period when Q fever has been a notifiable disease, only about 20% of the reported cases have been women (Figure 16). A similar difference in gender distribution has been described from other countries, but the cause is not clear.

Since the 1980s, few domestically acquired cases of Q fever have been reported apart from the cluster in 2010. Most reported cases have been infected in Mediterranean countries, including the Canary Islands.

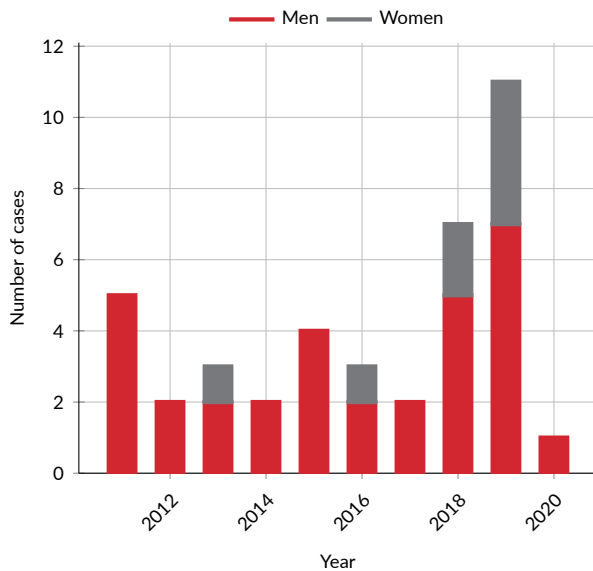


Figure 16: Number of human cases of Q fever by sex during the time period from 2011 to 2020.

DISEASE

Animals

Q fever in animals is usually asymptomatic but can also lead to reproductive failures such as abortions or still/weak born calves. In herds where the agent has been proven to be present, the investigation of reproductive problems should still exclude other causes before reproductive failures are attributed to *C. burnetii* infection.

Humans

In humans the infection can vary from asymptomatic or flu-like illness to acute pneumonia. Liver complications and obstetric complications can also occur. Most patients recover but some may develop a chronic illness. The incubation period varies likely depending on the number of organisms inhaled but is usually 2–3 weeks.

LEGISLATION

Animals

Q fever is a notifiable disease (SJVFS 2013:23). Notification of a primary case of Q fever in animals is based on detection of the agent *C. burnetii* or increased antibody levels in paired samples.

Humans

Q fever has been notifiable according to the Communicable Disease Act since 2004 (SFS 2004:168) with the amendments of SFS 2013:634.

SURVEILLANCE

Animals

Surveillance for Q fever in animals is passive.

Humans

Notification of human cases is mandatory and surveillance is based on identification of the disease by a treating physician or by laboratory diagnosis. Both are obligated to report identified cases to the regional and national level to enable further analyses and adequate intervention measures. For laboratory verification of the infection, serology and PCR are used.

RESULTS

Animals

Limited testing was done in 2020 on cattle mainly for import and export reasons. Blood samples from 11 cattle were analysed for the presence of antibodies by ELISA. As serological tests no longer are performed in Sweden the samples were sent to Denmark for analyses. Animals from one herd were tested for *C. burnetii* in bulk milk by PCR. In addition, one calf foetus was tested for the agent by PCR in conjunction with the surveillance in aborted foetuses. All samples that were submitted for testing were negative.

Humans

In 2020, one case of Q fever was reported, which is considerably less than the annual average over the last ten-year period 16. The case had been infected in Spain through animal contact. The very low number of imported Q-fever cases in 2020 can probably, to some extent, be explained by changed travel patterns during the COVID-19 pandemic.

DISCUSSION

Due to the nature of the infection with asymptomatic cases and unspecific clinical signs it is likely that Q fever is underreported in both humans and animals in Sweden. Only a few human cases are diagnosed every year, of which the majority are infected abroad. The surveillance in animals has been passive since 2012 and as a consequence of this, very few animals are being tested every year, mainly for export reasons. Based on the passive surveillance we know very little about the current prevalence of Q fever in the animal population.

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Rabies



Illegally imported dogs from endemic countries are probably the greatest threat to the rabies-free status of Sweden. Photo: MNSanthoshKumar/iStock.

BACKGROUND

Rabies is caused by a lyssavirus in the family *Rhabdoviridae*, which can infect all warm-blooded animals including humans. The disease occurs worldwide, with some exceptions. Rabies is transmitted through contact with saliva, typically via animal bites. Most human cases are caused by bites from infected dogs. The reservoir animal species for rabies in endemic countries are most notably among carnivores of the family *Canidae*. In Europe, the reservoir species are red foxes and raccoon dogs.

Bats in Europe may carry another type of lyssavirus called European Bat Lyssavirus (EBLV), which also can cause rabies-like disease in humans. Sweden has been free from classical animal rabies since 1886. Findings suggest that EBLV is present in Sweden, but virus has never been isolated.

DISEASE

Humans and animals

Rabies virus infects the central nervous system of humans and mammals. Early symptoms of rabies are non-specific, consisting of fever, headache, and general malaise. As the disease progresses, neurological symptoms appear and may include insomnia, severe anxiety, confusion, slight or partial paralysis, excitation, hallucinations, agitation, hypersalivation and difficulties in swallowing. The incubation period of rabies is usually 3–6 weeks but may vary from five days to

one year.

There are still knowledge gaps on how EBLV infections affect bats. Experimentally infected bats have shown clinical signs as weight loss, disorientation, lack of coordination, muscle spasms and aggression. Some infected bats may still be normal in behaviour.

LEGISLATION

Animals

Rabies is included in the Swedish Act of Epizootic diseases (SFS 1999:657 with amendments) and is notifiable on suspicion. If rabies is suspected or confirmed, measures will be taken to combat the disease and to prevent further spread.

To prevent the introduction of rabies, dogs and cats must be vaccinated against rabies before entering Sweden. In addition, depending on the country of origin, some must have their antibody titre tested. The rules are set in SJVFS 2011:49 (with amendments of SJVFS 2014:47) and in the EU Regulation 576/2013.

Humans

Rabies in humans is notifiable according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2013:634).

SURVEILLANCE

Animals

Passive surveillance

Animals with clinical signs where rabies cannot be excluded are euthanized and tested by fluorescent antibody test (FAT) and PCR.

Active surveillance

Some of the illegally imported pets that are detected and come from countries with endemic rabies are euthanized. They are examined for rabies using PCR to exclude the possible introduction of rabies in Sweden.

During a random check in 2020 in Poland a former stray dog from Russia on its way to Sweden, was found not to have reached the acceptable rabies antibody levels needed to prove effective rabies protection. In the follow-up investigation by Swedish authorities two shipments of a total of 32 dogs imported from Russia to Sweden were investigated for antibody concentration. The purpose was to investigate possible systematic deficiencies in vaccination protection.

Humans

The surveillance in humans is based on identification of the disease by treating physician and/or by laboratory diagnosis (i.e. passive surveillance). Contact tracing to find the source of a detected infection is mandatory in case of domestic transmission. Humans exposed to rabies virus will be evaluated for need of post-exposure vaccination and immunoglobulin treatment.

RESULTS

Animals

In 2020, seven dogs, three cats one red squirrel (*Sciurus vulgaris*) and one fox (*Vulpes Vulpes*) were examined for rabies due to clinical suspicion.

Three dead bats were examined for rabies. The investigations were requested and paid for by different individuals. Amongst them two cat-owners whose cats had been exposed to the bats.

In addition, 40 illegally introduced euthanized dogs and six cats were examined after decision by the Swedish Board of Agriculture. None of the animals had presented clinical signs associated with rabies.

In conclusion, all the above animals that were examined for rabies during 2020 tested negative.

17 of the 32 dogs imported from Russia to Sweden had a rabies antibody concentration below the international threshold of 0.5 IU/ml. Five of these dogs had values below 0.1 IU/ml.

Humans

No human cases were reported during the year.

DISCUSSION

During the last 50 years, two people have been hospitalised for rabies in Sweden, both of whom succumbed to the disease. In 1974, a Swedish man fell ill after having become infected in India. In 2000, a woman fell ill after a visit to Thailand. Both patients had most probably been infected by rabid dogs. Since Sweden is free from classical rabies, the risk of acquiring the disease from Swedish animals is negligible. However, since 2004, there has been an increasing problem with illegal importation of pets, mostly dogs. Illegally imported dogs from endemic countries are probably the greatest threat to the rabies-free status of Sweden.

During a random check in 2020 in Poland a former stray dog from Russia on its way to Sweden, was found not to have reached the acceptable rabies antibody levels needed to prove effective rabies protection. In the follow-up investigation five out of 32 dogs had antibody concentrations below 0.1 IU/ml and were euthanized after decision by The Board of Agriculture. Twelve dogs with titres between 0.1 and, 0.49 were isolated in their homes for a period of four months. The results are in line with investigations made in Norway and Finland. The recommendations from the authorities are to test dogs which are to be imported from Russia before they enter Sweden. Furthermore, the Board of Agriculture will carry out random checks on dogs from Russia to follow up the results from 2020.

However, the greatest risk to people is contact with dogs in countries with endemic dog rabies. In 2019 one woman in Norway died from rabies after having been exposed to a rabid puppy in the Philippines.

The rabies situation in many countries, especially in the EU, is improving due to control and eradication programmes. All countries in the EU are now considered rabies-free or low-risk countries. EU co-finances control, eradication and surveillance programmes in member states as well as in some third countries adjacent to EU. Russia is considered a high risk country with a lot of rabies cases in wild and domestic animals each year.

From 1998 to 2016, an enhanced passive surveillance programme where dead bats were examined for the presence of rabies was implemented almost every year. In addition, from 2008 to 2013 an active surveillance programme for EBLV was performed in different regions in Sweden.

Antibodies to EBLV have been detected in specimens from live Daubenton's bats as part of the active surveillance programme, suggesting that EBLV is present in Sweden. Daubenton's bats (*Myotis daubentonii*), associated with EBLV-2, are common and may be found from the south up to the county of Ångermanland in the north. Six other *Myotis* species may also be found in Sweden. The Serotine Bat (*Eptesicus serotinus*), associated with findings of EBLV-1 in Europe, is found in certain habitats in the south of Sweden. The Northern Bat (*Eptesicus nilssonii*), which is related to the Serotine Bat, is the most common bat in Sweden, and may be found all over the country.

Salmonellosis

BACKGROUND

Salmonellosis is one of the most important bacterial zoonoses. The genus is divided into two species: *S. enterica* and *S. bongori*. Most *Salmonella* belong to *S. enterica* subspecies *enterica*. More than 2500 different serovars belonging to this subspecies have been described. *Salmonella* can infect a multitude of animal species, including humans. Humans are infected by contaminated food products of various types, through contact with infected animals, via person-to-person transmission or via a contaminated environment.

A severe domestic outbreak of *S. Typhimurium* in 1953 with more than 9000 cases prompted the need for a control programme for *Salmonella* in Sweden. Since then, the strategy for control has been to prevent *Salmonella* in all parts of the production chain, from feed to food of animal origin. When Sweden joined the European Union in 1995, the Swedish *Salmonella* control programme was accepted. Sweden obtained additional guarantees for live animals, meat, and eggs from countries with a non-equivalent *Salmonella* status to be tested for the presence of *Salmonella* before entering the Swedish market. The control programme constitutes an important safeguard to Swedish public health.

In recent years, a total of 2000–3000 human cases of salmonellosis have been reported annually to the Public Health Agency of Sweden. A majority (60–80%) of these cases were infected abroad. During the last decade, the number of cases infected abroad has decreased, whereas the domestic incidence has remained stable. Yet, the proportion of domestic infections in Sweden is low compared to many other countries. The source of the verified outbreaks is often imported food. The contribution to the human disease burden from domestic food-producing animals is low. In 2020, the COVID-19 pandemic has resulted in both a record low incidence of salmonellosis and a record high proportion of domestic infections.

DISEASE

Animals

Infected animals are often asymptomatic. However, *Salmonella* can cause clinical illness with diarrhoea, abortions, and fever, and even lead to death. In Sweden, clinical signs are frequently seen in cattle, horses, cats and dogs, whereas infected poultry are most commonly asymptomatic.

Humans

Salmonella infects the gastrointestinal tract and causes an acute gastrointestinal illness. The symptoms can range from asymptomatic and mild to severe. The incubation period is typically between 1 and 3 days but can vary from 6 hours to 10 days. Most patients recover from the illness spontaneously but sequelae such as reactive arthritis occur in approximately 1–15% of the patients. Excretion of the pathogen normally lasts for four to six weeks but prolonged asymptomatic excretion occurs. In rare but severe cases the

infection can spread via the bloodstream to organs outside the gastrointestinal tract.

LEGISLATION

Feed

Control of animal feed is an integrated and essential part of the control programme for *Salmonella* in primary production. The feed business operator is responsible for producing *Salmonella*-free feed. Poultry feed must be heat treated according to the legislation. A major part of cattle and pig commercial feed is also heat-treated. The production of feed is supervised by the Swedish Board of Agriculture which carries out announced and unannounced inspections at feed mills and pet food producers. The control of *Salmonella* in feed is regulated in national legislation (SJVFS 2018:33) as well as in an EU regulation (Commission Regulation (EU) No142/2011).

Animals

Investigation is required upon clinical suspicion of salmonellosis and any finding of *Salmonella*, regardless of serovar, is notifiable. Action is taken to eliminate the infection or contamination except in cases of findings of *S. diarizonae* serovar 61:(k):1,5(7) in sheep. Vaccination is not used in Sweden. The *Salmonella* control programme is governed by the Swedish Act on Zoonoses (SFS 1999:658) and its regulations. The aim of the programme is that animals sent for slaughter and animal products should be free from *Salmonella*.

Food

Any finding of *Salmonella* in food is notifiable and a contaminated food product is considered unfit for human consumption. However, there is one exception, which is *S. diarizonae* serovar 61:(k):1,5(7) in sheep meat, as this serovar is not considered to be of public health importance (LIVFS 2005:20).

Laboratories analysing samples taken by authorities are obliged to send isolates of *Salmonella* from positive food samples to the National Reference Laboratory for serotyping (LIVFS 2005:21).

Humans

Salmonellosis in humans is notifiable according to the Communicable Disease Act (SFS 2004:168 with amendments, SFS 2013:634). Laboratory confirmed cases include cases with samples that are only positive by PCR i.e. where no isolate has been obtained.

MEASURES IN CASE OF FINDINGS OF SALMONELLA Isolates

All suspected isolates of *Salmonella* from non-human sources are sent to the National Veterinary Institute for confirmation, serotyping, resistance testing, and further typing.

Index cases are defined as the first isolate of *Salmonella* in a holding of pigs, cattle, goats, sheep, horses or a poultry flock during the period of restriction measures. For companion animals, index cases are defined as the first isolate of *Salmonella* from a companion animal in a household or a kennel of a specific species during a calendar year. For wild animals, the index case is defined as the first isolate from a wild animal species in a municipality or a locality during a calendar year. Index isolates from index cases as well as other index isolates (other serovars from the holding or the companion animal, findings of *Salmonella* at post-mortem or in a lymph node but not confirmed in a holding and *S. diarizonae* serovar 61:(k):1,5(7) in sheep) are resistance tested. From cats and passerine birds, however, a subset of isolates is resistance tested and typed. In addition, one isolate per holding from holdings under restrictions are resistance tested. Isolates of *S. Typhimurium* are further typed by MLVA. From 2020 onwards selected isolates of all serovars from food and animal sources are characterized by whole genome sequencing.

All isolates of *Salmonella* from domestic human cases are sent to the Public Health Agency of Sweden for typing using whole genome sequencing (WGS). A subset of isolates from travel-associated cases are also typed. Both serotype and resistance markers are identified from the sequence data. Clustering of isolates is also done to identify outbreaks and for source tracing.

Feed

Findings of *Salmonella* in intra-community traded or imported feed materials and compound feeds are reported in the Rapid Alert System for Food and Feed (RASFF) (https://ec.europa.eu/food/safety/rasff_en). Measures are always taken when *Salmonella* is detected in feed samples. *Salmonella* positive feed materials are usually treated with organic acids. After acid treatment the feed material must be re-tested negative before use in feed production. Finished feed containing *Salmonella* must be withdrawn from the market. Extended sampling and cleaning are done in the production line if *Salmonella* is detected in the weekly surveillance. If *Salmonella* is found before heat treatment, the contaminated part of the production line is thoroughly cleaned and disinfected, usually by dry cleaning, followed by disinfection. If *Salmonella* is found after heat treatment, the production will be stopped, and the feed mill must be thoroughly cleaned and disinfected. Environmental sampling must show negative results before production is resumed.

Animals

If *Salmonella* is suspected in an animal, a veterinarian is obligated to take samples and implement measures to prevent further transmission. When *Salmonella* is detected, the laboratory must notify the Swedish Board of Agriculture and the County Administrative Board. When detected in a food-producing animal, the County Veterinary Officer informs the official veterinarian at the abattoir involved.

When *Salmonella* is confirmed on a farm, the holding

is put under restrictions (except in cases of finding of *S. diarizonae* serovar 61:(k):1,5(7) in sheep), an epidemiological investigation is performed and a plan to eradicate *Salmonella* from the holding is defined. Animal movements to and from the holding are stopped.

All *Salmonella* positive poultry flocks are euthanised irrespective of serovar. The poultry house involved, and all possible contaminated areas are thoroughly cleaned and disinfected. Before introduction of new birds, all environmental samples must be negative for *Salmonella*.

In pigs and cattle, a combination of partial herd depopulation and hygienic measures controlled by repeated sampling is usually practiced. Cattle herds under restrictions for *Salmonella* are monitored by a combination of serological and bacteriological testing. Hygienic measures can include reducing the number of animals, control of animal feed and manure management on the farm and reduction of *Salmonella* contamination in the environment by cleaning and disinfection. Animals from restricted herds may be slaughtered after sampling with negative results. The restrictions are lifted when the cleaning and disinfection have been completed and *Salmonella* cannot be detected by culture from whole-herd sampling at two occasions performed four weeks apart.

If *Salmonella* is detected in companion animals, advice on hygienic measures to prevent further spread to other animals or humans is given to the owners. If *Salmonella* is detected in horses, the stables and/or the paddocks at risk are put under restrictions and follow up investigations are performed on the premises.

Food

Products released on the market will be withdrawn and contaminated products will be destroyed or sent for special treatment to eliminate the *Salmonella* bacteria, except for *Salmonella diarizonae* serovar 61:(k):1,5(7) in sheep meat.

Findings in imported consignments are reported in the RASFF system and the consignments will be returned to the country of origin, destroyed, or sent for special treatment as applicable. RASFF is also used for informing about contaminated Swedish food products released on the EU market or within Sweden.

In food enterprises where *Salmonella* has been detected, appropriate follow-up measures will be applied, such as careful cleaning and disinfection and environmental sampling.

SURVEILLANCE

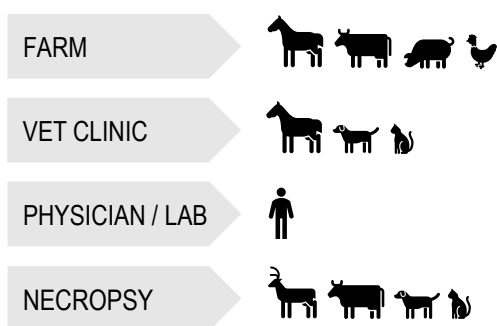
Feed

In the control programme for feed, the emphasis is on control of feed raw materials, the heat treatment process, and preventive measures to avoid recontamination of heat-treated feed. Suspected feed-borne infections are also investigated (Figure 17).

Scheduled sampling



Sampling upon disease suspicion



Voluntary sampling



Sampling following a confirmed case

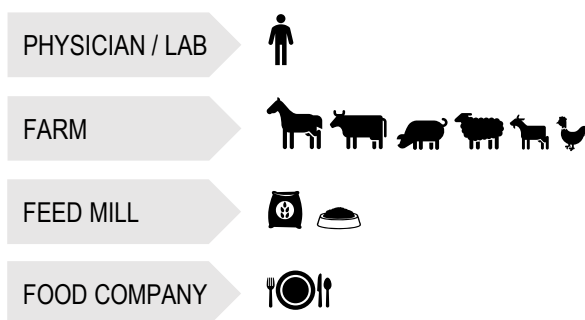


Figure 17: An illustration of the Swedish surveillance of *Salmonella* in feed, food, animals and humans. Infographic by Arianna Comin.

Surveillance of intra-community traded and imported compound feed and feed raw materials

Raw feed materials are the most important risk factor in feed production. In the domestic legislation, feed materials are classified according to the empirical risk of being contaminated, and high-risk feed materials must test negative for *Salmonella* contamination before being used in feed production. All consignments of intra-community traded or imported compound feed for cattle, pigs, poultry and reindeer and feed materials classified as a risk must be sampled and tested for *Salmonella*. The sampling plan is designed to detect a *Salmonella* contamination in 5% of the batch with 95% probability.

Surveillance of feed mills

The purpose of the surveillance is to ensure the absence of *Salmonella* in the production lines as well as in the feed mill environment. A safety management system is applied in the processing line according to HACCP (Hazard Analysis and Critical Control Points). The management system covers several specific GMP (Good Manufacturing Practices) requirements, according to the Swedish legislation. A minimum of five samples from feed mills that manufacture compound feedstuffs for poultry and a minimum of two samples from those manufacturing compound feedstuffs for other food-producing animals must be collected in the processing line on a weekly basis. These samples are analysed at the National Veterinary Institute (using the latest version of EN-ISO 6579-1) and any finding of *Salmonella* is reported to the Swedish Board of Agriculture. The feed manufacturers also take additional samples from the processing line and the feed mill environment as part of their own process quality control.

Pet food and dog chews

Sampling is performed by the feed business operators as part of their feed safety management system. Consignments of pet food and dog chews imported from third countries are sampled according to a sampling plan at the border inspection. The sampling plan is defined based on a risk assessment.

Animals

In all animal samples except for those taken within the control programme at abattoirs, detection of *Salmonella* is performed using the latest version of the EN-ISO 6579-1 method or a method validated against it. Measurement of antibodies against *Salmonella* in blood or milk samples of cattle is performed using commercial ELISA tests PrioCHECK® *Salmonella* Ab bovine ELISA and PrioCHECK® *Salmonella* Ab bovine Dublin.

Poultry

The programme comprises a compulsory part and a voluntary part. The purpose of the compulsory programme is to ensure that poultry sent for slaughter and meat products are free from *Salmonella*. All poultry species are included in the compulsory part, which sets the rules for mandatory sampling (Figure 17).

Compulsory programme

All breeding flocks with more than 250 birds are tested (Table 17). Grandparents of *Gallus gallus* broilers are imported as day-old chicks. Laying hens, turkeys, geese, and ducks are imported as parents. Samples consist of sock samples (free range systems) or faecal samples (cage systems) taken from all parts of the building or the department where the bird flock is kept. From rearing flocks, two pairs of sock samples are taken and pooled into one whereas five pairs pooled into two are taken from the breeding flocks in production.

All holdings that sell eggs for consumption are sampled (Table 17). All poultry flocks that have more than 500 birds, irrespective of species, must be tested. In practice, all poultry flocks are tested prior to slaughter and the results must be available before slaughter. According to the harmonised legislation, sampling needs to be performed within 3 weeks prior to slaughter.

The poultry producers pay the costs for laboratory analyses and the visits to the farms. Only accredited laboratories are allowed to perform the analyses. County Veterinary Officers supervise the poultry control programme regionally. The laboratory sends the test results to the County Veterinary Officer on a quarterly basis. According to regulations, the County Veterinary Officer must send a report on the test results of all poultry holdings to the Swedish Board of Agriculture once a year.

Voluntary programme

The aims of the voluntary programmes are to prevent introduction of *Salmonella* into the poultry holding and minimise the risk of spread of the infection to animals and humans. The voluntary programmes have been in place for more than 40 years.

All broiler and turkey producers belonging to the Swedish Poultry Meat Association are affiliated to the voluntary programme which represents approximately 99% of slaughtered broilers and 91% of turkeys. This voluntary preventive programme includes hygiene and biosecurity measures and a high standard for poultry house construction, such as biosecurity barriers between the clean and unclean parts. Purchases of animals may only occur from holdings affiliated to the voluntary programme and only heat-treated feed is allowed. The poultry houses must be cleaned and disinfected before introduction of a new flock. The poultry producer needs to make an application to be accepted into the voluntary programme and a veterinarian inspects the holding at least once a year.

The Swedish Egg Association is responsible for the voluntary programme of the egg line (laying hens, pullets, breeders). The voluntary programme of the egg line resembles that of the meat line. However, a voluntary programme is also available for holdings with outdoor access. Producers affiliated to the voluntary programmes of egg line receive higher financial compensation in case of a finding of *Salmonella*.

Cattle and pig herds

This programme includes a compulsory and a voluntary component (Figure 17).

Compulsory programme

The aim of the programme is to ensure a low prevalence of *Salmonella* in cattle and pig herds. The compulsory part consists of annual faecal sampling from breeding pig herds and gilt-producing herds and biannual sampling from sow pools. In cattle, *Salmonella* testing is performed in all calves <12 months of age that are submitted for necropsy. *Salmonella* testing is also performed in conjunction with necropsies if an infection is suspected based on macroscopic findings. All imported animals are also tested and on clinical suspicion, any herd or single animal should be tested for *Salmonella*.

Voluntary programme

The voluntary programme is a preventive biosecurity programme aiming at decreasing the risk of introduction of *Salmonella* and other infections. Holdings affiliated to the programme receive higher compensation in case of positive findings. In addition, affiliated holdings are entitled to apply for a commercial *Salmonella* insurance. Most breeding herds and many of the large dairy herds are affiliated to this programme.

In addition, there is a “Safe Trade” programme, including testing for *Salmonella* antibodies in bulk milk samples collected four times a year. All herds with test-positive results in this programme are offered veterinary consultations aiming at improved internal biosecurity to control and eradicate any *Salmonella* infection from the herd.

Salmonella screening in dairy herds

In 2020, regional bulk milk screenings were performed on the islands of Gotland and Öland in April and October, and in the county of Östergötland in October. Gotland and Öland were the regions with the highest proportion of test positive herds in the national screening in 2019, and herds in Östergötland were included due to new findings of *Salmonella* Dublin in this region. All samples were analysed with PrioCHECK® *Salmonella* Ab bovine ELISA (O antigens 1, 4, 5, 12 and 1, 9, 12). Samples with a PP-value higher than twenty (PP>20) in this first test were also analysed with PrioCHECK® *Salmonella* Ab bovine Dublin ELISA (JV Dnr 6.2.18-14893/2019).

Other animals

Animals are tested for *Salmonella* on clinical suspicion or as part of trace-back investigations (Figure 17). Wild animals necropsied at the National Veterinary Institute are also tested for *Salmonella* on suspicion (see chapter “Post mortem examinations in wildlife” on page 139).

Surveillance of *Salmonella* in wild boar was initiated during 2020 following the detection of *S. Choleraesuis* in a breeding herd of domestic swine. This serovar had been absent from domestic swine in Sweden for a period of more than 40 years. Samples from wild boar found dead and reported to the National Veterinary Institute from all of Sweden and a subset of apparently healthy shot wild boar from the counties of Skåne and Södermanland were analysed for *Salmonella* according to ISO 6579:1. Suspected isolates of

Table 17: Sampling scheme of poultry for *Salmonella*.

Category of poultry	Sampling frequency	Sample type	Sampling before slaughter	Official veterinarian
Breeders in rearing	1 d, 4 weeks, 2 weeks prior to rearing or moving	2 pairs of sock samples	Within 3 weeks before slaughter	Once a year
Breeders in production	every 2nd week	5 pairs of sock samples	Within 3 weeks before slaughter	3 times during production
Layers in rearing	2 weeks prior to moving	2 pairs of sock samples or 2 faecal samples of 75 g	Within 3 weeks before slaughter	Once a year
Layers in production	every 15th week (start at 22–26 weeks)	2 pairs of sock samples or 2 faecal samples of 75 g	Within 3 weeks before slaughter	Once a year
Poultry for meat production (all species)		2 pairs of sock samples or 2 faecal samples of 75 g	Within 3 weeks before slaughter	Once a year

S. Choleraesuis were whole genome sequenced for confirmation and further typing. The surveillance activity is ongoing.

Food

Control of *Salmonella* is an important part of in-house quality control programmes in many food enterprises in Sweden (Figure 17). All findings must be reported to the competent authority.

Between 500 and 1000 samples per year are tested as part of official sampling by local authorities at food enterprises, other than slaughterhouses and cutting plants. These samples are analysed mainly using NMKL (nr 71:1999) or a method validated against the NMKL method.

Isolates of *Salmonella* from samples of food taken by authorities are always sent for serotyping at the National Reference Laboratory for *Salmonella* (see Legislation). Although there are no legal requirements, laboratories most often also send isolates for confirmation from samples taken by food business operators. Serotyping and in some cases whole genome sequencing of these isolates is funded by the Swedish Board of Agriculture, provided that the food business operator agrees that the results are made available to the national authorities. Data from 2007 and onwards are stored in a database at the National Veterinary Institute.

Surveillance at slaughterhouses and cutting plants

According to the Swedish *Salmonella* control programme, samples from intestinal lymph nodes and swabs from carcasses are taken from cattle and swine and neck skin samples are taken from slaughtered poultry. Sampling at each slaughterhouse is proportional to the annual slaughter volume. The total number of samples taken is calculated to detect a prevalence of 0.1% with 95% confidence level in cattle, pig, and poultry carcasses at a national level. Altogether, approximately 21 000 samples from cattle, adult pigs, fattening pigs, and poultry are collected at abattoirs annually.

At red meat cutting plants, approximately 5000 samples are taken annually from meat residues. Similarly, approximately 1000 samples are taken in poultry meat cutting plants.

The samples within the control programme are analysed by commercial laboratories using the current edition of the NMKL (nr 71:1999) method, except for approximately 700 samples analysed by a method validated against the NMKL method. Up to 10 samples are allowed to be pooled into a pooled sample. If *Salmonella* is detected in the pool the samples included in the pool are analysed separately.

Food business operators are obliged to take swab samples from carcasses of sheep, goats, and horses at slaughterhouses for analyses of *Salmonella*, according to the regulation (EG) 2073/2005 on microbiological criteria for foodstuffs. The results of these analyses are not yet collected by the competent authority. In Sweden, the corresponding requirements of swab sampling of carcasses of cattle and pigs and sampling of neck skins of poultry carcasses are replaced by the sampling within the *Salmonella* control programme.

Humans

Surveillance in humans is based on identification of the disease by a treating physician and/or by laboratory diagnosis (i.e. passive surveillance) (Figure 17). Both treating physicians and laboratories are obligated to report to the regional and national level to enable further analyses and adequate intervention measures. *Salmonella* spp. is part of the microbial surveillance programme at the Public Health Agency of Sweden and domestic isolates are whole genome sequenced for serovar determination, assessment of diversity and cluster detection. The long-term goal is to use the data to evaluate efforts to lower the level of domestic incidence of *Salmonella* infection.

RESULTS

Feed

Fifteen major feed mills produce approximately 95% of the feed for food-producing animals. In the weekly surveillance of feed mills, 7359 samples were analysed for *Salmonella*; 14 of these samples (0.2%) were positive. Seven serovars were detected; *S. Typhimurium* was the most common (n=5) (Table 18).

In addition, *Salmonella* was detected in 18 out of 1906 analysed batches from feed materials of vegetable origin. The most common serovar was *S. Jerusalem* (n=6). *Salmonella* was detected in 2 out of 1583 batches from feed materials of animal origin and from pet food.

Table 18: Serovars of *Salmonella* isolated within feed control in 2020.

Serotype	Feed material of animal origin ^A	Pet food	Feed material of oil seed origin ^B	Feed material of cereal grain origin	Other plants ^C	Process control feed mills	Process control rapeseed crushing plant
S. Agona	-	-	-	-	-	2	-
S. Albany	-	-	-	1	-	-	-
S. Havana	-	-	-	-	-	1	-
S. Infantis	1	1	-	-	-	-	-
S. Jerusalem	-	-	6	-	-	-	-
S. Leeuwarden	-	-	1	-	-	-	-
S. Liverpool	-	-	1	-	-	-	-
S. Livingstone	-	-	1	-	-	-	-
S. Mbandaka	-	-	3	-	-	2	-
Monophasic S. Typhimurium	-	-	-	-	-	1	-
S. Ouakam	-	-	1	-	-	-	-
S. Senftenberg	-	-	4	-	-	-	-
S. Tennessee	-	-	-	-	-	1	-
S. Tunis	-	-	-	1	-	-	-
S. Typhimurium	-	-	-	-	-	5	-
S. enterica subspecies enterica	-	-	3	-	-	2	-
Total	1	1	18^D	2	0	14	0
Number of samples	1 467	116	1 131	715	60	7 359	686

^AMeat and bone meal, animal fat, fish meal, greaves, protein meal, meat meal, milk products, egg products, poultry offal meal and animal by-products.

^BDerived from palm kernel, rape seed, soya bean, linseed, and sunflower seed.

^CPeas, algae, leaves (dried), beans, lignin, herbs (dried), and berries.

^DIn two of the units positive for *Salmonella*, two other serotypes were found.

Sweden notified four findings of *Salmonella* in feed materials and pet food during 2020. All of these concerned intra-community traded or imported feed materials. Three of them had vegetable origin and the fourth one was of animal origin.

Animals

Poultry

Salmonella was not detected in any of the 4147 broiler flocks tested in routine sampling before slaughter (Table 19 and Figure 18). *Salmonella* was detected in 7 of the 646 flocks of layers tested. *Salmonella* was not detected in any breeding flocks, neither in any samples of commercially raised turkey flocks, quails, or ostriches. *Salmonella* was detected in one small-scale flock with laying hens, ducks and geese. As the poultry registries maintained by the Swedish Board of Agriculture are not sufficiently updated and a unique flock identification is lacking, the figures on the number of flocks within the programme and the number of flocks not sufficiently sampled, can only be considered estimates. It is estimated that approximately 20% of the poultry holdings lack an annual official sampling.

