SURVEILLANCE OF INFECTIOUS DISEASES IN ANIMALS AND HUMANS IN SWEDEN 2021

NATIONAL VETERINARY INSTITUTE

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Cover: Necropsy of a laying hen at the National Veterinary Institute (SVA). Photo: Désirée Jansson

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

Layout: The production of this report continues to be accomplished using a primarily open-source toolset. The method allows the source text to be edited independently of the template for the layout which can be modified and reused for future reports. Specifically, the chapter texts, tables and captions are authored in Microsoft Word and then converted 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 2021 has focused on migration of custom typesetting from R into the lua language which can be applied as a filter in the pandoc conversion process. 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.

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Contents

Figure 1: Group-housing of dry sows on deep straw bedding is common practice in Sweden. In areas where *Salmonella* Choleraesuis is present in wild boar, contaminated straw is a possible way of introduction into pig herds. Photo: Bengt Ekberg/SVA.

Introduction

Surveillance of infectious diseases in animals and humans 2021 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 again refers to the disease situation and surveillance implemented during the ongoing COVID-19 pandemic, with consequences both on surveillance efforts and their results. 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 fewer patients have presented to primary care with symptoms consistent with many of the common zoonoses during the pandemic. This is hypothesised to be related both to 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 resulted in extensive outbreaks of SARS-CoV-2 infections in mink in 2020, with vast consequences for the international mink fur industry and potential impact on public health. In Sweden, this prompted the ban on breeding of mink during 2021 along with restrictions to reduce the risk of the transmission of SARS-CoV-2 between humans and mink. At the EU level, surveillance for the presence of SARS-CoV-2 in mink became compulsory in all member states during the year.

The front cover of this year's report shows a hen on the necropsy table at the National Veterinary Institute, SVA; this to represent the most dramatic animal health event in Sweden during the last decades. The outbreak of avian influenza that affected domestic poultry and wild birds during the 2020–2021 season is the largest ever recorded in the country, with millions of birds lost to the disease or to measures implemented to reduce the risk of further spread (see more at page 49).

Following the first outbreak of *Salmonella* Choleraesuis in Sweden in 40 years, described in our previous report, an intensified surveillance of *Salmonella* in wild boar was carried out during 2021. The results from this surveillance suggest that *S.* Choleraesuis is widespread in parts of the country, posing a potential threat to the pig production. This is further described in the "In focus" section within the chapter on salmonellosis (page 76).

These major animal health events affecting the pig and poultry industries highlight the need for strengthened biosecurity measures at farms, directed towards avoiding introduction of pathogens from the environment.

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. The restrictions put in place to maintain trust between trading partners are also where the major costs appear in case of outbreaks of regulated diseases. 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 early action through preparedness are key for effective early warning and control. These are also vital factors to maintain trust and for joint European preparedness to which we actively contribute. In line with this, our understanding of the Swedish disease situation in 2021 is provided in this report.

Overview of active surveillance 2009–2021

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 116), 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 2021 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 during the last ten years (2012–2021). Filled circles (●) indicate that active surveillance was carried out.

Disease	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021
African swine fever	●	○	○	○	○	○	○	○	○	○
Atrophic rhinitis	●	●	●	●	●	●	●	●	●	●
Aujeszky's disease	●	●	●	●	●	●	●	●	●	●
Bluetongue	●	●	●	●	●	●	●	●	●	●
Bovine spongiform encephalopathy	●	●	●	●	●	●	●	●	●	●
Bovine viral diarrhoea	●	●	●	●	●	●	●	●	●	●
Brucellosis	●	●	●	●	●	●	●	●	●	●
Campylobacteriosis	●	●	●	●	●	●	●	●	●	●
Chronic wasting disease	○	○	○	○	●	●	●	●	●	●
Classical swine fever	●	●	●	●	●	●	○	●	●	●
Echinococcosis	●	●	●	●	●	●	●	●	●	●
Enzootic bovine leucosis	●	●	●	●	●	●	●	●	●	●
Footrot	●	●	●	●	●	●	●	●	●	●
Infectious bovine rhinotracheitis	●	●	●	●	●	●	●	●	●	●
Avian influenza	●	●	●	●	●	●	●	●	●	●
Swine influenza	○	○	○	●	○	●	○	○	○	○
Leptospirosis	●	●	○	○	●	○	○	●	○	○
Maedi-visna	●	●	●	●	●	●	●	●	●	●
Paratuberculosis	●	●	●	●	●	●	●	●	●	●
Porcine reproductive and respiratory syndrome	●	●	●	●	●	●	●	●	●	●
Rabies	●	●	●	●	●	●	●	●	●	●
Salmonellosis	●	●	●	●	●	●	●	●	●	●
Swine vesicular disease	○	●	○	○	○	○	○	○	○	○
Schmallenberg virus	●	○	○	○	○	○	○	○	○	○
Scrapie	●	●	●	●	●	●	●	●	●	●
Tick-borne encephalitis	○	○	○	●	○	○	○	●	○	○
Transmissible gastroenteritis	○	●	○	○	○	○	○	○	○	○
Trichinellosis	●	●	●	●	●	●	●	●	●	●
Tuberculosis	●	●	●	●	●	●	●	●	●	●
Tularaemia	○	○	○	●	○	○	○	○	○	○
Shigatoxin producing *Escherichia coli*	●	○	○	●	○	○	●	○	○	●
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 2, 3, 4 and 5 give an overview of the livestock population in Sweden 2021.

The numbers presented reflect 2021, if not otherwise stated. Published data is from the latest available date at the time of publishing.

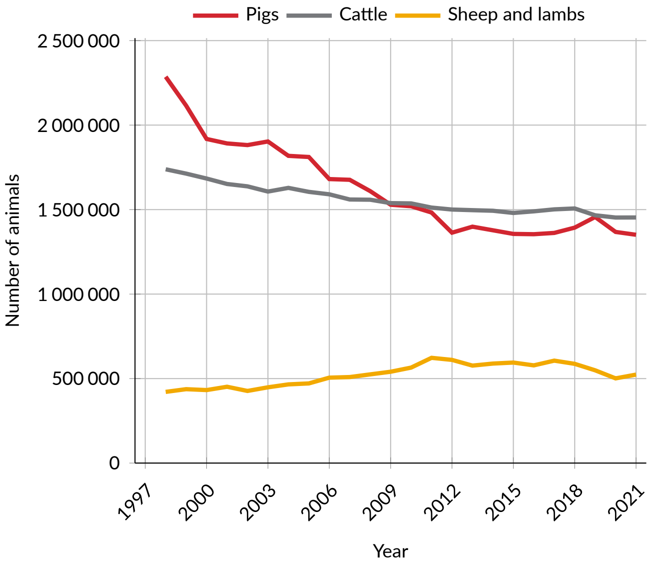

Figure 2: Number of Swedish livestock 1998–2021.

CATTLE

There are 15 227 holdings with a total of 1 453 303 cattle (dairy cows, beef cows, heifers, bulls, steers and calves younger than one year) in Sweden, see Figure 3 for the geographical distribution.

The number of holdings with dairy cows, as well as the number of dairy cows, has decreased consistently over a long period. There were 301 850 dairy cows in 2955 holdings, with an average of 102 cows per herd in 2021. Ten percent of the holdings have 200 or more dairy cows. The number of beef cows has been increasing consistently since the 1980s but has been quite stable during recent years. There were 209 745 beef cows, with an average herd size of 21 cows.

In total, approximately 400 140 adult cattle and 11 510 calves were slaughtered. The total milk delivered was approximately 2782 million kg.

PIGS

The total number of pigs was 1 350 947, see Figure 4 for the geographical distribution. For many years the number was decreasing, but more recently the population size has stabilised with little differences between years. There were 1190 holdings in 2021, of which 898 held fattening pigs and 749 held breeding pigs.

About 2 651 110 pigs were slaughtered.

SHEEP

There were 8479 sheep holdings with a total of 271 638 ewes and rams (see Figure 5 for the geographical distribution). Sheep holdings in Sweden are usually small-scale enterprises, with an average herd size of 32 adult sheep in 2021. During the last ten years there has been a slight decrease in number of sheep and holdings, see Figure 2.

During 2021, approximately 277 070 sheep were slaughtered, of which 195 970 were lambs.

GOATS

According to the farm registers there are approximately 15 800 goats (December 2021) in Sweden. In the Central Register of holdings there are about 5200 holdings registered for keeping goats, but only 2700 of them reported that they keep at least 1 goat.

The last census was carried out in 2018. A questionnaire was distributed in June 2018 to a random sample of 816 goat holdings. All goat holdings were eligible to be included in the sample, regardless of size. This is not the case for other livestock study populations, which are instead based on thresholds in the farm register. Based on results from the questionnaire, the total number of goat farmers was 2400, and the total number of goats was estimated to approximately 20 000. The results from the census show an increase compared to 2003, when the previous census was carried out. In 2018, most of the holdings (70%) had fewer than ten goats. More than half of the goats (60%) were kept as part of business activities. About 10% of the farmers milked their goats and the amount of produced milk was estimated to 1 471 000 kg in 2018.

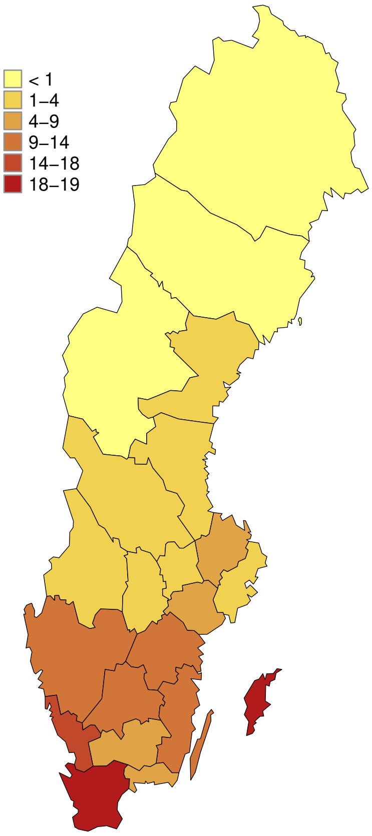

Figure 3: Number of cattle per km^2 in 21 Swedish counties as of June 2021.

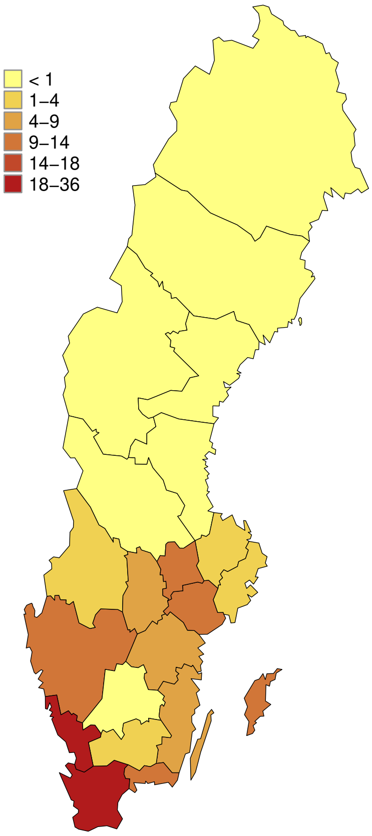

Figure 4: Number of pigs per km^2 in 21 Swedish counties as of June 2021.

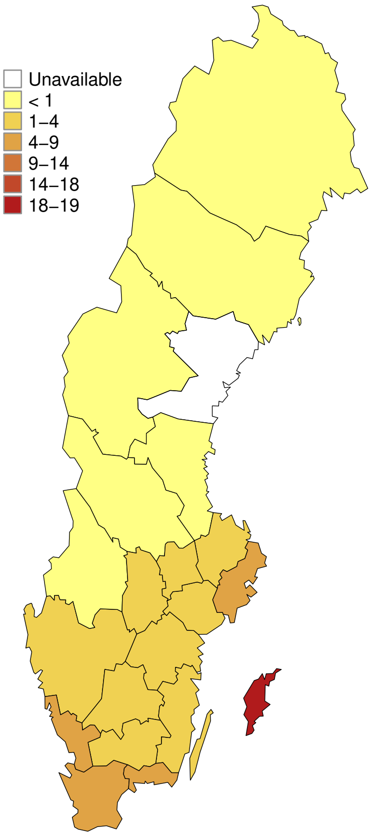

Figure 5: Number of sheep per km^2 in 21 Swedish counties as of June 2021.

POULTRY

To provide animals for the broiler industry, grandparent stock and parents (Ross and 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.

Poultry numbers have generally increased continuously during the last two decades. But in 2021, there were approximately 6.4 million hens over 20 weeks of age, in 2912 commercial holdings. This represents a significant decrease in population size compared to 2020. This decrease can be assumed to be an effect of the major avian influenza outbreak which occurred during winter and spring 2021, with significant impact on both broiler and egg industry.

Eggs delivered to wholesalers amounted to 111.5 million kg.

The number of holdings with broiler production in 2021 was 171 and approximately 116 million chickens were sent for slaughter during the year, an increase compared to 2020. During 2021, 528 360 turkeys were sent for slaughter.

The production of other poultry is very limited. In 2021, 9657 geese, 11 906 ducks, and no guineafowl were slaughtered.

FISH AND SHELLFISH

The numbers on fish and shellfish presented reflect 2020, if not otherwise stated.

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

Swedish shellfish production is dominated by cultivated blue mussels, of which 2297 tonnes were produced in 2020.

All mussel production and 14% 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 and eel is freshwater based. The most common aquaculture production system for food fish is cage culture, both in fresh and saltwater.

In 2020, there were 55 holdings producing food fish, 59 holdings with fish for restocking, four with crayfish for consumption and three with crayfish for restocking. There were 33 holdings with production of blue mussels, an increase compared with 2019.

In 2020, the production was 9900 metric tonnes, in fresh weight, of food fish, of which 91% was produced in northern Sweden. Production has decreased the last years due to closing of small holdings. Rainbow trout represented the largest production, with 88% of the total production of fish for consumption.