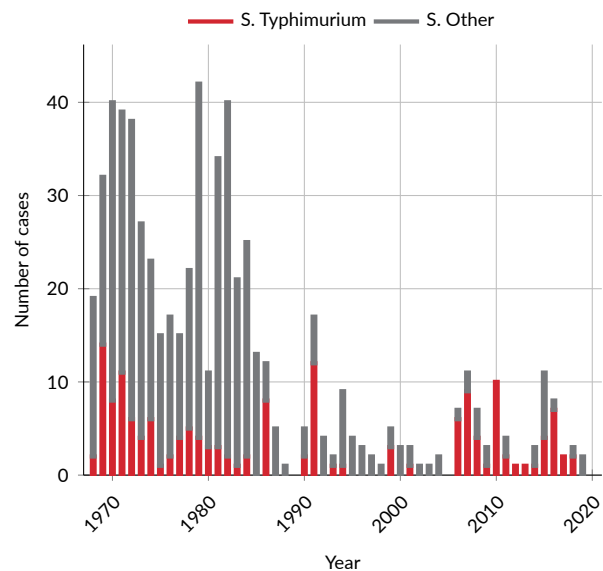


Figure 18: Annual notifications of *Salmonella* in broiler holdings during 1968–2020, breeding flocks included.

Table 19: Results from the *Salmonella* control programme in poultry flocks in 2020. The figures on the flocks tested are estimates due to the deficiencies in the Swedish poultry registries and the lack of a unique flock identification.

Animal species	Production type	Production stage	No. flocks tested	No. positives	Percentage	Serovar
<i>Gallus gallus</i>	Meat production	Adult Grand Parent	20	0	0.00%	-
<i>Gallus gallus</i>	Meat production	Adult Parent	139	0	0.00%	-
<i>Gallus gallus</i>	Meat production	Production	4147	0	0.00%	-
Turkeys	Meat production	Adult Parent	4	0	0.00%	-
Turkeys	Meat production	Production	159	0	0.00%	-
<i>Gallus gallus</i>	Egg production	Adult Parent	14	0	0.00%	-
<i>Gallus gallus</i>	Egg production	Production	646	7	1.08%	<i>S. Typhimurium</i> (n=7)
Geese	Meat production	Production	7	0	0.00%	-
Ducks	Meat production	Production	8	1	12.50%	<i>S. Enteritidis</i>

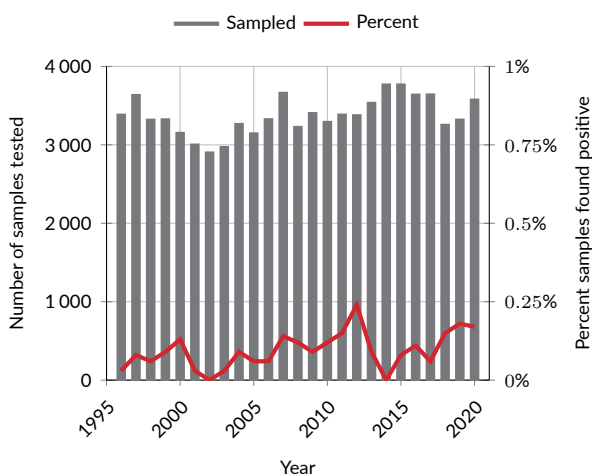


Figure 19: Samples tested (bars – left axis) and percentage of *Salmonella* found (line – right axis) in lymph node samples from **cattle**.

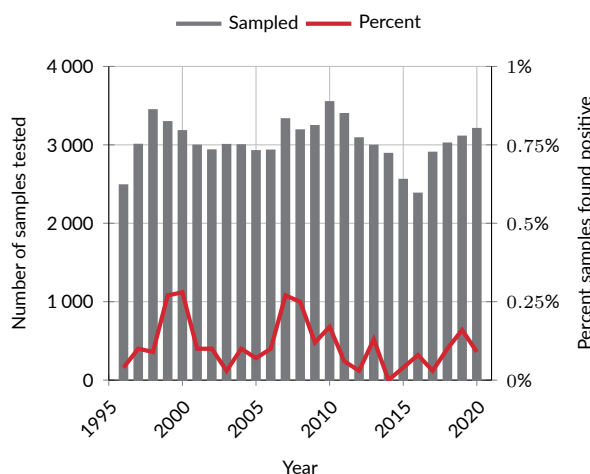


Figure 21: Samples tested (bars – left axis) and percentage of *Salmonella* found (line – right axis) in lymph node samples **fattening pigs** sampled at abattoirs.

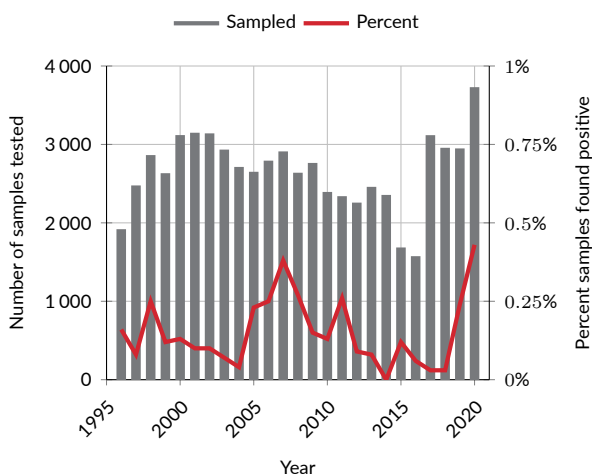


Figure 20: Samples tested (bars – left axis) and percentage of *Salmonella* found (line – right axis) in lymph node samples from **sows and boars**.

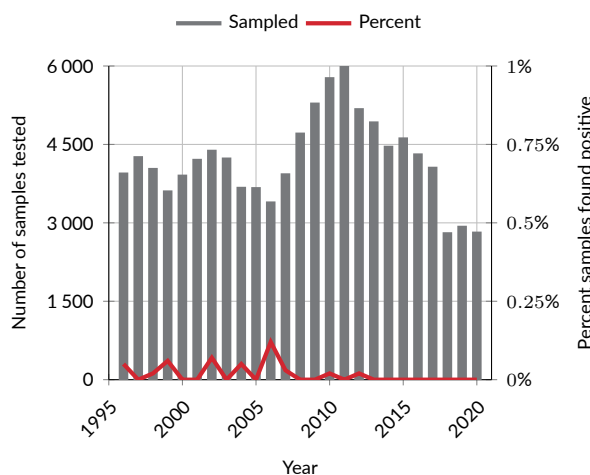


Figure 22: Samples tested (bars – left axis) and percentage of *Salmonella* found (line – right axis) in neck skin samples from **poultry** at major abattoirs.

Cattle

In total, *Salmonella* was detected in six new herds in 2020 (Figure 23). *Salmonella* was isolated from six (0.17%) of 3563 mesenteric lymph nodes from cattle at slaughter (Table 20 and Figure 19).

In the regional bulk milk screenings in Gotland, 3.0% of the tested herds were positive in April (4/132) and 5.5% in October (7/127), of which non were positive in the Dublin ELISA. This was a marked decrease compared to October 2019 when 22% (30/139) of the herds in Gotland had positive test results, but at the same level as seen in the national screening 2013 with 5.5% positive herds (12/218). Results in Öland were 16% (21/171) and 14.5% (19/131) test positive herds in April and October respectively, of which most were also positive in the Dublin ELISA. This confirms a continued endemic situation of *Salmonella* Dublin in Öland, but with a slightly lower level than expected in October when comparing to previous screenings. In the county of Östergötland 2.1% of the herds tested positive (4/194), of which most were also positive in the Dublin ELISA (n=3). These results were similar to previous results in 2013 and 2019. Regional screenings will continue to be performed in the following years to better understand variations between years and seasons and to follow the effect of a biosecurity program targeted on salmonella positive herds.

Pigs

Salmonella was detected in ten pig herds (Figure 24) and in 16 (0.43%) of 3703 lymph node samples taken from adult pigs and from three (0.09%) of 3189 lymph node samples from fattening pigs (Table 20, Figures 20 and 21).

In one of the herds, a breeding herd, the serovar

Salmonella Choleraesuis was detected. This was the first detection of *Salmonella* Choleraesuis in domestic pigs in Sweden in over 40 years. The serovar was also detected in gilts in isolation in one of the contact herds. An extensive repeated sampling of contact herds has been performed during 2020 and is ongoing. So far, no further spread has been detected.

Other animals

Salmonella was detected in two stables with horses, in 1207 cats, in 7 dogs, in 27 wild birds (mainly passerine) and in one squirrel and one porpoise (Table 21).

Salmonella was detected in wild boar in 12 municipalities in the counties of Skåne, Södermanland and Uppland and 19 index isolates were notified from these municipalities (Table 21). In total, *Salmonella* Choleraesuis was detected in three out of 16 wild boar found dead and in 20 out of 152 shot wild boar from the counties Skåne and Södermanland. In addition, other serovars were found in two wild boar found dead and in six shot wild boar. Whole genome sequencing of *S. Choleraesuis* from wild boar revealed a very high level of similarity between the wild boar isolates and the isolates from the two herds with domestic pigs.

Food

Within the Swedish *Salmonella* control programme, swab samples were taken from 6757 pig carcasses and 3557 cattle carcasses. Neck skin samples were taken from 2792 poultry carcasses. *Salmonella* was detected in swab samples from three pig carcasses and one cattle carcass (Table 20). At cutting plants, *Salmonella* was not detected in any of the 4916 red meat or the 1251 poultry meat samples taken. (Table 20 and Figure 22).

In addition to the sampling performed within the control programme, 418 samples were taken by national and local authorities.

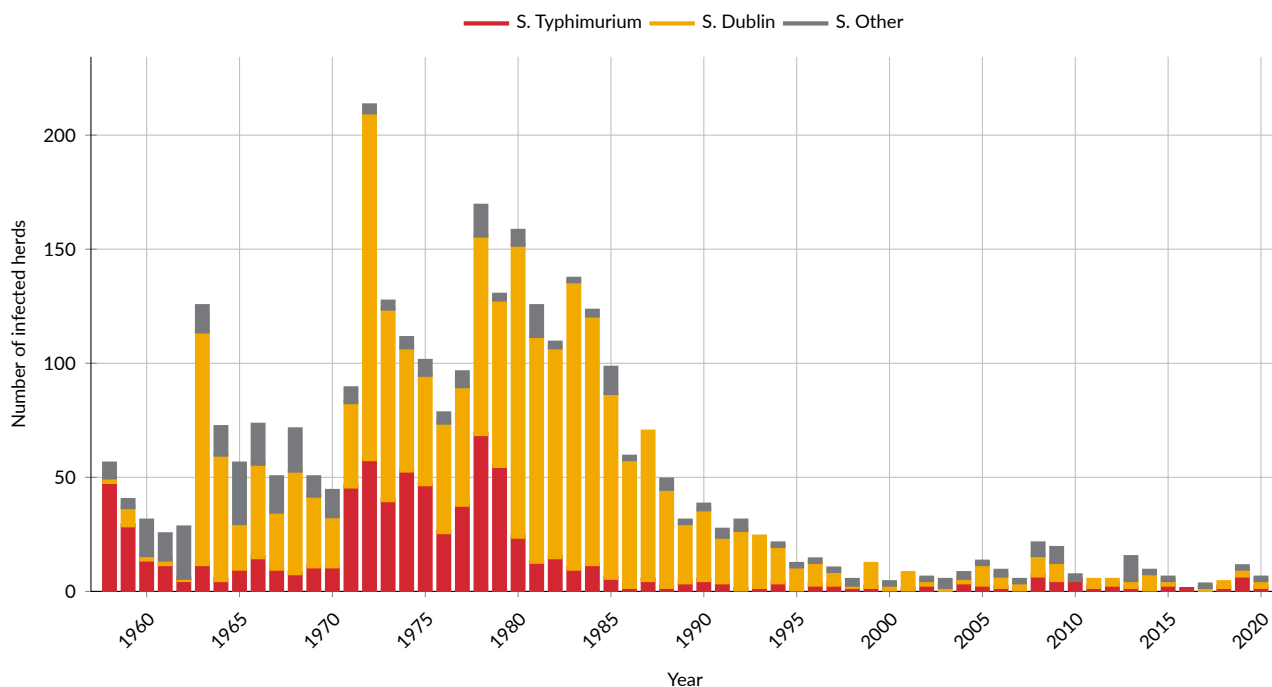


Figure 23: Annual notifications of *Salmonella* in Swedish cattle herds during 1958–2020. Data from 1958 through 1967 is extracted from a graph presented by J.Å. Robertsson (1985).

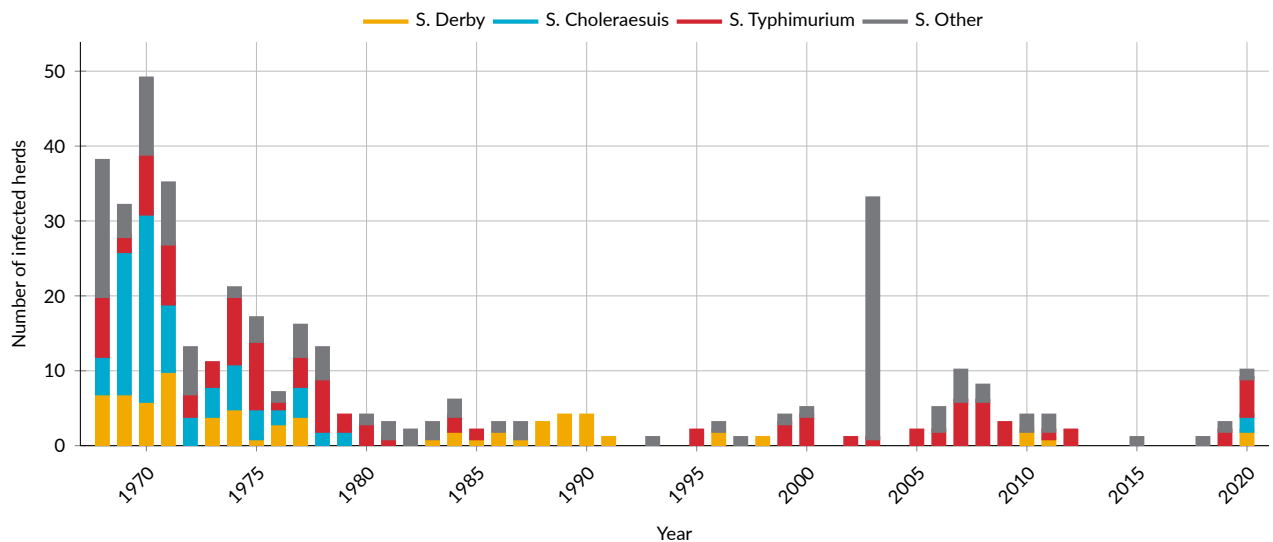


Figure 24: Annual notifications of *Salmonella* in swine herds during 1968–2020. In 2003, a feed borne outbreak of *S. Cubana* occurred in Sweden. In 2016 and 2017, *Salmonella* was not detected in any herd.

Table 20: Results from the *Salmonella* control programme at abattoirs and cutting plants in 2020.

Animal species	Sample type	No. samples	No. positive	Percentage	Serovar
Cattle	Lymph node	3563	6	0.17%	<i>S. Umbilo</i> (n=1), <i>S. Dublin</i> (n=1), <i>S. Typhimurium</i> (n=4)
	Carcass swab	3557	1	0.03%	<i>S. Choleraesuis</i>
Breeding swine	Lymph node	3703	16	0.43%	<i>S. Enteritidis</i> (n=1), <i>S. Stanley</i> (n=1), <i>S. Newport</i> (n=2), <i>S. Derby</i> (n=5), <i>S. Typhimurium</i> (n=8) ^A
	Carcass swab	3655	3	0.08%	<i>S. Derby</i> (n=1), <i>S. Typhimurium</i> (n=2)
Slaughter swine	Lymph node	3189	3	0.09%	<i>S. Livingstone</i> (n=1), <i>S. Typhimurium</i> (n=2)
	Carcass swab	3102	0	0.00%	-
Cattle and swine	Meat trimmings	4916	0	0.00%	-
	Meat trimmings	1251	0	0.00%	-

^AIn one sample of lymph node, two serovars, *S. Derby* and *S. Typhimurium* were detected.

Table 21: Notified index isolates of *Salmonella* in cats, dogs, horses, wild birds and wild mammals in 2020. For all animal species except for wild boar the number of index cases is the same as the number of index isolates. For wild boar, 12 of the notified index isolates were index cases.

Serovar	Cats	Dogs	Horses	Wild birds	Wild boar	Other wild animals
<i>S. Agona</i>	0	1	0	0	0	0
<i>S. Bovismorbificans</i>	0	1	0	0	0	0
<i>S. Choleraesuis</i>	0	0	0	0	10	0
<i>S. Coeln</i>	0	0	0	0	1	0
<i>S. Enteritidis</i>	0	0	0	0	1	0
<i>S. Lomita</i>	1	0	0	0	0	0
<i>S. Newport</i>	0	0	0	0	2	0
<i>S. Typhimurium</i>	172	5	2	12	2	0
<i>Salmonella enterica</i> sp <i>arizonae</i>	1	0	0	0	0	0
<i>Salmonella enterica</i> sp <i>diazona</i>	0	0	0	0	2	1 ^A
<i>Salmonella</i> , O:4,5:-:1,5	0	0	0	1	1	0
<i>Salmonella</i> , O:4	1033	0	0	14	0	1 ^B
Total	1207	7	2	27	19	2
Number of samples ^C	2210	152	60	57	22	20

^AA squirrel.

^BA porpoise.

^CNumber of samples tested per household (pets), stable (horses) or municipality or location (wild animals).

Table 22: Results of *Salmonella* analyses of food samples taken by the authorities in 2020.

Reason for sampling	Total no. of samples	No. of positive samples
Survey	54	1 ^A
Routine control	86	0
Suspected food poisoning or complaint	131	0
Border control	98	0
Other or not reported	49	0

^AS. Dublin, meat from bovine animals sampled at retail.

IN FOCUS: *Salmonella* cases associated with domestic beef

Findings of *Salmonella* in Swedish cattle and food with Swedish meat are uncommon and outbreaks in humans related to this are rare. Recently, however, an increasing number of human cases of salmonellosis linked to domestic beef have been observed. Between 2019 and early 2021, 27 cases belonging to four different outbreaks involving the serovars Agona, Dublin, Düsseldorf, and Reading have been investigated.

Salmonella Agona: In August 2020, indistinguishable isolates of *S. Agona* were detected in samples from six cases from five different regions. In early August *S. Agona* was also detected in both Swedish minced beef and Swedish minced pork and beef meat in an in-house quality control of a large food-chain. The meat had been sold at other food chains and several locations across the country but trace-back to a specific herd was not possible because large volumes of meat of different origins had been mixed. At least one of the cases had tasted raw minced meat and another of the cases used to give its dog raw minced meat, after which the dog had probably infected its owner who had contracted a wound infection. Another case where both dog and owner became infected was identified and where the dog died after suffering from a necrotic udder inflammation.

Salmonella Dublin: Since September 2019, ten cases from nine different regions have been identified. For seven of the cases, the bacterium was isolated from blood, which is seen more frequently with this serovar and indicates a higher degree of invasiveness. In April 2020, the outbreak strain was identified in a lymph node sample from a cattle at a slaughterhouse whereupon the infection was traced to a large meat producing cattle herd. The outbreak strain had been identified in another cattle herd in the same region in 2018, indicating that the strain may be endemic in that area. In August 2020, the same subtype of *S. Dublin* was identified in a sample from Swedish minced beef. Back-tracing led to meat from animals delivered to three different slaughterhouses.

Salmonella Düsseldorf: Five notified cases from two regions had diseased in the autumn of 2019. They all had purchased Swedish minced beef and fell ill after having tasted the minced meat raw. Back-tracing led to two possible slaughterhouses, but tracing to a specific herd was not possible. The outbreak strain was also found in an environmental sample taken at a feed factory using meat from Swedish slaughterhouses for production of pet feed.

Salmonella Reading: Between September 2019 and August 2020, six cases from four different regions with clustering isolates were reported. At least one of the cases had tasted raw minced beef. The outbreak strain has a clear connection to more than 20 human isolates from the years 2007–2011, where a majority of the cases were resident in or had visited the southernmost region of Sweden. From 2007 until 2020, *S. Reading* has been identified in various animal species (cattle, pigs, sheep, horse, turkey, duck, chicken) as well as feed, wild birds and the environment in Skåne, and also in domestic minced beef meat. Whole genome sequencing of a subset of isolates from animals, meat, feed, environment and case patients has shown a clear link between isolates from the entire time period, although a small genetic variation seems to have developed over time. The analyses indicate that the strain was initially introduced via imported feed in 2007 and has since become endemic in several parts of Skåne.

Continuous typing of *Salmonella* isolates and sharing data for comparison between sectors is central for identification of sources. However, it is often difficult to trace the source of the infection due to big volumes of meat and the time delay between the findings. With typing, domestic and endemic subtypes can be identified. Typing data can thereby be a tool for identifying where measures to reduce the spread can be set in place.

Salmonella was detected in one sample taken from bovine meat at retail within the framework of a control project. (Table 22). At the EU-level, Sweden notified eight findings of *Salmonella* in food during 2020. All these concerned intra-community traded batches within the food categories meat and vegetables. In addition, two findings of *Salmonella* in meat were notified at the national level.

In total, data from serotyped isolates from 586 batches of food or carcasses sampled at retail, slaughterhouses, or other food enterprises between 2010 and 2020 is available. Of these, 345 were from imported food batches, 146 of domestic origin (36 food batches and 108 carcasses) and 80 from food batches of mixed or unknown origin. The distribution of serovars differ between the major food categories (Figure 25). *S. Dublin* was the most common serovar in beef meat whereas *S. Typhimurium* and *S. Derby* were most common in pork meat. The composition of serovars from poultry meat was quite variable, but *S. Newport* and *S. Infantis* were the most common. Isolates from lamb meat (mainly originating from swab samples of carcasses) were almost exclusively *S. diarizonae* serovar 61:(k):1,5(7), whereas the composition of isolates from vegetables varied a lot.

Humans

In 2020, a total of 826 cases of salmonellosis were reported, compared to 1993 cases in 2019 (Figure 26). Domestic cases decreased by 45% from 763 cases in 2019 to 422 cases in 2020, resulting in an incidence of 4.1 cases per 100 000 inhabitants. The domestic incidence varies slightly from year to year but has been largely stable between 5 and 11 cases per 100 000 inhabitants over a long period. The sharp decrease in domestic cases from 2019 and the record low incidence in 2020 likely reflects drastic changes in behaviour due to the COVID-19 pandemic.

A total of 46% of the cases (n=382) were considered to have been infected abroad. Since the turn of the millennium, a nearly fourfold decrease in incidence per 100 000 inhabitants among travel-associated cases had been observed until 2019, despite an increase in international travel. From 2019 to 2020, the proportion of travel-associated cases decreased by more than two thirds from 11.8 (n=1215) to 3.7 cases per 100 000 inhabitants. As many as 85 percent (n=326) of the travel-associated cases in 2020 were reported during the first three months of the year. Of the travel-associated cases over half (52%, n=198) reported Southeast Asia as region of infection and 38% (n=145) had Thailand as reported country of infection.

Among the domestic cases, the median age was 44 years (0–96 years) and the incidence was highest for children younger than 5 years of age with 10.9 cases per 100 000 inhabitants followed by the age group of 70–79 years with an incidence of 6.0 per 100 000 inhabitants.

Of the isolates from domestic cases, 84% were serotyped and the most common serovars among these were *S. Typhimurium* (21%), *S. Enteritidis* (16%) and monophasic *S. Typhimurium* (14%). An additional 55 serovars were identified in domestic cases during 2020. Of the cases infected in other countries, 16% were serotyped and *S. Enteritidis* was the most common serovar (40% of the isolates that were typed).

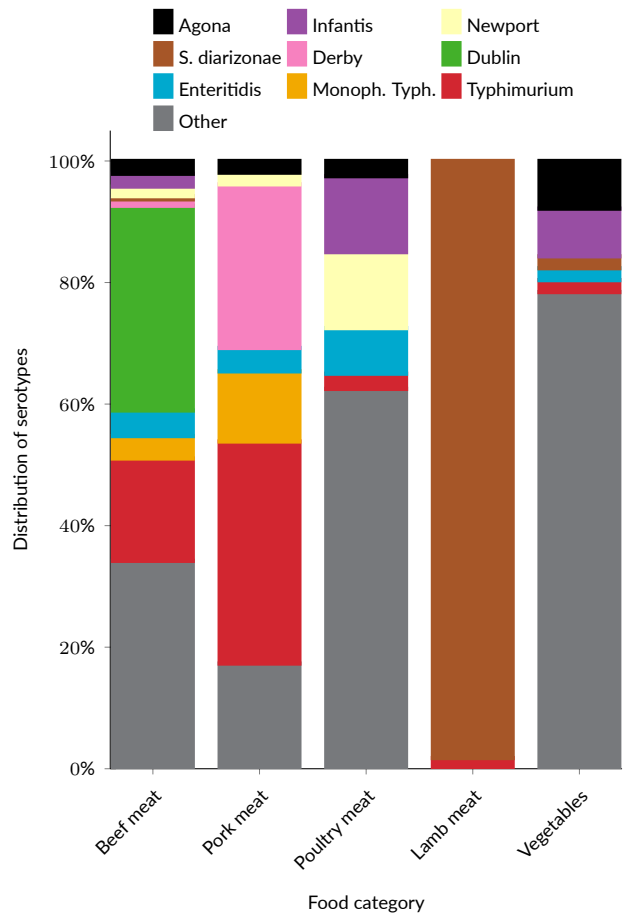


Figure 25: Distribution of *Salmonella* serovars in different food categories. Results of serotyping of isolates from samples taken at retail, slaughterhouses or other food enterprises by authorities or food business operators 2010 – 2020. In total, samples are from 447 batches of food or carcasses (beef meat 190, pork meat 52, poultry meat 40, lamb meat 114, vegetables 51). Food categories with isolates from samples of less than 20 batches of food are not included.

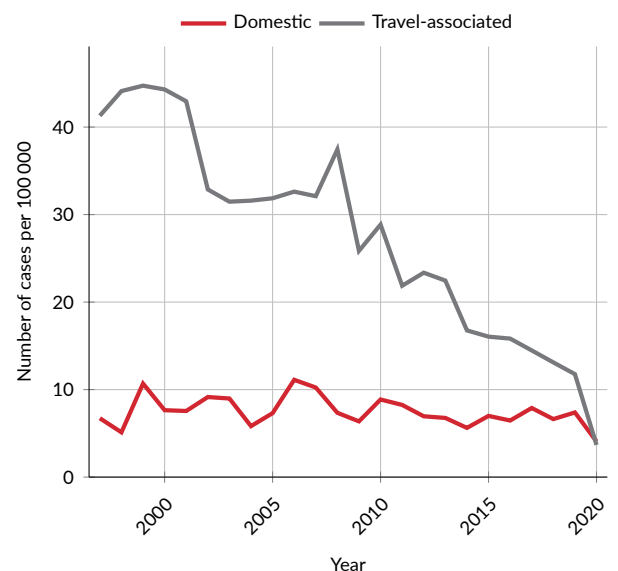


Figure 26: Incidence (per 100 000) of notified human cases of salmonellosis in Sweden, 1997–2020. Travel-associated cases are those where the patient has reported travel to another country during the incubation period prior to clinical presentation. Domestic cases are patients that have not travelled outside Sweden.

For domestic salmonellosis a clear seasonality is usually observed, with most cases occurring during late summer and early autumn. In 2020, the number of domestic cases followed normal seasonal levels until March after which the number of cases fell sharply. During the remainder of the year, a typical seasonal variation was seen, although with disease rates much lower than normal. Travel-related cases are usually the most common in summer and winter but in 2020 the numbers dropped sharply from April which coincides with extensive travel restrictions imposed in March (Figure 27).

Outbreaks

The low number of reported human cases of salmonellosis in 2020 is also reflected by a comparatively low number of outbreaks. In addition to a number of smaller clusters among isolates from cases, including some that could be linked to Swedish beef (see “In focus” section), five cases with *S. Newport* from late autumn could be linked to an outbreak investigated by Norwegian authorities. The probable source of the infection was iceberg lettuce. Only two outbreaks in which more than ten people were reported ill were identified. One of the outbreaks was caused by monophasic *S. Typhimurium*, in which 17 people fell ill between September and November and the source of infection remained unknown. The second outbreak was caused by the same types of *S. Typhimurium* as were found among wild birds, cats and dogs and affected 20 people (see below).

Outbreak of *S. Typhimurium* in wild birds, cats, dogs, and humans

In the early months of 2020, a large outbreak of *Salmonella* Typhimurium (MLVA profiles 2-[11-15]-[3-4]-NA-212) occurred among cats in Sweden. In total, *Salmonella* was detected in 1207 (54.6%) cats of 2210 tested. The number of index cases in cats was higher than before albeit close to the

levels of 2018 and 2019. Of the 174 fully serotyped cat isolates, 172 belonged to the serovar Typhimurium. Cases in infected cats were reported predominantly in March (57.9% of the cases) and throughout the country, but especially from the region of Västra Götaland (24.0% of the cases). Simultaneously, *S. Typhimurium* with the same MLVA profiles were detected in isolates from four passerine birds, and five dogs. In addition, comparisons between genomic sequences for isolates of *Salmonella* Typhimurium with MLVA profiles typical for wild birds and cats to genomic sequences of human cases revealed a match for 20 cases. A majority of the human cases were children 0–3 years (n=12) or persons above 70 years (n=5) and most cases were reported in February-April (n=14).

DISCUSSION

The low proportion of domestic *Salmonella* infections in humans is unique to Sweden, Norway and Finland when compared to most other European countries, where such data is collected. This reflects the low *Salmonella* burden in domestic animals and food. Despite a reduction in the incidence of domestically infected from 7.4 cases per 100 000 inhabitants in 2019 to 4.1 in 2020, which is possibly linked to changed behaviour during the pandemic, the proportion of domestically infected was for the first time higher than the travel-related cases. An explanation is the large effect that travel restrictions have had during the pandemic that has reduced the number of travel-related cases by more than two thirds.

In the feed sector, in 2020 as in previous years, several different serovars were isolated in the weekly surveillance of feed mills where *S. Typhimurium* was the most common serovar (n=5). The findings were from several different feed mills, and most of them from the feed material intake area. This illustrates the importance of handling feed materials in a proper way even if the feed materials have been negatively tested for *Salmonella*.

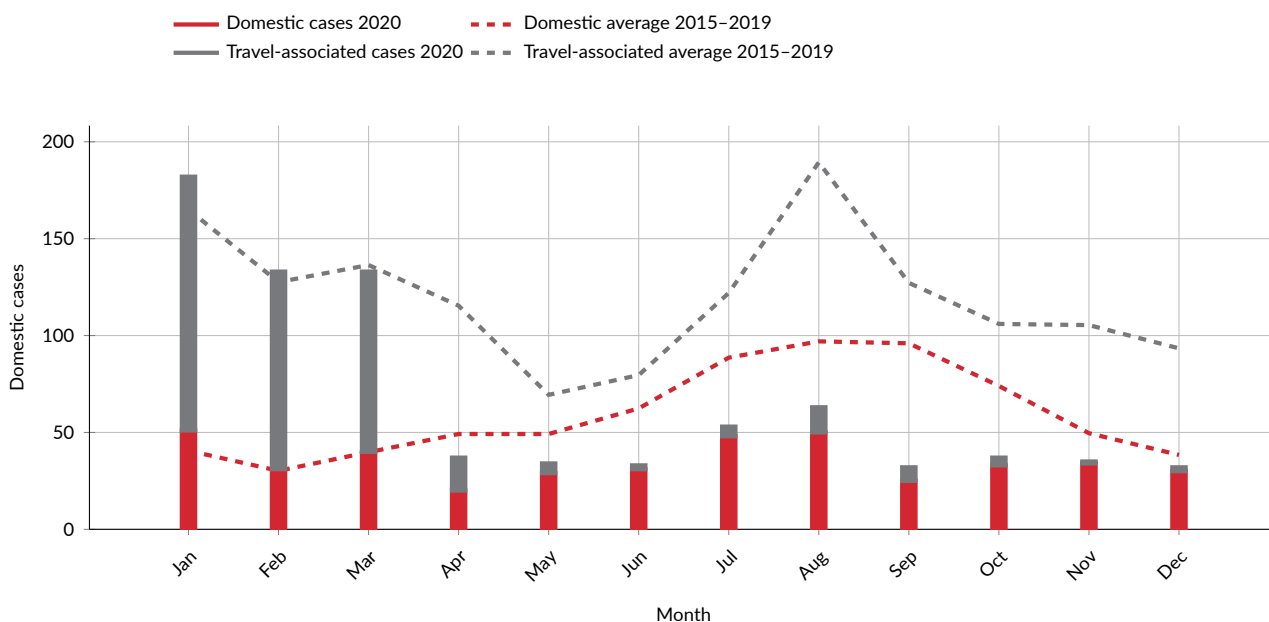


Figure 27: Monthly notifications of domestic and travel-associated human cases of salmonellosis in 2020 and a monthly average for domestic and travel-associated notifications in 2015–2019.

Salmonella was detected in ten pig herds during 2020. All these herds were geographically concentrated in one region in the south of Sweden. This is the highest number of detected herds since 2007 and the size and production structure of several of the herds made the control and eradication challenging and very costly. The detection of *Salmonella* Choleraesuis in a breeding herd called for thorough eradication and tracing plans to avoid a re-establishment of this serovar in the Swedish domestic pig population. These measures are ongoing including the surveillance of *Salmonella* Choleraesuis in wild boar. In addition, *S. Choleraesuis* was detected from a cattle carcass swab sample taken at a small abattoir that handles wild boar carcasses as well. Sequences of *S. Choleraesuis* isolates from wild boar and domestic pigs were very similar to the sequence of a human isolate from 2019. The findings so far, with high similarity between isolates from wild boar, domestic pigs and the human case indicate a common source and a recent introduction. The surveillance in wild boar is ongoing and will include all regions with a wild boar population.

In 2020, regional bulk milk screenings were used to follow up regions of special interest. This complements the national bulk milk screenings that are performed with several years interval, and will be continued in 2022.

The Swedish *Salmonella* control programme has been in place for decades and resulted in a very low *Salmonella* burden in domestic animals (Figures 23, 24 and 28). However, the programme is costly and could be modernised.

Good cooperation between the public health, food control and food safety and veterinary sectors is crucial in outbreak investigations, in control, in surveillance as well as in the further developments of the surveillance programmes.

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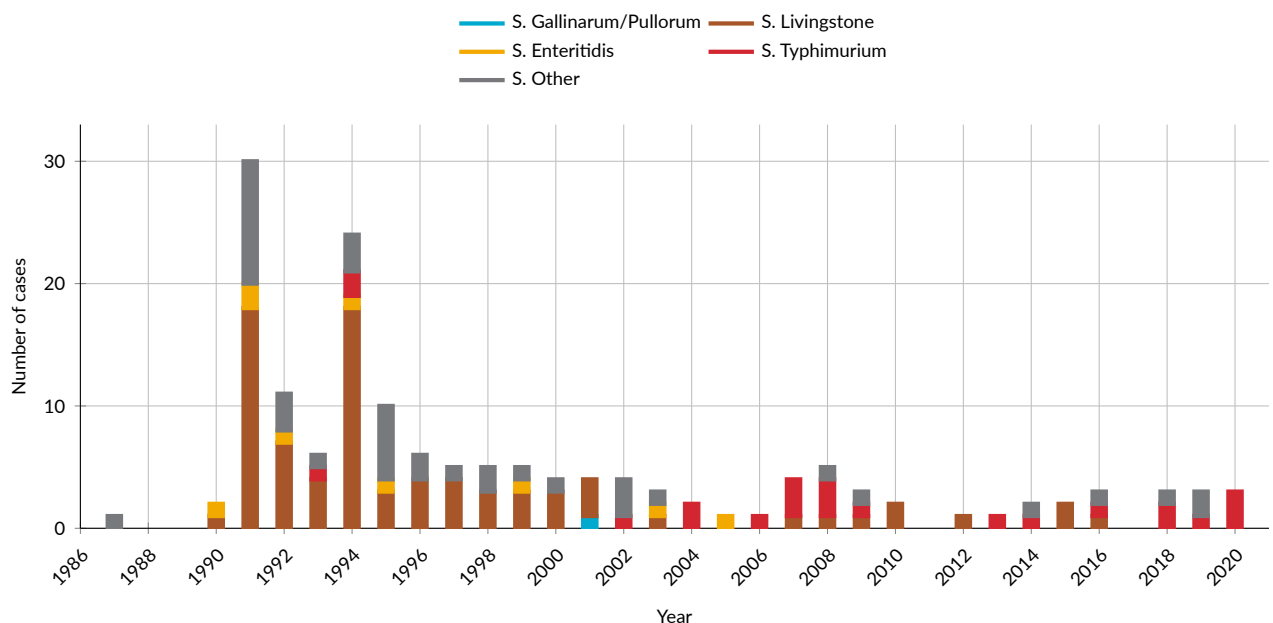


Figure 28: Annual notifications of *Salmonella* in layer holdings during 1987–2020.

Scrapie

BACKGROUND

Scrapie, which affects sheep and goats, belongs to a group of diseases called Transmissible Spongiform Encephalopathies (TSE) and was first described more than 250 years ago. The current theory about the causative agent is the protein-only hypothesis. This theory assumes that prions (misfolded and aggregated proteins) induce the same misfolded, aggregated, and pathological structure in normal prion-proteins of the host, resulting in accumulation of prions and cellular damage without involvement of any microorganism. Susceptibility to scrapie is genetically related and some countries have chosen to control the disease through specific breeding programs.

Scrapie occurs in different variants; classical and atypical scrapie/Nor98. Classical scrapie, which is clearly transmissible within flocks, has been detected in Sweden in a single flock in 1986. The whole flock was culled, and the farmer was not allowed to reintroduce sheep for seven years. The origin of the disease was never established.

In 1998, an atypical variant of scrapie was detected in Norway (Nor98), and this variant was also detected in Sweden for the first time in 2003. Since then, several cases have been detected in Sweden and worldwide. Although atypical scrapie is experimentally transmissible, cases occur sporadically and epidemiological studies on the European level indicate that atypical scrapie probably is a spontaneously (without known cause) occurring disease which does not seem to spread within or between flocks.

After classical BSE in cattle became a disease of public health concern (see chapter on BSE, page 19), and the existence of BSE in small ruminants was suspected, both surveillance and control of TSE in small ruminants was increased within the European Union in 2002. Since the start of the increased surveillance, more than 75 000 sheep have been tested in Sweden without any positive cases of classical scrapie detected. In 2014, Sweden sent an application to the European Commission to obtain status as country with negligible risk for classical scrapie. The dossier contained detailed information about the population, imports (which were limited), education about the disease, the EU-approved national control programme as well as results of estimates of the probability that Sweden is free from classical scrapie. The Commission evaluated the dossier and also asked the European Food Safety Authority (EFSA) for an opinion (doi:10.2903/j.efsa.2015.4292). In August 2016, the application was approved, and Sweden was granted the status negligible risk for classical scrapie through Commission regulation (EC) 2016/1396.

DISEASE

The incubation period is long, up to several years. Clinical signs of classical scrapie are related to the neurological system and include altered behaviour and sensation, affected movement and posture, as well as pruritus and skin lesions.

The disease is progressive and always fatal. All routes of transmission of classical scrapie have not been established, however, transmission of classical scrapie occurs horizontally within flocks and at lambing, and pastures can be contaminated for long periods of time. Scrapie has, based on epidemiological data, not been considered a zoonotic disease; however, the question is regularly raised. Many cases of atypical scrapie/Nor98 are detected in active surveillance and there are fewer descriptions of clinical signs, but among signs reported are ataxia, loss of body condition and abnormal behaviour. Atypical scrapie is believed to be spontaneously occurring (without known cause).

LEGISLATION

Surveillance and control of scrapie in sheep and goats is regulated through Regulation (EC) 999/2001 of the European Parliament and of the Council of 22 May 2001. At the national level, the surveillance scheme and control were, until 2016, also regulated by an EU-approved national scrapie control programme which from 2003 also formed the basis for additional guarantees related to trade within the union (Commission Regulation (EC) 546/2006).

Sweden was granted the status: “negligible risk” for classical scrapie through Commission regulation (EC) 2016/1396 amending Regulation (EC) 999/2001 and since then the rules in 999/2001 replace both the additional guarantees and previous surveillance scheme in the national program.

Scrapie is a notifiable disease under the Swedish Act of Epizootic diseases (SFS 1999:657, with amendments) and should be notified already on clinical suspicion. This legislation cover compensation to farmers for financial losses due to eradication measures. Sampling at the national level is regulated by SJVFS 2010:9, last amended through SJVFS 2013:3.

SURVEILLANCE

The Swedish Board of Agriculture is responsible for the surveillance programme. It is carried out in cooperation with the National Veterinary Institute, which is appointed the National Reference Laboratory (Regulation (EC) 999/2001). Samples are analysed at the National Veterinary Institute. Most samples are collected at rendering and there is therefore a close collaboration with Svensk Lantbrukstjänst and Konvex, the companies that collect and render carcasses.

Passive surveillance

All suspicions of scrapie, i.e. sheep or goats showing clinical signs or post mortem findings where scrapie cannot be excluded, must be reported to the authorities. The obligation to report applies to animal owners, veterinarians, and everyone else who is responsible for the animals. If the animal is still alive it is examined by a veterinarian who is in close



Classical scrapie has not been detected in Sweden since 1986 and after several years of intensive surveillance, Sweden has been granted the status “negligible risk” for classical scrapie. Photo: Ylva Persson.

contact with disease experts. If scrapie can still not be excluded the animals is euthanized. Brainstem samples from animals with clinical suspicion of scrapie are examined with Bio-Rad TeSeE short assay protocol (SAP). If inconclusive or positive the results are confirmed with Bio-Rad TeSeE Western Blot.

Active surveillance

From 2017, the basis of the active surveillance is Regulation (EC), 999/2001 Annex III, which states a minimum number of animals to be sampled based on population size. The minimum number to be sampled is 1500 fallen sheep and 100 fallen goats above the age of 18 months. The samples should be representative for the population.

The current national purpose of the surveillance is to maintain freedom (negligible risk) and to detect introduction. Regulation (EC) 999/2001 requires that for the preceding 7 years, sufficient numbers should have been tested annually to provide a 95% confidence of detecting classical scrapie if it is present in that population at a prevalence exceeding 0.1%.

Except for the northern parts of Sweden, where animal density is low (less than 10% of the sheep population are in this area), it is mandatory to send fallen animals for rendering. In the computerised system for collecting carcasses,

roughly every second or every third (adjusted by season) animal is “flagged” for sampling. The carcasses sent for rendering are sampled by employees at the rendering plants. All sheep and goats above 18 months of age sent for post mortem examinations are sampled. This is done by veterinarians or veterinary assistants.

Prior to 2017 sampling was based on an EU-approved national control program, which included sampling of all dead sheep and goats over 18 months of age that were not slaughtered for human consumption.

Farms with confirmed cases of atypical scrapie are obligated to have increased surveillance in the herd for two years (Regulation (EC) 999/2001). In addition to fallen stock, healthy slaughtered animals above 18 months of age are examined from these flocks. These animals are sampled at slaughterhouses by trained employees or inspectors employed by the National Food Agency.

The samples from active surveillance were examined with Bio-Rad TeSeE short assay protocol (SAP) at the National Veterinary Institute in accordance with Regulation (EC) 999/2001. In case of positive or inconclusive results the material was examined by Bio-Rad TeSeE Western Blot.

The number of samples and distribution between farms is followed up on a monthly basis.

RESULTS

Passive surveillance

In 2020, one sheep and one goat were tested due to clinical suspicion of scrapie, both with negative results. One further suspicion of scrapie in sheep was reported but based on the clinical history the animal was not euthanised for sampling, and later recovered.

Active surveillance

Sheep

In 2020, the National Veterinary Institute examined 1701 sheep from fallen stock and 79 sheep from flocks under increased surveillance due to Nor98 or under restrictions due to imports, sampled at slaughter. Out of these, all samples were negative for classical scrapie and one positive for atypical scrapie/Nor98. The northern part of the country is under-represented in the sampling and due to problems with rapid decomposition of carcasses during summertime, sampling is not evenly distributed throughout the year. Apart from this, sampling seems fairly representative.

Goats

In 2020, the National Veterinary Institute examined 121 goats from fallen stock for scrapie. All were negative both for classical scrapie and for atypical scrapie.

DISCUSSION

Classical scrapie

Classical scrapie is a challenging disease both to detect and eradicate, due to the long incubation period and persistence in the environment. Sweden has chosen not to breed for resistance and thus the sheep population is susceptible to classical scrapie. This means that introduction of the disease would potentially have negative consequences for the sheep industry. Imports of sheep and goats to Sweden have for many years been limited and in combination with trade requirements this has kept the risk for introduction at a low level. Within the European union, relaxation of current trade rules is being discussed. For Sweden, and other countries with a susceptible population and negligible risk, it is important that trade rules that minimise risk for introduction of classical scrapie to the country are kept in place.

Regarding the active surveillance, no positive cases have been detected. Continued efforts need to be made to increase samples from the northern parts of the country. From a surveillance point of view, a seasonal variation with less samples during summer is not deemed to have a systematic effect.

Atypical scrapie

Since the first case of atypical scrapie was confirmed in Sweden in 2003, more than 50 cases have been reported. Out of these, two were detected through passive surveillance and the rest through active surveillance. Currently, the flocks are put under intensified monitoring in accordance with Regulation (EC) 999/2001. At the European level, two epidemiological studies have concluded that the prevalence is similar in different countries and that the prevalence in positive flocks does not differ from the prevalence in the rest of the sampled population. This pattern differs from the way contagious disease are normally distributed in the population and supports the hypothesis that atypical scrapie is spontaneously (without known cause) occurring. Although within flock transmission between animals seems to be very low (if it exists) other routes of spread and the potential zoonotic aspect is regularly subject to discussion.

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Shigatoxin producing *Escherichia coli*

BACKGROUND

Shigatoxin producing *Escherichia coli* (STEC) or, synonymously, verotoxin producing *Escherichia coli* (VTEC), may cause serious intestinal infections in humans. The toxin can be divided into two main groups, shigatoxin 1 (Stx1) and shigatoxin 2 (Stx2), and the genes encoding the toxins can be further divided into several subtypes, for example, *stx1a*. Often the strains associated with severe disease carry the *stx2* gene.

STEC was only sporadically detected in Sweden before 1995, when 114 human cases of STEC O157:H7 were notified. In 1996, STEC O157 was isolated in Swedish cattle for the first time and human STEC O157 infection was traced to a cattle herd. Cattle are the main reservoir of STEC associated with human disease although other animal species may also carry the organism. Not only foods of bovine origin but also vegetable food items and drinking water have been implicated in outbreaks. The infection can also be transmitted through direct or indirect animal contact, via the environment or person-to-person contacts.

Since 2005, between 230–890 cases (2.4–8.7 cases per 100 000 inhabitants) of STEC infections have been reported in Sweden annually, of which 50%–80% are domestically acquired. Most of the domestic cases are reported during the period July to September.

DISEASE

Animals

Animals do not develop clinical disease.

Humans

The clinical picture can vary from asymptomatic infection to non-haemorrhagic or haemorrhagic diarrhoea associated with abdominal cramps. Most patients fully recover. However, a severe complication of the disease is haemorrhagic uremic syndrome, HUS. HUS is characterised by acute renal failure, thrombocytopenia, and microangiopathic haemolytic anaemia; a condition that may lead to death. In recent years, approximately 3% of the cases in Sweden have developed HUS. A large proportion of the patients are young children, and severe complications are most common in this age group, as well as among elderly people.

During 2015 to 2020, 122 cases with STEC were reported to develop HUS. When analysing which serotypes and *stx* profiles that have been associated with HUS during 2015 to 2020 the most prevalent serotype was the domestic serotype O157:H7 clade 8 with 42 (34%) cases, followed by O26 with 16 (13%) cases and O121 with 7 (8%) cases (Table 23). Almost 30 percent of the HUS cases did not have an isolate for typing.

LEGISLATION

Animals

Since 1999, STEC O157 findings in animals are notifiable when associated with human infection (SJVFS 2013:23).

Food

Detection of STEC in food is not notifiable.

Humans

STEC O157 has been notifiable for both clinicians and laboratories under the Swedish Communicable Disease Act since 1996. All EHEC serotypes have been notifiable since 1 July 2004 (SFS 2004:168 with the addition of SFS 2013:634). A laboratory confirmed case can also include cases that are only positive by PCR i.e., where no isolate has been obtained.

SURVEILLANCE

Animals

Surveillance of STEC in animals is both enhanced passive (i.e., traceback investigations from human STEC cases) and active, which consists of planned prevalence surveys of STEC in abattoirs.

Passive - Traceback from human cases

If a County Medical Officer suspects an association between a human case of STEC infection and animals, or a farm with animals, the County Veterinary Officer will be informed. A request will be made to the Swedish Board of Agriculture for a trace back investigation and sampling of suspected animals, and/or the environment of the animals.

Active

Prevalence studies of STEC O157 in cattle at abattoirs have been conducted annually between 1997 and 2002, and then every third year. The next study will be performed during 2020–2021. In these conducted studies, STEC O157 has predominantly been isolated from cattle originating from southern Sweden but rarely from the northern two thirds of the country. The collected samples during 2011–2012 were also analysed for STEC O26 and STEC O103. STEC O26 was detected in 8 of 1308 faecal samples (0.6%) and in 15 of 336 cattle ear samples (4.5%). STEC O103 was detected in three of 1000 faecal samples (0.3%) and in three of 500 ear samples (0.6%). Results from a slaughter prevalence survey from 1998 showed that 0.1% of the pigs were positive for STEC O157:H7.

Food

No official control programme exists for STEC. National and local authority may perform sampling as a part of extended official controls or targeted projects.

Table 23: Serotypes and shigatoxin (stx) profiles for reported cases with haemorrhagic uremic syndrome (HUS), 2015–2020.

Serotype	stx1	stx1+stx2	stx1a	stx1a+stx2a	stx1c+stx2b	stx2	stx2a	stx2a+stx2c	stx2a+stx2d	stx2b	stx2b+stx2d	stx2c	Unknown stx	Total
Untyped	-	-	-	-	-	1	-	-	-	-	-	-	33	34
ONT:H29	-	-	-	-	-	-	-	-	-	-	1	-	-	1
ONT:H2	-	-	-	-	-	-	1	-	-	-	-	-	-	1
O182:H25	-	-	1	-	-	-	-	-	-	-	-	-	-	1
O175:H21	-	-	-	1	-	-	-	-	-	-	-	-	-	1
O165:H25	-	-	-	-	-	-	-	1	-	-	-	-	-	1
O156	1	-	-	-	-	-	-	-	-	-	-	-	-	1
O153	-	-	-	-	-	1	-	-	-	-	-	-	-	1
O146:H21	-	-	-	-	-	-	-	-	-	1	-	-	-	1
O130:H11	-	-	-	-	-	-	1	-	-	-	-	-	-	1
O117:H7	-	-	1	-	-	-	-	-	-	-	-	-	-	1
O113:H21	-	-	-	-	-	-	-	-	1	-	-	-	-	1
O112ac:H19	-	-	-	-	-	-	-	-	-	-	-	1	-	1
O103	1	-	-	-	-	-	-	-	-	-	-	-	-	1
O77:H41	-	-	-	-	-	-	1	-	-	-	-	-	-	1
O145:H28	-	-	-	-	-	-	2	-	-	-	-	-	-	2
O113:H4	-	-	-	-	3	-	-	-	-	-	-	-	-	3
O157:H7	-	-	-	1	-	-	1	1	-	-	-	-	-	3
O121:H19	-	-	-	-	-	-	7	-	-	-	-	-	-	7
O26	-	1	3	5	-	-	7	-	-	-	-	-	-	16
O157:H7, clade 8	-	-	-	-	-	-	5	37	-	-	-	-	-	42
ONT:H6	-	-	-	-	-	-	-	-	-	1	-	-	-	1
Total	2	1	5	7	3	2	25	39	1	2	1	1	33	122

Humans

The surveillance in humans is based on identification of the disease by the treating physician and/or by laboratory diagnosis (i.e. passive surveillance). Both treating physicians and laboratories are obliged to report to the regional and national level to enable further analyses and adequate intervention measures.

Molecular surveillance

Isolates from human cases, food and animals are investigated by the national authorities using whole genome sequencing (WGS) to determine the molecular serotype, relevant virulence genes and for cluster detection. As a conventional nomenclature tool, the Multi Locus Sequence Typing (MLST) type, i.e. ST-type, is also defined by WGS. Single nucleotide polymorphism (SNP) analysis is used to compare human isolates to those recovered from suspected sources during outbreak investigations and traceback activities. WGS data is also used to monitor long-term trends, e.g. the population structure of STEC among Swedish animals and the types of STEC causing severe cases of illness among humans.

RESULTS

Animals

Passive - Traceback from human cases

See section “Investigations of outbreaks and single cases of infection of STEC” below.

Active

A one-year prevalence survey of STEC O26 and O157 in cattle at abattoirs was started in the fall 2020. In total, 1200 samples will be collected from 13 abattoirs.

Food

In 2020, 37 samples were taken by national and local authorities from different types of food and analysed for STEC. STEC was not found in any of these samples. Most samples (n=35) were taken at border control from bovine meat. The two other samples were taken to investigate complaints or suspected food poisonings.

Humans

In 2020, 491 human cases were reported of which 396 were domestically acquired (81%). The domestic incidence in 2020 was 3.8 (cases per 100 000 inhabitants), and over a longer period of time an increasing trend is seen (Figure 29). As in previous years, the incidence was highest in children.

STEC-associated HUS was reported in 10 cases of which 8 were domestically acquired infections. Six of the HUS cases were children under the age of 10. For 6 of the HUS cases an isolate could be retrieved and thereby serotyped. Three of the domestic HUS cases belonged to serotype O157:H7, clade 8 (Table 24).

For 56% of the domestically acquired STEC cases, an isolate could be retrieved and thereby serotyped. However, for the travel associated cases only 37% were typed. (Table 25). The reason for the low isolation frequency is not

known. It can be influenced by regional analysis algorithms, unusual serotypes that are difficult to isolate or that cases who are infected abroad are seeking care in a later stage of the infection where the concentration of the pathogen is too low for isolation. In total 68 different serotypes were identified. The most common serotypes were O26:H11, O157:H7 and O103:H2. 18 cases were diagnosed with the domestic clade 8 of O157:H7, stx2a and stx2c alternatively only stx2a. Three of these cases developed HUS. The third most common serotype in Sweden, O103:H2, normally carries stx1a and gives milder symptoms. In 2020 one case was infected with the more potentially virulent variant carrying both stx1a and stx2a. In total, 19 isolates (four percent) have been identified with this type in Sweden since 2012.

Table 24: Distribution of serotypes and shigatoxin-subtypes in haemorrhagic uremic syndrome (HUS) cases in 2020.

Serotype	stx1a	stx2a	stx2a + stx2c	stx2b	Unknown stx
O157:H7, clade 8	-	1	2	-	-
ONT:H6	-	-	-	1	-
O26:H11	1	-	-	-	-
O121:H19	-	1	-	-	-
Untyped	-	-	-	-	4
Total	1	2	2	1	4

Investigations of outbreaks and single cases of infection of STEC

In 2020, five farm investigations were carried out due to detection of human cases connected to farm animals. Three of the farms were positive for EHEC, while two were negative at sampling. At two of the farms, O26 was identified: H11, stx1a and stx2a, where one farm had sheep and the other cows and sheep. At the third farm there were goats and here the cause of infection was O157: H7 clade 8 stx2a. The most common cause of HUS cases in Sweden remains the O157:H7 variant known as clade 8, which is endemic in the southeast.

One national outbreak investigation was performed during 2020 with 7 cases of O103:H11 stx 1a. No source could be identified.

Table 25: Number of reported human cases of shigatoxin producing *Escherichia coli* (STEC) in comparison to number of cases where an isolate could be retrieved 2020.

Origin of infection	Number of reported cases	Number of isolates typed (%)
Domestically acquired infection	396	222 (56%)
Travel associated infection	78	118 (37%)
Unknown country of infection	17	3 (29%)
Total	491	256 (52%)



Figure 29: Incidence (per 100 000 inhabitants) of notified human shigatoxin producing *Escherichia coli* (STEC) cases in Sweden, 1997–2020. Prior to 2005, only O157 was required to be reported. In 2005, all serogroups of STEC including PCR findings became subject for notification. In 2005, 2016 and 2018, the number of cases increased due to one or more domestic outbreaks.

IN FOCUS: It only takes two to tango – clustering of STEC isolates

Outbreaks of STEC are seldom identified and the majority of cases are considered sporadic. Microbial surveillance of STEC is a tool for cluster detection, source tracing and outbreak investigation and it captures outbreak signals that could otherwise go undetected. Epidemiological typing of STEC isolates on national level in Sweden is done using whole genome sequencing. The sequencing data is used for e.g. species determination, identification of molecular serotype, virulence genes and other relevant genes such as antibiotic resistance markers. In addition, a cluster analysis is performed for all isolates within a defined serotype where a cluster is defined as two or more isolates. When a cluster is detected, regional health authorities are informed in order to interview cases and investigate the cluster. Small clusters can for example be cases within the same family, or it can be the first signal of a continuously growing cluster that will evolve to a national outbreak investigation. Each year a number of small and large clusters are investigated. Number of clusters, number of cases involved in clusters and proportion of isolates that are part of a cluster were summarised for 2018, 2019 and 2020 (Table 26). The majority of clusters were small in regard to number of isolates and most often reported as domestically acquired. The serotypes that were most often identified in clusters during this period were O157:H7 and O26:H11, which are also the most common serotypes identified in Sweden. In 2020 there were only three small clusters identified within O157:H7. In addition, there was a farm investigation where a human isolate and an isolate identified on a farm with goats clustered (Figure 30).

The number of clusters identified during 2018–2020 varied largely between years. In the pandemic year of 2020, relatively few clusters were identified (n=18) compared to 2018 and 2019 when 53 and 33 clusters were identified respectively (Table 26). Furthermore, the proportion of isolates involved in clusters varied between years. In 2018, when there was a large outbreak with 112 cases, 52 percent of all isolates were part of a cluster. If the large outbreak is not accounted for, this proportion was 30 percent. In 2019 and 2020 the proportion of isolates in clusters were 25 and 18 percent, respectively. This shows that a considerable proportion of isolates from cases with no known epidemiological links are connected by typing data. Possible explanations include exposure to shared sources of infection as well as the regional occurrence of genetically closely related domestic strains of STEC among animals on multiple farms.

Comparing isolates from patients, food, animals and the environment in cluster analyses is a powerful tool for investigating outbreaks and source tracing. In the longer perspective, analysing the duration, re-occurrence and possible seasonality of clusters can provide vital clues to determine the routes of infection for STEC in Sweden. However, cluster definition remains a challenge and appropriate thresholds for inclusion in a cluster are likely to be dependent on serotype and context.

Table 26: Distribution of human clinical Shigatoxin producing *Escherichia coli* (STEC) isolates in genomic clusters in 2018, 2019 and 2020. Clusters were assessed using single nucleotide polymorphisms (SNPs) of whole genome sequencing data.

Year	Total number of isolates	Isolates in clusters (n)	Isolates in clusters (%)	Total number of clusters	Clusters >=5 isolates	Clusters 2-4 isolates
2018	510	266 ^A	52	53	8	45
2019	361	92	25	33	4	28
2020	256	46	18	16	2	14

^AIn 2018, 112 isolates were part of a large outbreak.

Small ruminant lentiviruses

BACKGROUND

Small ruminant lentiviruses (SRLVs) include caprine arthritis-encephalitis virus (CAEV) and visna/maedi virus (VMV) in the retrovirus family. Maedi-visna (MV) is a globally distributed contagious disease in sheep, first described in Iceland in 1939. Caprine arthritis-encephalitis is a common disease in most goat producing countries all over the world. Transmission between animals occurs most commonly via the oral route (mainly via milk and colostrum) but may also occur via inhalation of infected aerosol droplets. The incubation period is long; often 4–5 years. The first case of MV in Swedish sheep was officially reported in 1974. Fifteen years later, the flock-level seroprevalence was 8.2% as demonstrated by sampling of randomly selected sheep at abattoirs. The prevalence of CAE in Sweden is not known, but in a pilot study from 2018, 30% of the herds were seropositive.

Voluntary control programmes for MV and CAE were launched by Farm & Animal Health in 1993 and 1999, respectively, and in 2005 an additional simplified version started, with single sampling of sheep and goats to identify diseased flocks and then in the next step enrol them into the control programme. From 2020, the simplified version is no longer available. The MV and CAE programmes were run in parallel, but from 2020, they are merged into one programme called the MV/CAE programme.

Data from all sampled and controlled flocks have been recorded since 1993.

DISEASE

Only the maedi form of MV is occurring in Swedish sheep flocks; a progressive viral pneumonia. The disease typically remains latent in the flock for several years before appearing with clinical manifestations. In an advanced stage of the disease the typical clinical signs are severe emaciation and respiratory distress in older ewes. After the appearance of clinical signs, the outcome is always fatal within weeks to months. CAE occurs in four different forms: arthritis, nervous form, pneumonia, and mastitis (hard udder). In Sweden, subclinical disease is probably most common.

LEGISLATION

MV and CAE are notifiable diseases (SJVFS 2013:23). The control programme is regulated through SJVFS 2015:17 (Jordbruksverkets föreskrifter om frivillig organiserad hälsokontroll av husdjur (K 152).

SURVEILLANCE

The purpose of the control programme is to detect and eradicate MV and CAE from Swedish sheep and goat flocks and to prevent introduction into free flocks. Documentation of the MV/CAE status in the flocks is essential. By identifying infected flocks and taking measures, the spread of MV/CAE stops, and eradication is possible. Prevention of introduction

of MV/CAE into flocks is crucial.

The programme is based on serological testing of sheep at farm level. A flock specific MV/CAE status is achieved by repeated blood sampling and testing. Participating farmers sign an agreement that all sheep and goats in the flock are individually identified (according to legislations) and recorded. Purchase of sheep and goats is only allowed from flocks with a similar or higher MV/CAE status.

Three consecutive serological tests are performed on all sheep and goats ≥ 12 months old with an interval of 12–16 months. All samples in each test must be negative for MV/CAE antibodies. Each test renders an MV/C-status; M1/C1, M2/C2 and M3/C3. M3/C3-status means that the flock is declared free from MV/CAE. 24–28 months after gaining the M3/C3-status a final test is performed on all sheep/goats ≥ 24 months old and the flock will render an MV/CAE free status. The MV/CAE free status is maintained by an assurance of the animal keeper every second year. An indirect control of the M3/C3/MV/CAE free status holdings is performed by testing of sheep and goats from holdings entering the programme as these new animals are mainly bought from M3/C3/MV/CAE free status flocks. If antibodies are detected in a flock, either the whole herd is culled or other control and eradication measures including selective slaughter is performed, depending on the prevalence of positive sheep and goats within the flock.

The programme is based on serological examination of blood samples for antibodies against MV or CAE virus with an ELISA test (CAEV/VMV Total Ab ELISA IDEXX). Samples with inconclusive or seropositive results are retested using the same ELISA-test and if the results are still seropositive a confirmatory test is performed using AGID (agar gel immunodiffusion) for which the antigen is purchased from the Animal and Plant Health Agency, Weybridge, UK.

Postmortem examinations and histopathology are additional important tools to detect MV. Diagnostic testing is performed at the National Veterinary Institute. Serum samples collected in the MV-programme are also used for other active surveillance activities in sheep (e.g., Brucellosis).

RESULTS

During 2020, approximately 7925 samples from sheep and goats were analysed in the MV/CAE control programme for antibodies against MV/CAE-virus.

At the end of 2020, 3412 sheep flocks with 122 316 sheep and 249 goat flocks with 2417 goats were enrolled in the programme. This corresponds to about 45% of the Swedish sheep population, and about 12% of the goat population. 3442 of the flocks were declared free from MV/CAE.

In 2020, 1 sheep flock and 1 goat flock were considered MV/CAE positive. The rest of the flocks was somewhere in the process from unknown to free, which normally takes 5 years and 4 sampling occasions.

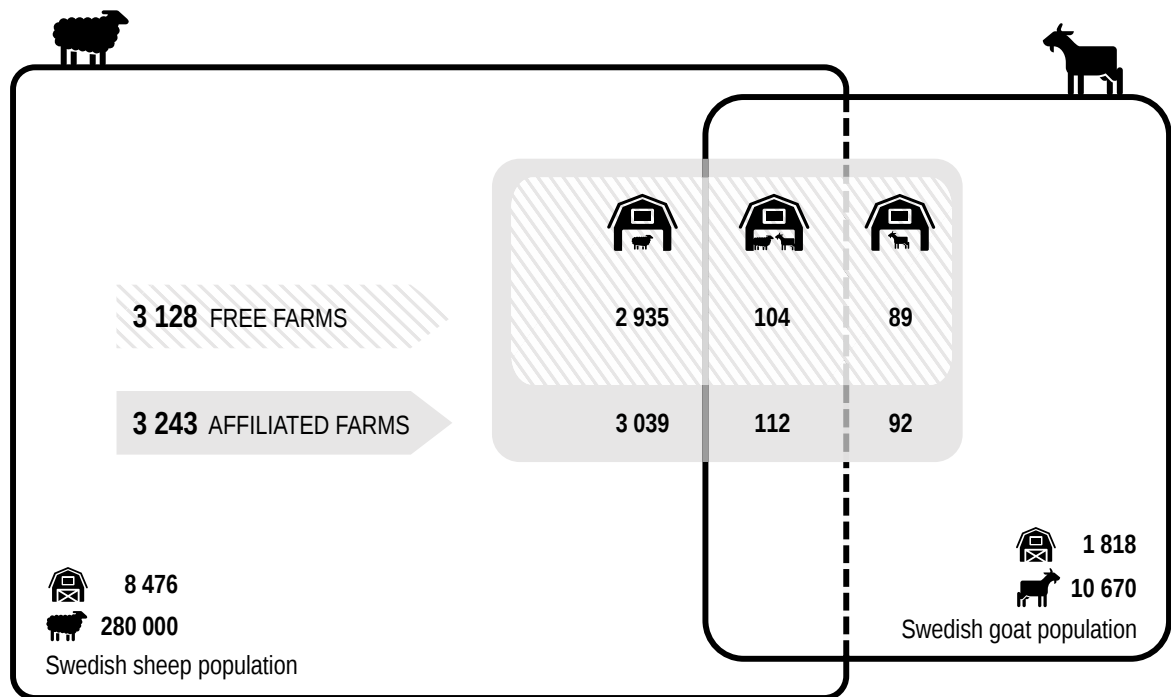


Figure 31: Coverage and achievements of the Swedish surveillance system for lentiviruses in 2019. Infographic by Arianna Comin.

DISCUSSION

It is now more than 25 years since the MV programme was launched. A series of measures have been taken to finalise the programme and to reach freedom from disease. A revision of the MV programme was made during 2013 by Farm & Animal Health and the National Veterinary Institute. Since July 2014, the programme has been further refined to improve efficacy and efficiency, e.g., by increasing sampling in risk areas and higher risk flocks and reducing sampling in long-term MV free and well-documented flocks. During 2020, the programme has been scrutinized for more cost-effective sampling, diagnostics, and control measures. Figure 31 shows an overview of the coverage and achievements of the Swedish surveillance system for lentiviruses in 2019. The updated program will be implemented during 2021–2022. Norway has after a successful programme declared most herds free from CAE, showing that it is possible to eradicate the disease.

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Strangles

BACKGROUND

Strangles is a very contagious disease in horses, caused by *Streptococcus equi subsp. equi* (*S. equi*), belonging to Lancefield's group C streptococci. The disease causes substantial losses for the Swedish equine industry, mainly from long standstills, which often lead to severe economic crisis for the infected establishment. There are several examples of strangles leaving riding schools in the threat of bankruptcy, often avoided by acute municipal aid. A survey from 2016–2017 indicates that most outbreaks are coupled to newly arrived, often imported horses.

Strangles normally resolves without antibiotic treatment but can cause severe complications or persistent infection. To control and eradicate strangles in a population, systematic surveillance by testing is necessary, and it is crucial that the equine industry implements preventive biosecurity strategies for high-risk-situations.

DISEASE

Strangles affects horses, including donkeys and zebras. Common clinical signs include fever, nasal discharge, depression, cough and enlarged submandibular or cervical lymph nodes. Other signs associated with strangles may include: inappetence, dysphagia, painful movements, ruptured abscesses, dyspnoea and swollen limbs; and less commonly: spread of infection to other organs, so called *bastard strangles*. Complications of strangles may be severe and lead to death.

So called *atypical strangles* with mild clinical signs is probably more typical than previously understood, which may lead to large outbreaks due to delayed diagnoses. Also, recent findings indicate that subclinical infections with *S. equi* after an acute outbreak may be far more common than previously understood, and microbiological confirmation of the absence of *S. equi* can be required to rule out the horse being a carrier.

LEGISLATION

Strangles is a notifiable disease in Sweden (SJVFS 2013:23). It is notifiable on clinical suspicion to the County Administrative Board in the county where the horse is residing.