The total production of fish for restocking was estimated to be 828 tonnes. The most common species produced for restocking was rainbow trout.

REINDEER

In 2020, there were 240 314 reindeer in Sweden, including 56 813 calves, with an average of 52 reindeer per owner. During the 2020/2021 season, 40 528 reindeer were slaughtered, and the average slaughter weight was 25.3 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 76 800.

Approximately 1200 horses were slaughtered in Sweden in 2021.

BEES

In 2021, the number of apiaries in Sweden was 20 054 and the number of colonies was 89 051, figures approximated by bee inspectors. Over the last ten years, these numbers have increased by 77 and 29 percent respectively.

TRADE IN LIVE ANIMALS (LIVESTOCK)

The trade of livestock into and out of Sweden is very limited. In 2021, 160 pigs from Norway, 87 pigs from Denmark and 18 pigs from Germany were brought into Sweden, as well as 49 cattle from Denmark, 35 cattle from Finland and three cattle from the Netherlands. Four sheep were brought from the Netherlands, and four sheep from Germany. One alpaca was brought from Denmark and two llamas were brought from Norway. Additionally, one reindeer came from the Netherlands.

Approximately 96 000 grandparent and parent animals as day-old chicks (*Gallus gallus*) entered Sweden, from the Netherlands, Spain, France, and Denmark as well as 6456 turkeys (*Meleagris gallopavo*) from Great Britain. In addition, 11 000 ducks (*Anas* spp.) were brought from Denmark and six geese (*Anser* spp.) from Germany. Thirteen consignments of hatching eggs (*Gallus gallus)* were sent to Sweden from Finland.

In total, 60 consignments of honeybees (*Apis mellifera*) were brought to Sweden from Austria, Croatia, Denmark, France, Germany, Slovenia, Spain, Italy, Malta, and Romania. Furthermore, 97 consignments of bumblebees (*Bombus* spp.) were brought to Sweden from the Netherlands and Belgium.

The number of animals that left Sweden for intra-Union trade during 2021 were: 139 bovine animals, 30 pigs, 149 sheep and 42 alpacas. In addition, 508 reindeer were sent from Sweden to Finland.

Approximately 2.6 million day-old chicks (*Gallus gallus*), 7400 ducks (*Anas* spp.) and 1.3 million live poultry (*Gallus gallus*) left Sweden for intra-Union trade in 2021.

Eighty-four consignments of hatching eggs fertilised for incubation (*Gallus gallus*) were sent for intra-union trade.

A total of 10 consignments of honeybees (*Apis mellifera*) left Sweden for intra-union trade to destinations in Poland, Germany, Belgium, and Austria.

REFERENCES

TRACES (**TRA**de **C**ontrol and **E**xpert **S**ystem), a trans-European network, developed by EU COM, for veterinary health which notifies, certifies and monitors imports, exports and trade in animals and animal products. Data from TRACES was extracted by Swedish Board of Agriculture.

Swedish Board of Agriculture (2022). Statistikdatabasen (available at 2022-03-25; https://statistik.sjv.se/PXWeb/pxweb/sv/Jordbruksverkets%20statistikdatabas)

Vattenbruk 2020, JO1201, SBA (available 2022-03-25 at: https://jordbruksverket.se/om-jordbruksverket/jordbruksverkets-officiella-statistik/jordbruksverkets-statistikrapporter/statistik/2021-08-31-vattenbruk-2020) (aquaculture)

Goats 2018; statistic report 2019:01, SBA (available 2022-03-25 at: https://jordbruksverket.se/om-jordbruksverket/jordbruksverkets-officiella-statistik/jordbruksverkets-statistikrapporter/statistik/2020-06-22-gethallning-2018)

Animal Register Unit, Swedish Board of Agriculture, communication by e-mail 2022-04-11 (goats 2021)

Horses and horse establishments in 2016, SBA (available 2022-03-25 at: https://jordbruksverket.se/om-jordbruksverket/jordbruksverkets-officiella-statistik/jordbruksverkets-statistikrapporter/statistik/2020-09-04-hastar-och-anlaggningar-med-hast-2016.-resultat-fran-intermittent-undersokning%23h-Rapport)

Livsmedelsverket, Fjäderfä statistik tillförda otjänligförklarade godkända 2021, (available 2022-03-16 by Livsmedelsverket) (statistics on poultry slaughter)

Sametinget (available 2022-03-25 at: https://www.sametinget.se/renstatistik) (statistics on reindeer)

Bitillsyn 2021 (available 2022-03-01 at: https://jordbruksverket.se/djur/ovriga-djur/bin-och-humlor%23h-Bitillsyn) (statistics on honeybees)

Databases used in animal surveillance

Figure 6: Registration of individual equine animals as well as the establishments where they are kept were introduced in 2021. Photo: Bengt Ekberg/SVA.

THE CENTRAL REGISTRY OF ESTABLISHMENTS

The Swedish Board of Agriculture is responsible for maintaining the Central Registry of Establishments (PLATS). All places where terrestrial animals are kept or where germinal products are collected, produced, processed or stored, except households where pet animals are kept and veterinary practices or clinics, must be registered as an establishment. Each establishment is assigned a unique registration number. It is required that the operators of establishments keeping terrestrial animals or collecting, producing, processing or storing germinal products register all information and all changes that occur at the establishment.

It is the responsibility of the operators of establishments keeping terrestrial animals or collecting, producing, processing or storing germinal products to fulfil the requirements and register according to the rules. The registry contains information on establishments for kept terrestrial animals and germinal products and laying hens. Details on unique registration number, address, type of production, capacity and the geographical coordinates of the establishments are included, as well as the name, address and telephone number of the operator among other information. All egg producers with a capacity of at least 350 laying hens must also register some extra information. The computer database contains specific information about production method, capacity and the number of houses and sections on the holding.

Every equine animal that is intended to be kept on one establishment for more than 30 days should also be registered at that establishment.

The computer databases are regulated through European and Swedish legislation: Regulation (EU) 2016/429, Delegated Regulation (EU) 2019/2035, Implementing Regulation (EU)2021/520 and The Swedish Board of Agricultures regulations SJVFS:2021:13., SJVFS 2016:25, Swedish Law SFS 2006:806, Swedish Regulations SFS 1999:1148, and SFS 2006:815. Owners of establishments with a capacity of at least 350 laying hens must register their establishment according to other kind of legislation, Directive 1999/74/EC and Directive 2002/4/EC and SJVFS 2003:20.

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 establishments with pigs, sheep and goats and their movements between establishments. The database contains information from the operators and the abattoirs, such as date of movement, address and unique registration number of the establishment as well as name and telephone number of the operator. 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 operator who dispatches the animals and the operator 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: Regulation (EU) 2016/429, Delegated Regulation (EU) 2019/2035, Implementing Regulation (EU) 2021/520 and The Swedish Board of Agricultures regulation SJVFS:2021:13.

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 computer database 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, 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 (EU) 2016/429, Delegated Regulation (EU) 2019/2035, Implementing Regulation (EU) 2021/520 and The Swedish Board of Agricultures regulation SJVFS:2021:13.

THE SLAUGHTER REGISTRY

The Slaughter Registry (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 registry is regulated through Swedish legislation (SJVFS 2016:25).

THE DATABASE OF DAIRY HERDS

The main national coordinating organisation for dairy and beef production is Växa (approved according to SJVFS 2015:17). 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 69% of all dairy herds in Sweden, covering approximately 66% 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.

CENTRAL AQUACULTURE REGISTRY

All aquaculture premises authorised by the County Administrative Boards are registered in the Central Aquaculture Registry. The registry 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 registry is regulated through European and Swedish legislation.

CENTRAL DATABASE OF THE INDIVIDUAL EQUINE ANIMALS

The Swedish Board of Agriculture is responsible for Central database of the individual equine animals (CHR). It contains data on Universal Equine Life Number (UELN) of each animal, chip number, birth date, name of the animal, breed society maintaining breeding books for purebred breeding animals of the equine species or organisation that do not manage a studbook but is authorised to issue horse passports where the animal is registered, if the animal is suitable for human consumption or not, among other information. There is a connection between every individual and the Central Registry of Establishments, by which it is possible to know on which establishment every individual animal is.

The computer database is regulated through implementing Regulation (EU) 2021/963.

SVALA

SVALA is the Laboratory Information Management System (LIMS) used at the National Veterinary Institute (SVA) 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.

REFERENCES

Erik Eriksson, SVA (SVALA)

Andrea Holmström, Växa (The Database of Dairy Herds)

Milan Mirosavljevic, 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.

The SBA promotes animal health through the prevention and control of contagious animal diseases. SBA is the competent authority for official controls on animal health and veterinary issues, 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. The 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.

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 web address of Swedish Food Agency is www.livsmedelsverket.se.

SWEDISH AGENCY FOR MARINE AND WATER MANAGEMENT

Swedish Agency of Marine and Water Management (SwAM) is responsible for managing the use and preventing the overuse of Sweden's marine and freshwater environments. SwAM takes into consideration the requirements of the ecosystem and people, both now and in the future. The agency does this by gathering knowledge, planning, and making decisions about actions to improve the environment. To be successful in these efforts, SwAM coordinates and establishes its efforts among everyone involved, both nationally and internationally. The wild fish surveillance programme and the programme for health and disease surveillance of marine mammals are commissioned by and financed from SwAM.

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 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.

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

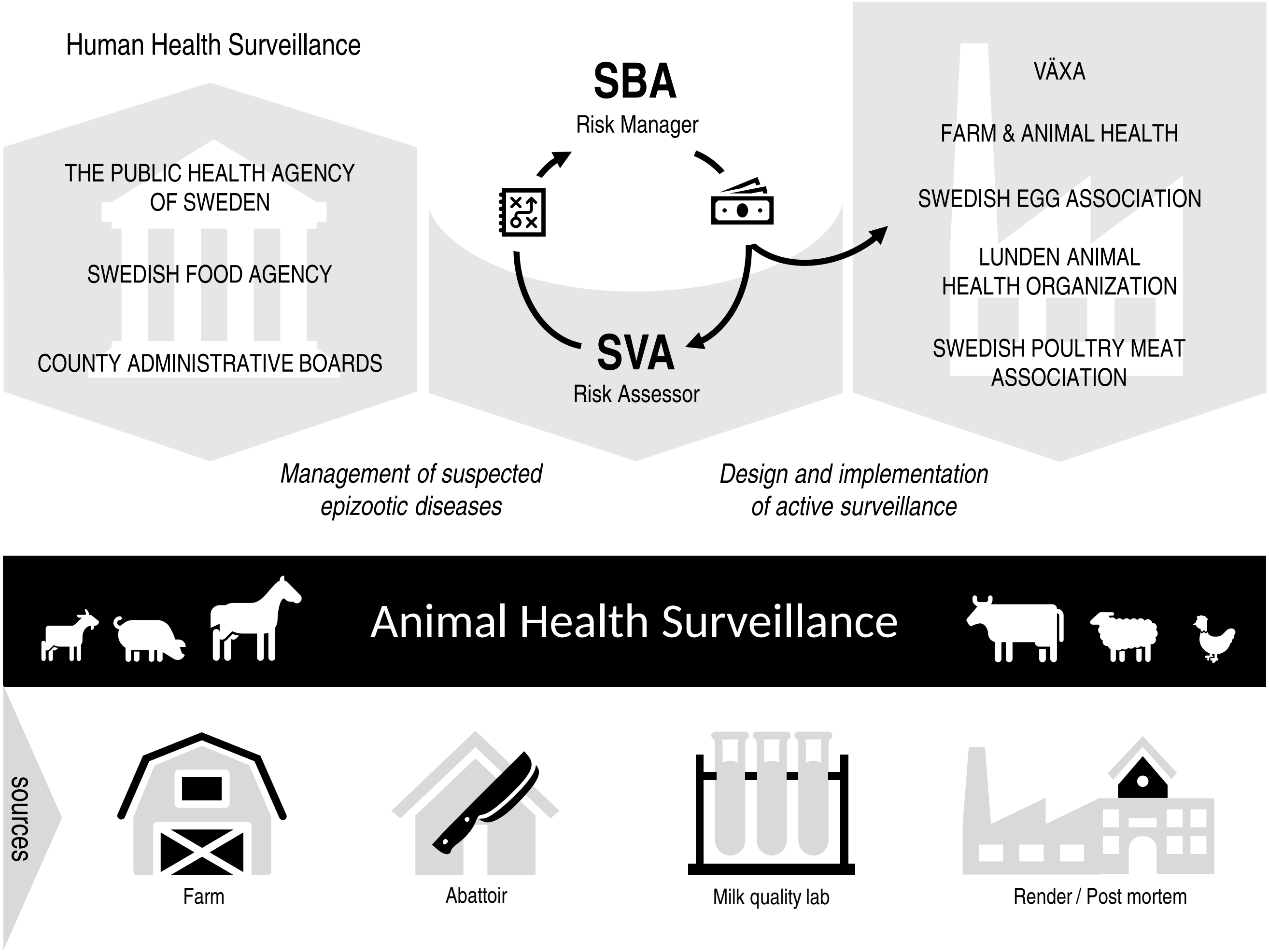

Figure 7: Roles, responsibilities and relationships between organisations involved in active surveillance in domestic livestock populations (cattle, pigs, poultry, sheep and goat), and their sources of animal health information. Infographic by Arianna Comin.

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.

VÄXA

Växa is Sweden's largest cattle farmers association, and their vision is a sustainable dairy and meat production with low antibiotic use and healthy animals. Växa is owned by 6000 farmers and provides a variety of advisory services for farmers.

Växa is a co-owner of the Nordic breeding company Viking Genetics and provides insemination and breeding advice. Växa also supports development of agricultural businesses through economic guidance as well as innovation by collaborations with universities and other stakeholders.