SURVEILLANCE

In Sweden, surveillance for strangles is passive. Sampling and diagnostic testing are performed on clinical suspicion. Typically, samples from upper airways or ruptured abscesses are submitted for bacterial analysis (culture or qPCR).

A yearly summary of notified, confirmed cases of strangles per county is produced by the Board of Agriculture; Figure 32 illustrates the number of notified cases per year.

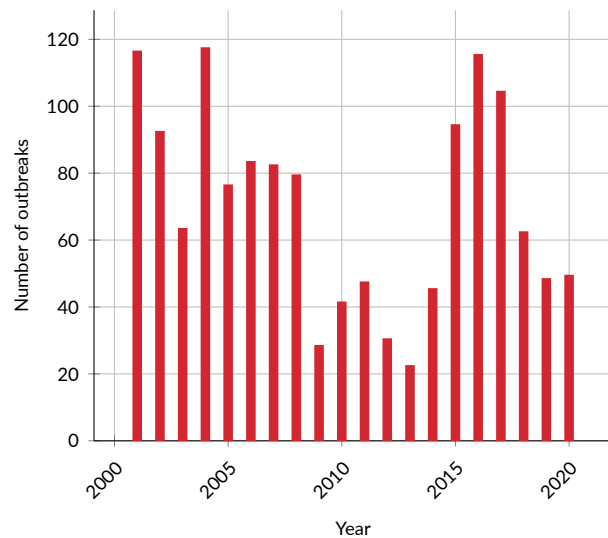


Figure 32: Reported index cases (farm outbreaks) of *Streptococcus equi* infections in horses in Sweden during years 2001–2020. Source: Swedish Board of Agriculture.

RESULTS

In 2020, there were 49 officially reported index cases of strangles in Sweden, each representing an outbreak in a farm. The number of reported cases have varied from year to year, with an observed decreasing trend since 2016 when 115 index cases were reported (Figure 32).

DISCUSSION

The passive surveillance results indicate that strangles is endemic in the Swedish horse population. However, newly arrived horses, often from international trade, appear to be involved in most of the investigated acute outbreaks. A programme for tracing the spread of strangles, by DNA characterisation of different isolates, would provide an effective tool for control.

Veterinary practitioners should be made aware that the probability of detecting *S. equi* in an infected horse is influenced by several factors: site of specimen collection (nasal passage, nasopharynx, guttural pouch or abscess), method of sampling (flocked swab, rayon swab, or wash), and type of diagnostic test (culture or qPCR), as well as target gene for the PCR and the DNA amplification method that is performed. Timing of sampling is also crucial. Serology for serum antibodies against antigens A and C of *S. equi* has been suggested for screening of subclinical *S. equi* carriers but has limitations in both sensitivity and specificity.

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Swine dysentery



Swedish domestic pig production. Photo: Marie Sjölund.

BACKGROUND

Swine dysentery (SD) is a severe disease affecting the large intestine of pigs that is caused by *Brachyspira hyodysenteriae* (*B. hyodysenteriae*). SD was rare in Sweden prior to the ban of the use of low dose antibiotics for growth promotion in Sweden. Following this ban in 1986, post weaning diarrhoea (PWD) increased and SD was also more frequently diagnosed, especially in grower pigs.

Since then, improvements in biosecurity and non-antibiotic feed adaption for weaners have improved the situation considerably. SD has also successfully been eradicated from affected herds following special sanitation protocols. Despite this, SD is still diagnosed in a few herds annually. The reason for this is, to a large extent, that the disease is not notifiable and thereby not actively monitored. Therefore, herds may trade pigs despite the presence of subclinical SD. Herd owners may also choose to change abattoir or animal-health organisation without informing the new organisation of their existing SD status.

In 2016, tiamulin-resistant SD was identified for the first time in Sweden. This is particularly problematic as tiamulin

is the drug-of-choice for controlling SD. Fortunately, the tiamulin resistant strain of SD was successfully eradicated, but this incident awakened a national interest in national eradication of SD. However, SD still escapes detection, at the population level, due to the lack of knowledge about the status of individual production herds.

DISEASE

Clinical signs of SD include mucohaemorrhagic diarrhoea, occasionally with blood, ill-thrift, inappetence and weight loss. Mortality can be significant, but the largest economical losses are induced by a reduced weight gain and cost of treatment.

LEGISLATION

SD is not a notifiable disease, but due to the severity of the disease, an improved control of SD would be valuable for the pig producers.

SURVEILLANCE

Nucleus and multiplying herds have been actively tested for the presence of SD since the 1990s. A national network with the aim of eradicating SD at the national level was established in the autumn of 2019 and became active on the 1st of January 2020. It included the pig producers' organisation, abattoirs, pig health organisations and SVA. The work is co-ordinated from SVA, and all diagnosed cases of SD during the period 2016–2019 as well as the present status of these herds were defined. From the 1st of January 2020, all herds where SD can be suspected are to be tested through rectal swabs and cultured at SVA and all information shared with the network.

Herds previously diagnosed with SD and not officially declared free from the infection on the 1st of January 2020 received transport restrictions and were to be transported in ways that reduced the risk for infecting other herds. Similarly, new herds diagnosed with SD receive transport restrictions until declared free from the infection. To achieve this, all organisations reported to SVA who in turn continuously informed all members of the network of the current national SD status.

Table 27: Number of herds positive for swine dysentery (SD) at end of 2020.

Herds with SD on 2020-01-01	9
New herds diagnosed during 2020	5
Herds declared free from SD during 2020	5
Herds with SD on 2020-12-31	9

RESULTS AND DISCUSSION

During 2016–2019, SD was diagnosed in 25 herds, whereof nine still had not been declared free by the 31st of December 2019.

In 2020, a total number of 147 herds were tested for SD (Table 28). Of these, 53 were nucleus or multiplying herds tested for freedom of SD with negative results and 82 herds were tested upon suspicion. SD was detected in five of these 82 herds. In total, 14 Swedish pig herds were diagnosed with

SD during 2020; of these, 5 were diagnosed for the first time during 2020. As of the 31st of December 2020, five of these 14 detected herds were subsequently declared free from SD, 6 were under sanitation and 3 remained with SD.

It is important to maintain a high proportion of sampled herds over time to support future declarations of freedom from this disease in the Swedish pig population. By the end of 2020, there was an equal number of pig herds (9) with SD as there was at the beginning of that year (Table 27). Despite the similar number of positive herds at the end of 2020 compared to the previous year, the Swedish SD situation has improved due to a better certainty of the disease status with more testing of the population.

Table 28: Herds monitored for swine dysentery (SD) in Sweden during 2020.

Reason for testing	Number of herds sampled	Number of positive herds
Certification testing of breeding stock herds	53	0
Testing of herds due to first clinical suspicion during 2020	82	5
Retested herds due to previous positive result during or before 2020	12	7

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Tick-borne encephalitis

BACKGROUND

Tick-borne encephalitis virus (TBEV) belongs to the genus flavivirus in the family *Flaviviridae*. TBEV is endemic in an area ranging from northern China and Japan, through far-eastern Russia to Europe. The virus may cause a neurological infection which may lead to long-term sequelae in the affected patients. The virus is spread by ticks (*Ixodes ricinus* and *I. persulcatus*), which become infected when they suck blood from infected rodents. Wild rodents are the natural reservoir for TBEV. The virus also circulates in the tick population through transovarial transmission without involvement of vertebrate hosts. Large mammals, predominantly ungulates, are important for the maintenance of large tick populations. Humans typically become infected via ticks, although unpasteurised cow, goat and sheep milk and milk products have also been reported as sources. Vaccination of persons living, visiting or working in endemic areas is recommended.

Three sub-types of TBEV are described: the “Western”, “Siberian” and “Far eastern” subtypes. In Sweden, only the “Western” subtype has been identified.

The first case of TBE infection in Sweden was reported in 1954. During the following three decades, 10–40 annual cases were reported. From the mid-1980s a clearly increasing trend has been observed. In recent years about 150–400 cases have been reported annually. A majority of the cases acquire their infections in Sweden. Most have been infected on the east coast of Sweden and in the Stockholm archipelago but in recent decades cases have been observed regularly on the west coast of the country and the infection occurs from the region of Skåne in the south to the regions of Gävleborg and Dalarna in the north. The age distribution is wide but most of the cases are between 30 and 70 years. There is a slight over-representation of men. A majority of the patients are diagnosed in July to October.

DISEASE

Animals

In general, animals develop a subclinical infection. However, confirmed clinical cases have been reported in dogs and horses. Seroconversion has been demonstrated in grazing domestic animals such as goats, cattle and sheep as well as in wild ungulates. Ruminants may excrete the virus in milk. Wild rodents are considered the natural reservoir for TBEV but are not reported to contract the disease. Serological testing of wild animals, such as moose and deer, has been suggested as an indicator of the circulation of the virus.

Humans

In humans, a biphasic course of the disease is common. The first, viraemic phase lasts for about four days. After an interval of about a week, a meningoencephalitic phase appears in about one third of the patients. The symptoms may include fever, headache, nausea, cognitive dysfunctions or spinal paresis. The mortality is low, about 0.5%. The incubation period of TBE is usually between 7 and 14 days.

LEGISLATION

Animals

TBE is not a notifiable disease in animals in Sweden.

Humans

TBE in humans is notifiable as a viral meningoencephalitis since 2004, according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2013:634).

SURVEILLANCE

Animals

The surveillance in animals is passive.

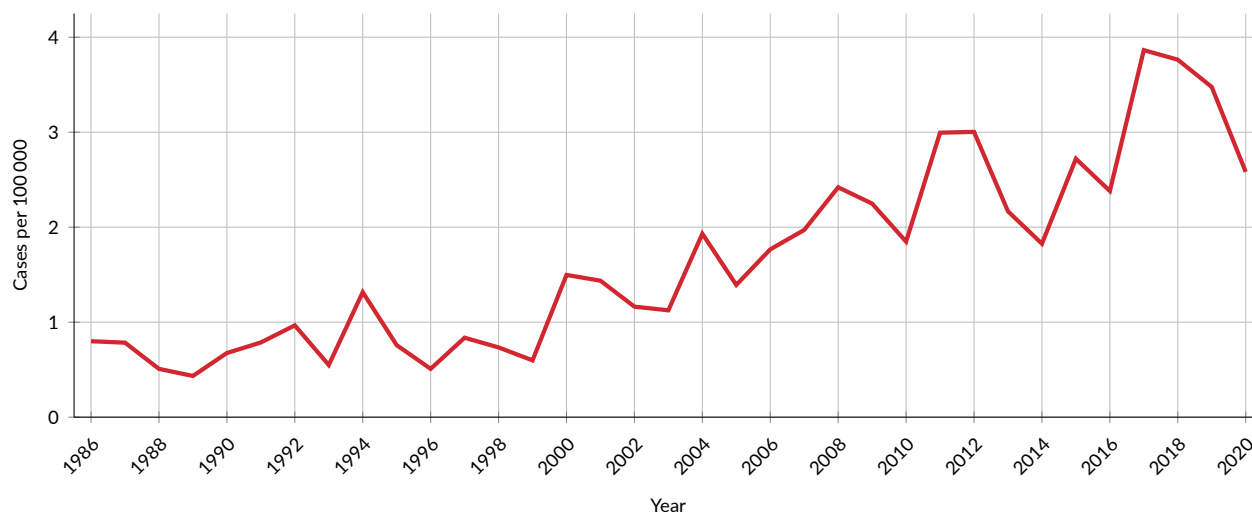


Figure 33: Incidence (per 100 000 inhabitants) of notified cases of tick-borne encephalitis in humans 1986–2020.

Humans

TBE is notifiable based on identification of the disease by a treating physician or by laboratory diagnosis. Both are obligated to report identified cases to the regional and national level to enable further analyses and adequate intervention measures.

RESULTS

Animals

No surveys on TBE in animals were performed in 2020.

Humans

In 2020, 268 cases of TBE were reported. This is a relatively large decrease since the year before (n=359) (Figure 33).

More men (63%) than women were reported with TBE. The incidence was highest among people in the age group 30–79 years, but there were cases reported from 0 to 83 years of age. Normally, there are few young children reported with TBE and this was the case also in 2020 with only four cases among children below the age of 5.

All but nine cases had acquired their infections in Sweden. One person was infected in Lithuania and one in Poland. For seven cases the countries of infection were unknown. The first TBE case became ill as early as in late January and the last in November. The peak occurred in August, when most people fell ill. As before, the majority of cases were infected in a geographic area that runs like a belt across Sweden, from the regions of Stockholm, Södermanland, Uppsala and Östergötland in the east to Västra Götaland and Värmland in the west (Figure 34). In addition, TBE is widely distributed in several parts of the rest of southern and central Sweden. Cases were reported from the region of Skåne in the south to Gävleborg and Dalarna in the north. In 2020, the incidence decreased in almost all regions. One of the exceptions was the region of Örebro, where the incidence on the contrary doubled.

DISCUSSION

Despite the decrease in number of TBE cases in 2020, the overall picture shows a significantly increasing trend of the incidence since the reporting started.

Although most human cases acquire the TBE infection via tick bites the infection can be food-borne. Outbreaks and clusters of cases of TBE caused by consumption of unpasteurised milk or milk products have been described in Baltic, Balkanise and central European countries. National surveys performed in Sweden in 2013 and 2019 show that the virus circulates in the Swedish population of dairy cattle.

The long-term increase in TBE incidence is probably due to several interacting factors. The most important cause is presumably the very dense population of ticks, a consequence of a large roe deer population from the 1980s up until the recent snowy winters. This situation in combination with a high population of small host animals such as bank voles, and optimal weather for both virus spread and humans spending time outdoors, could explain the large number of cases reported.

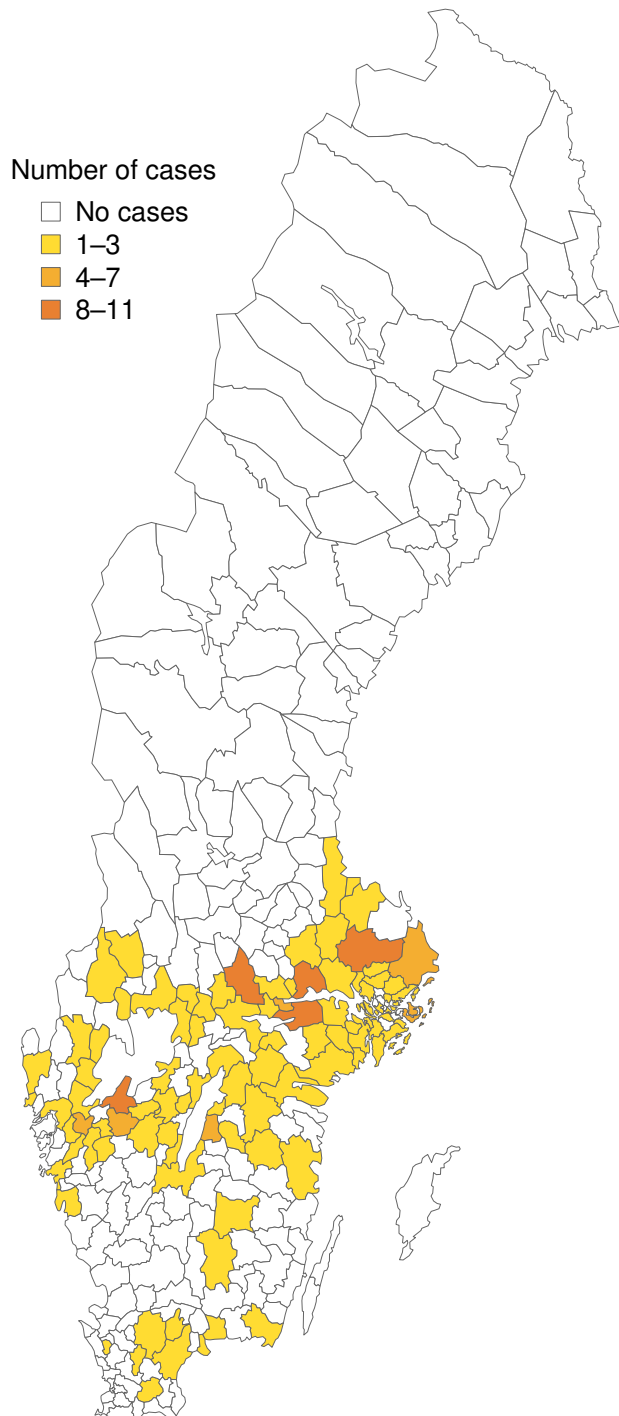


Figure 34: Geographical distribution of notified cases of tick-borne encephalitis in humans in 2020, based on the municipality of infection.

Trichinellosis

BACKGROUND

Trichinellosis is caused by parasitic nematodes of the genus *Trichinella*. The parasites can be hosted by different mammals including domestic pigs and horses, but the main reservoirs are wild carnivores and omnivores. Humans typically acquire the infection by eating raw or inadequately heated infected meat or meat products, for example cold-smoked, fermented sausages. In the gut, the *Trichinella* larvae develop into adult worms and mate. After mating, the female releases new larvae which penetrate the intestinal mucosa and travel via the bloodstream to various organs and muscles. In striated muscle cells the larvae may survive in an encapsulated form for years. There are several *Trichinella* species of which *T. spiralis* is the most widespread and most common in domestic pigs and as a cause of human disease.

In Europe today, trichinellosis is a rare disease that occurs predominantly in a few countries, mainly Bulgaria and Romania. Human cases are often associated with food-borne outbreaks and thus the reported numbers of cases fluctuate between years, but the trend has been declining during the period 2015–2019. Most outbreaks are caused by meat/meat products from pigs, but wild boar meat is also an important source of infection. *Trichinella spiralis* followed by *T. britovi* are the dominant causes of human disease. According to EU legislation all slaughtered pigs, horses and wild boars should be tested for *Trichinella*, with the possible exemption for pigs raised under controlled housing conditions (EU 2015/1375). While many EU Member states have not detected any infected pigs since long back, positive cases occur in others. For example, in 2019 positive pigs were reported from Spain, Romania, Poland, Croatia, Bulgaria and France. These infected pigs were all free-range and backyard pigs reared in rural regions.

In Sweden, *Trichinella* has been monitored at slaughter in domestic pigs since the beginning of the 20th century. From 1970–1990 sporadic cases were detected in domestic pigs, but since 1994 there has not been any positive pigs. The parasite is endemic at a low level in Swedish wildlife. The species most often detected in wild boars are *T. britovi* and *T. pseudospiralis*, while the freeze-resistant *T. nativa* is dominant in wild carnivores, especially those from the northern part of the country. In contrast, *T. spiralis* has been a rare finding in Swedish wildlife during the last decade.

The disease is extremely rare in Sweden and detected human cases are usually infected abroad. Since 2004 only seven human cases with confirmed infection with *Trichinella* have been reported; all except one (in 2013) were infected abroad.

DISEASE

Animals

Animals rarely develop a clinical infection, although both pigs and rodents can exhibit clinical signs.



Trichinella occurs in wild carnivores in Sweden, but the risk of getting infected with the parasite from Swedish food-producing animals is negligible. During 2020, the parasite was found in 6 out of 91 tested lynx. Photo: Bengt Ekberg/SVA.

Humans

In humans, the disease can range from subclinical infection to fatal disease. The incubation period varies from 5–15 days. Symptoms initially involve diarrhoea and abdominal pain and later muscle pain, fever, oedema of the upper eyelids and photosensitivity. Intestinal stages of the disease respond well to treatment. Cardiac and neurological complications may occur 3–6 weeks post infection. *Trichinella* is not transmitted between humans.

LEGISLATION

Animals

Trichinella is notifiable in animals according to SJVFS 2013:23. Official controls for *Trichinella* in meat is regulated by Commission Implementing Regulation EU 2015/1375 of 10 August 2015.

Humans

Trichinellosis is notifiable according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2013:634).

SURVEILLANCE

Animals

Testing for *Trichinella* is part of routine meat inspection for domestic pigs, horses, wild boars and other animal species that can become infected. Since 2014, Sweden applies reduced testing of domestic pigs from holdings officially recognized to apply controlled housing conditions (EU 2015/2013). The risk of *Trichinella* infection in pigs from such production sites is considered as negligible and only certain categories of pigs have to be tested. In Sweden, all carcasses of breeding sows and boars sent for slaughter are examined, while fattening pigs originating from controlled holdings are not obligated to test for *Trichinella*. Pig production sites without controlled housing conditions should test all their slaughtered domestic pigs. The digestion method is the only method applied in testing for *Trichinella*.

All slaughtered horses, and all wild boars and bears delivered to game handling establishments, are tested for *Trichinella*. Also, most hunters test wild boars and bears consumed in private households. In addition, to monitor the occurrence of *Trichinella* in the environment several species of wild animals are tested for *Trichinella*, including foxes, lynxes, wolves, wolverines, badgers and birds of prey. Testing of *Trichinella* in animals was performed by six laboratories during 2020.

Humans

Notification of human cases is mandatory and surveillance is based on identification of the disease by a treating physician or by laboratory diagnosis. Both are obligated to report identified cases to the regional and national level to enable further analyses and adequate intervention measures.

RESULTS

Animals

In 2020, the number of tested pigs from controlled housing conditions were 29 744 breeding sows, 508 boars and 1 469 068 fattening pigs. In addition, 480 206 slaughtered pigs (all categories) from uncontrolled housing conditions were tested. The number of slaughtered and tested horses was 1425. *Trichinella* was not detected in domestic pigs or horses.

Trichinella spp. was detected in 9 out of a total of 161 072 (0.006%) wild boar samples and also in 6 lynx, see Table 29. These figures are based on results from examination of samples from animals submitted to wild game establishments (16 639 wild boars and 109 bears) as well as samples submitted for testing by private hunters. In addition, samples were taken from selected wildlife species (primarily carnivores) sent to the National Veterinary Institute within the general surveillance programme for wildlife diseases.

Humans

No human case of trichinellosis was reported in 2020.

DISCUSSION

Trichinellosis is extremely rare in Swedish food-producing animals and a majority of the few human cases detected during the last decades were infected abroad. The *Trichinella* situation in the Swedish animal population seems to be stable. *Trichinella* occurs in wild carnivores and wild boar but the risk of getting *Trichinella* from domestic pigs and horses is negligible.

Table 29: Findings of *Trichinella* in wild animals 2020.

Animal species	No. samples	No. positives	Percentage (%)	<i>T. britovi</i>	<i>T. nativa</i>	<i>T. pseudospiralis</i>
Badgers	13	0	0.00%	-	-	-
Bears	222	0	0.00%	-	-	-
Beavers	64	0	0.00%	-	-	-
Lynx	91	6	6.59%	1	5	-
Seals	20	0	0.00%	-	-	-
Wild boars	161 072	9	0.006%	4	-	5
Wolves	1	0	0.00%	-	-	-
Total	-	15	-	5	5	5

Tuberculosis



Import of alpacas is identified as a potential route of introduction of tuberculosis. There is a voluntary control programme for alpacas to enable detection and confirm absence of tuberculosis in the population. Photo: norr08/iStock.

BACKGROUND

Tuberculosis (TB) is a serious disease in humans and animals caused by bacteria included in the *Mycobacterium tuberculosis* complex. *Mycobacterium bovis* causes bovine TB in several animal species as well as in humans. Historically, the reservoir has been cattle, but many other wild and domestic species can also maintain the infection. Wildlife reservoirs including badgers, deer and wild boar cause persistent problems in some countries. Humans usually acquire *M. bovis* infection via unpasteurised milk or via inhalation. The predominant cause of human TB globally is however *Mycobacterium tuberculosis*. In countries where human TB caused by *M. tuberculosis* is common, this bacterium is also frequently isolated from various species of animals.

Bovine TB was introduced to the Swedish cattle population through imports in the first half of the 19th century. In 1958, after a successful control programme, Sweden was declared officially free from bovine TB. Since then, sporadic cases have occurred in cattle, the most recent in 1978. Compulsory tuberculin testing of all cattle was abolished in 1970 and the national TB control in cattle is now based on meat

inspection and clinical surveillance.

When Sweden joined the European Union in 1995, the status of OTF (officially tuberculosis free) was obtained.

In 1987, *M. bovis* infection was introduced into the farmed deer population through imports. A control programme for TB in farmed deer was introduced in 1994 and made compulsory in 2003. The last case of TB in farmed deer was identified in 1997.

The yearly incidence among humans in Sweden in the early 1940s was above 300 per 100 000 inhabitants. This was followed by a rapid decline, beginning before effective treatment was available in the early 1950s. Currently, the yearly incidence is 4.8 per 100 000 inhabitants, which is among the lowest in the world. Around 90% of the cases are born outside of Sweden and the vast majority of them are immigrants originating from countries that still have a high incidence of TB. The yearly incidence among people born in Sweden is 1 per 100 000 inhabitants. A large majority of the cases detected in humans in Sweden are caused by *M. tuberculosis* and only a few cases per year are caused by *M. bovis*.

DISEASE

The clinical signs caused by TB in both humans and animals depend largely on the localisation of the infection. The disease progresses slowly, and clinical signs may take a long time to develop, even in cases with substantial lesions. Weight loss and sometimes coughing (in cases with respiratory tract infection), ascites (due to infection in intestinal lymph nodes or liver) or mastitis (mainly in cattle with udder infection) can be seen. The incubation period varies from weeks to years.

LEGISLATION

Animals

Suspect and confirmed cases of infection with *Mycobacterium bovis* or *M. tuberculosis*, are notifiable in all animal species according to the Swedish Act of Epizootic diseases (SFS 1999:657, with amendments), other mycobacteria in the *M. tuberculosis*-complex are notifiable according to the Swedish act on notifiable animal diseases and pathogens (SJVFS 2012:24).

Humans

Tuberculosis in humans is a notifiable disease according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2013:634). Contact tracing is compulsory, and the treatment is free of charge. Refusing treatment as a patient when being contagious can lead to detention.

SURVEILLANCE

Passive surveillance

Animals

TB is notifiable both on suspicion and confirmed diagnosis and farmers and veterinarians are obliged to report suspicion of TB. Clinical signs in animals or lesions detected at slaughter, surgery or postmortem of an animal prompt investigation, which may include sampling for histopathology, bacteriology, PCR, tuberculin testing of contact animals and epidemiological investigations.

Surveillance for TB is mainly performed by meat inspection at slaughter of food producing animals. Official inspectors from the Swedish Food Agency perform the inspections. Suspect lesions are sent to the National Veterinary Institute for histology and bacteriology, as described above. For tissue from macroscopic lesions indicating TB, histology and direct smears are performed. If TB cannot be ruled out by histology or if direct smears are positive, culture is performed. Cultures are performed on solid media (Löwenstein-Jensen and Stonebrink's) at the National Veterinary Institute and cultured for up to twelve weeks. Suspected colonies are tested with PCR and, if necessary, with sequencing of a specific gene. Isolates suspected to belong to the *M. tuberculosis*-complex or where the *M. tuberculosis*-complex cannot be ruled out are sent for confirmation, e.g. to the Norwegian Veterinary Institute or the Public Health Agency of Sweden. Positive isolates are further sub-typed.

Skin fold tuberculin tests are performed according to EC 1226/2002 (amending annex B of EC 64/432) and SJVFS

2003:33, (K62). The comparative intradermal test is used, mostly at the neck site. In case of positive tuberculin test reactors, the animal is culled and samples from organs with macroscopic lesions and lymph nodes from five different areas (retropharyngeal, submandibular, mediastinal, mesenteric and inguinal) are collected and examined as described above.

A positive finding of mycobacteria belonging to the *M. tuberculosis*-complex in animals, either detected through active or passive surveillance, will generate contacts with public health representatives to ensure that possible exposure of humans can be investigated.

Humans

The surveillance in humans is mainly passive but contact tracing from diagnosed cases is compulsory and asylum seekers from high incidence countries are offered health examination where screening for TB is included, mainly with IGRA.

In humans, culture on sputum smear is the standard test when pulmonary TB is suspected. Otherwise culture from urine, faeces, blood or liquor is also a possibility, or biopsies from suspected site of infection. All isolates from humans are genotyped with whole genome sequencing, mainly to detect clustering of cases that could indicate ongoing transmission, but also to look for genetic mutations associated with resistance.

Active surveillance

Animals

The control programme in farmed deer was initially, until October 2012, based on regular whole-herd tuberculin testing, or whole-herd slaughter and meat inspection. Since October 2012, tuberculin tests are no longer performed in TB-free herds, but inspections at slaughter and postmortem of animals found dead or euthanized are still required.

A voluntary control programme in alpacas was launched by Farm & Animal Health in 2015. Testing of alpacas for TB is done using a serological test (Enferplex) instead of an intradermal test as the intradermal test has a demonstrated low sensitivity in alpacas. All adult animals in the herd are serologically tested and all animal purchases and contacts with other herds are recorded.

Furthermore, tuberculin tests are performed at artificial insemination centres and prior to export of animals as required according to EU-legislation (Council Directive 64/432/EEC). Positive animals are treated as suspect cases of TB as described above.

RESULTS

Animals

Due to lesions detected at slaughter, 2 sheep, 7 pigs, 4 red deer and 3 fallow deer were investigated by histology or, where relevant, by culture and/or PCR. From these samples NTM (Non-tuberculous mycobacteria), from the *Mycobacterium avium/intracellulare*-complex were isolated from 4 red deer and 2 fallow deer (all in the same flock), and 2 pigs. No other slaughterhouse samples yielded any mycobacteria.

Due to clinical suspicions, macroscopic lesions, or findings of acid-fast bacteria, samples from one dog, one cat, one horse, and one cattle were investigated. From these samples NTM (Non-tuberculous mycobacteria), from the *Mycobacterium avium/intracellulare*-complex were isolated from one horse, one dog, and one cat. No other sample yielded any mycobacteria.

During 2020, 13 alpacas, were tested serologically in relation to export or import, and one brown fur seal (*Arctocephalus pusillus*) from a zoo was tested with PCR on a pharyngeal swab prior to export. Within the voluntary control program, 102 alpacas, 4 camels and 3 llama were tested. All with negative final results.

In 2020, there were approximately 300 holdings with farmed deer that were considered active. All except one had obtained TB free status. The remaining herd was exempted from regular testing and following the alternative track to obtain a free status; slaughter of at least 20% of the herd yearly, for 15 years, without findings of TB at meat inspections and necropsies. TB was not detected in any farmed deer in Sweden during 2020.

Humans

The total number of detected cases of tuberculosis in humans in 2020 was 335. Out of these, six cases of *M. bovis* were reported in humans in 2020, two cases with pulmonary TB and four cases with extrapulmonary TB, and all six most probably infected in their respective country of origin: Syria (4), Afghanistan (1) and Eritrea (1). All six isolates were unique when analysed with whole genome sequencing.

DISCUSSION

In summary, the overall TB situation in animals and humans remains favourable.

No cases of TB were detected in Swedish livestock during 2020. The officially free status for bovine TB in cattle has been maintained during 2020. Although the surveillance is mainly dependent on inspections of slaughtered animals, this has been considered sufficient. However, the rate of submission of lesions from slaughtered ruminants has decreased over the years and work has been initiated in 2019 and continued in 2020 to increase submissions. Work is also ongoing to introduce PCR as initial analytic test. Passive surveillance based on clinical suspicions and post mortem findings

will always have a low sensitivity as clinical symptoms and massive lesions are mainly seen in late stages of the infection. The eradication efforts in farmed deer have been successful and the probability that Swedish farmed deer are TB free is high. The aim is to eventually declare all deer herds officially free. Livestock imports to Sweden are very limited, and TB is an internationally regulated disease which means that precautionary measures are taken.

The rapid decline of TB in humans in the 1940s coincided with the eradication of TB in cattle and started before the introduction of effective treatment in the 1950s. A much larger part of the human population lived in close contact with domestic animals at the time, and the successful control of TB in cattle is likely to have contributed to the decline in human incidence of TB. Today, Sweden has one of the lowest incidences of human TB in the world and there are no signs of ongoing transmission between humans and animals, neither from animals to humans nor from humans to animals.

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Tularaemia



The number of reported dead positive hares from the County of Norrbotten was high for the second year in a row which coincided with a large number of human cases. Photo: Karin Bernodt.

BACKGROUND

The bacterium *Francisella tularensis* is the causative agent of tularaemia, a disease affecting many animal species, including humans. Although many different animal species can be infected, tularaemia is typically found in hares and small rodents. There are several subtypes of *F. tularensis* of variable virulence. *F. tularensis* subsp. *holarctica* (type B) is the main subspecies responsible for human and animal infection in Europe. *F. tularensis* is capable of surviving for weeks at low temperatures in water, moist soil, or decaying plant and animal matter.

Humans become infected through a variety of mechanisms such as bites of infected insects or other arthropods, handling infected or dead animals, ingesting contaminated food or water, and inhaling aerosols of bacteria. Clinical disease is variable and dependent on the route of transmission. The age group of 40–79 years is the most affected in both sexes. Tularaemia may occur during the whole year, but elevated number of cases are commonly seen during late summer and early autumn.

Hares and other animals are probably infected by the same routes as humans even if it is difficult to prove. Lesions in the skin are difficult to find in furred animals, but in some hare cases the infection sites have been confirmed

by finding still attached ticks and pathology corresponding to tularaemia. In hares with pneumonia a respiratory route might be suspected. In wildlife species that are more resistant to developing disease upon infection, e.g. carnivores and omnivores, *F. tularensis* has been found in lymph nodes in the jaw region suggesting infection through contaminated food or water.

Sweden has reported cases of tularaemia in humans and animals since 1931. Ever since the first Swedish tularaemia case was reported, endemic areas have been identified in northern and central Sweden.

The mountain hare and the European brown hare are the animal species in which tularaemia has most frequently been identified. Diseased animals have been found in the traditionally endemic areas in northern and central Sweden, as well as in regions south of these areas.

The annual numbers of reported human cases range from a few cases to more than 2700 cases in 1967.

DISEASE

Animals

In Swedish hares, and in many rodent species that die of tularaemia, a common pathological presentation of the disease is a disseminated multi-organ septicaemia. Some of the hares have lesions corresponding to a somewhat more prolonged course of disease, but ultimately the infection resumes a more acute course ending in septicaemia. Carnivores and omnivores are animal species that develop no or mild disease. Studies of several wild carnivore and omnivore species in Sweden and other countries have detected antibodies but no signs of disease.

Humans

Tularaemia can be manifested in different forms depending on the route of transmission and on the virulence of the organism. The ulceroglandular form is the most commonly diagnosed form and is more frequently seen than the typhoidal form. The pneumonic, oculoglandular and oropharyngeal forms are rarely diagnosed. In the ulceroglandular form, a local ulcer usually appears at the site of infection and the adjacent lymph nodes are enlarged. The general symptoms of tularaemia are high fever, headache and nausea.