The organisation is responsible for the official milk recording scheme and lineage recording for dairy cows, Kodatabasen, which is managed in accordance to the Global Standard for Livestock Data (ICAR) recommendations). The database includes milk recordings, calvings, cullings, inseminations, registered observations at claw trimming 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 farmers, advisors 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.

Växa is the principal organiser of the surveillance programmes for bovine leucosis, infectious bovine rhinotracheitis and bovine viral diarrhoea virus. In addition, Växa is the organiser of a general biosecurity programme for cattle ("Smittsäkrad besättning"). 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.

Farm & Animal Health is an established stakeholder when it comes to national animal health surveillance as well as on-farm issues relating to disease control, animal health and animal welfare. Originating in the 1960s, the company has decades of experience conducting animal health care and control programs for pigs, cattle and sheep and the consulting services are available to all farmers.

Farm & Animal Health is assigned by the Swedish Board of Agriculture to implement specific disease control and surveillance programs. The company runs several control programs including the control of Footrot and Contagious Ovine Digital Dermatitis in sheep, Maedi-visna/caprine arthritis-encephalitis (CAE) in sheep and goats and Paratuberculosis (Johne's disease) in cattle, Biosecurity program for pigs and Tuberculosis monitoring program for camelids.

Farm and Animal Health is responsible for surveillance in place for maintaining the national disease status of Aujezky's disease (AD), Porcine reproductive and respiratory syndrome (PRRS) and paratuberculosis, where the latter two are covered by national regulations from 2021. The company also contributes to the maintenance of the Swedish *Salmonella* guarantees through collection of *Salmonella* samples on pigs and calves.

Furthermore, Farm and Animal Health coordinates the national postmortem services for livestock and runs four necropsy laboratories throughout Sweden. The postmortem services not only provide a valuable tool for individual veterinarians and producers in emergency and preventive disease interventions, but is also an important platform for disease surveillance and epizootic preparedness

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.

REFERENCES

Anders Wallensten, The Public Health Agency of Sweden

Andrea Holmström, Växa

Ebba Schwan, Farm & Animal Health

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Mikael Krysell, Swedish Agency of Marine and Water Management

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Pernilla Stridh, County Administration Östergötland (County Administrative Boards)

Surveillance of infectious diseases in animals and humans in Sweden 2020, National Veterinary Institute (SVA), Uppsala, Sweden. SVA:s rapportserie 68 1654-7098. (Lunden animal health organisation, The Swedish egg association)

Disease Surveillance 2021

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 decline in occurrence. 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. The programme is administered by the branch organisation Farm & Animal Health and diagnostic testing within the programme is performed at the National Veterinary Institute (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 2021:10.

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 2020, all 606 samples from 31 test occasions were negative regarding toxigenic *P. multocida*.

In 2021, samples from 27 herds were analysed. In addition, samples from eight batches of imported boars were analysed. Eight out of 24 boars in a batch imported from Norway tested positive in quarantine. When all boars were re-tested, two of the boars were still positive for *P. multocida* toxin (PMT). These two boars were culled and the remaining 22 boars were moved to a boar station as intended. Moreover, five out of 20 pigs in a multiplying herd tested positive for PMT. In a follow-up test scheme of the herd, it was concluded that PMT-positive pigs only were present in the age group initially tested. That group was allocated to a specialised fattening herd (to a dead end) instead of being sold as breeding stock to piglet producers. In a final test round of this herd, there were no positive samples and the herd was concluded to be healthy.

Table 2: The total number of samples and the outcome of laboratory analyses for *P. multocida* 2005–2021 at SVA. Nasal swab samples were collected from all nucleus and multiplying herds, as well as in production herds where clinical signs indicative of atrophic rhinitis (AR)were seen. When individual samples from a herd test positive, further sampling is performed in the herd to evaluate if the herd is truly affected, or can be 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
2021	767	11	3

Aujeszky's disease

Figure 8: In 2021, 2176 samples from 433 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.

BACKGROUND

Aujeszky's disease (AD) is caused by a herpes virus that has the capacity to infect many species, but for which 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.

LEGISLATION

AD is a listed disease (category C, D and E) in the Animal Health Law, (EU) 2016/429. Sweden is officially free from the disease in accordance with (EU) 2021/620 and surveillance to demonstrate freedom from AD is implemented in accordance with (EU) 2020/689. AD is notifiable on clinical suspicion as described in SJVFS 2021/10 (K12).

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, Uppsala, Sweden). Samples that test positive are analysed with a second ELISA (SVANOVIR® PRV-gE-AB/PRV-gE-Ak, Svanova, Uppsala, Sweden) 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 (SVA).

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 2021, 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 67), 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 2021, 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 boar" on page 121), with the exception of 2018 when testing was not undertaken due to a redistribution of funding.

RESULTS

Passive surveillance

In 2021, one clinical suspicion of AD was investigated. The investigation was prompted after the herd experienced an increase in piglet and weaned pig mortality, with several affected animals showing neurological signs prior to death. During the investigation, four piglets were examined by post-mortem and tissues samples 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 2021, 2176 samples from pigs from 433 herds taken on 726 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 2010–2021.

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
2021	2176	433

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 2021, the probability of freedom from AD was calculated and found to be >99%.

REFERENCES

Robertsson JÅ, Wierup M (2000) The eradication of Aujeszky's disease from pig production in Sweden. Vet Rec 31(1):152–153

Meier RK, Ruis-Fons F, Ryser-Degiorgis MP (2015) A picture of trends in Aujeszky's disease virus exposure in wild boar in the Swiss and European contexts. BMC Vet Res 11:277

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 has been carried out annually. Until 20th April 2021 according to Commission Regulation (EC) No 1266/2007 with amendments, and following that according to the Animal Health Law, Regulation (EU) 2016/429 and the Commission Delegated Regulation (EU) 2020/689.

Vector surveillance was initiated in 2007to 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 infection 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 may 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 surveillance, eradication programmes, and disease-free status for certain listed and emerging diseases are governed by Commission Delegated Regulation (EU) 2020/689. 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 (SVA) with the purpose of demonstrating sustained freedom from BTV in Swedish cattle.

Bluetongue virus infection cycle

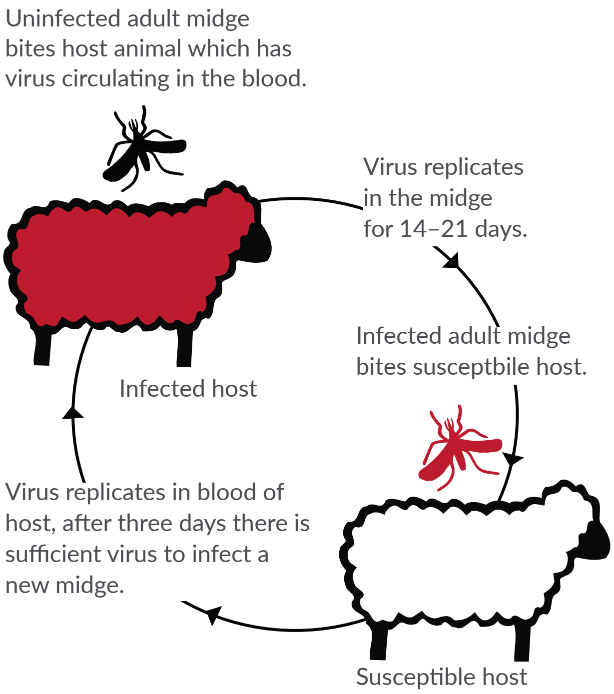


Figure 9: Transmission of Bluetongue virus involves insect vectors (midges) and a ruminant host. Virus replication in the midge is highly dependent on the surrounding temperature and is thought not to happen at all below 14°C. Infographic by Erika Chenais.

Bulk milk samples were analysed with an indirect ELISA (ID Screen Bluetongue Milk Indirect, Innovative Diagnostics, Grabels, France) and serum samples were analysed with a competitive ELISA (ID Screen Bluetongue Competition ELISA, Innovative Diagnostics, Grabels, France). For clinical suspicions, organs or blood were analysed with real-time pan-PCR detecting 27 serotypes.

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

Suspicions 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 2021 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 2021. 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 188 holdings were tested in the field surveillance, all with negative results. Three clinically suspect cases were investigated and tested during 2021 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 2021, 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. Recent research suggests the reappearance may have resulted from accidental release of virus originating from material, e.g. bull semen, that had been kept frozen since the time of the original outbreak. Between 2015 and 2020 several thousand cases (defined as animal found positive for BTV with real-time PCR) were reported by France every year. Most of these cases were animals found positive within active surveillance activities; few were 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. In 2021 only a handful of cases of BTV-8 were reported from France, three from Belgium and one from Germany. During 2021, 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 livestock 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.

REFERENCES

Pascall DJ, Nomikou K, Breard E, Zientara S, et al. 2020. “Frozen evolution” of an RNA virus suggests accidental release as a potential cause of arbovirus reemergence. PLoS Biology 18(4): e3000673

Hulten C, Frössling J, Chenais E, Sternberg Lewerin S. 2012. Seroprevalence after Vaccination of Cattle and Sheep against Bluetongue Virus (BTV) Serotype 8 in Sweden. Transboundary Emerging Diseases 60(5):438–47.

Ågren EC, Burgin L, Sternberg Lewerin S, Gloster J, Elvander M. 2010. Possible means of introduction of bluetongue virus serotype 8 (BTV-8) to Sweden in August 2008 - comparison of results from two models for atmospheric transport of the Culicoides vector. Veterinary Record 167:484–488

Sternberg Lewerin S, Hallgren G, Mieziewska K, Treiberg Berndtsson L, Chirico J, Elvander M. 2010. Infection with bluetongue serotype 8 in Sweden 2008. Veterinary Record 167:165–170

Nielsen SA, Nielsen BO, Chirico J. 2009. Monitoring of biting midges (Diptera: Ceratopogonidae: Culicoides Latreille) on farms in Sweden during the emergence of the 2008 epidemic of bluetongue. Parasitology Research 106:1197–1203

Bovine spongiform encephalopathy

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 United Kingdom 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 banned, 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 including the removal of specified risk material (such as brain and spinal cord) from cattle at slaughter and restrictions related to feed, to avoid recycling of infectious material to ruminants through infected MBM. It also included 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. This due to an early ban on the use of fallen stock in the production of livestock feed as well as 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.

Figure 10: Classical bovine spongiform encephalopathy has never been detected in cattle in Sweden. Photo: Mia Holmberg.

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

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 farm level and further 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 the responsible authorities. Samples are selected 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 (SVA), which also is the National Reference Laboratory (Regulation (EC) 999/2001). Samples are analysed at SVA.

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 clinical 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 the TeSeE^{TM} SAP Combi kit (short assay protocol; Bio-Rad Laboratories, Hercules, California, United States). In case of positive or inconclusive results, the material is prepared and examined with the TeSeE^{TM} Western Blot kit (Bio-Rad Laboratories, Hercules, California, United States).

Clinical suspicions 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 in 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 on antemortem inspection at slaughter, or are emergency slaughtered.
- Cattle of other than Swedish origin above 24 months of age that have remarks on antemortem inspection at 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. Fallen stock are sampled by employees at the rendering plants, or by veterinarians or veterinary assistants at post mortem examinations.

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

RESULTS

Feed

In 2021, 19 feed samples were taken at feed mills; 18 of these were from feed (12 were cattle feed) and one from raw material for feed production. All of these samples were negative for PAP, except two samples of pig feed which contained fish particles.

Animals

Passive surveillance

In 2021, 13 bovines were examined due to clinical suspicion, all with negative results.

Active surveillance

In 2021, 8564 samples were examined for BSE. All samples were negative. Of these samples 8378 were from fallen stock, 14 samples were from animals with remarks on antemortem inspection at slaughter and 159 samples were from emergency slaughtered animals.

DISCUSSION

No cases of BSE were detected in Sweden in 2021. The increased number of clinical suspicions in the past four years compared to previous years is the result of substantial efforts made to detect and notify authorities of animals with clinical signs that could be compatible with BSE. Previously there has been a long trend of a decreasing number of clinical suspicions when compared to the years of the peaks of the BSE crisis. This can be explained by a lesser degree of awareness among farmers and veterinarians when media reporting on the disease is reduced.

The source of the large classical BSE epidemic of has not been determined and atypical cases cannot be excluded as the source. Atypical cases could hence be a potential source of a new epidemic. As the number of cases of classical BSE is decreasing within the EU, surveillance is also declining. Suggestions have been made to once again allow the use of MBM and processed animal protein (PAP) in feed within the EU. However, strict separation of feed materials during production, to avoid cross-contamination, and bans of these feeding practices must be kept in place. This to avoid any possibility of BSE-prions recirculating, if the disease agent was to enter the feed 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 the 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 the preventive measures, resulting in a significant decrease of cases of classical BSE on a European and global level, a revision of the current surveillance requirements on EU and OIE-levels 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 the potential recirculation of prions is still relevant to avoid a new BSE crisis.

REFERENCES

Gavier-Widén D, Nöremark M, Langeveld JP, Stack M, Biacabe AG, Vulin J, Chaplin M, Richt JA, Jacobs J, Acín C, Monleón E, Renström L, Klingeborn B, Baron TG (2008) Bovine spongiform encephalopathy in Sweden: an H-type variant., J Vet Diagn Invest 20:2–10.

Capobianco R, Casalone C, Suardi S, Mangieri M, Miccolo C, Limido L, Catania M, Rossi G, Di Fede G, Giaccone G, Bruzzone MG, Minati L, Corona C, Acutis P, Gelmetti D, Lombardi G, Groschup MH, Buschmann A, Zanusso G, Monaco S, Caramelli M, Tagliavini F (2007) Conversion of the BASE prion strain into the BSE strain: the origin of BSE? PLoS Pathog 3(3):e31.