LEGISLATION

Animals

Tularaemia is notifiable in animals (SJVFS 2013:23).

Humans

Tularaemia has been a notifiable disease since 1970 according to the Communicable Disease Act (SFS 2004:168) with the amendments of SFS 2013:634.

SURVEILLANCE

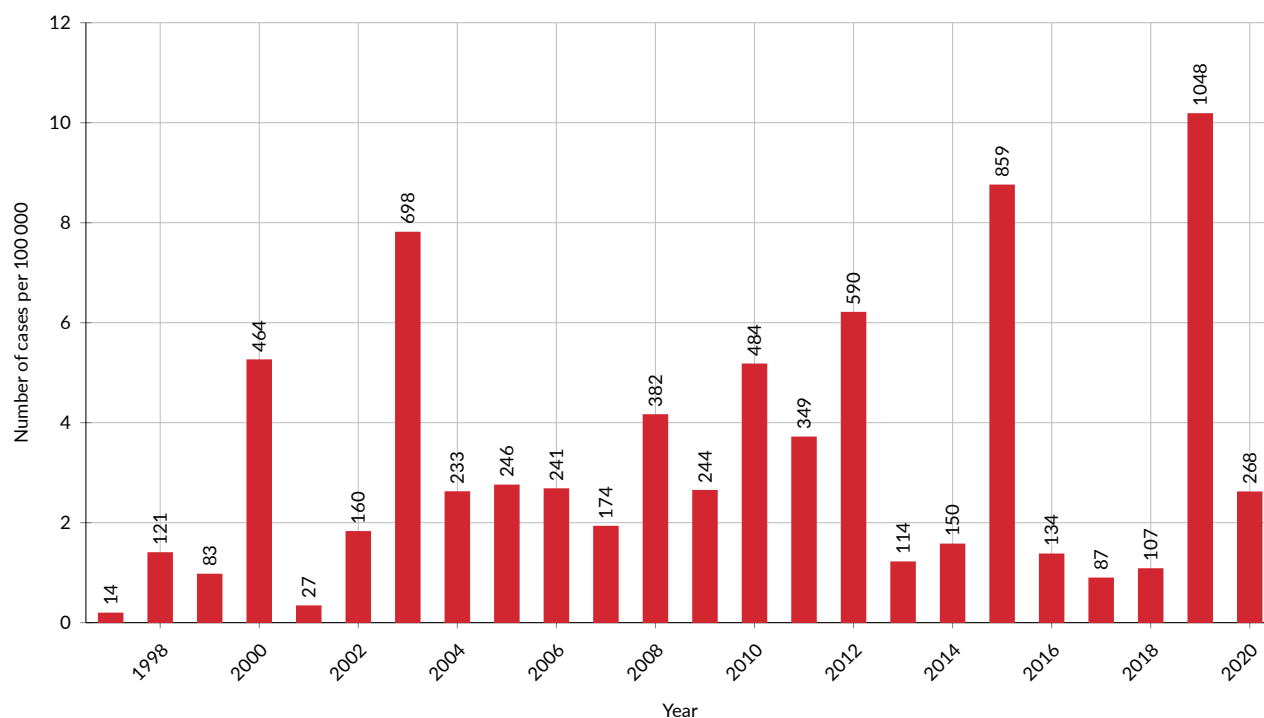


Figure 35: Incidence of notified human cases of tularaemia in Sweden 1997–2020. Bars indicate the incidence per 100 000 inhabitants and adjacent numbers the total number of cases reported.

Animals

Surveillance in animals is passive. It is based on voluntary submission of animals found dead or euthanised by hunters and the general public. Detection is based on PCR or immunohistochemistry of the animal sample. Laboratories are required to report identified tularaemia cases in animals to the authorities.

Humans

Notification of human cases is mandatory and surveillance is based on identification of the disease by a treating physician or by laboratory diagnosis. Both are obligated to report identified cases to the regional and national level to enable further analyses and adequate intervention measures. For laboratory verification of the infection, serology, PCR and isolation of the bacteria are used.

RESULTS

Animals

In 2020, 54 European brown hares, 22 mountain hares, one red squirrel and four dogs were investigated. The number of reported dead hares and the number submitted for examination was lower than in the outbreak year 2019. *F. tularaemia* subsp. *holarctica* was detected in 11 European brown hares and 21 mountain hares. The number of tularaemic hares peaked during August and September due to a high number of cases from the county of Norrbotten (19 cases). In the remaining counties where tularaemia was found (Västerbotten, Dalarna, Värmland, Örebro, Uppsala, Stockholm and Södermanland), the number of cases ranged from one to four. One investigated dog from Uppsala was serologically positive for tularaemia.

Humans

In 2020, 268 human cases of tularaemia were reported, which is approximately a quarter of the number of cases reported during the outbreak year 2019 (n=1048) (Figure 35). Of the cases, all but 14 were reported as infected in Sweden. For the population as a whole, the incidence was 2.6 per 100 000 inhabitants. However, as in previous years, there were considerable regional differences with a larger proportion of cases in the central and northern parts of the country (Figure 36). During 2020, the incidence was highest in the County of Norrbotten with 34.9 cases per 100 000 inhabitants, followed by the County of Värmland with 14.1 cases per 100 000 inhabitants. The reasons behind the annual and regional fluctuations observed are not known.

More men (63%) than women were reported to be infected in 2020, which is in accordance with previous years. The incidence of tularaemia was highest in the age group 40 years and older, which is also similar to previous years. The uneven distribution among age groups and sexes might partially be attributed to the demographic distribution of people who work or practice leisure activities outdoors in high-risk rural areas.

As in previous years, the number of cases started to increase in July and peaked at the end of August and the beginning of September (Figure 37).

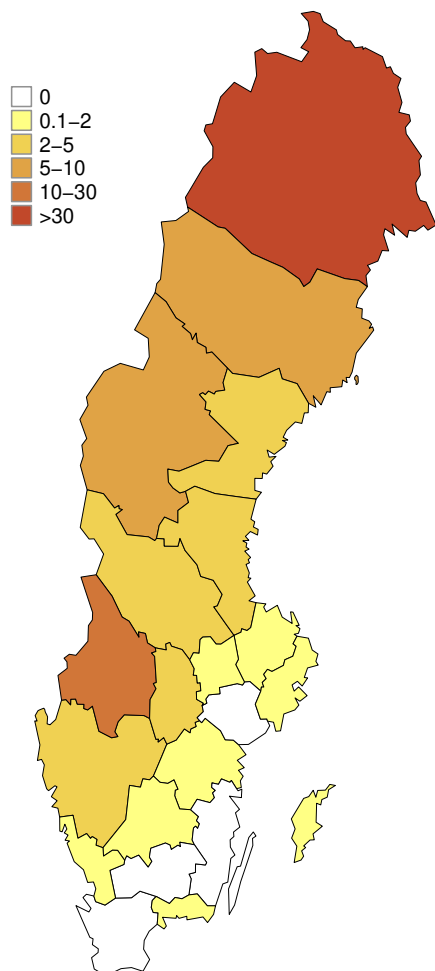


Figure 36: Incidence of reported human tularaemia cases by County in Sweden 2020. The colour scale represents the number of cases per 100 000 inhabitants.

DISCUSSION

Tularaemia has been endemic in northern and central Sweden at least since the early 20th century with a marked annual variation. Years with high numbers of cases are often followed by periods when the disease is virtually absent. There is no obvious explanation for these fluctuations. Probably, variations in population sizes of host animals and insect vectors that can transmit infection to humans play a major role which in turn is influenced by factors such as predators, diseases, weather and climate.

During the last two decades, the epidemiology of tularaemia has changed and the number of reported cases in humans and animals, mainly hares, infected south of the previous endemic region is increasing. Since the information on diseased and dead hares is dependent on voluntary reporting and submitting animals for investigation the true numbers are not known. However, it is noteworthy that the numbers of reported dead hares and examined positive hares from the County of Norrbotten was high for the second year in a row. It is also notable that this high number of reported dead hares coincides with where the largest number of human cases were reported in 2020.

The reservoir for the bacterium between outbreaks has not been clearly identified. In some countries, outbreaks of tularaemia in animals have been associated with a rise in rodent and hare populations, but this has not been confirmed in Sweden. The epidemiological role of the hare as a possible carrier of *F. tularensis* is unclear.

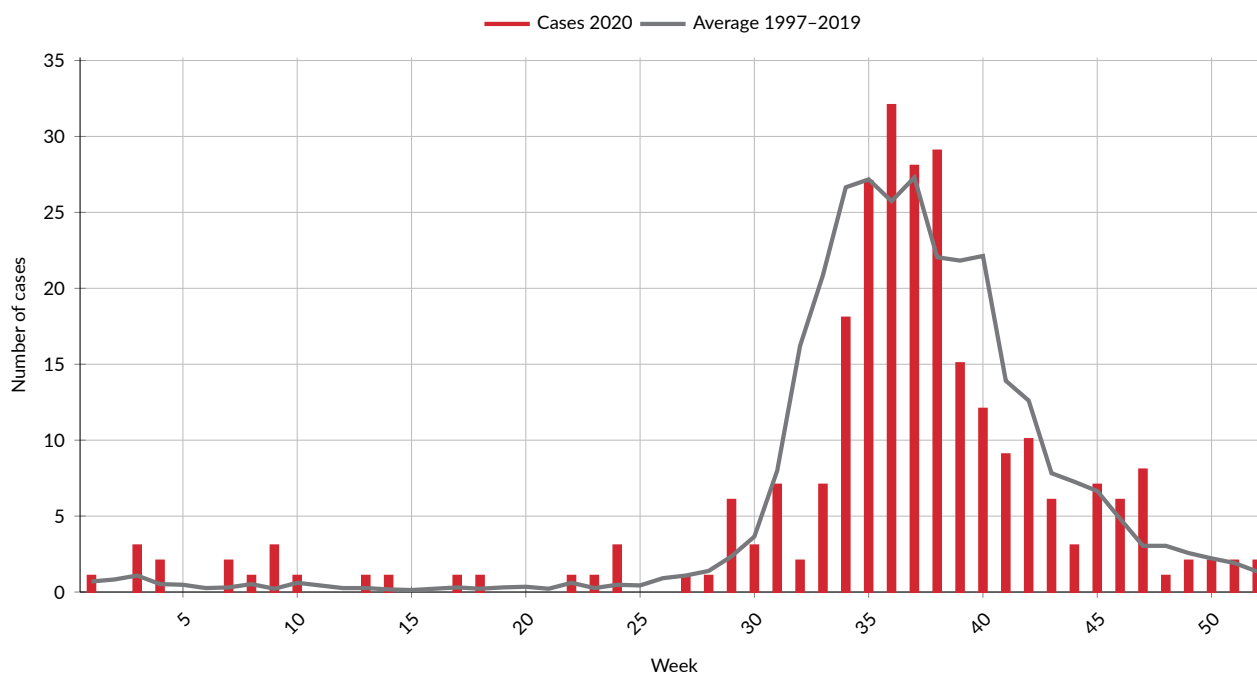


Figure 37: Number of reported human cases of tularaemia per week in 2020 and as an average 1997-2019.

Yersiniosis

BACKGROUND

The genus *Yersinia* is associated with human and animal diseases and was first identified in the late 19th century and classified into its own genus in the mid-20th century. Two enteropathogenic species of the genus are zoonotic: *Yersinia enterocolitica* and *Yersinia pseudotuberculosis*. Pigs are considered the main reservoir of *Y. enterocolitica*. *Yersinia* bacteria are widespread in nature, among which nonpathogenic strains are most frequent. The most common human pathogenic bioserotype is *Y. enterocolitica* 4/O:3.

Wild animals, especially rodents and birds are considered the principal reservoir of *Y. pseudotuberculosis*. Both *Y. enterocolitica* and *Y. pseudotuberculosis* are frequently found in pig tonsils and porcine intestinal contents. Infections caused by *Y. enterocolitica* are thought to be foodborne and pigs are considered the main source of infection. The sources and vehicles of *Y. pseudotuberculosis* infections in humans are not well understood but infections caused by consumption of contaminated carrots and iceberg lettuce have been described in Finland. *Yersinia* bacteria are destroyed by heating (pasteurisation and cooking) but can grow at refrigerator temperature and in vacuum and modified atmosphere packaging.

The latest information from 2014–2015, indicates that the prevalence of *Y. enterocolitica* in the Swedish domestic pig population (30.5% of herds) is similar to the other pig producing countries in Europe. Human yersiniosis is primarily a domestic infection and normally about three quarters of the cases are reported to be infected in Sweden.

DISEASE

Animals

Pigs are asymptomatic intestinal carriers of pathogenic *Y. enterocolitica* and *Y. pseudotuberculosis*. Infection with *Y. pseudotuberculosis* in other animals may vary from asymptomatic to severe mesenteric lymphadenitis and lead to septicæmia and death. *Y. enterocolitica* has occasionally been isolated from cats and dogs with diarrhoea.

Humans

Y. enterocolitica causes gastrointestinal symptoms in humans ranging from mild self-limiting diarrhoea to acute mesenteric lymphadenitis, which might be difficult to differentiate from appendicitis. *Y. pseudotuberculosis* causes primarily abdominal pain, fever headache and erythema nodosum, a skin reaction. The infection can be complicated by long-term sequelae including reactive arthritis, uveitis and glomerulonephritis (kidney disease).

LEGISLATION

Animals

Y. enterocolitica and *Y. pseudotuberculosis* are not notifiable in animals.

Food

Detection of *Y. enterocolitica* and *Y. pseudotuberculosis* in food is not notifiable.

Humans

Yersiniosis (isolation or identification by PCR of *Y. enterocolitica* (other than biotype 1A) or *Y. pseudotuberculosis* from a clinical sample) is notifiable according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2013:634). Diagnosis of yersiniosis by serology is not notifiable.

SURVEILLANCE

Animals

Active surveillance for *Yersinia* was not conducted during 2020, but some materials were submitted for routine health examinations or because of clinical disease.

Food

No official control programme exists for *Yersinia spp.* National and local authority may perform sampling as a part of extended official controls or targeted projects. Sampling may be performed by food business operators, but analysis results are not normally reported to the authorities.

Humans

The surveillance in humans is based on identification of the disease by treating physician and/or by laboratory diagnosis (i.e. passive surveillance). Both treating physicians and laboratories are obligated to report to the regional and national level to enable further analyses and adequate intervention measures.

RESULTS

Animals

In 2020, *Y. pseudotuberculosis* was isolated at SVA from 17 wild animals (14 hares, 1 fallow deer, 1 roe deer, 1 pigeon), three pet animals (2 cats and 1 dog) and from four zoo animals (2 primates, 1 antelope, 1 rodent). *Yersinia spp.* was detected from one moose.

Food

In 2020, no samples taken by national and local authorities were analysed for *Yersinia*.

Humans

During 2020, 220 cases were reported (2.1 cases per 100 000 inhabitants). This is the lowest incidence since at least 1997. The proportion reported as infected in Sweden was 78% while travel-associated infections were a record low 13% of the cases (Figure 38).

Like previous years, the incidence was high among children younger than five years. The incidence was 4.4 (cases per 100 000 inhabitants) for infants and 5.8 for children 1–4 years old, compared to 2.1 for all cases. In 2020, the incidence was also higher than average among persons 15–29 years old (3.3).

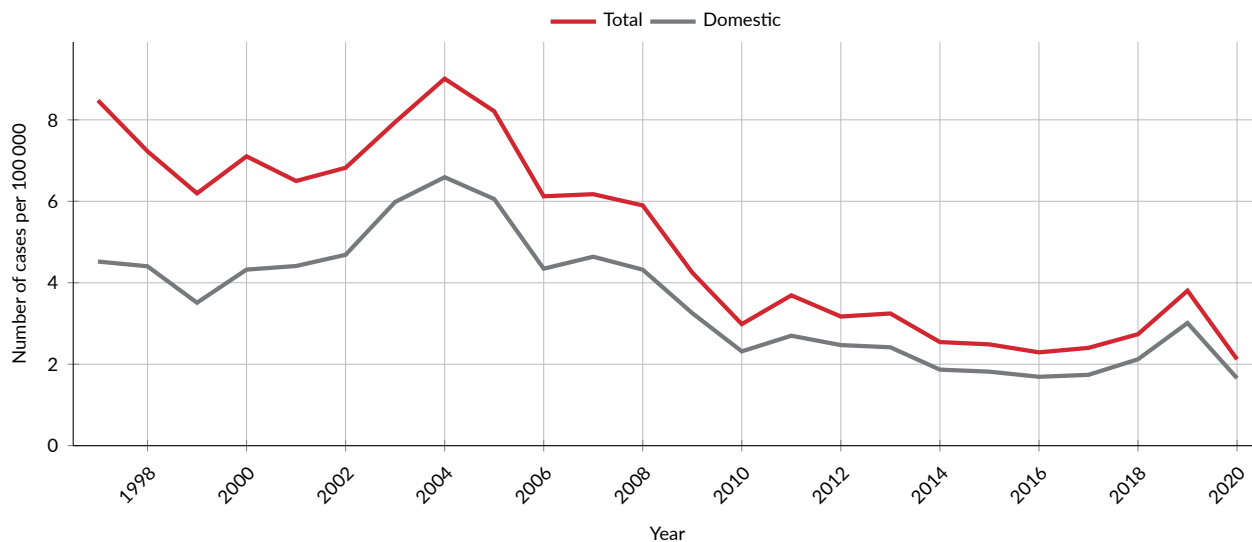


Figure 38: Notified incidence (per 100 000 inhabitants) of human cases of yersiniosis in Sweden, 1997–2020.

IN FOCUS: *Yersinia* – what you detect and how to detect it

Yersiniosis in humans has been on the rise in Sweden the last few years, after a historical decrease in cases. Notification of laboratory confirmed cases includes the species *Y. pseudotuberculosis* (YP) and *Y. enterocolitica* (YE), however excluding the biotype (BT) 1A of YE which does not cause typical yersiniosis but may be the cause of milder gastrointestinal symptoms in humans. Pork, and products thereof, have been the main source of *Y. enterocolitica*. In recent years, however, several outbreaks of YE and YP have occurred with contaminated vegetables such as lettuce and spinach as the probable cause.

Detection and isolation of YE and YP from samples from human faeces, food, environment, and animals can be challenging. It is complicated by the poor selectivity of the current methods, low levels of YE/YP (especially in food and environmental samples) and competing background flora including other species of *Yersinia* and avirulent variants. It is estimated that approximately 30 percent or more can be lost during cultivation. During the last ten years in Sweden there has been a transition process for the clinical microbiological laboratories from cultivation-based detection methods to molecular-based using PCR panels, a process that is still ongoing. In animals, YP causes an infection that can vary from asymptomatic to severe. Generally, detection of YP from a clinically diseased animal is easier due to higher levels of the bacteria than in an asymptotically infected animal or in food and environmental samples. To reach detectable levels of pathogenic YE or YP in food, environmental and animal samples, long incubation periods (up to 21 days) may be needed, since this is often done by enrichment in culture broth at 4 °C employing the psychrotrophic ability of YE and YP. Also, same methods may not be optimal for detection of both YE and YP, or even different strains of YE.

The PCR panels used in clinical microbiology can often be used as a first screening method for pathogens to be targeted for cultivation. However, depending on the epidemiological setting further isolation attempts are not necessarily being made and it is the PCR finding that is notified. Depending on PCR panel and target genes used, the outcome of what types of *Yersinia* that are detected varies. The target genes can be situated on the chromosome or on the virulence plasmid of *Yersinia*. The chromosomal marker gene *ail* is one of the most used for detection of both YE and YP in human, food, environmental and animal samples. It excludes YE BT1A, with few exceptions; meaning only notifiable yersiniosis cases are reported. *VirF* also excludes YE BT1A, however this target is situated on the virulence plasmid which can be lost during cultivation. Other common targets that are used are *invA* and *ystB*, chromosomal genes that are also present in YE BT1A.

It is important to have awareness when reporting and communicating results on what variants that can be detected or not detected within the specific system used, in addition to the diagnostic challenges on the food and veterinary side.

Yersiniosis follows a minor seasonal variation with the highest number of cases infected during the summer. However, during 2020, such seasonal trend was reversed with the highest number of reported cases during the first quarter, a decline during the summer months and a smaller increase during the autumn (Figure 39). As the large majority of *Yersinia* cases are usually domestic (Figure 38), travel restrictions after the first months of the year due to the pandemic explain only a small part of this pattern. Instead, there was a large decrease in domestic cases, mainly from April to September, that is behind the deviating seasonal pattern. This decrease is most probably related to the COVID-19 pandemic, but the impact of specific factors related to behavioural changes, societal restrictions and reduced health care visits remain to be investigated. For the majority of cases species was reported, with 143 being *Y. enterocolitica* and twelve *Y. pseudotuberculosis*.

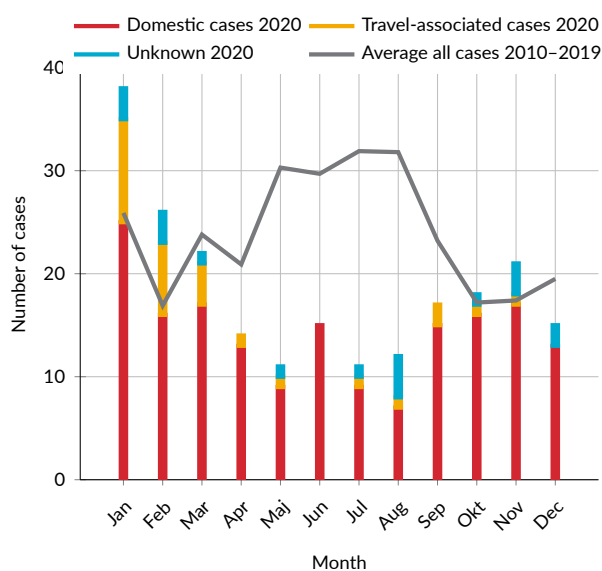


Figure 39: The monthly number of notified cases of yersiniosis of domestic, travel-associated and unknown country of origin in 2020 and the mean monthly number of all cases in 2010–2019.

The majority of yersiniosis cases are considered sporadic. However, *Yersinia* spp. is not part of the national microbial surveillance programme in Sweden. Therefore, there is no national monitoring of circulating subtypes and a limited ability to capture cross-regional outbreaks.

Outbreaks

No outbreaks in humans were identified during 2020.

DISCUSSION

In the beginning of the 2000s, the number of reported cases of yersiniosis decreased not only in Sweden but also in the other European countries. This decrease occurred without any active interventions in the food chain. In recent years, this trend has been broken with increases both in 2018 and 2019. However, the decreasing numbers for 2020 are difficult to assess due to the impact of the pandemic.

Yersiniosis in humans is considered foodborne and most infected cases are of domestic origin. Outbreaks in humans are rarely detected but most recently in 2019 outbreaks due

to imported leafy greens were notified. Most infections are considered sporadic but under-reporting may be considerable. Case-control studies suggest that consumption of pork products is a risk factor, however vegetables should be considered as a route for transmission as shown, for example, in the Swedish-Danish outbreak in 2019. In 2020, more cases of yersiniosis in hares (caused by *Yersinia pseudotuberculosis*) were detected but the reasons for this are unclear. Recent information on the prevalence of enteropathogenic *Yersinia* in Swedish production animals is lacking, the most recent in 2015. Similarly, recent studies in Swedish food have not been done. Good agricultural practices, as well as good slaughter hygiene and good manufacturing practices in food processing are essential for control of *Yersinia*.

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Additional Surveillance 2020

Mink-associated infections with SARS-CoV-2

BACKGROUND

Severe Acute Respiratory Syndrome Coronavirus type 2 (SARS-CoV-2) is an emerging zoonotic coronavirus initially described as the causative agent of a cluster of cases of viral pneumonia in the city of Wuhan, China, in December 2019. Since then, SARS-CoV-2 has caused the COVID-19 pandemic in humans, with over 160 million confirmed human cases worldwide and over 3.5 million deaths to date (end of May 2021).

Coronavirus infections are common in both animals and humans, and some are known to be zoonotic. In humans, previously known coronaviruses can cause illness ranging from the common cold to more severe diseases such as Middle East Respiratory Syndrome (caused by MERS-CoV), and SARS (caused by SARS-CoV). SARS-CoV and MERS-CoV as well as SARS-CoV-2 belong to the genus *Betacoronavirus*, and all are believed to have viral ancestors with bats as the original host. Whereas investigations suggest that MERS-CoV and SARS-CoV were transmitted to humans from intermediary animal hosts (dromedary camels and civet cats, respectively), there is not enough scientific evidence to identify a possible intermediate host of SARS-CoV-2 or to explain the original route of transmission to humans, which may or may not have involved an intermediate host.

Susceptibility to SARS-CoV-2 has been demonstrated in several animal species, including, e.g. cats and other felines, ferrets, mink, dogs and non-human primates either through experimental infection or by identification of cases in natural settings after contact with infected humans. With the exception of mink, however, natural infection in animals has been limited to sporadic spill-over events from humans. In farmed mink, on the other hand, SARS-CoV-2 has caused extensive outbreaks with significant between-animal and between-farm spread in several countries with a vast impact on the international mink fur sector. Moreover, cases of mink to human transmission have been reported, including spillovers into society of new SARS-CoV-2 variants associated with mink. Concerns have therefore been raised concerning the risk that mink farms could represent a serious animal reservoir for SARS-CoV-2 resulting in the introduction and circulation of new virus strains in humans potentially with modifications of transmissibility or virulence and decreased treatment and vaccine efficacy and thus with potential future public health impact.

In 2020, before pelting, the Swedish mink fur sector was composed of approximately 35 farms with in-total 600–650,000 animals. Eighteen of these farms were located in the municipality of Sölvesborg, the County of Blekinge, in the south-eastern part of the country.



After pelting in 2020, approximately 90 000 breeding mink remained in the Swedish population and a decision was made to ban mink breeding during 2021. Photo: Svensk Mink.

DISEASE

Animals

Clinical signs of SARS-CoV-2 in mink are often non-specific and present only in a variable proportion of outbreaks. They can include increased mortality, mild respiratory signs, a slight drop in feed intake and occasionally mild gastrointestinal signs.

Humans

In humans according to WHO, infection with SARS-CoV-2 causes COVID-19, a disease characterized by mild to moderate respiratory illness in most people. Among those who develop symptoms, most recover from the disease without needing hospital treatment. About 15% become seriously ill and require oxygen, and 5% become critically ill and need intensive care.

Complications leading to death may include respiratory failure, acute respiratory distress syndrome, sepsis and septic shock, thromboembolism, and/or multiorgan failure, including injury of the heart, liver or kidneys. Older people

and those with underlying medical problems like cardiovascular disease, diabetes, chronic respiratory disease, and cancer are more likely to develop serious illness.

LEGISLATION

Animals

Infection with SARS-CoV-2 in animals is notifiable as an emerging infection in animals (SJVFS 2013:23).

Humans

COVID-19 in humans is notifiable according to the Communicable Disease Act (SFS 2004:168 with amendments, SFS 2013:634)

SURVEILLANCE

Animals

Following the first reports of outbreaks of SARS-CoV-2 in mink in the Netherlands in April and Denmark in June 2020, a dialogue between the competent authority and representatives from the Swedish mink sector was initiated to raise awareness, to ensure enhanced on-farm biosecurity practices and to raise vigilance regarding increased morbidity and mortality. In early October, given the absence of any reports of morbidity/mortality from the Swedish mink farms, an active surveillance scheme was initiated based on sampling up to five dead mink per farm per week. Within the scheme, mink found dead were submitted to the National Veterinary Institute in Uppsala, where they were sampled with swabs from the oral cavity and pharynx and analysed by qRT-PCR. Positive cases were further analysed through whole genome sequencing.

In December, after pelting, a serological screening was conducted targeting breeding animals. Blood was collected on filter papers from 24 animals per farm and sent to the National Veterinary Institute for the detection of SARS-CoV-2 specific antibodies using a commercially available ELISA (ID Screen SARS-CoV-2 double antigen multiple species ELISA).

The surveillance scheme was voluntary and organised in close collaboration with the industry.

Humans

In parallel to the surveillance of mink, an active surveillance program was launched for mink farmworkers in Sölvesborg and Skara municipalities at the end of November. The surveillance program encompassed 21 of the mink farms in Sweden. The program included voluntary screening of ongoing infection, where samples from farmworkers were screened by PCR weekly. The purpose of the program was to identify infected workers to prevent transmission from workers to mink. Moreover, the system provided early warning of mutations of concern that could arise within the animal population and subsequently be introduced to the human community. The surveillance of virus variants was achieved by performing whole-genome sequencing of SARS-CoV-2 PCR-positive samples. In addition to the screening for ongoing infection, voluntary serological surveys of the participating mink farmworkers were conducted.

RESULTS

Animals

Between mid-October and mid-November, the National Veterinary Institute received 74 submissions of between 3–5 dead mink, representing between 1 and 4 submissions per farm. Thirteen farms gave positive results for SARS-CoV-2 nucleic acids using qRT-PCR. All positive farms were located in Sölvesborg, the County of Blekinge, in the south-eastern part of the country. None of the positive farms had reported increased morbidity or mortality before testing positive but, retrospectively, a slight increase in daily mortalities could be observed in the records from several of the farms. All sequences from mink belonged to sub-lineage B.1.1.39, a sub-lineage only seen once in Sweden before the outbreak.

From the serological screening, 24 samples per farm were received from 26 out of the 28 mink farms that remained after the pelting. Specific SARS-CoV-2 antibodies were detected in the vast majority of samples from 23 farms, including in all farms that previously had been tested positive for SARS-CoV-2 nucleic acids. In the remaining three farms, all samples tested negative.

Humans

A total of 100 persons have been registered in the program, but due to the seasonal mode of work, and changes in the workforce, the number of participants has varied. The 317 samples that have been taken and analysed for ongoing viral infection within the surveillance program have resulted in 8 positive persons. In addition to samples from these persons another 14 samples from mink farmworkers that was tested positive before the surveillance was launched were collected. All 22 samples were whole-genome sequenced (WGS). In the serological survey, 78 persons participated, among whom 27 tested positive.

The resulting sequences from WGS were analysed using pangolin. Generally, two main groups were seen, one representing sequences with a pangolin classification similar to that of sequences recovered from WGS of samples from minks (B.1.1.39) and the second group representing sequences with a pangolin classification identical to those circulating in Sweden at the time. The sequences were further analysed by aligning them towards the reference sequence NC_045512. A phylogenetic tree was calculated, and the subtree representing sequences with the pangolin classification B.1.1.39 was studied separately as new sequences were added. A majority of sequences from human cases had clear phylogenetic relationships to sequences recovered from mink samples. Sequences from humans and mink from the same mink farms clustered closely together, suggesting within-farm human-to-mink and/or mink-to-human transmission. In sequences from two human samples from one of the negative mink farms the mutation Y453F, considered as an adaptation to mink, was observed.

DISCUSSION

Whereas a number of animal species have been shown to be susceptible to infection with SARS-CoV-2, and have the capacity to transmit the virus, extensive outbreaks in animals have only been seen in farmed mink. Once introduced into a farm, SARS-CoV-2 appears to spread efficiently among the animals. The high animal density that is typically present in a mink farm, provides ideal conditions for viral replication and transmission, also increasing the risk of virus evolution. Furthermore, experience from e.g. the Netherlands and Denmark demonstrates that once SARS-CoV-2 has been introduced into an area with high density of mink farms, farm-to-farm transmission is likely to occur, with potential spill over to people associated to the farms and to human communities close to the farms. Also, in Sweden extensive spread within and between farms occurred in spite of implemented biosecurity measures, as shown by the results from the surveillance carried out. A clear association was also observed between presence of SARS-CoV-2 among the mink and COVID-19 in people associated to mink, supported by the results of the whole genome sequencing. In contrast to e.g. Denmark, however, no community spread within the communities close to the affected farms was observed.

In Sweden, none of the affected farms was culled. The Swedish outbreak coincided with the annual pelting, when approximately 80% of the mink are killed as part of the production cycle. According to the assessment made, culling of affected farms as part of disease control measures would

not speed up the process of reducing the number of susceptible animals compared with the annual pelting and killing, and would therefore not contribute to any significant reduction in the risk of further spread of the disease. Pelting was carried out from mid-November to early December, under strict biosecurity recommendations, to prevent mink-to-human SARS-CoV-2 transmission. After pelting, approximately 90 000 breeding animals remained in Sweden.

Given the extensive spread of SARS-CoV-2 among Swedish mink experienced during the fall, with spill-over to people associated to the affected farms, a concern was raised regarding the potential public health risk of allowing breeding to occur during the following season (i.e. spring 2021). With this in mind, and based on a risk assessment, a decision was taken to ban mink breeding during 2021.

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Clinical surveillance



Clinical surveillance constitutes a fundamental part of the animal disease surveillance system in Sweden. Photo: Åsa Lundberg.

BACKGROUND

Clinical (also referred to as passive) surveillance is a fundamental component of disease surveillance for both endemic and epizootic diseases. For epizootic diseases with severe and obvious clinical signs, such as foot-and-mouth disease, African swine fever and anthrax, clinical surveillance is in fact the most efficient means for early detection, which is of utmost importance in order to prevent spread and reduce the impact. For other diseases of importance, clinical surveillance is complementary to active surveillance activities. In this chapter, clinical surveillance of epizootic diseases is described. Specifically, clinical surveillance approaches to foot-and-mouth disease, African swine fever, anthrax and Newcastle disease are described in more detail. Diseases with both passive and active surveillance components are presented in specific chapters.

DISEASES

African swine fever

African swine fever (ASF) is a contagious disease of domestic pigs and wild boar, in its acute form characterised by haemorrhagic fever and high case fatality rates. The disease is endemic in large parts of sub-Saharan Africa. In 2007 an incursion into Europe occurred and since then the geographical distribution has expanded in spite of extensive disease control measures being implemented. ASF is currently present in large parts of Europe, in particular among wild boar populations. To date two of the affected countries (the Czech Republic and Belgium) have eliminated the infection, but in other parts of Europe the disease continues to spread affecting new countries every year. In 2018 the disease emerged for the first time in China, the largest pig producer in the world accounting for almost half of the world's pork production. It has since spread to large parts of Asia. With these developments, ASF is currently considered a global threat.

Anthrax

Anthrax is a serious zoonotic disease that may affect most mammals, especially herbivores. It is caused by *Bacillus anthracis*, a spore forming bacterium. The spores are highly resistant and may survive in the soil for decades. The disease was common in Swedish livestock in the beginning of the 20th century, with a significant reduction in frequency of outbreaks during the latter part of the century. During the last decade, however, the disease has re-emerged in the country with reported outbreaks in 2008, 2011, 2013 and 2016. The disease is endemic in most countries of the world.