EFSA Panel on Biological Hazards, 2004. Scientific Report of the European Food Safety Authority on the Assessment of the Geographical BSE Risk (GBR) of Sweden. EFSA Journal 2004; 2(8):RN-7, 27 pp. https://doi.org/10.2903/j.efsa.2004.7r

Requena JR, Kristensson K, Korth C, Zurzolo C, Simmons M, Aguilar-Calvo P, Aguzzi A, Andreoletti O, Benestad SL, Böhm R, Brown K, Calgua B, Del Río JA, Espinosa JC, Girones R, Godsave S, Hoelzle LE, Knittler MR, Kuhn F, Legname G, Laeven P, Mabbott N, Mitrova E, Müller-Schiffmann A, Nuvolone M, Peters PJ, Raeber A, Roth K, Schmitz M, Schroeder B, Sonati T, Stitz L, Taraboulos A, Torres JM, Yan ZX, Zerr I. The Priority position paper: Protecting Europe's food chain from prions. Prion. 2016 May 3;10(3):165–81.

Bovine viral diarrhoea

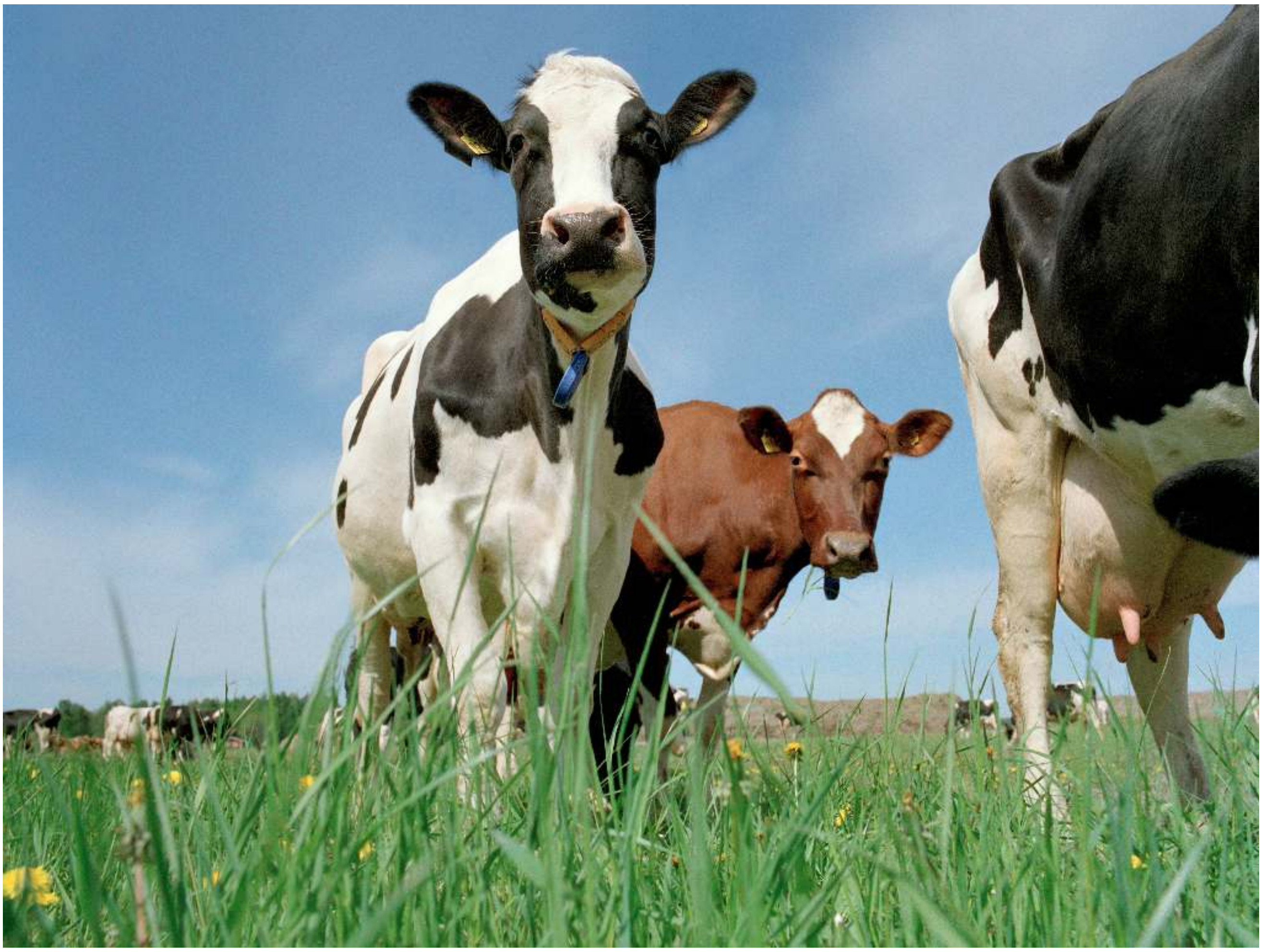


Figure 11: The fact that Sweden has been free from bovine viral diarrhoea since 2014 is very important for cattle health in the country. Photo: Bengt Ekberg/SVA.

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. 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. Sweden has been considered free from BVD since 2014.

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 listed disease (category C, D and E) in the Animal Health Law (EU) 2016/429. Since 2022 Sweden is officially free from the disease in accordance with (EU) 2021/620. BVD is notifiable on clinical suspicion as described in SJVFS 2021/10 (K12).

During the reporting year for this report, 2021, the voluntary control was regulated through SJVFS 2015:17 and the compulsory control regulated 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 (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.

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

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

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 2021 are given in Tables 5 and 6.

Table 5: Total numbers of samples with different contents of bovine viral diarrhoea virus antibodies tested in 2021.

Sample type	Class/Finding	Herds	Animals
Bulk milk	0–1[A]	2432	-
Bulk milk	2–3[A]	0	-
Blood sample at slaughter	Negative	-	6609
Blood sample at slaughter	Positive	-	4
Field sample	Negative	-	0
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)

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

Table 6: Dairy and beef herd results from testing of bovine viral diarrhoea virus antibodies in bulk milk or blood samples in 2021 divided by herd level risk.

		Production type	
Herd level risk[A]	Herd numbers (N)	Dairy	Beef
Low risk	N of herds	1528	7615
	N of herds tested	656	1617
	N positive	0	2
Medium risk	N of herds	1086	2087
	N of herds tested	1074	958
	N positive	0	0
High risk	N of herds	285	579
	N of herds tested	278	260
	N positive	0	1

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

RESULTS

The outcome of antibody testing of bulk milk, slaughter, and field samples tested in 2021 is given in Table 5. As shown in Table 5, four blood samples from slaughtered cattle from three herds (Table 6) were antibody positive during the year. The positive blood samples came from older animals that had been infected as young and had also been previously tested as antibody positive. In 2021, 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 2021. At the end of the year, no herd was diagnosed as having an ongoing BVDV-infection. During 2021, the Swedish Board of Agriculture applied for official declaration of freedom from BVD to the EU Commission, and in February 2022 Sweden was declared free from the disease. Hence, there will no longer be a compulsory BVDV programme. Continued surveillance to demonstrate freedom from the disease will continue as regulated in (EU) 2020/89.

REFERENCES

Växa, Statistics for 2021.

Niskanen, R. (1993). Relationship between the levels of antibodies to bovine viral diarrhoea virus in bulk tank milk and the prevalence of cows exposed to the virus. Vet Record 133: 341–344.

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 not been reported from Sweden since 1957. Brucellosis in humans has been a notifiable disease in Sweden since 2004. Between 4 and 19 human cases have been reported annually, the majority of these 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%.

Figure 12: *Brucella melitensis* is common in many countries in southern and eastern Europe. Photo: Erika Chenais.

LEGISLATION

Animals

Brucellosis caused by infection with *Brucella abortus, B. melitensis* or *B. suis* is a listed disease (category B, D and E in cattle, sheep and goats, and D and E in pigs and other cloven-hoofed mammals) in the Animal Health Law, (EU) 2016/429. Sweden is officially free from infection with *Brucella abortus, B. melitensis* or *B. suis* in cattle, sheep and goats in accordance with (EU) 2021/620, and surveillance to demonstrate freedom is implemented in accordance with (EU) 2020/689. Brucellosis (here defined as infection with *Brucella abortus, B. melitensis*, *B. suis* or *B. ovis)* in food-producing animals is included in the Swedish Act of Epizootic diseases (SFS 1999:657 with amendments) and notifiable as described in SJVFS 2021/10 (K12). Brucellosis (also including infection with *B. canis)* 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 2022:217).

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 (SVA). Since the start of the screenings, no samples have been confirmed positive. All diagnostic testing is performed at SVA. Bovine samples (serum and milk) are tested with an indirect ELISA (IDEXX Brucellosis Serum Antibody Test Kit, IDEXX Laboratories, Westbrook, Maine, United States), 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 135) 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.

Passive surveillance

Animals

Suspicions 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 foetuses of ruminants and pigs, see the chapter “Examinations of abortions in food producing animals” (page 135).

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 2021. 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 2021 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, this sampling was performed in 2021. Serum samples are collected at slaughter 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 2021, three clinical suspicions of brucellosis were reported in food-producing animal species and one in wild boar.

Within the surveillance of aborted foetuses, 22 bovine, 26 ovine, no caprine, and 14 porcine foetuses were examined for *Brucella* spp. All samples were negative.

Humans

In 2021, ten 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 57 years, spread 25–78 years, four female cases) were comparable with previous years. Two cases were reported to have acquired their infections in Iraq, two in Somalia, one in Afghanistan and one in Ethiopia and for three cases the country of infection was unknown. There was one domestic case reported for which the source of infection was never established. For five 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. One isolate was resistant to streptomycin, while the rest were sensitive to the antibiotics commonly used for treating brucellosis.

Active surveillance

Animals

During 2021, 2052 ovine and caprine serum samples from 422 individual holdings were analysed for *B. melitensis.* All these samples were negative, assuring sustained freedom from *B. melitensis* in the ovine and caprine population. 717 porcine serum samples from 431 individual holdings were analysed for *B. suis.* As samples are taken at slaughter some holdings were sampled several times, but on different occasions. All these samples were negative, assuring sustained freedom from *B. suis* in the porcine 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 2021. 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 ten 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

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.

During 1997–2019 the incidence of human campylobacteriosis in Sweden has varied between 65 and 110 cases per 100 000 inhabitants (Figure 13). 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 in 2020–2021 and a record high proportion of domestic infections in relation to infections retrieved abroad in 2020–2021.

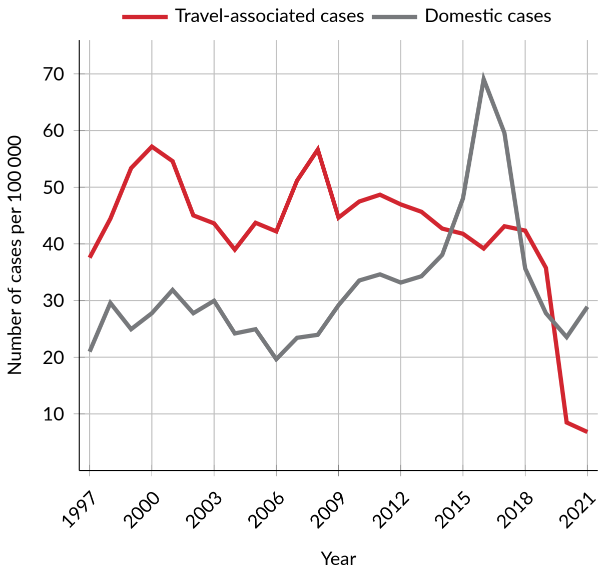


Figure 13: Incidence (per 100 000 inhabitants) of notified human cases of campylobacteriosis in Sweden, 1997–2021. Travel-associated cases are those where the patient has reported travel to another country during the incubation period prior to clinical presentation. Domestic cases are patients that have not recently travelled outside Sweden.

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.

LEGISLATION

Animals

Findings of thermophilic *Campylobacter* spp. in meat-producing poultry are notifiable in Sweden, according to SJVFS 2021:10. 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 abattoirs are obliged to sample neck skins of broilers for quantitative analyses of *Campylobacter* according to regulation (EG) 2073/2005 on microbiological criteria for foodstuffs. 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 2022:217). 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 2021, the guidelines for the programme were reviewed.

The programme covers more than 99% of the broilers slaughtered in Sweden. Since 2006, sampling is performed

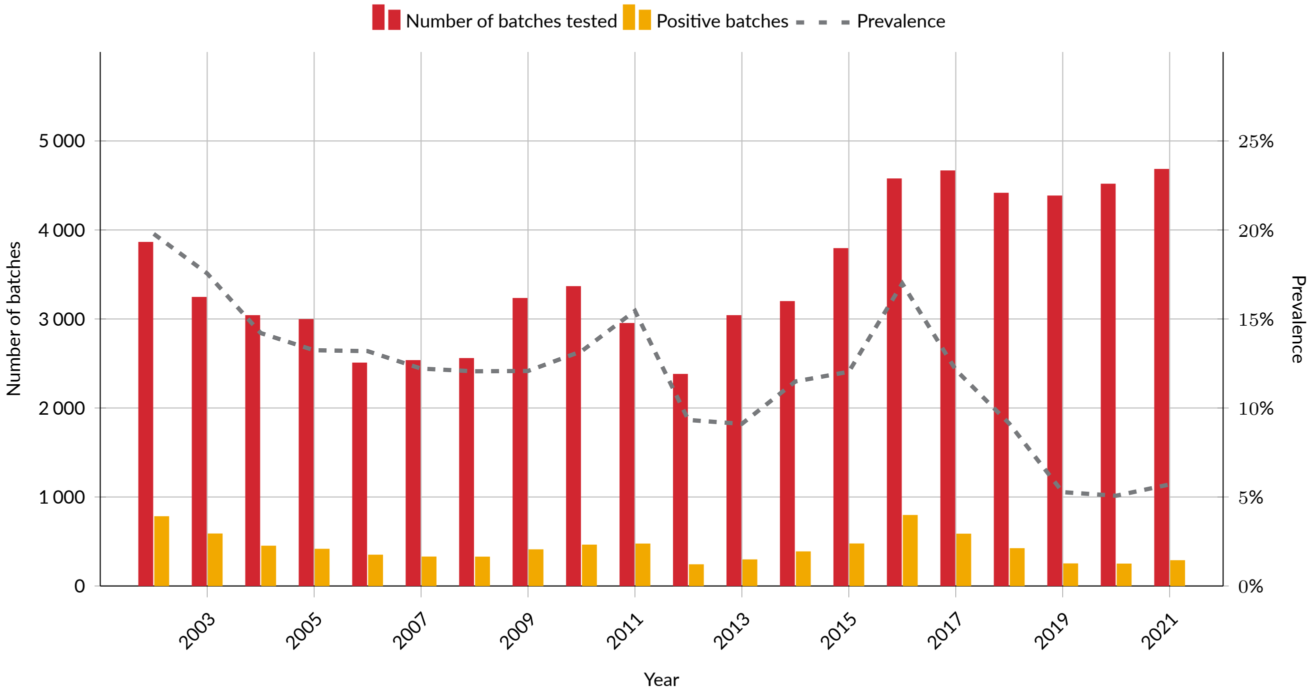


Figure 14: Prevalence of *Campylobacter* in slaughter batches of broiler chicken in 2002–2021.

by collecting intact caeca from 10 birds per sampled slaughter batch at the major abattoirs. In 2021, seven abattoirs 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 for detection of *Campylobacter* spp. according to EN ISO 10272-1.