Foot-and-mouth disease

Foot-and-mouth disease (FMD) is a highly contagious disease of cloven-hoofed animals such as pigs, cattle, sheep and goats. The case fatality rate in FMD is low, but morbidity very high and convalescence is extended, which cause severe production losses. The cost of disease eradication in countries previously free from the disease is extremely high. FMD is endemic in many parts of the world, but since 2011 the disease is absent in Europe. However, the major FMD epidemics that affected several European countries during the last twenty years demonstrated that the continent is continuously at risk for FMD virus introduction, and that early detection is crucial.

Newcastle disease

Newcastle disease (ND) is a highly contagious and often severe disease of domestic poultry and other birds, caused by virulent strains of avian paramyxovirus type 1. Wild birds are important reservoirs of the virus, which is transmitted through direct and indirect contacts between infected and non-infected birds. Since 1995, twenty outbreaks of ND have occurred in Sweden, all of which have been successfully eradicated. Sweden has status of ND free without vaccination (Commission Decision 95/98/EEC).

LEGISLATION

Clinical suspicions of epizootic diseases, including ASF, anthrax, FMD and ND, must be notified to the Swedish Board of Agriculture in accordance with the Swedish Act of Epizootic diseases (SFS 1999:657 with amendments). This obligation applies to animal keepers, official and private veterinarians, veterinary laboratories, and other relevant stakeholders. Suspicions are investigated after consultation with disease experts at the National Veterinary Institute and following notification to the Swedish Board of Agriculture, and sampling and analysis carried out in accordance with diagnostic manuals of the EC as applicable (ASF 2003/422/EC; FMD 2003/85/EC annex XIII; ND 92/66/EEC annex III). In addition, a number of other infectious diseases are notifiable to the Board of Agriculture and/or the relevant County Administrative Board based on laboratory confirmation or clinical suspicion (SJVFS 2013:23).

SURVEILLANCE

Every year, hundreds of suspicions of serious infectious diseases are reported by field veterinarians, animal owners or private veterinary pathologists to the experts at the National Veterinary Institute. Many of these suspicions can be ruled out already based on anamnesis and initial clinical investigation, whereas others require notification to the Swedish Board of Agriculture and further investigation including sampling of sick or dead animals, with movement restrictions imposed on the farms during the investigation. Also, in cases in which an epizootic disease is not primarily suspected, but where it cannot be excluded based on clinical investigation, samples can be submitted for laboratory investigation to exclude a diagnosis. This can only be done after discussions with experts at the National Veterinary Institute and in consultation with the Swedish Board of Agriculture. This approach serves to reduce the threshold for submitting samples for analysis of notifiable diseases, and thereby increasing the sensitivity of the system. The Swedish Board of Agriculture covers all costs for veterinary visits, transports, and diagnostic analyses related to the investigation.

African swine fever

Reported cases of increased mortality or serious morbidity, with clinical signs such as haemorrhagic disorders or reproductive failures in pigs are considered suspicions of ASF until ruled out through further clinical investigation. Samples are sent to the National Veterinary Institute for laboratory analyses. Due to clinical similarity, samples from domestic

pigs collected for ASF are also analysed for CSF. This strategy is strongly recommended by the EU.

Given the current situation in Europe as regards ASF in wild boar, the surveillance is enhanced, and Swedish public are encouraged to report all findings of dead wild boar. If possible, carcasses or samples are taken in and investigated to rule out ASF as the cause of death (see also specific chapter on infectious diseases in wild boars, page 123). Reports of two or more wild boar found dead in the same location, or of wild boar found dead with signs suggesting ASF, are included in the surveillance as clinical suspicions.

Anthrax

Cases with a history of sudden deaths in more than one animal on the premise are considered suspicions of anthrax. Clinical signs such as fever, bloody discharges from the nose, mouth, anus or vagina, uncoagulated blood, subcutaneous oedematous swellings and lack of rigor mortis, as well as recent landscape interventions such as dredging or digging in areas accessible to the animals, strengthens the suspicion. In addition, cases with gross pathological lesions suggestive of anthrax found at postmortem are considered suspicions of anthrax. Samples from suspected cases are sent to the National Veterinary Institute for laboratory analyses.

The surveillance in the two areas affected by anthrax the last ten years has been enhanced since the outbreaks. The aim is to investigate all cattle, sheep and wild ruminants found dead in the area, with no obvious cause of death to rule out anthrax.

Table 30: Suspicions of epizootic diseases reported and further investigated between 2014–2020, based on sampling of sick or dead animals.

Disease	Investigated ^A (Confirmed)							
	2013	2014	2015	2016	2017	2018	2019	2020
African swine fever ^B	17 (0)	6 (0)	17 (0)	20 (0)	18 (0)	18 (0)	38 (0)	80 (0)
Anthrax ^C	18 (1)	18 (0)	11 (0)	74 (15)	34 (0)	16 (0)	15 (0)	10 (0)
Aujesky's disease	2 (0)	2 (0)	1 (0)	2 (0)	0 (0)	1 (0)	2 (0)	1 (0)
Avian influenza ^D	12 (1)	16 (0)	15 (0)	17 (2)	28 (4)	9 (1)	9 (0)	8 (2)
Bluetongue	2 (0)	2 (0)	2 (0)	2 (0)	2 (0)	2 (0)	2 (0)	4 (0)
Brucellosis	5 (0)	2 (0)	1 (0)	0 (0)	0 (0)	1 (0)	1 (0)	0 (0)
BSE ^E	4 (0)	3 (0)	1 (0)	2 (0)	2 (0)	42 (0)	18 (0)	10 (0)
CWD ^F	0 (0)	0 (0)	0 (0)	0 (0)	1 (0)	17(0)	31 (2)	27 (1)
Classical swine fever	4 (0)	5 (0)	3 (0)	5 (0)	3 (0)	4 (0)	5 (0)	8 (0)
FMD	2 (0)	1 (0)	1 (0)	1 (0)	0 (0)	0 (0)	0 (0)	0 (0)
IBR	3 (0)	1 (0)	0 (0)	0 (0)	0 (0)	2 (0)	1 (0)	3 (0)
Lumpy skin disease	0 (0)	0 (0)	1 (0)	1 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Newcastle disease ^G	15 (0)	25 (3)	15 (0)	17 (1)	29 (3)	8 (1)	11 (0)	9 (1)
Paratuberculosis	4 (0)	7 (0)	3 (0)	5 (0)	5 (0)	1 (0)	4 (0)	4 (0)
PRRS	9 (0)	4 (0)	5 (0)	5 (0)	2 (0)	2 (0)	12 (0)	5 (0)
Rabies	8 (0)	5 (0)	10 (0)	3 (0)	6 (0)	9 (0)	5 (0)	12 (0)
Tuberculosis ^H	8 (0)	14 (0)	8 (0)	6 (0)	9 (0)	7(0)	15 (0)	20 (0)
West Nile fever	2 (0)	1 (0)	2 (0)	1 (0)	2 (0)	0 (0)	5 (0)	4 (0)

^AIn many cases clinical suspicions were investigated for several diseases with similar clinical picture (e.g. ASF/CSF/PRRS, AI/ND).

^BIncludes wild boar found dead, also described in the specific chapter on infectious diseases in wild boars (page 123).

^CIncludes one sheep from the intensified surveillance.

^DDoes not include surveillance of, or cases in, wild birds.

^EThe increased number of clinical suspicions in 2018 and 2019 compared to previous years is the result of substantial efforts to detect and notify animals with clinical signs compatible with BSE.

^FDoes not include surveillance of, or cases, in the intensified sampling.

^GOne case was negative after autopsy.

^HReported as cases per herd or owner, surveillance at slaughter included.

Foot-and-mouth disease

Reported cases of disease in cattle, pigs, sheep or goats which presents with vesicular lesions of the feet, buccal mucosa or mammary glands, are considered suspicions of FMD. Samples are sent to the National Veterinary Institute for analyses.

Newcastle disease

Reported cases of disease in poultry, or other birds kept in captivity, that present a significant reduction in egg production (egg drop) and deterioration of eggshell quality are considered suspicions of ND, even without more severe clinical signs such as increased mortality, nervous signs and respiratory distress. Samples are sent to the National Veterinary Institute for analyses. Due to clinical similarity, samples from poultry collected for ND are in general also analysed for avian influenza.

In addition, an active ND surveillance component is present within the Poultry Health Control Programme targeting breeding flocks (described in the specific chapter related to this programme, page 121).

RESULTS

The suspicions of epizootic diseases that were reported and further investigated based on sampling of sick or dead animals between 2014–2020 are compiled in Table 30.

In 2020, ten clinical suspicions of ASF in domestic pigs and one in wild boar were investigated, with negative results. Samples from eight of the suspicions in domestic pigs were also analysed for CSF, and one for *Salmonella choleraesuis*, all with negative results. In addition, sixty-nine samples from wild boar found dead were analysed for ASF, as part of the enhanced passive surveillance, all with negative results.

Six clinical suspicions of anthrax in cattle, two in sheep and one in a horse were reported and investigated. In addition, one cattle was investigated as part of the enhanced passive surveillance in the area affected by anthrax during 2016. In none of the cases, anthrax could be confirmed.

Two clinical suspicions of FMD were investigated during 2020, but could be ruled out after further clinical investigation. No sampling for FMD was conducted.

Nine clinical suspicions of ND were investigated of which one, in domestic pigeons, was positive for Newcastle disease virus (avian paramyxovirus-1). Samples from six of the suspicions were also analysed for avian influenza with negative results.

DISCUSSION

Clinical surveillance constitutes a fundamental part of the animal disease surveillance system and is particularly important as regards early detection of epizootic and/or emerging diseases. This surveillance component depends on the

level of cooperation and trust between the relevant stakeholders in the field (including animal keepers and official and private veterinarians, among others) and the central veterinary authorities, but also on the level of knowledge and awareness among all involved. In Sweden, cooperation between the relevant stakeholders is long-standing at a high level, and the level of knowledge and awareness as regards epizootic diseases as well as the obligation to report suspicions thereof is considered good. Based on this and given the relatively high numbers of suspicions of epizootic diseases investigated each year, the performance of the clinical surveillance is considered adequate. However, a systematic evaluation of this performance has never been carried out. Therefore, to get a better understanding of the coverage and representativeness of the clinical surveillance and thus the performance, and to identify gaps, an evaluation of the clinical surveillance using data from the last ten years is currently underway.

As regards ASF, given the current situation in Europe and globally, the risk for introduction to Swedish wild boar is considered increased. In case of introduction, early detection is crucial in order to prevent a longer-term establishment of the disease. The timeline of detection depends, to a large extent, on the capacity of Swedish hunters to detect, and their willingness to report, findings of dead wild boar. The number of wild boars submitted by the public during 2020 in the enhanced passive surveillance has almost doubled compared to 2019. The steady rise of submitted wild boar is probably to some extent a result of increased awareness of ASF among hunters and the general public. However, given the population size of Swedish wild boar (estimated to at least 250 000–300 000) and the expected number of wild boar that would die from other causes than hunting and road kills, and thus constitute the potential sampling frame for the surveillance, this number is still not adequate. Further measures are therefore being taken to increase the numbers.

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Poultry Health Control Programme

BACKGROUND

The aim of the Poultry Health Control Programme is to document freedom from the included diseases, to prevent the introduction and further spread of diseases and to allow trade from the participating companies.

The Poultry Health Control Programme is based on provisions (SJVFS 2010:58) issued by the Swedish Board of Agriculture. The programme is mandatory for all Swedish hatcheries producing more than 50 000 day-old chicks per year and all breeding establishments (grandparent and parent flocks of layers, broilers and turkeys) delivering hatching eggs to these hatcheries. In addition to serological sampling for several infectious diseases, the programme consists of biosecurity requirements, standards for poultry houses, management and clinical surveillance.

LEGISLATION AND DISEASES

All diseases covered by the programme, except for *Mycoplasma synoviae*, are notifiable according to provisions issued by the Swedish Board of Agriculture (SJVFS 2013:23). The diseases included in the programme during 2020 are briefly described below.

Fowl typhoid and pullorum disease

Fowl typhoid and pullorum disease are two poultry diseases caused by *Salmonella enterica* subspecies *enterica* serovar Gallinarum biovar Gallinarum (*Salmonella* Gallinarum, fowl typhoid) and biovar Pullorum (*Salmonella* Pullorum, pullorum disease), respectively. These two biovars of the same serovar are specifically adapted to poultry, and vertical transmission (from the hen to the chicken via the egg) is an important feature, in addition to the common horizontal spread. Pullorum disease mainly affects fetuses and chickens up to 3 weeks of age while *Salmonella* Gallinarum commonly infects and causes disease (diarrhoea, inappetence, production losses and mortality) in older birds. Both biovars are included in the Swedish zoonosis legislation (SJVFS 2004:2) as well as in the European legislation on trade in poultry and hatching eggs (Council Directive 2009/158/EC). The diseases were eradicated from the Swedish commercial poultry population in the beginning of the 1960s. A single case of fowl typhoid (*Salmonella* Gallinarum) was detected in a backyard flock in 1984 but has not been diagnosed since then. *Salmonella* Pullorum is however present in the Swedish backyard poultry population; the last outbreak was diagnosed in 2017.

Mycoplasma gallisepticum, *Mycoplasma synoviae* and *Mycoplasma meleagridis*

Mycoplasma gallisepticum, *M. synoviae* and *M. meleagridis* are important poultry pathogens. However, *M. meleagridis* is only pathogenic for turkeys. These three mycoplasmas can spread both horizontally and vertically. They mainly cause respiratory disease and egg production losses. *Mycoplasma*

gallisepticum and *M. synoviae* may also cause arthritis and are present in the backyard poultry population in Sweden. Testing of breeding flocks for *M. gallisepticum* and *M. meleagridis* (only turkey flocks) is included in the European legislation on trade in poultry and hatching eggs (Council Directive 2009/158/EC). Due to its potential to cause disease and production losses, testing for *M. synoviae* was included in the programme between 1995 and 2010. During a revision of the programme the agent was excluded but is since 1 June 2015 included again. In 2016, testing for *M. synoviae* was further intensified.

Paramyxovirus type 1

Paramyxovirus type 1 may cause outbreaks of Newcastle disease, with egg production losses, increased mortality, nervous signs and respiratory disease; the severity of the disease may vary. The virus is transmitted through direct and indirect contacts with infected birds and for shorter distances also with the wind. Wild birds are an important reservoir. Since 1995, twenty outbreaks of Newcastle disease have occurred in Sweden. The disease is included in the Swedish Act of Epizootic diseases (SFS 1999:657 with amendments). Since all outbreaks have been successfully eradicated, Sweden has a status of Newcastle disease free country without vaccination according to Commission Decision 95/98/EEC.

Egg drop syndrome

Egg drop syndrome virus is a naturally occurring adenovirus in waterfowl (including the wild population) in which it does not cause any clinical disease. In chickens, the clinical signs are only seen during the production period as decreased egg production in an otherwise clinically healthy flock. The virus is able to spread both vertically and horizontally. The Swedish poultry breeding population is free from the disease.

SURVEILLANCE

Serological screening within the programme is administered by the National Veterinary Institute and financed by the Swedish Board of Agriculture and the participating companies. In 2020, eight breeding companies participated in the programme: five broiler, three laying hen and one turkey breeding company (one company with both broiler and laying hen parent flocks). In accordance with the provisions (SJVFS 2010:58), sixty blood samples were taken from the breeding flocks included in the programme, once during the rearing period and several times during the production period. In the majority of the flocks, blood samples are taken by the breeding companies' personnel after delegation from the official veterinarian. In the remaining flocks the official veterinarian takes the samples. The blood samples were sent by mail to the National Veterinary Institute where serological tests were performed. The sampling and testing schemes are presented in tables 32 and 31.

Table 31: Sampling schedule for turkey parent flocks. Number of blood samples tested at different weeks of age.

Agent	Age in weeks			
	20	32	44	56
<i>S. Pullorum/ S. Gallinarum</i>	-	60	-	-
<i>Mycoplasma gallisepticum</i>	60	60	60	60
<i>Mycoplasma meleagridis</i>	60	60	60	60
<i>Mycoplasma synoviae</i>	60	60	60	60
Paramyxovirus type 1	-	-	-	60

Table 32: Sampling schedule for chicken grandparent and parent flocks. Number of blood samples tested at different weeks of age.

Agent	Age in weeks				
	16	24	36	48	60
<i>S. Pullorum/ S. Gallinarum</i>	-	60	-	-	-
<i>Mycoplasma gallisepticum</i>	60	60	60	60	60
<i>Mycoplasma synoviae</i>	60	60	60	60	60
Paramyxovirus type 1	-	-	-	60	-
Egg drop syndrome virus	-	30	-	-	-

RESULTS

Table 33 gives an overview of all samples taken in breeding flocks of chickens and turkeys, and the laboratory methods used, during 2020. All analysed samples tested negative for paramyxovirus type 1.

During 2020, antibodies to *Mycoplasma meleagridis* were detected in samples from one turkey parent flock. The number of positive samples had increased when new samples obtained two weeks later were analysed.

Serological reactions to *M. synoviae* were detected in eleven chicken parent flocks, one chicken grandparent flock and one turkey parent flock. All thirteen flocks were considered free from *M. synoviae* based on clinical status and testing of new samples.

Two chicken parent flocks were further investigated due to a few positive samples for *M. gallisepticum*. In addition, two chicken parent flocks were investigated due to a few positive samples for *Salmonella Gallinarum/Salmonella Pullorum* and one chicken grandparent flock investigated based on a few positive samples for Egg Drop Syndrome. No clinical signs were seen in these flocks and after testing new samples from these flocks, the previous positive samples were considered as unspecific serological reactions.

DISCUSSION

In conclusion, the results from the serological screening in the Poultry Health Control Programme in 2020 support the status of freedom from several important infectious diseases in the Swedish breeding poultry population. In 2020, all flocks were free from *M. synoviae*. Antibodies to *M. synoviae* have been detected in chicken breeding flocks in previous years (2016, 2017 and 2019).

The finding of *M. meleagridis* antibodies in a turkey breeding flock this year (2020) was the first time that antibodies to *M. meleagridis* were detected in a flock in the Poultry Health Control Programme since the start of the programme in the 1990s. Possible implications on animal health and production both in the breeding and in offspring flocks need to be further considered. *Mycoplasma meleagridis* may spread both horizontally and vertically (from the hen to the chicken via the egg), hence infection in breeders may have consequences for the next generation as well. Infection may result in respiratory signs, decreased hatchability, skeletal disorders and impaired growth. Based on national provisions and EU legislation the approval for trade of the establishment in question was withdrawn by the Swedish Board of Agriculture.

Finally, the clinical surveillance of the poultry breeding population is also of utmost importance.

Table 33: Number of sampling occasions for grandparent (GP) and parent (P) flocks of chickens and turkeys and total number of samples tested during 2020.

Agent	No. of sampling occasions			No. of samples			Method
	Chickens		Turkeys	Chickens		Turkeys	
	GP	P	P	GP	P	P	
<i>S. Pullorum / S. Gallinarum</i>	13	100	4	780	6000	240	Serum plate agglutination test, antigen, Ceva Biovac
<i>Mycoplasma gallisepticum / Mycoplasma synoviae</i>	58	439	15	3480	26340	900	<i>Mycoplasma gallisepticum/synoviae</i> Antibody Test Kit, BioChek
<i>Mycoplasma meleagridis</i>	0	0	15	0	0		Serum plate agglutination test, antigen, Ceva Biovac
Paramyxovirus type 1	13	106	4	780	6360	240	NDV screen competition ELISA, ID.Vet
Egg drop syndrome virus	13	100	0	390	3000	0	Antibody haemagglutination inhibition test, antigen, GD Animal Health

Infectious diseases in wild boar



Surveillance of infectious diseases in wild boar, which has been ongoing since 2000, provides evidence that the Swedish wild boar population remains free from several important diseases, including African swine fever, Classical swine fever and Aujeszky's Disease. Photo: SVA.

BACKGROUND

Wild boars are susceptible to contagious diseases that affect domestic pigs, and they can therefore play a role in spreading disease to and from domestic pigs. For example, Aujeszky's Disease (AD) is present in several wild boar populations in the EU, which has led to the sporadic transmission of the disease to domestic pig herds. Wild boars were involved in the spread of Classical swine fever (CSF) during outbreaks in domestic pigs in several EU countries in the 1990s and early 2000s. In recent years, African swine fever (ASF) has spread in Europe and in 2020, cases of the disease were reported in the wild boar population of ten EU countries.

The Swedish wild boar population is increasing rapidly and is now estimated to be 250 000–300 000 animals. Established wild boar populations are found primarily in the southern parts of the country, but the northern border of the wild boar's range in Sweden is extending and it has, at present, passed the level of the river Dalälven. Surveillance of infectious diseases in Swedish wild boar has been ongoing since 2000. The purposes of this monitoring are to provide

evidence that Sweden is free from several important infectious pig diseases and to enable early detection of new introductions of these diseases into the country.

LEGISLATION

Several diseases capable of infecting wild boar, including ASF, CSF, AD, brucellosis and Porcine reproductive and respiratory syndrome (PRRS), are included in the Swedish Act of Epizootic Diseases (SFS 1999:657 with amendments) and are therefore notifiable upon clinical suspicion. If any of these diseases are suspected or confirmed, measures will be taken to control the disease and to prevent further spread.

SURVEILLANCE

Passive surveillance

Any sick or dead wild boar that is reported to have shown clinical signs, or found to have post mortem lesions consistent with a disease included in the Swedish Act of Epizootic Diseases, is sampled and investigated.

Additionally, an enhanced passive surveillance programme for ASF in wild boars has been in place since 2013. Anyone who finds a dead wild boar can voluntarily submit the whole carcass or samples from it to the National Veterinary Institute for post mortem examination. All submitted samples are analysed for the presence of ASF virus genome with PCR, whether lesions suggestive of the disease are present or not.

Active surveillance

Since 2000, hunted wild boars throughout Sweden have been sampled yearly for surveillance purposes. Hunters voluntarily collect blood samples when free-living wild boars are harvested.

The samples are sent to the National Veterinary Institute for analysis for the presence of antibodies to infectious agents that are of importance to domestic pig production. In 2020, the samples were used for the active surveillance of AD and CSF. The samples were tested for antibodies against AD and CSF using ELISA kits (SVANOVIR® PRV-gB-Ab ELISA, Svanova and IDEXX™ HerdChek CSFV Ab Test Kit, respectively). The surveillance was designed to detect these diseases at a 1% prevalence with a 99% confidence level. To reach this level of confidence, it was calculated that 500 samples would need to be submitted for analysis.

RESULTS

Passive surveillance

Sixty-nine wild boar that were found dead were submitted by members of the public for examination for the presence of ASF virus genome in 2020. This represents an approximate doubling in the number of animals submitted for analysis as compared to the previous year. This increase is likely a result of several awareness campaigns that were carried out to increase voluntary reporting of dead wild boar findings, as well as heightened awareness and concern about ASF among the general public as a direct result of the spread of the disease in the EU in recent years. The geographic distribution of the sampled dead wild boars is shown in Figure 40. All

samples from the submitted wild boars were negative for ASF. Additional post mortem findings in these wild boars are reported in the chapter “Post mortem examinations in wildlife” (page 139) in this report.

During 2020, no clinical suspicions of any disease included in the Swedish Act of Epizootic Diseases were investigated in free-living wild boar. One suspicion of ASF/CSF was investigated in a herd of captive wild boar. The investigation was initiated after the post mortem examination of a sick, euthanized sow from the herd showed an enlarged spleen and haemorrhages in the lungs and heart. Samples from the sow were analysed for the presence of ASF and CSF virus. These were found negative and the herd was declared free from both ASF and CSF. *Salmonella choleraesuis* was subsequently identified in samples from this sow and other animals in the herd.

Active surveillance

In 2020, 108 blood samples were collected from hunted wild boar and analysed for the presence of antibodies against AD and CSF. All samples were negative. The geographical distribution of sampled wild boar was roughly correlated to the distribution and density of the Swedish wild boar population (Figure 40) (location information was not available for 21 of the hunted wild boar). The goal of analysing 500 samples for antibodies against these two diseases was not met. However, the surveillance evidence collected in 2020 is sufficient to indicate that the prevalence of AD and CSF in the Swedish wild boar population is <3% with a certainty of 95%.

DISCUSSION

The Swedish wild boar population is growing, and the boundary of the population is moving north. In areas where wild boars are already present, the population is also becoming more dense, which increases the risk of direct and indirect contact between wild boars and domestic pigs. The area in Sweden inhabited by wild boars is surrounded by the sea so there is no risk of wild boars migrating into Sweden. Instead, the role of the wild boar in disease spread might be to pick up infectious agents introduced into Sweden by other routes. For example, wild boars could gain access to infected meat or other animal products in garbage or following indirect spread by other means from people, vehicles or equipment. The unfavourable development of the global ASF situation is of special concern and calls for efficient approaches to early detection of disease in the wild boar population. As such, methods to further increase the number of wild boars found dead that are voluntarily submitted by the public for postmortem and ASF testing are currently being investigated.

In the fall of 2020, for the first time in over 40 years, *Salmonella choleraesuis* was identified in Sweden, first in a domestic pig herd and then in the captive wild boar herd described above (see chapter “Salmonellosis” (page 75) for more information about this outbreak). Because the *Salmonella choleraesuis* status of the Swedish wild boar population has not previously been well-examined, and to help determine the role wild boar may play in its spread, a surveillance program for *Salmonella choleraesuis* in wild boar is being developed.

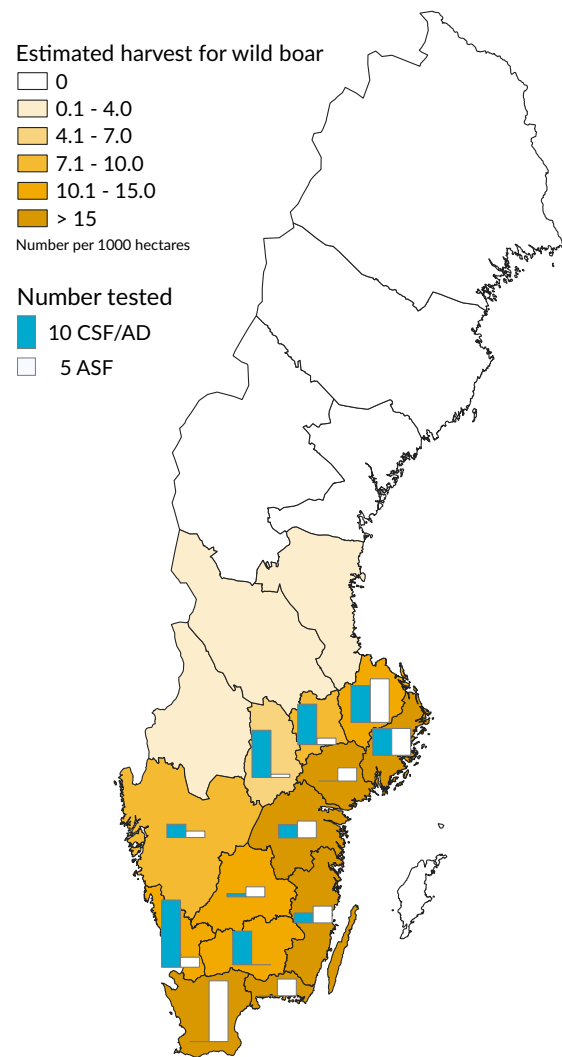


Figure 40: Geographical distribution by county of origin of wild boar samples included in the surveillance. The blue bars indicate the number of hunted wild boar sampled and tested for antibodies against Aujeszky's Disease (AD) and Classical Swine Fever (CSF) in 2020 (total 87). The white bars indicate the number of wild boar found dead and tested for ASF (total 69). The background colours indicate wild boar density based on hunting statistics from 2019–2020 (Swedish Association for Hunting and Wildlife Management, game monitoring).

Beginning in late 2020, all wild boar found dead and submitted to SVA for ASF analysis have also been tested for the presence of *Salmonella choleraesuis*, provided appropriate material for the analysis is received. Additionally, hunters hunting wild boar in the areas surrounding the *Salmonella choleraesuis* positive herds have been provided with sampling kits so that they can voluntarily submit samples from healthy, hunted wild boar for *Salmonella* testing. While it is too soon to draw any conclusions about its prevalence in the Swedish wild boar population, early results have identified *Salmonella choleraesuis* in both wild boar found dead and in apparently healthy, hunted wild boar. This surveillance program will continue in 2021 and be expanded to cover all areas in Sweden where wild boar are found.

Infectious diseases and parasites in honeybees

BACKGROUND

Every beekeeper in Sweden has the responsibility to prevent the spread of bee diseases and is obliged to register the location of their apiaries to the responsible County Administrative Boards (CABs). There is no national bee register, but the number of apiaries and colonies is estimated by the local bee inspectors and reported to the respective CABs. The health of honeybees is supervised by local bee inspectors, appointed and given the responsibility over local inspection districts by seven of the CABs. Sweden was in 2020 divided in 327 bee districts and local bee inspectors are responsible for the practical control of the apiaries located in their designated district. The Swedish Board of Agriculture (SBA) is the central competent authority for the control of bee diseases. The SBA is responsible for the regulations and guidelines for management and control of the honeybee diseases regulated in SJVFS 1992:38 (amendment regulation number 2018:47) including American foulbrood, Varroa and tracheal mite infestations. There are regulations for the movements of bees, bee-related products and beekeeping equipment to prevent contagious bee diseases from entering the country and to reduce further spread. Applications for permits to import bees from countries outside the EU must be made to the SBA at each point of entry. The conditions for import are the same in all EU Member States. If bees are introduced without permission, it is considered a violation of the law on smuggling goods.

DISEASES AND LEGISLATION

All veterinarians as well as laboratories analysing samples from honeybee colonies, are obliged to notify the SBA if American or European foulbrood (AFB and EFB, respectively), tracheal mite infestation/acariosis (*Acarapis woodi*), Varroa mite infestation/varroosis (*Varroa destructor*), Tropilaelaps mite infestation (*Tropilaelaps* spp) or the small hive beetle (*Aethina tumida*) are found. This is regulated in the bee diseases act (1974:211), the ordinance of bee diseases (1974:212) and the SBA's regulation (SJVFS 1992:38) on the control of American foulbrood, Varroa and tracheal mites in honeybees, as well as the SBA's regulation on notification of animal diseases and infectious agents (SJVFS 2012:24). A beekeeper needs a permit issued by a bee inspector to move the bees out of an area that has been declared infected with AFB by the SBA. Visual inspection of clinical signs of AFB and Varroa mites is carried out at the same time. In case of an outbreak of AFB, or if *Varroa* mites are reported from an area or region where it has not been detected earlier, the bee inspector notifies the CAB, which in turn notifies the SBA. The SBA then declares the area in which the apiary is situated infected/infested. Bee inspectors can send samples of diseased brood, larvae, pupae or adult bees to the National Reference Laboratory for Bee Health

(NRL) at the Swedish University of Agricultural Sciences (SLU), where the diagnosis of honeybee diseases included in the legislation is performed on behalf of the SBA. This is a yearly, laboratory-based, passive surveillance of honeybee diseases.

American foulbrood

American foulbrood (AFB) of honeybees is a contagious bacterial disease caused by the spore-forming bacterium, *Paenibacillus larvae*. The disease is widely distributed across the world causing great economic losses in apiculture and is notifiable in most countries. As the name indicates, the disease only affects the larval stages of honeybees (brood refers to the eggs, larvae and pupae of honeybees). AFB is highly infectious, lethal to the individual honeybee larva and potentially lethal to infected colonies. AFB is a statutory notifiable disease in the European Union in the framework of trade and export requirements (Directive 92/65/EEC). In many European countries, Sweden included, the disease is controlled through burning of colonies with clinical disease and the use of beekeeping management techniques to avoid the spread of the infectious agent to uninfected hives. Current legislation does not allow European beekeepers to use antibiotics since there is no maximum residue limit (MRL) set for the antibiotic substances used to control AFB (oxytetracycline and tylosin). No antibiotics can be legally used since there is a zero-tolerance limit to antibiotic residues in honey. Sweden has strict rules for the movement of bees, apiculture equipment and honeybee products from areas where AFB has been reported. The bee inspectors burn any colony with clinical signs of American foulbrood and inspect and/or use samples of adult bees to track all other colonies with clinical disease within a 3 km radius from the infected apiary. In addition, apiaries outside the 3 km radius that have been in contact with infected colonies through beekeeping management are inspected and sampled.

European foulbrood

European foulbrood (EFB), is a serious disease of honeybees caused by the bacterium *Melissococcus plutonius*. EFB affects mainly young honeybee larvae usually between 4 and 5 days old. A massive loss of brood resulting from severe infection weakens the colony and can lead to its collapse. Regional variations in disease burden have been reported and recent decades have seen dramatic increases in the incidence of EFB in parts of Europe. Large disease outbreaks have been identified in areas previously thought to be disease free, such as Norway.

Tracheal mite infestation (acariosis)

The honeybee tracheal mite *Acarapis woodi* is an internal parasite of the respiratory system of adult honeybees. The tracheal mite has spread through global beekeeping exchanges and has been reported from all European countries except Sweden. It is therefore regulated in Swedish legislation.

Varroa mite infestation (varroosis) and associated virus infections

The honeybee parasitic mite, *Varroa destructor*, was originally confined to the Eastern honeybee (*Apis cerana*), where a stable host-parasite relationship exists due to a long period of coevolution. After a shift in the last century, from the native host to the Western honeybee (*Apis mellifera*), the mite dispersed around the globe and is currently considered the greatest threat to honeybees and apiculture worldwide. The mite was reported in Europe in the late 1970s, and was found on Gotland in 1987 and in the county of Skåne in 1991. The regulations from the SBA have since been aimed at limiting the spread of the *Varroa* mite in the country. There are still areas in northern Sweden where *Varroa* mites have so far not been reported (parts of Dalarna, Västerbotten, Jämtland, Västernorrland and Norrbotten), but there were several reports of findings of the mite in hitherto free areas during 2020.

Honeybee viruses such as *Deformed wing virus* (DWV) and *Acute bee paralysis virus* (ABPV) are associated with the *Varroa* mite, and DWV is the actual cause of the clinical signs observed in connection with high *Varroa* numbers. The mite acts as a biological vector for both viruses.