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, abattoirs 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. Since 2020, the regulation has 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.

During 2017–2021, the Public Health Agency of Sweden have requested isolates from all domestic cases reported during selected periods of weeks (in March and in August) for WGS analysis. 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 2021, thermophilic *Campylobacter* spp. were detected in 266 (5.7%) of the 4662 broiler chicken batches tested at slaughter (Figure 14), which is at the same level as in 2020 and less than in years prior to 2020. Among the slaughter batches at the four largest abattoirs, which cover 97.5% of the slaughtered chicken, *Campylobacter* spp., was detected in 4.9% of them. The monthly prevalence of *Campylobacter* in chicken slaughter batches varied between 0.8% (March) and 14.2% with the highest prevalence in July (Figure 15). The prevalence of *Campylobacter* in incoming batches varied between abattoirs. The monthly number of chickens from *Campylobacter* positive slaughter batches varied as well.

IN FOCUS: Antimicrobial resistance in *Campylobacter* — comparison between isolates from chicken meat and from Swedish patients

A total of 103 *Campylobacter jejuni* isolates from meat, and 272 isolates from patients, were collected and sequenced in 2018 and 2019.

Antimicrobial resistance of all isolates was assessed by bioinformatics analysis of sequencing data at the Public Health Agency of Sweden and Swedish Food Agency. The aim was to investigate the presence of described genetic determinants (genes and chromosomal mutations) encoding antimicrobial resistance in *Campylobacter*. A further aim was also to investigate the extent to which different resistance determinants of *Campylobacter* from chicken meat and from patients overlap, and whether related *Campylobacter* from these two sample types could be linked to a certain antimicrobial resistance profile.

In 67 (85%) of the 79 isolates of *C. jejuni* from Swedish chicken meat, no mutations or genes encoding resistance to the clinically important antimicrobial classes macrolides, quinolones, tetracyclines, or aminoglycosides were identified, whereas 14 (58%) of the 24 isolates from meat obtained from other countries lacked such resistance determinants. For *C. jejuni* from patients, 162 (76%) of the 212 isolates from domestically acquired infections and 11 (21%) of the 53 isolates from travel-related cases contained no such determinants. None of the isolates from either meat or patients contained determinants for resistance to macrolides, which are first-line antimicrobials in Sweden to treat severe *Campylobacter* infections. Multidrug resistance, i.e., determinants for at least three of these classes of antimicrobials, was identified only in three isolates from patients, two of whom had likely been infected abroad.

The overall most common resistance determinant in isolates from both chicken meat and patients was bla_{OXA} genes for resistance to beta-lactams, which are not recommended for treatment of *Campylobacter* infections. The most prevalent resistance determinant identified among the clinically important antimicrobial classes was the gyrA_T86I mutation, which confers resistance to quinolones, followed by the tetracycline resistance gene tet(O) and the aminoglycoside resistance gene aph(3')-IIIa.

The same types of determinants for resistance to clinically important antimicrobials were identified in isolates from both chicken meat and patients, regardless of origin, or where the infections were acquired, respectively. However, the determinants were most frequently identified in isolates from patients infected abroad, followed by chicken meat from other countries. One of the reasons for the relatively higher proportion of antimicrobial resistance in *C. jejuni* from such meat and this type of patient could be the generally lower usage of antimicrobial drugs in Sweden compared to other countries, both in food-producing animals and in humans.

Food

In 2021, national and local authorities took 49 samples from different types of food. *Campylobacter* was detected in one sample taken at retail within routine control. The sample was from fresh broiler meat.

Food business operators at seven abattoirs collected 1046 pooled neck skin samples according to regulation (EC) No. 2073/2005. Test results at all abattoirs were satisfactory according to the legislation, and only 15 (1.4%) of the 1046 samples exceeded the limit of 1000 CFU/g.

Humans

A total of 4059 cases of campylobacteriosis were reported in 2021. Of the reported cases, 75% (3025 cases) were domestic. The incidence of domestic cases was 28.9 per 100 000 inhabitants, an increase with 23% from the year before. The incidence of travel-related cases was a record low, 6.8 cases per 100 000 inhabitants, a decrease by 20% which makes the overall incidence the second lowest (33.1) since the current reporting system was introduced in 1997 (Figure 13). The reported domestic cases followed the typical yearly pattern with more cases during the summer months, peaked in July and August during 2021 when 39% (n=1184) of all domestic cases were reported. Very few travel-related cases were reported during the first half of the year, a minor increase from July-December, but still to a very low level compared to before 2019 and before the COVID-19 pandemic.

For the domestic cases in 2021, the median age was 49 years with a range from 0–98 years. The incidence was highest in the age group 50–69 years followed by 1–4 years, both of which are age groups that historically tend to have comparatively high proportions of cases. More men (55%) than women were reported with campylobacteriosis.

In the microbial surveillance programme at the Public Health Agency of Sweden, isolates from human cases were collected during weeks 34–37. A total of 293 isolates were characterised and 46% (n=135) were included in 26 tight genetic clusters. The diversity was high and 85 different sequence types (ST) were identified. Isolates from domestically infected patient isolates (n=257) were compared with domestic chicken isolates (n=89) from the same time span. Of the patient isolates, 22% (n=56) were included in 12 tight genetic clusters with chicken isolates (n=25) consisting of 12 different sequence types (ST) where the largest cluster belonged to ST 7516.

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 2021. 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 15).

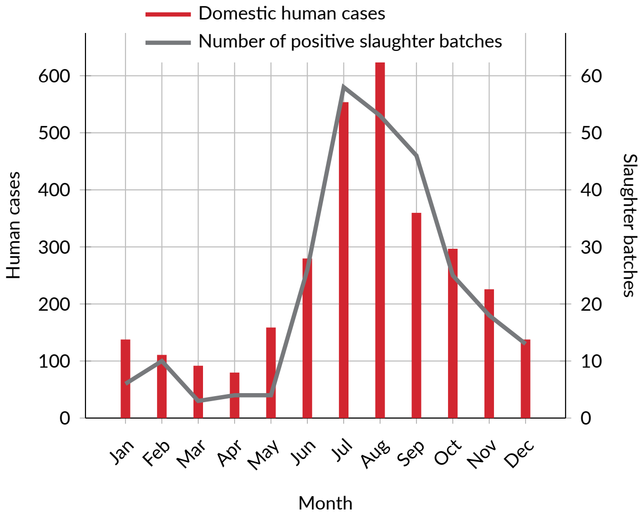


Figure 15: Number of notified domestic cases of human campylobacteriosis, along with the number of broiler batches positive for Campylobacter, broken down per month in 2021.

OUTBREAKS

From having been at low levels in the beginning of the year, a large increase in the number of people infected with *Campylobacter* was noticed in June with a peak in July-August. Also, in the surveillance programme in chickens, a higher prevalence was noted during the period July–October. In 2021, it was not possible to identify a specific dominating genotype or cluster of *Campylobacter* found both in human and chicken isolates as shown in earlier years. The ST-clusters were dispersed and no specific abattoir was found to be responsible for the majority of cases during the sampling period in August. However, the STs with high numbers of human cases in clusters were also common STs in chickens and overlapped in sampling period. About 20% of clusters were found in both chickens and humans during the period of four weeks: weeks 34–37. The largest human cluster was a new ST 7516, which also was detected in five sequenced chicken isolates in 2021. The sampling period restricted to four weeks does not give the full picture, and other unknown sources of infections are probably also responsible for some of the domestic cases.

DISCUSSION

The domestic incidence of campylobacteriosis was low in 2021 compared to the period 2009–2019, but higher than 2020. 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 were part of outbreaks. Many of these outbreaks appear genetically linked to isolates from retail poultry meat.

In 2021, the annual prevalence of *Campylobacter* in chicken slaughter batches was at the same level as in 2020 but lower than in previous years (Figure 14). The correlation between human cases of campylobacteriosis and *Campylobacter*-positive broiler batches further underscores the need for preventive measures. *Campylobacter* prevalence varies considerably between abattoirs, 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 on 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 abattoirs concerned. The results show that no abattoir in Sweden had any difficulties in meeting the process hygiene 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 as well as the measures taken at slaughter decreases the risk of human infection. 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 the 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.

REFERENCES

Folkhälsomyndigheten (2019) Mikrobiologisk övervakning av campylobacter. https://www.folkhalsomyndigheten.se/mikrobiologi-laboratorieanalyser/mikrobiella-och-immunologiska-overvakningsprogram/overvakning-av-campylobacter/.

Livsmedelsverket, Folkhälsomyndigheten. Dryselius R, Jernberg C (2019) S 2019 nr 01: Campylobacter från butik och klinik. Livsmedelsverkets samarbetsrapport, Uppsala

Newell DG, Elvers KT, Dopfer D, Hansson I, Jones P, James S, Gittins J, Stern NJ, Davies R, Connerton I, Pearson D, Salvat G, Allen VM (2011) Biosecurity-based interventions and strategies to reduce *Campylobacter* spp. on poultry farms. Appl Environ Microbiol 77:8605–8614

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 30 states in the USA, and in four Canadian provinces (USGS, 2022). 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 (April 2022) resulted in the detection of the disease in 20 reindeer in two different wild reindeer areas. In addition, CWD has been found in 11 elderly moose (*Alces alces*) and in three 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, positive lymph nodes, although not identical. The cases in moose and red deer have been shown to differ from the cases in reindeer (cases found in older animals, samples test positive in the brain but negative in the lymph nodes). 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 cases may be spontaneously occurring in older animals (Pirisinu et al., 2018). The cases in moose are sometimes referred to as “atypical”, as they differ from previously described cases.

Due to the detection of CWD in Norway, surveillance for CWD was mandatory in several EU member states, including 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 of age, was detected within the intensified sampling. Although shot during the normal hunting, the moose was showing altered behaviour and standing still in a mire.

Figure 16: The EU-regulated surveillance of chronic wasting disease (CWD) finished in 2021 but the passive clinical surveillance continues. Photo: SVA.

The fourth 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. When approached by hunters, she did not attempt to escape. The moose was positive in the brainstem sample but negative in the lymph nodes.

These cases all showed 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 cross the border between the countries as part of seasonal migration, i.e., the cervid populations in Sweden and Norway are not separated by geographical borders.

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 investigation 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 (i.e., without known cause) 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 to not 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 and owners 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

Passive surveillance

Since 2016, efforts have been made to increase awareness among hunters, reindeer owners and owners of farmed deer to notify and react on suspected clinical signs of CWD.

Active surveillance

The time-limited EU-regulated surveillance programme, mentioned under "Legislation" above, started in January 2018. For the member states concerned, a minimum of 6000 animals were to be tested between the years 2018 and 2020. Samples were collected from wild, semi-domesticated and farmed/captive cervids. In Sweden, moose, red deer, roe deer and reindeer were included in the surveillance programme. Samples from wild cervids (moose, red deer, roe deer) were collected from fifty primary sampling units (PSU) covering the whole country. Samples from farmed cervids (red deer) and semi-domesticated cervids (reindeer) were collected from all red deer farms (n=137) 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 were over twelve months of age and preferably from a risk category, i.e., cervids found dead or diseased or road/train killed cervids which are assumed to have a higher probability of infection. Because the sampling target had not been reached by the end of 2020, the surveillance was extended throughout 2021.

Intensified active surveillance

In accordance with EU legislation, an intensified sampling was carried out in the areas surrounding the previously positive cases. The size of the areas 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 slaughtered and healthy hunted animals were included to increase the number of animals that were tested in the area. In 2019–2021 (moose 2019–2020, reindeer 2019–2021) intensified sampling was done around the cases detected in Arvidsjaur and Arjeplog and in 2020–2021 Robertsfors was included. The 2018–2020 CWD surveillance programme was run in a collaboration between the National Veterinary Institute (SVA) and the Swedish Board of Agriculture and was financed by the latter.

All samples, from the passive surveillance as well as the active and intensified surveillance, are analysed at SVA, Uppsala, which also is the national reference laboratory (Regulation (EC) 999/2001) for TSEs. For analysis, brainstem and retropharyngeal lymph node samples are screened separately with the TeSeE^{TM} SAP Combi kit (short assay protocol; Bio-Rad Laboratories, Hercules, California, United States), using the CWD addendum. The TeSeE ^{TM} Western Blot kit (Bio-Rad Laboratories, Hercules, California, United States) is used for confirmation of positive or inconclusive screening results. Test results are reported to the European Food Safety Authority by the Swedish Board of Agriculture, based on data provided by SVA.

RESULTS

The number of samples tested from 2016 to 2021 is detailed in Table 7.

In 2021, 17 cervids were sampled due to a clinical suspicion of CWD (11 moose and 6 roe deer). In total, 433 moose, 290 red deer, 63 roe deer, 3 fallow deer and 2527 reindeer were examined for CWD at SVA during 2021. 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 2021, 1485 reindeer and 1 moose were sampled within the intensified sampling in Norrbotten and 283 moose and 9 reindeer were sampled within the intensified sampling in Västerbotten. No positive cases were found during 2021. Further analysis of the surveillance results is ongoing on both a national and a European level.

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 and 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 cervids is quite high in Sweden and was initially planned to constitute the backbone of the surveillance. However, divergent interpretations of legislation made sampling of these animals difficult or even impossible. Work has been ongoing to ease this legislation to allow for the routine sampling of road kills. Since the sampling targets were not reached the national surveillance was prolonged during 2021, with the aim to collect more samples in general and a hope that the problem with road kills would have been solved. This resulted in an overall increase in the number of samples, however the problem with legislation was not solved and the sampling target was not reached.

In contrast, sampling of healthy hunted moose and healthy slaughtered reindeer within the intensified surveillance has been more successful despite logistical challenges.

As mentioned, the cases in moose in Norway, Finland and Sweden differ from "classical" CWD cases; all have been detected in old female animals and prions have only

Table 7: The number of animals tested for CWD per year in Sweden 2016–2021, 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}
2021	433^{B}	290	63	3	2527^{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 and 283 of the moose sampled in 2020 and 2021, respectively, were sampled within the intensified sampling in the county of Västerbotten.

[C] 896 and 1485 of the reindeer sampled in 2020 and 2021 respectively were sampled within the intensified sampling in the county of Norrbotten.

been detected in samples from the brain and not in lymph nodes. Further studies are ongoing to characterise these strains and to understand more about the epidemiology. 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 the screening tests, while not in lymph nodes, still fits the hypothesis of spontaneous (without known cause) 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 a type of CWD with the characteristics of "classical" CWD would be present or introduced into Sweden, it would potentially 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 (without known cause) 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.

REFERENCES

U.S. Geological Survey and Centers for Disease Control and Prevention, https://www.cdc.gov/prions/cwd/occurrence.html https://www.usgs.gov/media/images/distribution-chronic-wasting-disease-north-america-0 (accessed 2022-05-05)

Benestad SL, Mitchell G, Simmons M, Ytrehus B, Vikøren T (2016) First case of chronic wasting disease in Europe in a Norwegian free-ranging reindeer. Vet Res 47:88

Pirisinu L, Tran L, Chiappini B, Vanni I, Di Bari MA, Vaccari G, Vikøren T, Madslien KI, Våge J, Spraker T, Mitchell G, Balachandran A, Baron T, Casalone C, Rolandsen CM, Røed KH, Agrimi U, Nonno R, Benestad SL (2018) Novel Type of Chronic Wasting Disease Detected in Moose (Alces alces), Norway. Emerg Infect Dis 24:2210–2218

Ruokavirasto, https://www.ruokavirasto.fi/viljelijat/elaintenpito/elainten-terveys-ja-elaintaudit/elaintaudit/luonnonvaraiset-elaimet/hirvielainten-naivetystauti-cwd/ (accessed 2020-03-16)

VKM (2016) CWD in Norway. Opinion of the Panel on biological hazards, ISBN: 978-82-8259-216-1, Oslo, Norway

VKM (2017) CWD – update statement. Opinion of the Panel on biological hazards, ISBN: 978-82-8259-283-3, Oslo, Norway

Vikøren T, Våge J, Madslien KI, Røed KH, Rolandsen CM, Tran L, Hopp P, Veiberg V, Heum M, Moldal T, Neves CGD, Handeland K, Ytrehus B, Kolbjørnsen Ø, Wisløff H, Terland R, Saure B, Dessen KM, Svendsen SG, Nordvik BS, Benestad SL. First Detection of Chronic Wasting Disease in a Wild Red Deer (Cervus elaphus) in Europe. J Wildl Dis. 2019 Oct;55(4):970-972. Epub 2019 Mar 28. PMID: 30920905

Waddell L, Greig J, Mascarenhas M, Otten A, Corrin T, Hierlihy K (2018) Current evidence on the transmissibility of chronic wasting disease prions to humans-A systematic review. Transbound Emerg Dis 65:37–49

Ågren EO, Sörén K, Gavier-Widén D, Benestad SL, Tran L, Wall K, Averhed G, Doose N, Våge J, Nöremark M. First Detection of Chronic Wasting Disease in Moose (Alces alces) in Sweden. J Wildl Dis. 2021 Apr 1;57(2):461-463. doi: 10.7589/JWD-D-20-00141. PMID: 33822167

Classical swine fever

Figure 17: 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 2021, 2131 pigs were tested and found negative for the disease. Photo: Bengt Ekberg/SVA.

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°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 a listed disease (category A, D and E) in the Animal Health Law, Regulation (EU) 2016/429. The disease is notifiable on clinical suspicion as described in SJVFS 2021/10 (K12).

SURVEILLANCE

The purpose of the surveillance for CSF is to ensure early detection in case of an introduction to the Swedish pig population and thus to contribute to the maintenance of freedom from the disease. The National Veterinary Institute (SVA) 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 SVA. CSF serology is done using a commercial kit (IDEXX HerdChek® CSFV Antibody Test Kit, IDEXX Laboratories, Westbrook, Maine, United States) 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 typically 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 135).

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 2021, 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 67), 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 boar" on page 121).

RESULTS

Passive surveillance

Four herd investigations following clinical suspicions of CSF in domestic pigs were carried out during 2021. In two herds, the primary clinical sign was the sudden, unexplained death of multiple animals within a short period of time. In one herd, findings during a postmortem examination, including haemorrhages in multiple organs, prompted the herd investigation. In one herd, an increase in the number of abortions and sows with bluish skin discolouration initiated the CSF investigation. During all investigations, 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, 14 foetuses from 11 herds were examined for the presence of CSF virus genome and all samples were negative.

Active surveillance

Serum samples from 2131 domestic pigs were analysed for the presence of antibodies for CSF in 2021. All samples were negative. Taking the surveillance outcome from previous years into account, the probability of freedom from CSF during 2021 was >99%.

DISCUSSION

The results from the active and passive surveillance for CSF in Sweden in 2021 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.

REFERENCES

Postel A, Austermann-Busch S, Petrov A, Moennig V, Becher P (2018) Epidemiology, diagnosis and control of classical swine fever: recent developments and future challenges. Transbound Emerg Dis. 65:248–261

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 transmissive 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 to 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.

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. Beginning 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 2022:217.

RESULTS

Humans

In 2021, a total of 524 cryptosporidiosis cases were reported corresponding to an incidence of 5.0 cases per 100 000 inhabitants. (Figure 18). Among reported cases the median age was 36 years (0–97 years) and 59 percent were women (n=308/5241). In 2021, the majority of cases were reported infected in Sweden (n=411), 83 cases were infected abroad and for 30 cases information was missing. Nearly half of the reported domestic cases (49%) were reported during July-October (n=201) and most in August (n=70). A peak is usually seen especially in late summer. Many domestic cases were also reported in January (n=42) due to a local outbreak with vegetables as the suspected source of infection. Out of 83 travel-related cases, 58% (n=48) were reported July-September. Due to COVID-19 restrictions the incidence of travel-related cases was low with 1.8 per 100 000 inhabitants. The most common destination was Somalia (n= 11) followed by Pakistan (n=7) and Ethiopia (n=7).

As part of the microbiological surveillance program 155 *Cryptosporidium* positive samples were further analysed for species and subtype. The majority of samples were *C. parvum* (82 %; n=128). The second most common cause of

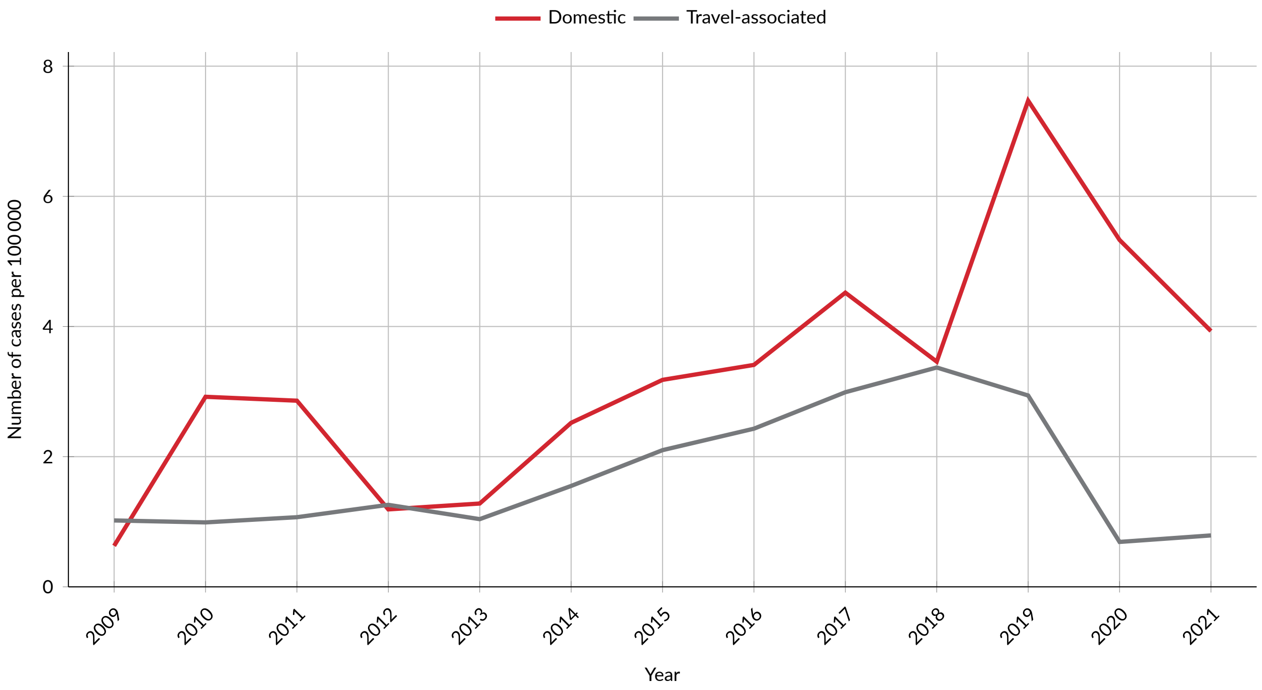


Figure 18: Number of notified human cases of cryptosporidiosis per 100 000 inhabitants from 2009 to 2021.

cryptosporidiosis was *C. hominis* (n=9) followed by *Cryptosporidium* chipmunk genotype I (n=7). The most common *C. parvum* subtypes were IIdA24G1 (n=17), IIaA16G1R1b (n=15), IIdA22G1c (n=15) and IIaA15G2R1 (n=11).

Two samples of *Cryptosporidium cuniculus*, one sample each of *Cryptosporidium erinacei* and *Cryptosporidium ubiquitum* were also detected.

In January, several cases of cryptosporidiosis were detected in a retirement home followed by cases in March among students and personnel at two different schools in Jönköping county. 14 cases were analysed and all cases were positive for *C. parvum*. 11 cases were subtype IIdA23G1, two cases were IIaA18G1R1b_variant and one case was IIdA21G1. Kale and cabbage were suspected as the probable cause of infection in January and March respectively. Kale was analysed and *C. parvum* was detected. Faecal matter from rodents and deer from the farm was sampled, but the source of contamination of the vegetables was not established.

DISCUSSION

Most domestic human cases are reported during the end of summer and this was also the case in 2021. Due to COVID-19 pandemic restrictions the travel-related cases were approximately one third compared to before the pandemic, but approximately the same as in 2020. The increase of reported cases of cryptosporidiosis over time is primarily a result of altered laboratory methods and increased awareness of the disease in primary care. 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 they 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 of finding *E. multilocularis* in foxes in Denmark in 2000 an active monitoring programme of red foxes (*Vulpes vulpes*) was implemented in Sweden. From 2000 to 2010 approximately 300 foxes per year were examined, all with negative results, until E. *multilocularis* was found in a fox shot in December 2010 in the county of Västra Götaland.

In the spring of 2011, a national screening was performed in which 2985 hunter-harvested 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. The national screening continued in 2012 – 2014 and 2779 fox scat samples were analysed by magnetic capture probe-based DNA extraction and real-time PCR (MC-PCR). Three samples were positive; one from Gnesta, one from Katrineholm (both in Södermanland) and one from

Figure 19: A new national screening for *Echinococcus multilocularis* in red foxes started in 2021. The parasite was detected in Kungsbacka, Halland in south-west Sweden, an area where it has not previously been detected. Photo: Schaef1/iStock.

Västra Götaland. During this period the parasite was also detected in fox scats from an area near the town Växjö in the county of Kronoberg (within the Emiro/SLU-project described below).

To obtain a better prevalence estimate in a known infected area, fox scats were collected in 2011, by a systematic sampling procedure from a circular area with a diameter of 25 km surrounding a positive finding in Södermanland. Six out of 790 (0.8%) faecal samples were positive. Also, to follow up the positive findings from the five areas where the parasite had been detected so far, hunters were asked to submit 30 foxes from an area with a diameter of 40 km. The sampling started in 2012 and continued to 2016. In Västra Götaland two foxes were positive, in Södermanland three foxes from Katrineholm and one from Gnesta were positive, whereas all tested foxes from Dalarna and Kronoberg were negative.

In 2020, fox scats were collected again from the areas in Uddevalla, Gnesta, and Katrineholm where the parasite has been previously found. The results 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 tested positive.