Tropilaelaps mite infestation

Mites of the genus *Tropilaelaps* affect both developing brood and adult bees mainly in Asia. *Tropilaelaps mercedesae* and *Tropilaelaps clareae* are the only species found reproducing on brood of *A. mellifera*. The distribution of the emerging mite is currently restricted to tropical and subtropical regions of Asia and Africa but is regulated within the EU, and honeybee queen imports from outside EU are visually inspected for the occurrence of *Tropilaelaps* mites. The mite has not been reported as being present in Europe.

The small hive beetle

The small hive beetle (*Aethina tumida*) is endemic to sub-Saharan Africa, but has spread to many other locations, including North America, Australia and the Philippines, and was detected in Europe in 2014, in Calabria and Sicily. The European Commission has defined protective measures to prevent the spread of the beetle and the incidence is still limited to these areas in southern Italy.

The small hive beetle can be a destructive pest of honeybee colonies, causing damage to comb, stored honey and pollen. The primary damage to colonies and stored honey is caused through the activity of the larvae tunnelling through honeycombs, feeding and defecating, causing discolouration and fermentation of the honey. If a beetle infestation is sufficiently heavy, they may cause bees to abandon their hive.

SURVEILLANCE

Passive surveillance

Passive disease surveillance of honeybee diseases and parasites is done through diagnostics related to disease outbreaks, and results are reported by the NRL to the SBA yearly.

Enhanced passive surveillance by visual inspection of clinical signs of AFB is done when a beekeeper needs a permit issued by the bee inspector in order to move the bees out of an area which is declared infected by the SBA. All inspections during which diseases are detected are reported by the bee inspectors to the CABs. For results over time, see Figure 41.

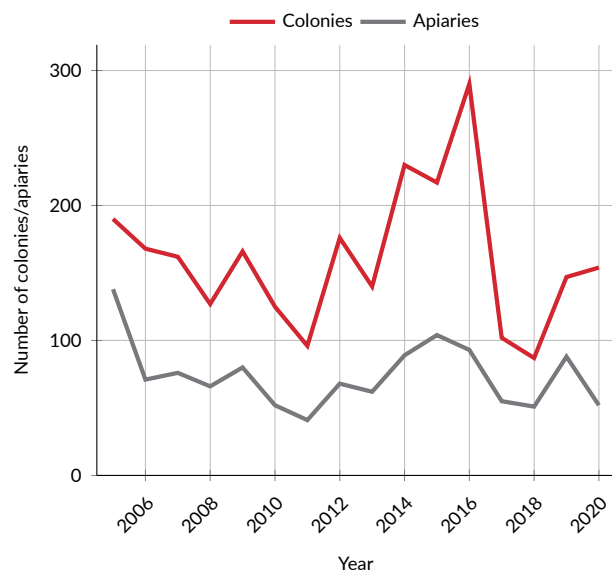


Figure 41: Number of new cases of American foulbrood in 2005–2020 in bee colonies and apiaries, based on reports from bee inspectors to the County Administrative Boards. A total of 5217 colonies in 1258 apiaries were inspected in 2020.

RESULTS

Samples from a total of 2797 bee colonies in 264 beekeeping operations were analysed by the NRL for bee health in 2020. The results are shown in (Table 34). European foulbrood was detected in 12 colonies from six beekeeping operations.

The national bee inspectors performed visual inspection of disease symptoms in 5217 colonies in 1258 apiaries and reported symptoms of AFB in 154 colonies in 52 apiaries. See Figure 41.

No active surveillance was conducted during 2020.

DISCUSSION

The reporting of AFB incidence before January 2019 was based on the information that the bee inspectors report to the CABs based on visual observation of clinical signs (Figure 41). In a 2016 baseline study of honeybee diseases (presented in “Surveillance of infectious diseases in animals and humans in Sweden 2017” and Silva de Oliveira et al., 2021), microbiological cultivation of *P. larvae* from samples of adult bees was used. This method has previously proved to be well correlated with clinical signs of disease (Nordström et al., 2002; Locke et al., 2019). Only young larvae

Table 34: Number of samples from the Swedish honeybee population analysed at the national reference laboratory for bee health during 2020. Testing conducted based mainly on clinical suspicions.

Disease/parasite	No. of tested beekeeping operations	No. of infected/infested operations	No. of operations with symptomatic brood	No. of tested colonies	No. of infected/infested colonies	No. of colonies with symptomatic brood
AFB	264	68	33	2797	457	122
EFB	8	6	6	19	17	17
<i>A. woodi</i>	0	0		0	0	-
<i>V. destructor</i>	56	16	3	122	35	12
<i>Tropilaelaps</i> spp.	0	0	-	1	0	0
<i>A. tumida</i>	0	0	-	0	0	0

develop clinical signs, but adult bees are carriers of the bacterium. In the 2016 baseline study, the subclinical presence of the bacterium in a selection of the country's apiaries was investigated. The bacteria could not be detected in a majority of the examined apiaries (94%).

Starting January 2019, the bee inspectors have the option to send samples of adult bees to the NRL for the detection of *P. larvae*, in connection with a disease outbreak and tracking. This led to a more than 10-fold increase in the number of hives analysed for the presence of *P. larvae* in 2019 and 2020 compared to earlier years (Table 34). This complement to visual inspection of honeybee colonies in connection with outbreaks of AFB is a useful tool for the bee inspectors to track symptomatic colonies.

The bacterium *Melissococcus plutonius*, which causes EFB, was detected in only two apiaries in Östergötland in the 2016 baseline study, and only one additional confirmed case was reported during 2017–2019. However, during the 2020 beekeeping season, symptomatic brood samples from 17 bee colonies from six beekeeping operations in Västra Götaland, Halland and Skåne were diagnosed with EFB. Historically, EFB has been considered less serious than AFB but reports of more aggressive forms of the bacterium and more serious disease outbreaks have become increasingly common, which highlights the value of continued disease monitoring to prevent future outbreaks in Sweden.

After the introduction of the *Varroa* mite in Sweden, the SBA introduced regulations to prevent or at least slow down the spread of the mite in the country. This has not completely prevented the spread but has led to the fact that we still have apiaries and areas in the northern parts of the country that are apparently free from *Varroa* mites. This was further confirmed by the results of the 2016 baseline survey reinforcing earlier observations and reports from bee inspectors. New reports of *Varroa* mites in 2020, however, came from areas in Boden and Luleå in Norrbotten. In the 2016 baseline survey, DWV was detected in all counties except Västernorrland, Jämtland, Västerbotten and Norrbotten. The spread of DWV coincides with the presence of *Varroa* and follows the spread of the mite. Another virus associated with *Varroa* is ABPV, which was detected only in a single apiary on Gotland and one in Skåne in the 2016 baseline study. A possible explanation for the sparse occurrence is that the virus is so virulent

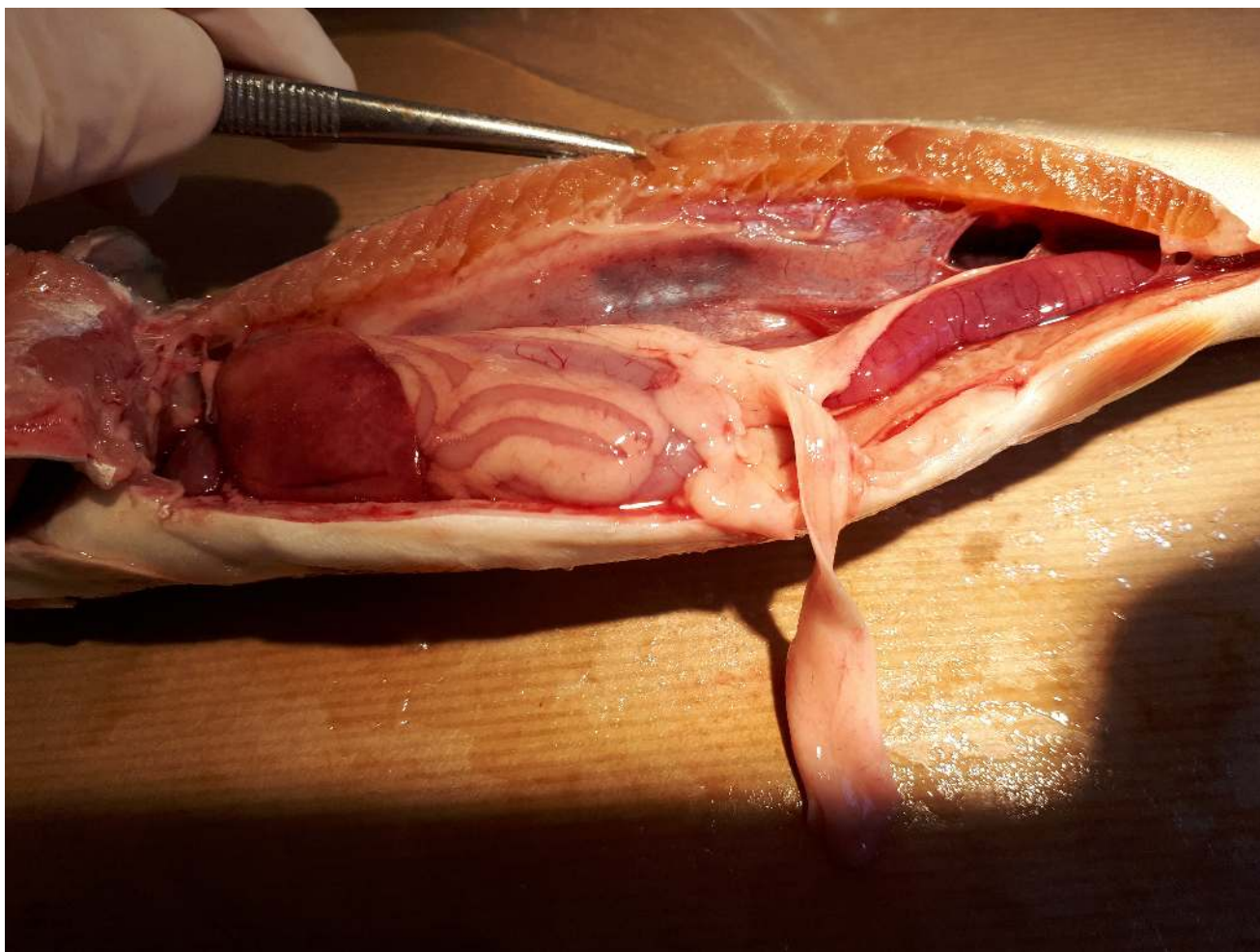
that it kills its host faster than it can effectively spread. This could explain why the less virulent virus DWV has such a high incidence while ABPV is rare. It is also worth noting that the counties where ABPV is detected, Gotland and Skåne, are the counties where *Varroa* was first introduced into the country. At that time (late 80s, early 90s), ABPV was the most dominant *Varroa*-associated virus in Europe before being surpassed by DWV. Perhaps it is that ABPV was established in parts of the honeybee population in these counties before DWV became more widely spread.

The lack of a national bee register makes it difficult to organise sampling of honeybees. As part of the new EU legislation on animal health, Regulation (EU) 2016/429 (the Animal Health Law), however, registers of all animals kept in husbandry for food production will be mandatory. This will facilitate disease surveillance in the future and is a prerequisite for being able to follow the contingency plans for certain exotic pests in honeybees. In summary, the health situation for Swedish honeybees is good and we should continue to promote regular disease monitoring to maintain it.

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Infectious diseases in fish, crustaceans and molluscs



Necropsy of an Arctic char (*Salvelinus alpinus*) with furunculosis. There are multiple petechial haemorrhages in the swim bladder wall. Photo: Charlotte Axén.

BACKGROUND

All registered aquaculture farms are obligated to participate in the Official Health Control Programme, regulated in accordance with SJVFS 2014:4 and by Council Directive 2006/88/EG. Sweden has a very good health status in aquaculture as well as in wild populations of fish and shellfish in the aspect that none of the serious viral diseases that occur in other European countries are prevalent in Sweden. A restrictive approach to imports of live fish for restocking/farming, an early introduction of health control in farms and the presence of hydroelectric power dams in most Swedish rivers (acting as migration barriers for feral fish from the coastal zone) all contribute to maintaining this health status. The presence of dams also results in a different health status at the coast compared to the more disease-free continental zone. To maintain this situation, all transport of live fish from the coast to the inland zone is forbidden and Sweden has a national restocking programme for salmonids to maintain populations that cannot migrate and spawn in nature.

LEGISLATION AND DISEASES

All Swedish fish farms have participated in surveillance for the diseases mentioned below since the late 1980s in accordance with Commission Implementing Decision (EU) 2015/1554) and Council Directive 2006/88/EC. Sweden has an approved disease-free zone status (2002/308/EC) for Viral haemorrhagic septicaemia (VHS) and Infectious haematopoietic necrosis (IHN) (2008/427/ EC). Additional guarantees are in place for the whole country for Spring Viraemia of Carp (SVC), and for the inland zone for Infectious Pancreatic Necrosis (IPN) (2010/221/EU). The inland zone has an eradication programme for Renibacteriosis/bacterial kidney disease (BKD) and the coastal zone for IPN (2010/221/EU). These diseases are included in the Swedish legislation on notifiable diseases (SJVFS 2013:23). Further, IHN, VHS, IPN (other than genogroup 2) and SVC are included in the Swedish Act on epizootic diseases (SFS 1999:657 with amendments). In addition, testing is routinely done for Koi herpes virus (KHV) in imported, quarantined koi, and for Crayfish plague in crayfish. These diseases are also regulated by the Swedish legislation on notifiable

diseases (SJVFS 2013:23). Other notifiable diseases such as furunculosis (*Aeromonas salmonicida salmonicida*/ASS), yersiniosis/Enteric redmouth disease (ERM), Marteiliosis and Bonamiosis (shellfish) and Whitespot disease (crayfish) are not actively tested for within surveillance programmes.

Epizootic haematopoietic necrosis (EHN)

EHN is caused by a ranavirus. The disease is considered exotic to EU. Susceptible species present in Sweden are rainbow trout, European/redfin perch, Northern pike and pike-perch. Fish is susceptible at all ages. Farm outbreaks have occurred at 11–20°C with a rapid onset of high mortality rates and there is no evidence of a carrier state.

Infectious haematopoietic necrosis (IHN) and viral haemorrhagic septicaemia (VHS)

Both diseases are caused by rhabdoviruses and occur frequently in Europe. They are transferred horizontally, but vertical transmission cannot be completely ruled out for IHN. Both diseases have greatest impact in freshwater rainbow trout (*Oncorhynchus mykiss*) aquaculture but have also been detected in several other species. Infected fish exhibit behavioural changes, lethargy and abnormal swimming (whirling). The fish are anaemic with varying degrees of haemorrhage in multiple organs. VHS also exists in a marine form, and a low prevalence in wild populations of sensitive species cannot be excluded in the Swedish coastal zone since the virus has been identified in wild fish from Skagerrak and the Bornholm basin. IHN was found in two Bothnian bay farms in Finland in 2017, but the virus has not yet been identified in Sweden.

Infectious pancreatic necrosis (IPN)

IPN is caused by an Aquabirnavirus which is highly infectious to juvenile salmonids. Susceptibility declines with increasing age. Fish that survive infection become subclinical carriers. In addition to salmonids, the virus has been detected in several other species. The virus is transmitted both horizontally and vertically.

There are seven genogroups with varying virulence. Some genogroups cause up to 90% mortality in fry, and IPN is considered one of the costliest fish diseases in several European countries. Symptoms include darkening, abdominal distension and corkscrew swimming. Petechial haemorrhage in abdominal fat and internal organs are the most common internal disease signs. IPN appears sporadically in Swedish east coast farms.

Renibacteriosis (BKD)

BKD is caused by a gram-positive bacterium, *Renibacterium salmoninarum*. The infection can be transmitted both horizontally and vertically. The disease favours low water temperatures, and outbreaks mainly occur at temperatures between 7 and 15°C.

Salmon and Arctic char are most susceptible to BKD and mortality can reach 80%. In rainbow trout, the disease is chronic with a continuous low mortality of about 5–10%,

however outbreaks of up to 40% mortality can occur. Infected fish may have reduced growth and disease can result in a deterioration of the meat quality. BKD is present in a few farms in the Swedish inland zone.

Spring viraemia of carp (SVC)

SVC is caused by a rhabdovirus. The disease occurs in Asia and several European countries. SVC is not present in Sweden. Several species within the cyprinid family are susceptible to infection and the virus is transmitted horizontally. Clinical signs are usually general, such as darkening, exophthalmia and slow breathing. The fish swim lazily with sporadic periods of hyperactivity. Other common findings are pale gills, ascites and skin and gill haemorrhage. Internally, haemorrhage is found in various organs including muscle, swim bladder and the brain.

Koi herpes virus (KHV) infection

KHV is a herpesvirus and affects common carp (*Cyprinus carpio*) and variants thereof, including koi. The virus was first detected in 1998 and has since then been reported from all continents except Australia. Transmission is horizontal. KHV can cause severe problems and is associated with high mortality. Infected fish usually swim at the surface and have an increased breathing frequency. Disease signs include enophthalmia, gill necrosis and secondary bacterial or parasitic infections on gills and skin. Surviving carps can become subclinical carriers. The prevalence in Sweden is unknown. Koi is frequently imported, but only a few farms use quarantine and sampling. Two outbreaks in koi, with 90–100% mortality, occurred in 2018.

Crayfish plague

Crayfish plague is caused by an aquatic fungus (*Aphanomyces astaci*) that spread with live crayfish from the United States to Europe in the late 1800s. The disease occurs throughout Europe and North America. The fungus reproduces by spores spread in the water. When the spores infect crayfish, they grow through the skin and attack the underlying tissues.

The signal crayfish becomes subclinically infected and may exhibit black (melanised) areas in the shell adjacent to the presence of the fungus in the skin. The spots disappear when the shell is shed but may gradually reappear.

When noble crayfish are infected, the first sign is high mortality in affected populations. Disease in the individual is characterised by behavioural changes such as movement during daytime and, reduced coordination and balance.

Crayfish plague is spread in the southern parts of Sweden.

White spot syndrome (WSS)

WSS is caused by White spot syndrome virus (WSSV), a *Whispovirus* that can infect a wide range of aquatic crustaceans, including marine, brackish and freshwater shrimps, crabs, crayfish and lobsters. Outbreaks with high mortality occur at water temperatures of 18–30°C. The most common clinical sign in penaeid/giant shrimps is white spots in the

exoskeleton. In species with a thicker exoskeleton the disease can occur without obvious external signs.

The virus is transmitted both horizontally and vertically and has a long survival time outside the host animal. Viable virus can be present in imported frozen raw giant shrimps. There is a non-negligible risk that the virus will be introduced to the aquatic environment by anglers using these shrimps for bait. The consequences are difficult to predict but the virus may have a negative impact on Swedish crustacean populations. WSSV has never been detected in Sweden.

Marteiliosis

Marteiliosis, a disease in oysters and blue mussels, is caused by a unicellular parasite (*Marteilia refringens* in oysters and *M. pararefringens* in blue mussels). The parasite needs a crustacean (*Paracartia grani*) as an intermediate host. The disease causes reduced fitness, impaired growth and resorption of the gonads and hence reduced reproductive capacity. *M. pararefringens* is present on the Swedish west coast.

Bonamiosis

Bonamiosis is a disease in oysters caused by the protistan parasite *Bonamia ostreae*. The parasite invades and destroys the haemocytes. Usually, the only sign of disease is increased mortality in the infected oyster population. *B. ostreae* is found along the European Atlantic coast as far up as Denmark, where it has been found in Limfjorden.

SURVEILLANCE

Within the Official Health Control Programme, there is active surveillance for the viruses causing EHN, IHN, VHS, IPN and SVC, and for renibacteriosis/BKD. Sampling frequency is based on classification of each farm into one of three categories (high (I), medium (II) or low risk (III)) after a risk analysis, based on the risk for the farm becoming infected, the risk that the farm will further spread the pathogen and the impact of the pathogen. The risk categorisation is performed by the Swedish Board of Agriculture. Farms within risk categories I and II are tested every year and every second year, respectively, whereas farms within risk category III are only tested upon suspicion of disease. The aim of the Official Health Control Programme is to document freedom from disease and to contribute to the maintenance of this status.

There is also active surveillance in imported quarantined fish (eel - IPN and koi/carp - KHV). Active surveillance is also done when potential invasive alien species - like the marble crayfish - are discovered.

Passive disease surveillance has been done through diagnostics related to disease outbreaks in farms and wild fish.

Crayfish plague is monitored by passive surveillance and testing is done based on suspicion of disease outbreaks.

DIAGNOSTIC PROCEDURES

All diagnostic virus analyses are performed according to recommendations by the EU (EU 2015/1554) or the OIE aquatic manual at the Swedish reference laboratory for fish diseases at the National Veterinary Institute. Pooled organ material (for EHN, VHS, IHN and IPN spleen, kidney, heart/brain are tested, for SVC spleen, kidney, brain and gill are tested) by cell culturing. A pool consists of organs from up to ten fish (up to five fish for SVC). A cell culture is defined as virus-positive if a cytopathogenic effect is detected within two weeks, after which the virus is identified by ELISA and confirmed by real-time PCR, or in some cases by serum neutralisation (SN) test. Thirty fish are sampled in regular fish farms, and in restocking farms all females are sampled after stripping of roe. In eel quarantine, 120 glass eels are sampled at arrival, and after two months 120 cohabitated rainbow trout are sampled for detection of virus. In the case of carp/koi, only a few fish may be sampled. KHV is tested on individual fish (pooled gill and kidney) by PCR.

BKD is tested on kidney tissue from individual fish and demonstrated by an ELISA method. Verification is done by real-time-PCR. Thirty fish are sampled in regular farms, and in restocking farms all females are sampled after stripping of roe.

A. astaci and WSSV are detected with real-time PCR. The number of sampled animals varies from case to case.

RESULTS

Official health control programme for fish farms and crustacean surveillance

The number of samples analysed during 2020 and results are shown in Table 35. In summary, the active surveillance detected two cases of BKD (one case = one outbreak). The BKD cases were reinfections of recently sanitised farms.

Voluntary health control programme for fish farms

There were seven recorded outbreaks of “other” notifiable diseases in fish during 2020. Furunculosis (ASS) was detected in six cases. One farm had recurrent disease and concurrent BKD infection. In 2019 another production site within the same company also got infected with ASS and in 2020 the disease was spread to two more production sites. Another farm also had recurrent disease and one case was detected in wild spawning salmon with saprolegniosis. Yersiniosis was detected in one restocking farm.

Few cases (n=6) of flavobacteriosis due to *Flavobacterium psychrophilum*, usually the predominant production disease, were detected compared to previous years (15–30 cases in the last 10 years). Instead, *Aeromonas* bacteria other than *A. salmonicida salmonicida* or *A. salmonicida* atypically dominated with 16 cases. The cause for this shift is unknown. *Flavobacterium columnare* was detected in five disease cases during the summer.

OUTBREAKS IN WILD FISH, CRUSTACEANS AND MOLLUSCS

During 2020, suspicion of crayfish plague was investigated in ten outbreaks of mortality in noble crayfish. Crayfish plague was detected in six cases. Mortality cases that could not be attributed to crayfish plague were investigated for presence of WSSV but the virus was not identified. Further analyses will be performed during 2021 as a PCR for *Thelohania contijeani* (causing porcelain disease) is currently being evaluated.

DISCUSSION

The number of farms that were sampled during 2020 are listed in Table 35. Swedish aquaculture has a good health status, where all severe diseases of EU/OIE importance are absent. This is confirmed by the surveillance results from 2020.

The most problematic disease to control is renibacteriosis/BKD, due to its vertical transmission and variable clinical presentation. In 2020 only two cases were detected, one

recurring in an on-growth farm and one in wild broodstock. More farms are currently known to be infected and thus not sampled. Prolonged time from diagnosis to slaughter can lead to secondary health issues and increased antibiotic use, as well as decreased welfare. As an example: in the last five years, ASS has been causing problems in one BKD infected farm and there is an apparent lack of treatment effect. The reason is probably the underlying BKD infection, facilitating the ASS infection and itself being accelerated by the concurrent ASS infection. The farm has also managed to spread both BKD and ASS between production sites. Control of BKD could be improved by modified sampling and improved methodology, from today's post mortem sampling to an *in vivo* method. Also, rapid slaughter to avoid manifestation of the bacterium in wild fish is imperative to avoid reinfection in farms and secondary bacterial diseases that require antibiotic treatment. Additional resources must be invested in risk-based analysis of individual aquaculture farms to get a more reliable assessment for health surveillance.

Table 35: Samples taken in the Swedish surveillance programmes for notifiable diseases in fish, crustaceans and molluscs during 2020. One case = one outbreak.

Disease	No. of sampled production sites	No. of infected production sites	No. of tested individuals	No. of tested pools	No. of infected individuals/pools
Fish					
VHS	68	0	-	509	-/0
IHN	68	0	-	509	-/0
IPN	68	0	-	509	-/0
SVC	2	0	5 ^A	3	0/0
KHV	3 ^B	0	7	0	0/0
BKD	64	2	3194	-	4/-
Crustaceans					
<i>Aphanomyces astaci</i>	10 ^C	6 ^C	17	-	9/-
WSSv	0	0	8	-	0/-
Molluscs					
<i>Bonamia ostreae</i> ^D	4	0	150	0	0/-
<i>Marteilia refringens</i> ^D	4	0	150	0	0/-

^A One koi import company tests individual fish

^B One koi import company, two private fish owners (diseased koi).

^C A total of 10 locations were sampled, representing 10 separate waterways with wild crayfish. Six waterways were positive.

^D This sampling was performed as part of a project within the European Sea and Fisheries Fund.

Abbreviations:

EHN	Epizootic haematopoietic necrosis
VHS	Viral haemorrhagic septicemia
IHN	Infectious haematopoietic necrosis
IPN	Infectious pancreatic necrosis
SVC	Spring viraemia of carp
KHV	Koi herpesvirus
BKD	Bacterial kidney disease

Wild fish surveillance programme

BACKGROUND

In 2020, a general surveillance programme for wild fish, crustacean and mollusc health was launched, organized by the National Veterinary Institute by commission from the Swedish Marine and Water Agency. Previously, wild fish had only been investigated through short term projects or in cases of acute disease, except for eel which had been monitored since 2018. Crayfish plague has been monitored for several years, and wild molluscs have been included in bonamiosis and marteilosis projects for farmed molluscs. The surveillance programme started in 2020 aims to cover several ecological niches and important diseases for each of these three animal groups. To manage this, several programmes are currently under development, including both active and passive surveillance. The programmes and summary results from 2020 are described below.

SPECIES INDEPENDENT TOOLS

In addition to the specific fish, crustacean and mollusc programmes, other surveillance components are available that are used as complements to cover acute disease events and species not covered by the active surveillance programmes.

Reporting site

A reporting site (rapporteratfisk.sva.se) was set up in 2016 to enable passive surveillance, mainly of returning salmonids. It has since been expanded but salmon is still the main species reported.

Emergency funding

The emergency funding allows the investigation of cases identified through passive surveillance (e.g. the reporting site, phone calls or email correspondence).

Invasive alien species

Upon specific request from the Swedish Marine and Water Agency, risk assessments are made regarding introduction of pathogens with invasive alien species that are identified in Sweden or are considered at high risk of being introduced. Invasive alien species like the American lobster (*Homarus americanus*), are also investigated for the presence of pathogens at the National Veterinary Institute using emergency funding.

FISH

Anadromous fish

Salmonids and lampreys are anadromous (breed in freshwater and mature in salt/brackish water). The programme focuses on salmonid health because of ongoing health issues in the Baltic salmon (*S. salar*) population. The disease problems started in 2014, with fresh run salmon showing ventral skin haemorrhages followed by fungal infections. The cause of this is still unknown. In 2019, a similar disease started appearing in rivers emptying to the Atlantic Ocean (Sweden, Norway, British Islands). The syndrome has been named red skin disease. In addition, many rivers have problems with fungal infections in both salmon and trout (*S. trutta*) in the period around spawning (October-December). Summer

samplings are performed in specific rivers to investigate the disease cause. Active surveillance is also done for autumn problems by monitoring spawning grounds and recording health problems in broodstock (restocking farm).

In 2020, a total of 148 salmon were sampled in the summer. Analysis of histopathological samples, thiamine, thyroid status and whole metabolism are ongoing. Spawning grounds were successfully monitored in some rivers but could not be performed due to high water flow in other rivers. In all, it is considered a valuable monitoring tool given that the environmental conditions are good. The health trends for broodstock will be evaluated after a few years of data collection.

Catadromous fish

The European eel (*Anguilla anguilla*) is an endangered species and Sweden is working to restore the population. Glass eels are imported annually and quarantined before being released at different locations. Assisted migration for juveniles that have migrated naturally to Sweden is conducted at hydroelectric power dams in Southern Sweden. Health monitoring started in 2018 at some of these dams and in larger eels collected during the coastal fishing performed by the Swedish University of Agricultural Sciences. Ten to 20 eels per site are investigated for the presence of Infectious pancreatic necrosis virus (IPNV), Eel virus European X (EVEX) and eel herpes virus (AngHV-1). In addition, fish >10 cm are checked for the eel swim bladder worm *Anguillicoloides crassus*. If skin haemorrhage, wounds or internal signs of infectious disease are present, bacterial culture is also performed.

In 2020, a total of 155 eels were sampled. Generally, they were in good condition. Of 120 eels examined for the presence of swim bladder worm, 49 were infected. Eel herpes was the only virus detected and it was found in 11 of 49 organ pools, with each pool containing 2–3 eels. All eels in herpesvirus positive pools were >33 cm.

Saltwater fish

Active surveillance is performed through sampling of cod (*Gadus morhua*), flounder (*Platichthys flesus*) and dab (*Limanda limanda*) in the Southern Baltic and Kattegat. Sampling is done during international trawl surveys performed by the Swedish University of Agricultural Sciences. In the Baltic, 100 cod and 100 flounder were collected in the first quarter of the year, and in Kattegat 100 cod and a total of 1000 flounder and dabs were collected in the third quarter of the year. External signs of disease were noted according to an internationally used schedule. Internal signs of disease were also noted. Histopathology was performed on liver and gonads. Sampling for virus or bacterial culture was done if deemed necessary. In cod, livers from 50 fish >35 cm per sampling were digested and the number of cod worms (*Contracaecum* sp.) were counted. The results are currently being evaluated.

Freshwater fish

For freshwater fish, no specific programme has been established. Instead, annual projects that focus on ‘hot topics’ are selected. In 2020, renibacteriosis (BKD), caused by *Renibacterium salmoninarum*, in wild fish was investigated. Until 30 June 2021, Sweden has additional guarantees for BKD. On-growing of salmonids is usually performed in open net pens, and without stamping out of infected fish, the disease could easily spread to the surroundings and become established in wild salmonids. The disease is present or has recently been present in farms in four different rivers (see chapter “Infectious diseases in fish crustaceans and molluscs” on page 128). In the decision-making process to determine if Sweden should apply for national measures according to the new animal health law (Article 226, (EU) 2016/429) or not, a study was performed to investigate the status of wild salmonids (Arctic char (*Salvelinus alpinus*), Brown trout (*Salmo trutta*), Whitefish (*Coregonus* sp.) and grayling (*Thymallus thymallus*)) in these four rivers. The county boards selected nine sampling points upstream and downstream from affected farms as well as a reference sampling point outside the river system. The reference point was situated in a lake or river where anthropogenic movement of fish had not occurred. With 10 sampling points representing each river, there were a total of 40 sampling points, with 30 salmonids collected at each sampling point, generating 1200 fish for analysis. In addition, water was collected at each sampling point to test for *Renibacterium salmoninarum* eDNA using real-time PCR. Detection of *Renibacterium salmoninarum* in fish was done by an antigenic ELISA, with confirmation through real-time PCR.

A total of 1059 fish could be sampled in 38 sampling points and all four designated species were represented. Of the 1059 fish, 52 (4.9%) were positive for *Renibacterium salmoninarum* by ELISA. Of these, 50 came from one river. Whitefish was the main species infected (n=43), whereas only 6 graylings, 2 trout and one Arctic char were positive. Active infection could only be confirmed in one fish by real-time PCR. Water samples were positive for *Renibacterium salmoninarum* eDNA at only two sampling points and this was not associated with the presence of *Renibacterium salmoninarum* infected fish from the same sampling point.

It is apparent that there is a chain of *Renibacterium salmoninarum* transfer between farmed and wild fish. Within a farm, high fish density can cause high infection pressure and the subsequent spread of pathogens from net pens to surrounding wild fish. If the pathogen becomes established in the wild fish, there is a high risk of reinfection of the site after sanitation and restocking.

The river where 50/52 *Renibacterium salmoninarum* positive fish were collected is small with shallow lakes and slow water flow in comparison to the other three rivers. We believe that the water properties of this smaller river allow for a higher infection pressure to build up around a farm. Little is known about the virulence of *Renibacterium salmoninarum* to whitefish and grayling. It is apparent that whitefish

are readily infected, but the lack of active infection suggests high survival rates. This could be problematic as they could represent a reservoir for the disease for Arctic char that can suffer high mortalities. The lack of eDNA positive water samples could possibly be attributed to the lack of active infection in the wild fish, but it may also be that bacteria adhere to particles in the water and sink. Thus, it might be necessary to use equipment that allows for water sampling at the river bottom. Interestingly, both *Renibacterium salmoninarum* positive sampling points were situated a few km downstream from fish farms, one of which tested positive for *Renibacterium salmoninarum* a few months later. The other farm tested negative. However, this site had been recently sanitised due to BKD so it is probable that wild fish adjacent to the farm harbour the infection.

CRUSTACEANS

Saltwater crustaceans

Saltwater crustaceans are monitored by passive surveillance. For example, the Swedish University for Agricultural Sciences fishes for Norwegian lobster (*Nephrops norvegicus*) and if any disease signs are detected, animals are sent for analysis. The university also reports if the invasive alien species American lobster is caught on the west coast.

Freshwater crustaceans

Freshwater crayfish has been monitored for crayfish plague for many years. This surveillance is passive, with investigations upon suspicion of disease. White spot syndrome virus and porcelain disease, caused by the parasite *Thelohanania contigitjeani*, are investigated if crayfish plague is ruled out as the cause of mortality. Results for 2020 are included in the chapter “Infectious diseases in fish, crustaceans and molluscs” (page 128).

In recent years, the use of eDNA for detection of crayfish plague and the presence of noble crayfish (*Astacus astacus*) and the invasive alien species signal crayfish (*Pacifastacus leniusculus*) under Swedish conditions has been evaluated. In 2021, a pilot will be run to begin active surveillance of crayfish plague and crayfish species using eDNA analysis.

MOLLUSCS

Saltwater molluscs

Saltwater molluscs will be included in the surveillance from 2021. Samplings in 2020 were included in a project funded by the European sea and fisheries fund, and results are presented in the chapter “Infectious diseases in fish, crustaceans and molluscs”(page 128).

Freshwater molluscs

The river pearl mussel (*Margaritifera margaritifera*) is an endangered species, and in some Swedish rivers there have been sharp population declines in the last years. Research to identify the cause is ongoing. Because of the endangered state of the species, annual samplings of a number of individuals per population is not an alternative. A monitoring programme will be developed as soon as there is more knowledge about the cause.

Examination of abortions in food producing animals

BACKGROUND

Post mortem examinations are considered important for early detection and national surveillance for infectious and emerging diseases. As mentioned in the chapter “Post mortem examinations in food producing animals” (page 136), the Swedish Board of Agriculture has financed a programme to encourage such examinations for the past 20 years. However, some infections do not produce lesions that can be detected at postmortem or cause only non-specific macroscopic changes. Brucellosis, porcine reproductive and respiratory syndrome (PRRS) and classical swine fever (CSF) are examples of infections that may be present without specific macroscopic findings at postmortem. Moreover, the clinical picture in herds affected by these diseases can be non-specific, which may cause a delay before the suspicion of these infections occurs in clinical surveillance.

SURVEILLANCE

This surveillance component was introduced in 2008. It includes examinations for brucellosis in all ruminant foetuses and for brucellosis, PRRS and CSF in all pig foetuses submitted for postmortem through the post mortem examination programme. These infections often cause abortion, so by sampling aborted foetuses the sampling occurs within a risk group. This increases the chance of detecting the infectious agents, if present. The Swedish Board of Agriculture finances the sampling and testing of foetuses for *Brucella*, PRRS and CSF. The National Veterinary Institute (SVA) is responsible for the organisation of the aborted foetus examination programme. Samples from aborted foetuses are either submitted to SVA by veterinarians performing post-mortem at regional laboratories or are taken from foetuses submitted directly to SVA for post mortem examination. All diagnostic testing is performed at SVA. Testing for the presence of CSF virus and PRRS genome is done by PCR, and for *Brucella* by bacterial culture.



Examination of aborted foetuses is an important part of the national surveillance for infectious and emerging diseases. Photo: Bengt Ekberg/SVA.

Table 36: The number of fetuses investigated and the number of investigated herds (in parentheses) by species 2010–2020 through the aborted fetus examination programme. The number of investigated herds were not available prior to 2014.

Species	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020
Cattle	62	21	63	114	32 (27)	29 (23)	34 (23)	20 (18)	34 (28)	21 (20)	22 (20)
Goat	9	3	5	4	2 (2)	0	2 (2)	2 (1)	5 (3)	3 (2)	2 (2)
Sheep	70	45	79	89	28 (14)	31 (21)	16 (13)	22 (15)	23 (16)	12 (8)	7 (5)
Alpaca	5	0	0	0	0	2 (1)	1 (1)	0	0	0	0
Bison	0	0	1	0	0	0	1 (1)	0	0	0	0
Wisent	0	2	1	0	0	0	0	0	0	0	0
Gnu	0	0	0	1	0	0	0	0	0	0	0
Pig	61	51	54	46	31 (12)	17 (10)	43 (22)	6 (4)	16 (9)	31 (14)	21 (11)
Water buffalo	0	0	0	0	0	0	0	1 (1)	0	0	0
Total	207	122	203	259	93 (55)	79 (55)	97 (62)	51 (39)	78 (56)	67 (44)	52 (38)

RESULTS

In 2020, a total of 52 fetuses from 38 herds were examined (Table 36). This number represents a decrease in submissions when compared to the previous two years and is similar to 2017, when the lowest number of fetuses was submitted for postmortem since the surveillance programme started in 2008. This number is well below the 140 fetuses that were expected to be examined during the year. All analysed samples were negative for *Brucella*, PRRS and CSF.

DISCUSSION

The post mortem examination and sampling of aborted fetuses is an important part of the national surveillance for infectious and emerging diseases. This was demonstrated in 2012–2013, when the then newly-identified Schmallenberg virus (SBV) was detected in Sweden through the surveillance of aborted fetuses. At that time, in addition to testing for *Brucella*, ruminant fetuses were also examined for the presence of SBV. Testing for SBV did not continue beyond 2013, because the disease became established in Sweden and elsewhere in the EU with limited economic impact and was therefore delisted at EU level.

Since 2008, the number of fetuses of different species submitted for examination has varied from year to year. In 2013, the number of ruminant fetuses submitted was extraordinarily high, most likely because of concerns about

SBV. For the last seven years, the number of submissions has been less than anticipated across all species (Table 36). The reasons for this decrease are concerning and not yet well-understood. It is of interest to note that the number of food-producing animals submitted for post-mortem examination has also dropped over the years (see chapter “Post mortem examinations in food producing animals”, page 136) which is likely due in part to the overall decrease in the number of livestock-producing farms in Sweden. The number of sheep fetuses submitted in the last 2 years has been particularly low. This may be partly due to the drought of 2018, during which many sheep producers were forced to reduce or entirely cull their herds. It has also been speculated that stricter packaging requirements for shipping samples via mail that have come about in recent years may have contributed to the drop in submissions of aborted fetuses for post mortem examination. Producers often do not have the necessary shipping supplies on hand and it can take several days for them to receive shipping items once they have been ordered. This waiting time, during which the aborted fetuses must be stored on the farm, may discourage producers from sending fetuses for postmortem. To combat this problem, producers are now being encouraged to pre-order shipping supplies so that they are always on hand in case they are needed.

Post mortem examinations in food producing animals



The total number of post mortem examinations in 2020 was lower than in recent years and particularly low for cattle. This may be partially explained by the decrease in the number of farms with food producing animals. Photo: Bengt Ekberg/SVA.

BACKGROUND

Early detection of infectious diseases is of utmost importance to prevent negative consequences. For diseases with severe clinical signs, the first line of defence is the detection of disease by animal owners, field veterinarians and pathologists. International and national experiences show that post mortem examinations remain a vital part in disease control and detection of emerging diseases.

As post mortem examinations are considered an important part of early detection and national disease surveillance, a specific programme for such examinations started in the early 1990s. The Swedish Board of Agriculture finances the programme, complemented by fees from animal owners. Farm & Animal Health is responsible for the organisation of the post mortem examination programme.

SURVEILLANCE

The programme subsidises post mortem examinations in all food producing animals, poultry and exotic ungulates. Poultry were included in the programme in 2007, domesticated exotic ungulates in 2008, and reindeer in 2017. Each year, between 2000–3000 animals are examined within the

programme. In conjunction with post mortem examinations, samples are collected from defined categories of animals for surveillance of antimicrobial resistance, salmonellosis, transmissible spongiform encephalopathies (TSE) and paratuberculosis. Aborted ruminant and pig fetuses submitted for post mortem examination are sampled for brucellosis, porcine reproductive and respiratory syndrome (PRRS) and classical swine fever (CSF) (see chapter “Examinations of abortions in food producing animals” on page 134).

Transportation of the carcasses to the laboratories is arranged and financed by the animal owner. This can be a problem for large animals, particularly during the summer months when high temperatures lead to rapid carcass putrefaction especially when the distance between the farm and post mortem examination facility is large.

The programme also includes training for large animal practitioners and veterinary employees of the post mortem examination facilities. In the spring, webinars are held for veterinarians in the field to facilitate their skill development and help ensure the freshness of materials that are sent in for analysis during the warm summer months.

RESULTS

In 2020, post mortem examinations were performed at six different laboratories, all located in the southern half of Sweden: Skara (Farm & Animal Health), Kävlinge (Farm & Animal Health), Uppsala (the National Veterinary Institute (SVA) and the Swedish University of Agricultural Sciences (SLU)), Visby (Farm & Animal Health) and Karlskoga (Farm & Animal Health). To facilitate post mortem examination of large animals in the area around Skara, a pilot programme was started in 2019 to have necropsies of all animals weighing more than 10kg performed by an experienced ambulatory veterinarian on the farm, instead of transporting carcasses long distances to other laboratories. This programme has been successful and has now become a routine part of the post mortem examination programme.

Since 2017, a Remote Digital Autopsy (RDA) method has been used in a pilot study to facilitate timely post-mortems of large animals in remote areas of Sweden. This method utilizes a process where a simplified gross post mortem examination is done at the farm by either a field veterinarian or the animal owner. When the method was first implemented, digital photographs of key organs were taken and, together with available anamnestic information, sent to a pathologist for a presumptive diagnosis. During 2020, this method was further developed into a live digital technique where the person in the field is guided through the post-mortem and sample taking process by personnel experienced in doing post mortems using virtual meeting platforms. These digital post mortem examinations are not designed to replace traditional post mortem examinations carried out at laboratories, but rather to facilitate post mortem examination in cases where a post mortem examination would not otherwise be conducted due to the remote location of the farm or to avoid the cadaverous changes that would otherwise occur when transportation distances are long. The technique has primarily been used for the postmortem of reindeer, but the aim is to increase its use for all large animals when immediate transport to a laboratory is not possible.

A total of 2050 post mortem examinations were performed within the programme during 2020. The distribution of species examined over the last 16 years is shown in Table 37. In 2020, 67 cases were diagnosed with a notifiable disease at post mortem examination (Table 38).

DISCUSSION

Post mortem examinations are a vital part of the national surveillance for infectious and emerging diseases, as illustrated by the detection of 67 index cases of notifiable disease in 2020. Post mortem examination is also an important tool that helps veterinarians solve animal health problems at the individual farm. The number of post mortem examinations performed each year varies but has remained at between 2000–3000 per year over the last decade. Some of the

yearly variation in submissions over all species can be explained by the occurrence of outbreaks or other animal disease situations that lead to periods of increased post mortem examination. The total number of examinations in 2020 was lower than in recent years and was caused primarily by a drop in the number of sheep, cattle and poultry carcasses submitted for postmortem. Poultry submissions have typically shown large variations from year to year but the number of cattle and sheep examined had previously been relatively stable at around 800 and 500 animals per year, respectively. However, for the last four years, the number of sheep undergoing post mortem examination has declined, with 2020 seeing the lowest number of submissions since 2005. Similarly, cattle submissions during 2020 were particularly low. The reasons for these decreases are not well understood but they may be partially explained by the decrease in the number of farms with food producing animals.

A regional imbalance can be seen in that more examinations are done in regions closer to post mortem examination facilities. The highest numbers of examinations are performed in regions with high animal density and access to a regional laboratory performing post mortem examinations. With the exception of reindeer, the relatively new RDA and live digital methods have yet to increase the number of large animal post mortem examinations performed. However, these techniques did contribute to the largest number of reindeer postmortems being performed since reindeer were added to the programme in 2017. It is hoped that the new on-farm post mortem examination programme started in 2019 in the area around Skara, a region with high animal density but without a large animal post mortem examination facility, will increase the number of post mortem examinations performed in the region. Performing post mortem examinations on-farm has allowed for fresher material to be examined and collected for further diagnostics, which improves the chances of reaching a diagnosis. The programme has been appreciated by both producers and veterinarians and will therefore continue in 2021.

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Redovisning av uppdrag om veterinär obduktionsverksamhet. veterinär obduktionsverksamhet (SJV Dnr 33-10225/10)

Personal communication, Ulrika Rockström Swedish Farm & Animal Health.

Table 37: Number of food producing species submitted for post mortem examination, 2005–2020.

Year	Pigs	Cattle	Sheep	Goat	Farmed deer	Poultry	Exotic ungulates	Reindeer	Other	Total
2005	2190	839	550	13	26	49	1	0	-	3668
2006	2543	733	630	7	38	39	-	0	-	3990
2007	1434	660	545	17	39	80	7	0	-	2782
2008	1173	646	613	15	43	480	10	0	1	2981
2009	1112	655	510	11	10	656	18	0	5	2977
2010	932	773	637	24	13	391	25	0	2	2797
2011	737	707	611	23	11	460	28	0	1	2578
2012	862	826	749	35	11	630	37	0	1	3151
2013	667	983	840	34	18	749	43	0	2	3338
2014	502	747	548	14	11	1006	40	0	0	2868
2015	529	707	557	21	3	778	42	0	3	2640
2016	651	845	617	34	17	642	31	0	0	2837
2017	498	777	458	17	15	1478	36	4	0	3283
2018	481	785	414	35	19	609	12	5	0	2360
2019	448	725	306	19	1	700	10	4	1	2214
2020	464	597	272	29	4	601	9	71	3	2050

Table 38: Number of index cases of a notifiable disease diagnosed from samples taken at post mortem examination, 2013–2020. Statistics from Farm & Animal Health.

Disease	2013	2014	2015	2016	2017	2018	2019	2020
Anthrax	0	0	0	1	0	0	0	0
Avian rhinotracheitis	1	0	0	0	0	0	0	0
Blackleg	7	4	19	26	25	24	25	9
Bovine Malignant Catarrhal fever	3	1	1	6	6	2	2	3
Chorioptes (sheep/goat)	-	-	-	-	1	0	0	0
Duck Viral Enteritis ^A	-	1	0	0	0	0	0	0
<i>Dichelobacter nodosus</i>	-	-	-	-	-	-	-	2
Fowl Cholera (pasteurellosis)	0	0	0	3	4	2	0	0
Fowl typhoid (<i>S. Gallinarum</i>)	0	0	0	0	3	0	0	0
Gumboro (Very virulent IBDV)	-	-	-	-	5	4	0	1
Infectious Bronchitis	0	0	0	0	0	0	0	1
Infectious laryngotracheitis	36	35	26	26	17	20	21	16
Influenza, pigs	1	1	0	0	1	0	0	0
Influenza A typ (H1N1) 2009	3	0	0	0	1	0	0	0
Listeriosis	49	31	22	20	22	22	9	14
Lymphoma (not EBL)	0	0	0	2	0	0	0	0
<i>Mycoplasma gallisepticum</i>	0	4	4	0	1	7	32	15
<i>Mycoplasma</i> , poultry (not <i>gallisepticum</i>)	0	0	0	2	0	0	0	0
Necrotic haemorrhagic enteritis (<i>Clostridium perfringens</i> type C)	0	0	0	0	0	0	0	0
Salmonellosis	2	3	3	1	2	2	5	6
Total	102	80	75	87	88	83	94	67

^AThis disease was not diagnosed in Sweden prior to 2014.

Post mortem examinations in wildlife

BACKGROUND

The national general wildlife disease surveillance programme is based on pathology and ancillary testing at SVA. The surveillance programme is financed partly by annual state hunting permit fees, and partly by governmental funding. The aim is to monitor the wildlife disease situation in Sweden and to diagnose and acquire knowledge on present and emerging diseases in Swedish wildlife. Results from the disease surveillance provides key information for wildlife management. It is also part of zoonotic and epizootic disease surveillance efforts, including surveillance for new and potentially emerging diseases, and can also serve as an indicator of environmental and ecosystem health. The OIE national focal point for wildlife is located at SVA and reports OIE listed diseases in wildlife, as well as OIE specified non-listed wildlife diseases.

SURVEILLANCE

The public, local authorities, and especially hunters submit wildlife that is found dead, or found sick and then euthanised, to SVA for diagnostic examination. Standard samples are collected for bio-banking from suitable submitted carcasses. Hunter-harvested wild boar and brown bear (*Ursus arctos*) samples for *Trichinella* analysis are not included in these numbers, as these can be tested at various commercial labs as well as SVA. All large carnivores: brown bear, lynx (*Lynx lynx*), wolf (*Canis lupus*) and wolverine (*Gulo gulo*) found dead, euthanised, or hunter harvested must be submitted to SVA for examination, as skinned carcasses or tissue samples.

RESULTS

In 2020, whole carcasses or parts of 2510 free-ranging wildlife were submitted to the Department of Pathology and Wildlife Diseases, not including examined farmed or captive wildlife species. The most important wildlife disease events in 2020 are mentioned below.

The finding of a fourth case of chronic wasting disease (CWD, a prion disease of cervids), in yet another old female moose, but from a second county; Västerbotten. An intensified surveillance during the moose hunt in the local area did not discover any further cases. For more details, see the CWD chapter (page 32).

The beginning of the largest outbreak of avian influenza so far started late in 2020, caused by highly pathogenic H5N8 and H5N5 strains.

The reporting and surveillance of African swine fever virus in found dead wild boar has increased, but so far, the disease has not been found in Sweden. But a re-emerging disease was discovered in wild boar in 2020, when *Salmonella choleraesuis* was found in several areas in Sweden.



The necropsy room at SVA where submitted dead wildlife is examined within the general and the targeted wildlife disease surveillance programmes. The dead wolf in the image is first radiographed and body measurements are taken before skinning and postmortem, to decide cause of death, underlying diseases, as well as routine health surveillance sampling for parasites or other infections. Photo: Bengt Ekberg/SVA.

This bacterium has not been identified in Swedish wild boar previously, but after an outbreak in a domestic pig farm, surveillance has revealed that also wild boar both can carry and be affected clinically by this type of pig-associated *Salmonella*. For details, see the chapter about infectious diseases in wild boars (page 123).

A retrospective study of the intestinal tapeworm *Echinococcus granulosus* in stored samples from necropsied wolves, using a new specific PCR-analysis, identified the first two positive cases in wolves in Sweden. Both wolves had died in 2012. The parasite has previously only rarely been found in intermediate hosts such as moose and semi-domesticated reindeer. The parasite seems to be present at a very low prevalence in wildlife.

A programme for health and disease surveillance of marine mammals has been initiated in 2020, together with the Museum of Natural History, and is financed by the Swedish Agency for Marine and Water Management. A coastal network to report and handle stranded marine mammals has been expanded and a limited number of seals and whales

have been necropsied and sampled to improve knowledge about these key species that also act as indicators of marine ecosystem health.

Use of the SVA online form (rapporteravilt.sva.se) to report sick or dead wildlife has steadily increased. This is an easily available tool for reporting that helps SVA to map the disease situation in wildlife, and to access suitable samples with the help of the public.

DISCUSSION

The general disease surveillance in wildlife is based on citizen science, with the interested public and hunters especially, reporting and submitting samples. A high public interest in wildlife health and conservation continues

to make this work possible, together with state financing. Among scientists and relevant authorities, it is well recognised that wildlife disease surveillance is an integral part of the One Health concept. The surveillance results regarding reportable infectious diseases (Table 39) show that there are only few serious infectious disease threats to wildlife.

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Table 39: Reportable infectious diseases in wildlife and number of outbreaks/cases diagnosed at SVA in 2020. Here, individual cases are listed, and may differ from other official numbers of disease outbreaks or number of index cases.

Disease	Cases	Species
Avian pox	1	Hooded crow
Chronic wasting disease	1	Moose
Chytrid disease	1	Moor frog
<i>Echinococcus multilocularis</i>	1	Red fox
European brown hare disease	7	European brown hare
Highly pathogenic avian influenza	6	Barnacle goose (4), Great horned owl (1), Peregrine falcon (1)
Malignant catarrhal fever	1	Moose
Myxomatosis	4	Wild rabbit
Pasteurellosis	1	Fallow deer
Pigeon paramyxovirus	5	Rock pigeon
Pseudotuberculosis	8	European brown hare
Rabbit haemorrhagic disease	5	Wild rabbit
Salmonellosis	69	Black-headed gull (4), Bullfinch (8), Porpoise (1), Red poll (2), Siskin (23), Wild boar (31)
Sarcoptic mange	5	Lynx (3), Red fox (1), Wild boar (1)
Toxoplasmosis	3	European brown hare
Trichomoniasis	15	Bullfinch (1), Chaffinch (4), Greenfinch (4), Hawfinch (4), Rock pigeon (1), Siskin (1)
Trichinosis	15	Lynx (6), Wild boar (9)
Tularaemia	30	European brown hare (10), Mountain hare (20)
Total	178	

Antibiotic resistance in bacteria from animals and food

BACKGROUND

The National Veterinary Institute (SVA) has the mission to monitor and analyse the development of antimicrobial resistance in bacteria from animals and food of animal origin. This also includes implementation of the mandatory harmonised monitoring of antibiotic resistance in bacteria from food-producing animals and food thereof, dictated by EU legislation. The monitoring activities are carried out through the Swedish Veterinary Antibiotic Resistance Monitoring Programme (Svarm), which has been running since 2000.

The objectives of Svarm are to detect changes in trends in resistance and to provide a basis for recommendations on the use of antibiotics in animals. Three types of bacteria are monitored: zoonotic bacteria, specific animal pathogens and indicator bacteria from healthy animals and meat. In addition, both intestinal content from healthy farm animals and fresh meat are screened for *E. coli* producing extended spectrum beta-lactamases (ESBL), AmpC-enzymes and carbapenemases. The rationale for monitoring indicator bacteria, i.e. commensal *Escherichia coli* and *Enterococcus* spp. from the normal intestinal flora of healthy animals, is that resistance among these bacteria reflects the selection pressure caused by the use of antibiotics in an animal population. These commensal bacteria can also be a reservoir of mobile resistance genes that can reach humans through the food chain. Thus, the prevalence of resistance in bacteria that contaminate meat reflects the magnitude of the potential human exposure to such reservoirs in food-producing animals.

The Svarm programme conforms to directive (2003/99/EG) and subsequent decisions (2013/652/EU, from 2021 replaced by 2020/1729/EU). According to the directive, resistance in *Salmonella*, *Campylobacter jejuni* and indicator bacteria shall be regularly monitored in broilers, turkeys, pigs and cattle using harmonised methodologies. Briefly, for Sweden, this implies that each year, isolates of *Salmonella* from all notified outbreaks in food-producing animals, as well as 170 isolates of *Campylobacter* from either broilers or pigs, are tested for antibiotic susceptibility. Also, 170 isolates of *E. coli* from intestinal content of healthy broilers or pigs are tested each year. In addition, each year 300 samples of intestinal content and 300 samples of fresh retail meat from either broilers or from pigs and cattle are screened for ESBL/AmpC- and carbapenemase producing *E. coli*. Due to small production volumes, it is not mandatory for Sweden to investigate *Campylobacter* or indicator bacteria from healthy turkeys or cattle. It is not mandatory to screen for ESBL/AmpC- or carbapenemase producing *E. coli* in these animal categories either. However, sometimes such investigations are still performed, on

a voluntary basis. Starting from 2021, sampling of turkey meat and sampling of meat from countries outside EU at border control posts are also included in the monitoring.

In addition to the mandatory monitoring described above, Svarm is complemented with data on resistance in clinical isolates of bacteria from the routine testing of clinical submissions at SVA. Svarm is also complemented with data from research projects and specifically from the Svarm-Pat project focusing on resistance in animal pathogens from farm animals. SvarmPat is run in cooperation with Farm & Animal Health and is financed by the Swedish Board of Agriculture.

Sales of antibiotics for use in animals is also monitored. The primary data source is sales from pharmacies to animal owners (prescriptions dispensed) and to veterinarians (requisition for use in own practice). In Sweden, all veterinary medicinal products are sold by pharmacies and they are obliged to report all sales of medicinal and veterinary medicinal products to the eHealth Agency. Data on sales of antibiotics are calculated to kg active substance. For prescriptions, animal species is also recorded and can be included in the analyses.

Data on antibiotic resistance in bacteria from animals and food as well as data on sales of antibiotics for use in animals are presented in a yearly report together with corresponding data for human medicine compiled by the Public Health Agency of Sweden in an integrated report - Swedres-Svarm - available at www.folkhalsomyndigheten.se or at www.sva.se/swedres-svarm. The different data sources compiled in this report are illustrated schematically in Figure 42.

LEGISLATION

As mentioned above, parts of the antibiotic resistance monitoring performed in Sweden are regulated by EU legislations (2003/99/EG and 2013/652/EU which from 2021 is replaced by 2020/1729/EU). Furthermore, there is also national legislation indirectly affecting the antibiotic resistance monitoring. More precisely, findings of carbapenemase producing Enterobacteriaceae (ESBL_{CARBA}) and methicillin-resistant coagulase-positive staphylococci (e.g. MRSA and MRSP) in animals are notifiable in Sweden (SJVFS 2021:10 and previously SJVFS 2012:24 with amendments).

SUMMARY OF RESULTS

From an international perspective, Sweden still has a favourable situation regarding antibiotic resistance in bacteria in humans and animals. This confirms that our strategies to promote the rational use of antibiotics and to limit the spread of antibiotic resistance are effective. In the last decades, the sales of antibiotics in Sweden have decreased

for both humans and for animals. In addition, the distribution between broad- and narrow-spectrum antibiotics has changed and the proportion of narrow-spectrum antibiotics has increased. Among bacteria from animals, the occurrence of resistance has generally been stable at low or moderate levels. For some substances and in some bacteria occurrence of resistance is even declining. One example of this is the occurrence of ESBL producing *E. coli* among broilers that has declined significantly. There are however exceptions, and for example resistance to ampicillin, sulphonamides, and trimethoprim has increased in indicator *E. coli* from both broilers and pigs.

Antibiotic sales for veterinary use

In 2020, reported sales of antibiotics for animals were 9306 kg, of which 54% were penicillins with narrow spectrum. The corresponding figures for 2011 were 12 220 kg and 52%, respectively. Since the withdrawal of growth-promoting antibiotics from the Swedish market in 1986, the total sales of antibiotics have decreased by more than two thirds when

corrected for population sizes over time. During the 1990s, sales of veterinary products for medication of groups of animals decreased, and in the past decade there has also been a decrease in sales of products for use in individual animals. (Figure 43).

Extended spectrum beta-lactamase (ESBL) producing Enterobacterales (previously Enterobacteriaceae)

ESBL-producing Enterobacterales (previously Enterobacteriaceae) are rare among animals in Sweden. Previously, the occurrence in intestinal samples from broilers was high but it has decreased in recent years. In 2020, the occurrence of ESBL-producing *E. coli* in intestinal samples from broilers and turkeys, as well as samples of broiler meat was investigated with screening methods. Such bacteria were isolated from 3 and 0% of the intestinal samples from broilers and turkeys respectively, and 2% of the broiler meat samples of Swedish origin. Bacteria that form ESBL_{CARBA} have not been confirmed from animals in Sweden.

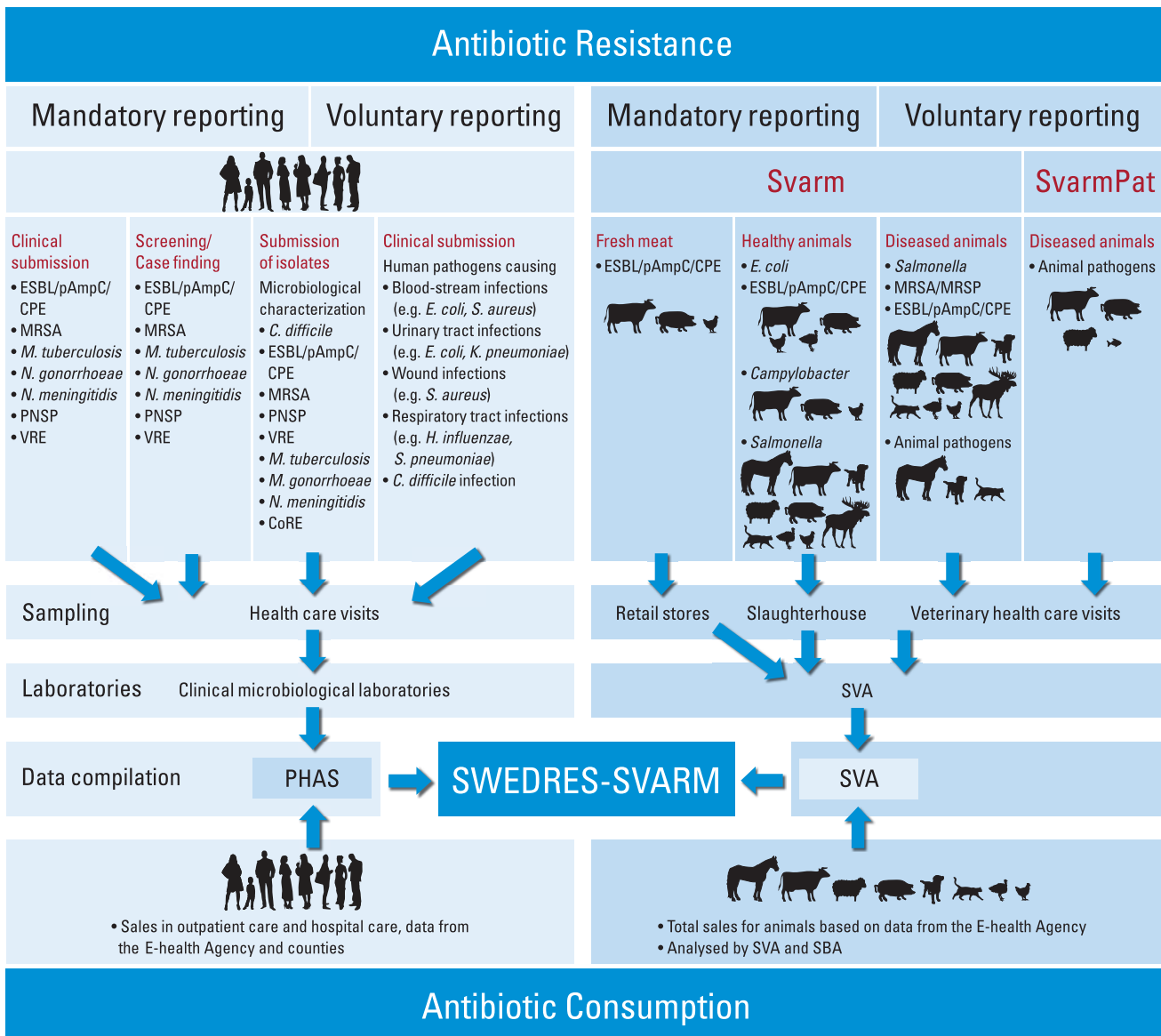


Figure 42: A schematic illustration of data included in the Swedres-Svarm report.

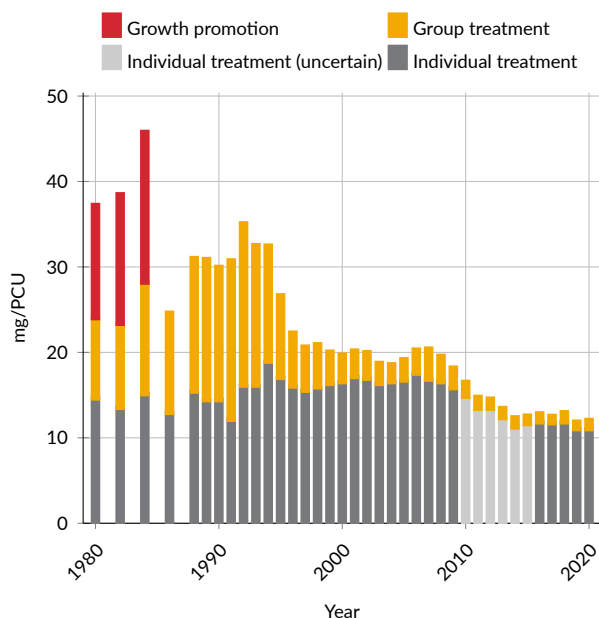


Figure 43: Sales of antibiotics for animals expressed as mg per population correction unit (PCU). Data from 2010–2015 are uncertain because of a lack of completeness mainly affecting injectable products (indicated in a lighter grey). In the present figure, all products (including tablets) are included while in data presented in the European surveillance of veterinary antimicrobial consumption tablets are excluded when calculating mg/PCU.

Methicillin-resistant *Staphylococcus aureus* (MRSA)

The occurrence of MRSA in animals in Sweden is still low, which limits the spread from animals to humans. MRSA was found sporadically in horse, dog, and cat. However, the number of MRSA cases in horses was tripled in 2020, compared to earlier highest figure of nine cases in 2014. The increase could be explained by outbreaks in two equine hospitals with a total of 18 cases. In companion animals, the same types of MRSA as in humans dominate, indicating a human source of MRSA in these animals. In horses, livestock-associated MRSA clonal complex 398 used to be most common, but in 2020 *spa*-type t1971 dominated (14 of 27 cases). This variant is since 2019 a new finding in horses in Sweden.

Methicillin-resistant *Staphylococcus pseudintermedius* (MRSP)

In 2020, the number of reported cases of methicillin-resistant *Staphylococcus pseudintermedius* (MRSP) in animals was around the same level as in previous years. In total 49 cases of MRSP were notified to the Swedish Board of Agriculture, and isolates from 47 cases from dogs were available for further investigations. All but two of the investigated isolates were resistant to three or more substances,

i.e. multi-resistant. The epidemiology of MRSP is more diverse compared to earlier years with several sequence types occurring.

Vancomycin-resistant enterococci (VRE)

In 2020, the occurrence of vancomycin resistant enterococci (VRE) in intestinal samples from broilers was investigated with screening methods. Such bacteria were isolated from 6% of the samples. That shows that the decrease in occurrence of VRE among broilers in Sweden that has been since 2005 continues. All the isolates belonged to the clone of *E. faecium* with *vanA* which is the most common VRE in broilers in Sweden.

Resistance in zoonotic pathogens

Salmonella is rare in animals in Sweden. Furthermore, only a few of the incidents involve antibiotic-resistant strains. Resistance to fluoroquinolones is rare. Isolates from human invasive infections with *Salmonella* are markedly more resistant, probably due to the large proportion of cases acquired abroad.

Campylobacter from animals in Sweden are generally susceptible to relevant antibiotics, and resistance to erythromycin, for example, is most uncommon.

Infections, either in humans or in animals, caused by *Salmonella* and *Campylobacter* are usually not treated with antibiotics.

Resistance in animal clinical isolates

Bacteria causing clinical disease in animals are mostly susceptible to antibiotics relevant for treatment. Respiratory pathogens from farm animals and horses are generally susceptible to benzylpenicillin, but penicillin resistance is common in *Staphylococcus pseudintermedius* from dogs and occurs in *S. aureus* from horses and *S. felis* from cats. Resistance in *E. coli* occurs in all animals but is most prominent in enteric isolates from young calves and pigs. Susceptibility testing for guidance in antibiotic therapy is warranted, especially for staphylococci, *E. coli* and, *Brachyspira* spp.

Resistance in indicator bacteria from healthy animals

Antibiotic resistance in *E. coli* from the intestinal flora of healthy animals serves as an indicator for the presence of resistance in an animal population. The prevalence of acquired resistance in such commensal bacteria also indirectly indicates the magnitude of the selective pressure from the use of antibiotics in an animal population. The prevalence of resistance in indicator bacteria from animals in Sweden is low, and the situation is favourable in an international perspective.