Potential intermediate hosts were examined 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 metacestode 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).

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 zero 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 2021:10).

Humans

Infection with *Echinococcus spp.* has been notifiable since 2004 according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2022:217). 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. Since 2012, all free-living wolves submitted to necropsy at the National Veterinary Institute (SVA) have been tested with MC-PCR, without any positive finding. In 2021 a follow-up targeted screening of fox scats was conducted in the previously known infected areas in Uddevalla and Gnesta. This study was financed by the Environmental Protection Agency.

Furthermore, in 2021 a second national screening funded by the Board of Agriculture was initiated. During this three-year project, up to 3000 samples (faecal samples from dead foxes and fox scats) will be collected and analysed with MC-PCR. Collaboration with field staff from the Swedish Association for Hunting and Wildlife Management and calls to the public to contribute with samples in this citizen science project is used to receive samples from the entire country.

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

In 2021, intensified sampling of fox scats was conducted in two focal areas, Gnesta and Uddevalla, where *E. multilocularis* was known to be present since the 2011–2014 screening. In 2020, positive fox scats were again found in both of these locations. During 2021, the geographic area for sampling was widened to investigate potential spatial spread from the previously known hot spots. A circular area, up to 5 km from each of the original finding sites was sampled, and

10 of 63 samples from Gnesta and 5 of 102 samples from Uddevalla were positive.

Within the newly initiated national screening, a total of 178 samples were collected during 2021, and one tested positive. Thereby a new infected area was identified in Kungsbacka, the county of Halland in the south-west of Sweden.

In addition, 51 wolves (*Canis lupus lupus*) and one pine marten (*Martes martes*) were tested with the MC-PCR and all were negative.

Humans

In 2021, no cases of alveolar echinococcosis were reported.

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 future trends 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 was initiated and will run for three years. So far this has resulted in identification of a new infected area in Kungsbacka in the county of Halland in south-west Sweden.

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 common voles (*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 become infected by 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, except sporadic cases in horses imported from Great Britain or Ireland where they most likely had acquired the infection. However, in a retrospective study of biobank material from 116 wolves submitted to SVA during 2012–2020, faecal samples from two wolves culled 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 2021:10).

Humans

Echinococcosis has been notifiable according to the Communicable Disease Act since 2004 (SFS 2004:168 with the amendments of SFS 2022:217). 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 SVA 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

In 2021, one case of equine echinococcosis was discovered at slaughter. Multiple hydatid cysts were found in the liver of a 13-year old horse imported from Ireland in 2015. The horse had no clinical symptoms related to the finding. Parasite material was genotyped as *E. equinus* (G4) by multiplex PCR at the European Reference Laboratory for Parasites (EURL-P) in Rome.

In addition to the routine inspection at slaughter, 51 wolves, one red fox and one pine marten were tested by MC-PCR detecting *E. canadensis* genotype G8 and G10 as well as *E. ortleppi,* and all were negative.

Humans

In 2021, 26 cases of echinococcosis were reported. For fourteen 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 had cystic echinococcosis. Annually around 15–30 cases are reported in Sweden. In 2021, the reported cases ranged in age from 11 to 63 years (median 33 years). Fourteen cases were women,10 were men and for two cases the sex was unknown. They were all considered to have been infected abroad in areas where the parasite is endemic. The most frequently specified country of infection was Syria (6 cases).

Discussion

E. granulosus s.l. is very rarely detected in animal intermediate hosts in Sweden. In reindeer it has not been detected 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 culled 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* (G10). Retrospective analysis of one of the three above mentioned Swedish reindeer revealed the same genotype. This species is considered as less pathogenic, and possibly with a lower zoonotic potential, than *E. granulosus* s.s. that is prevalent in some other parts of Europe and identified mainly in a cycle between dogs and farm animals.

In 2021, hydatid cysts were found at slaughter in a horse imported from Ireland in 2015, and parasite material was genotyped as *E. equinus* (G4, horse strain). Cystic equine echinococcosis is a very rare finding in Sweden with the latest previous case reported in 2011. Furthermore, there is no indication of any transmission in Sweden, since the infection has only been diagnosed in imported horses. The absolute majority of these have been from the United Kingdom or Ireland, where *E. equinus* in known to be endemic. This species is regarded as specific for equids as intermediate hosts, and with a very low zoonotic potential.

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.

REFERENCES

Isaksson M, Hagström A, Armua-Fernandez M, Wahlström H, Ågren E, Miller A, Holmberg A, Lukacs M, Casulli A, Deplazes P, Juremalm M (2014) A semi-automated magnetic capture probe based DNA extraction and real-time PCR method applied in the Swedish surveillance of *Echinococcus multilocularis* in red fox (*Vulpes vulpes*) faecal samples. Parasit Vectors 7:583

Miller, A. The role of rodents in the transmission of *Echinococcus multilocularis* and other tapeworms in a low endemic area. Doctoral Thesis 2016. Faculty of Veterinary Medicine and Animal Sciences, Swedish University of Agricultural Sciences, Uppsala, Sweden

Wahlström H, Comin A, Isaksson M, Deplazes P (2016) Detection of *Echinococcus multilocularis* by MC-PCR: evaluation of diagnostic sensitivity and specificity without gold standard. Infect Ecol Epidemiol 6:30173

Wahlström H, Lindberg A, Lindh J, Wallensten A, Lindqvist R, Plym-Forshell L, Osterman Lind E, Ågren EO, Widgren S, Carlsson U, Christensson D, Cedersmyg M, Lindström E, Olsson GE, Hörnfeldt B, Barragan A, Davelid C, Hjertqvist M, Elvander M (2012) Investigations and actions taken during 2011 due to the first finding of *Echinococcus multilocularis* in Sweden. Eurosurveillance 17:28

Davison KR, Lavikainen A, Konyaev S, Schurer J, Miller AL, Oksanen A, Skirnisson K, Jenkins E (2016) *Echinococcus* across the north: Current knowledge, future challenges. Food Waterborne Parasitol 4:39

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 is officially free from EBL since January 2001. 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 a listed disease (category C, D and E) in the Animal Health Law, (EU) 2016/429. Sweden is officially free from the disease in accordance with (EU) 2021/620 and surveillance to demonstrate freedom from EBL is implemented in accordance with (EU) 2020/689. EBL is notifiable on clinical suspicion as described in SJVFS 2021/10 (K12).

SURVEILLANCE

The purpose of the active surveillance is to document freedom from EBL in accordance with Directive 64/432/EEC. The Swedish cattle farmers association Växa 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 2021 are given in Table 8.

Diagnostic testing is performed at the National Veterinary Institute (SVA). Milk is analysed using the IDEXX Leukosis Milk Screening Ab test kit (IDEXX Laboratories, Westbrook, Maine, United States) and serum is analysed using the IDEXX Leukosis Serum X2 Ab Test kit (IDEXX Laboratories, Westbrook, Maine, United States).

Table 8: Total numbers of herds and animals tested for bovine leukaemia virus antibodies in 2021.

Herd type (sample type)	Herds	Animals
Dairy herds (one bulk milk sample per herd)	2056	-
Beef herds (blood from 1–3 animals per herd)	2925	6673
Beef herds with at least three tested animals	504	-
Beef herds with two tested animals	1883	-
Beef herds with one tested animal	538	-

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

Two bulk milk samples were tested antibody positive in 2021. After further investigations of these herds the conclusion was that the results from these samples were falsely positive.

Samples from two cases of tumours in lymph nodes were analysed for EBL at SVA using PCR in 2021 and both 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.

REFERENCES

Ballagi-Pordány A, Belák S. The use of mimics as internal standards to avoid false negatives in diagnostic PCR. Mol Cell Probes. 1996;10: 159–164. doi:10.1006/mcpr.1996.0022

Enzootic Bovine Leukosis, OIE Terrestrial Manual 2018. (https://www.oie.int).

Växa, Statistics for 2021.

WAHIS Interface. (https://www.oie.int). Accessed 2020-03-19.

Footrot

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 (virulent strains of *D. nodosus*) is a notifiable disease in Sweden (SJVFS 2021:10).

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

Figure 20: Lameness is a common sign of footrot. Photo: Ylva Persson.

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.

385 (out of a total of 8480) sheep flocks are affiliated to the control programme. Most of the top pedigree flocks in Sweden are affiliated to the programme.

RESULTS

In 2021, footrot was confirmed in 2 new flocks within the control programme. (Figure 21). In both flocks, benign strains of *D. nodosus* were detected. In the programme, 383 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%.

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. During 2021, the control programme was evaluated by the National Veterinary Institute (SVA) and Farm & Animal Health for more cost-effective sampling, diagnostics, and control measures.

REFERENCES

Albinsson R (2021) Förekomst av klinisk fotröta och *Dichelobacter nodosus* hos svenska slaktlamm/Prevalence of clinical footrot and *Dichelobacter nodosus* in Swedish slaughter lambs. Master thesis SLU.

Frosth S, König U, Nyman AK, Aspán A (2017) Sample pooling for real-time PCR detection and virulence determination of the footrot pathogen *Dichelobacter nodosus*. Vet Res Comm 41:189–193

Frosth S, König U, Nyman AK, Pringle M, Aspán A (2015) Characterisation of *Dichelobacter nodosus* and detection of *Fusobacterium necrophorum* and *Treponema* spp. in sheep with different clinical manifestations of footrot. Vet Microbiol 179:82–90

Frosth S, Slettemeås JS, Jørgensen HJ, Angen O, Aspán A (2012) Development and comparison of a real-time PCR assay for detection of *Dichelobacter nodosus* with culturing and conventional PCR: harmonisation between three laboratories. Acta Vet Scand 54:6

König U, Nyman AKJ, de Verdier K (2011) Prevalence of footrot in Swedish slaughter lambs. Acta Vet Scand 53:27

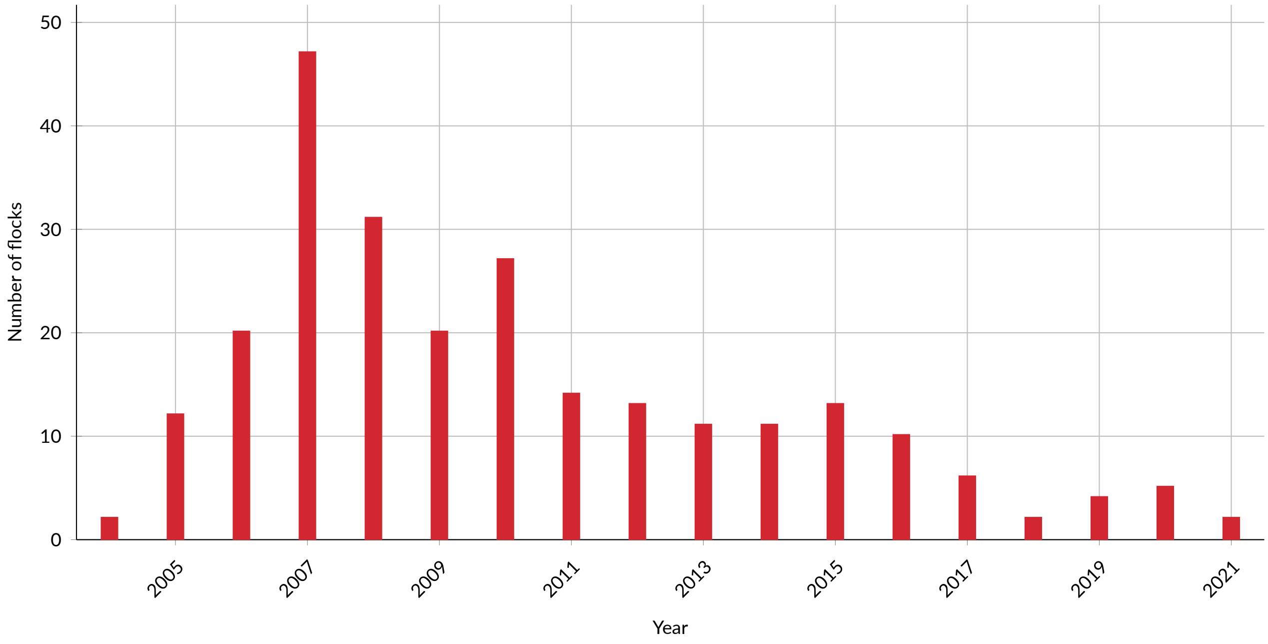


Figure 21: Number of sheep flocks detected with footrot within the programme, 2004–2021.

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

IBR is a listed disease (category C, D and E) in the Animal Health Law, (EU) 2016/429. Sweden is officially free from the disease in accordance with (EU) 2021/620 and surveillance to demonstrate freedom from IBR is implemented in accordance with (EU) 2020/689. IBR is notifiable on clinical suspicion as described in SJVFS 2021/10 (K12).

SURVEILLANCE

During 2021 all diagnostic testing was performed at the National Veterinary Institute (SVA). Milk samples were analysed for the presence of antibodies using an indirect ELISA (ID screen IBR Milk indirect, Innovative Diagnostics, Grabels, France), and serum samples were analysed with a blocking ELISA (IDEXX BHV1 gB AB test kit x3, IDEXX Laboratories, Westbrook, Maine, United States). Positive milk samples were confirmed with a blocking ELISA (IDEXX BHV1 gB AB test kit x3, IDEXX Laboratories, Westbrook, Maine, United States), 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

Suspicions 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, Sweden's largest cattle farmer association, 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 2021, 2687 bulk milk samples and 6536 serum samples from beef cattle were examined. Of these, 1 serum sample tested positive in the screening test but negative in the confirmatory test. In addition, 172 cattle, 11 fallow deer, 1 musk ox, 2 reindeer, 2 European bison and 1 moose were tested as part of health schemes or prior to export or import. All samples were negative.

DISCUSSION

In summary, no herd or individual animal was diagnosed with IBR infection during 2021. This supports Sweden's IBR-free status.

REFERENCES

Wang J, O'Keefe J, Orr D, Loth L, Banks M, Wakeley P, West D, Card R, Ibata G, Van Maanen K, Thoren P, Isaksson M, Kerkhofs P (2007) Validation of a real-time PCR assay for the detection of bovine herpesvirus 1 in bovine semen. J Virol Methods 144:103–108

Influenza

Influenza viruses are members of the *Orthomyxoviridae* family and are divided into four genera: *Alphainfluenzavirus* (species; influenza A virus [IAV]), *Betainfluenzavirus* (influenza B virus [IBV]), *Gammainfluenzavirus* (influenza C virus [ICV]), and *Deltainfluenzavirus* (influenza D virus [IDV]), 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.

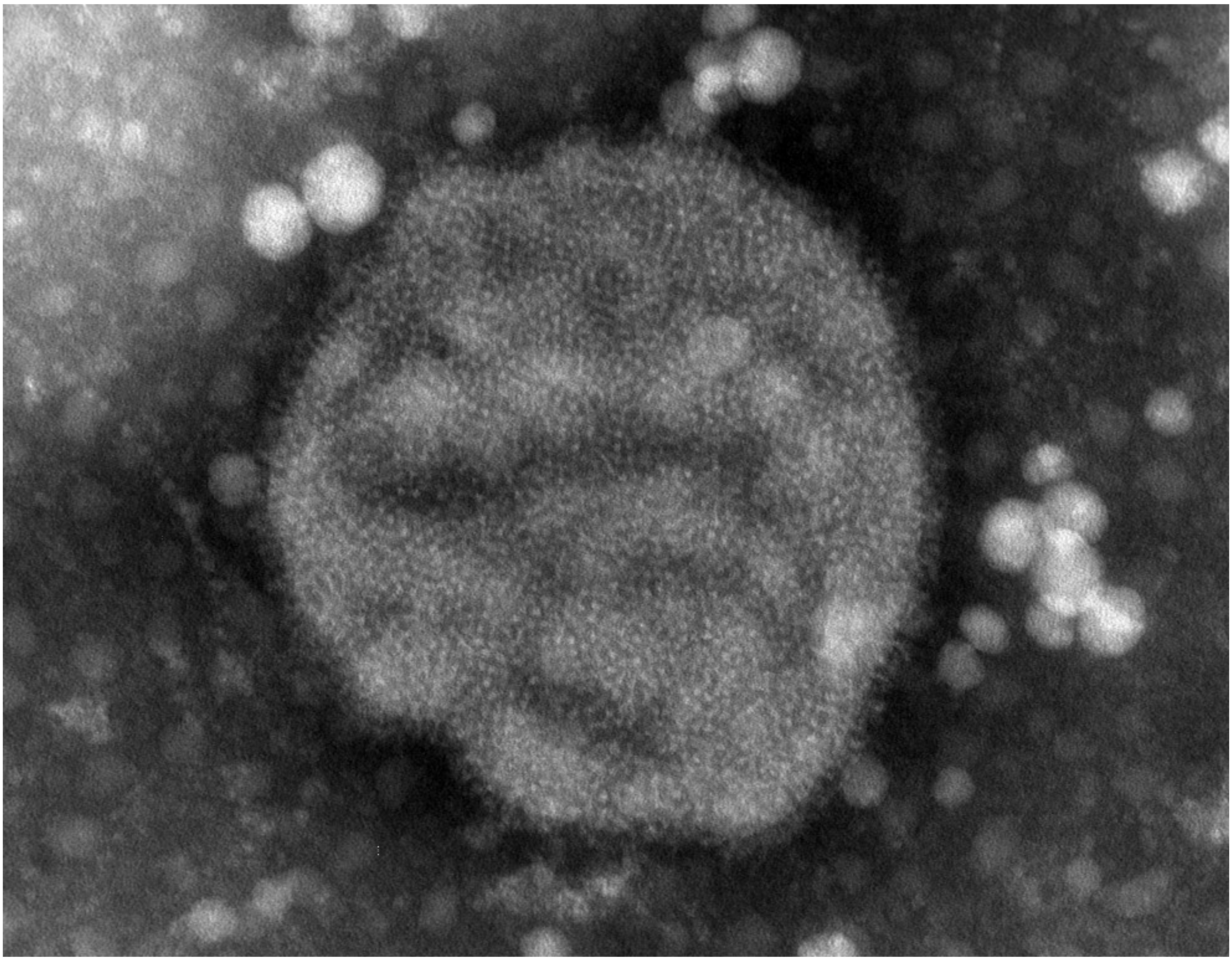


Figure 22: Electron microscopy of low pathogenic H2N2 influenza A virus. Photo: SVA & Public Health Agency of Sweden.

Avian influenza

BACKGROUND

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

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

The detection of highly pathogenic avian influenza (HPAI) H5N1 in Hong Kong in 1997, with the ability to cause disease in humans, highlighted the potential threat of AI to animal and human health. Since then, the resurgence of extensive outbreaks of HPAI viruses of the goose/Guangdong/96 (Gs/ Gd) lineage has continued in various regions in Asia, Africa, and Europe.

Historically, there have been four recorded outbreaks of avian influenza in Sweden: in 2006, 2015, 2016–2017 and 2020–2021. The 2006 and 2015 outbreaks were limited to findings among wild birds. The 2016–2017 outbreak was more extensive and besides affecting the wild bird population resulted in the depopulation of several thousand domestic birds (Figure 24).

The 2020–2021 outbreak of HPAI caused the largest poultry disease outbreak ever recorded in Sweden, where millions of birds were lost to the disease itself or culled to prevent further spread of the virus.

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.

Figure 23: Whooper swan with typical symptoms of highly pathogenic avian influenza including torticollis (twisting of the neck), photographed in Malmö during the 2021 outbreak. Photo: Kenneth Bengtsson/Fågelskydd Spillepeng.

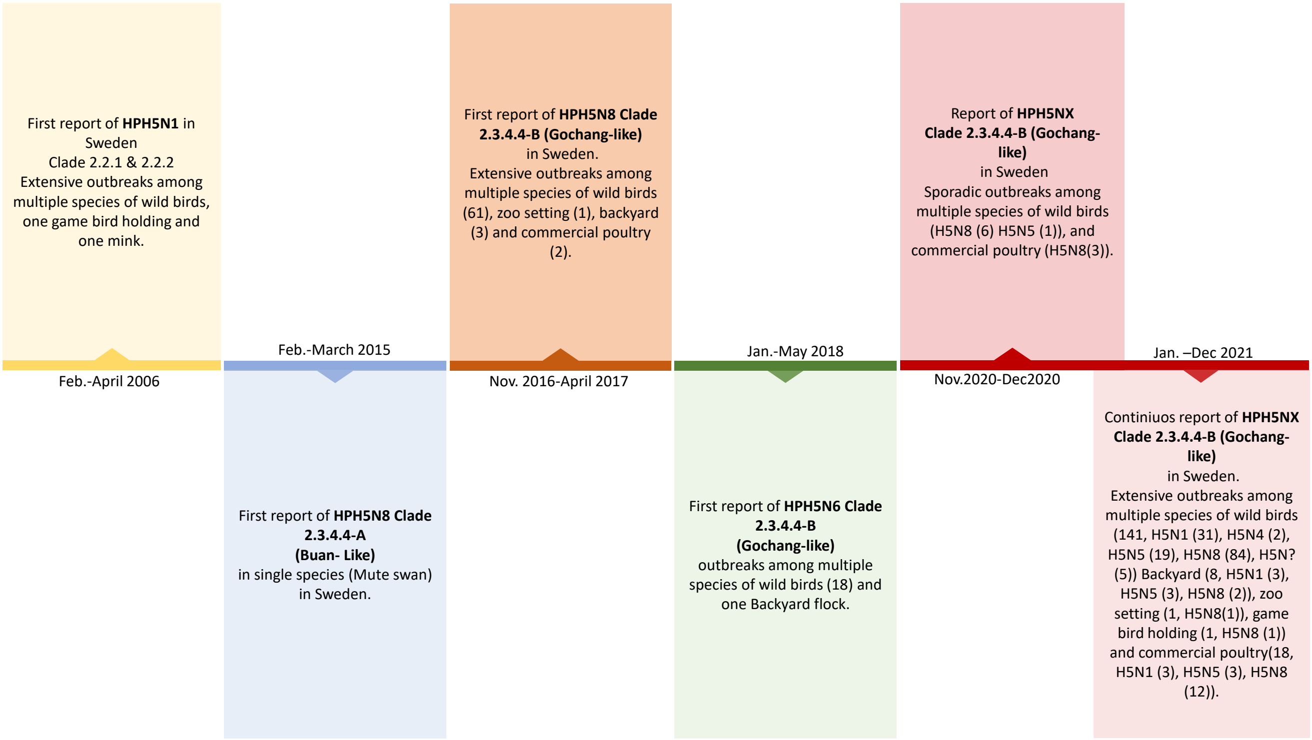
Humans

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. In rare cases, human infections with HPAIV can lead to severe pneumonia and death.

Since 2003, 863 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 close direct or indirect contact with infected live or dead poultry. One human case of asymptomatic infection with HPAI H5N1 of HA Clade 2.3.4.4 was identified in December 2021 in the UK associated with the handling of infected birds. Prior to outbreak confirmation, the owner had contact with infected Muscovy ducks without protective material (Oliver et al, 2022). New human infections associated with H5N6 activity have been detected in China. From 2014 to December 2021, 58 laboratory-confirmed cases of human infection with HPAI H5N6, including 25 with fatal outcomes, (57 in China and 1 in Laos) have been reported. In all cases, there was a known exposure to sick animals or a contaminated environment and there was no link between individuals. It should be noted that these viruses are not related to the HPAI H5N6 viruses that circulated in wild birds in the EU in 2017–2018.

H5N8 human cases were reported from Russia in 2020 but no new cases have been identified.

More than 1568 laboratory-confirmed cases of human infection with H7N9 viruses, including 39% deaths, have


Feb.-April 2006

First report of **HPH5N1** in Sweden
Clade 2.2.1 & 2.2.2
Extensive outbreaks among multiple species of wild birds, one game bird holding and one mink.

Feb.-March 2015

First report of **HPH5N8 Clade 2.3.4.4-A (Buan- Like)** in single species (Mute swan) in Sweden.

Nov. 2016-April 2017

First report of **HPH5N8 Clade 2.3.4.4-B (Gochang-like)** in Sweden.
Extensive outbreaks among multiple species of wild birds (61), zoo setting (1), backyard (3) and commercial poultry (2).

Jan.-May 2018

First report of **HPH5N6 Clade 2.3.4.4-B (Gochang-like)** outbreaks among multiple species of wild birds (18) and one Backyard flock.

Nov.2020-Dec2020

Report of **HPH5NX Clade 2.3.4.4-B (Gochang-like)** in Sweden
Sporadic outbreaks among multiple species of wild birds (H5N8 (6) H5N5 (1)), and commercial poultry (H5N8(3)).

Jan. –Dec 2021

Continiuos report of **HPH5NX Clade 2.3.4.4-B (Gochang-like)** in Sweden.
Extensive outbreaks among multiple species of wild birds (141, H5N1 (31), H5N4 (2), H5N5 (19), H5N8 (84), H5N? (5)) Backyard (8, H5N1 (3), H5N5 (3), H5N8 (2)), zoo setting (1, H5N8(1)), game bird holding (1, H5N8 (1)) and commercial poultry(18, H5N1 (3), H5N5 (3), H5N8 (12)).

Figure 24: Timeline of highly pathogenic avian influenza outbreaks in Sweden 2006–2021. Infographic by Siamak Zohari.

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 33 human cases, 13 of them fatal, have been due to infection with HPAI H7N9. Since March 2019 no case of H7N9 was reported. As for the other avian strains, there is no evidence of human-to-human transmission of H7N9. The decrease in human cases of H7N9 is due to the introduction of control measures, including a mass vaccination programme in poultry in China.

From 1998 to December 2021, 95 laboratory-confirmed cases of human infection with LPAI H9N2, including two fatal cases, have been reported globally. Cases occurred in China (83), Egypt (4), Bangladesh (3), India (1), Cambodia (1), Oman (1), Pakistan (1), and Senegal (1). Most of the infections were mild and were detected in children aged 10 or younger with known exposure to poultry or contaminated environment.

One human case of H10N3 was reported from China in 2021. The H10N3 has been detected in poultry and may be detected in humans exposed to infected birds.

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 Delegated regulation 2020/687 supplementing Regulation (EU) 2016/429 as regards rules for the prevention and control of certain listed diseases that came into force on April 21, 2021. Before that, measures according to Council Directive 2005/94/EC were implemented.

The Swedish avian influenza surveillance programme in poultry and wild birds 2021 is based on Council directive 2005/94/EC and Commission decision 2010/367/EU. A gradual transition to delegated regulation 2020/689 supplementing Regulation (EU) 2016/429 as regards rules for surveillance, eradication programmes, and disease-free status for certain listed and emerging diseases starts in 2022.

Humans

All laboratory-confirmed cases of influenza are notifiable, and avian influenza H5N1 is classified as a high consequence pathogen according to the Communicable Disease Act (SFS 2004:168 with amendments).

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 the subtypes H5 and H7 in particular.

Poultry

The surveillance programme in poultry for 2021 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 holding were collected. In holdings with fewer individuals than the abovementioned sample size, all individuals were sampled. In addition to the surveillance programme, samples were taken on clinical suspicion. On clinical suspicion of AI or Newcastle disease, laboratory analyses for both diseases are generally performed.

The surveillance programme for 2021 was based on representative sampling and the serological analyses were performed at the National Veterinary Institute (SVA). 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, IDEXX Laboratories, Westbrook, Maine, United States). Positive results were confirmed with haemagglutination inhibition tests (for subtypes H5, H7 and H5N8) in accordance with the OIE guidelines.

Wild birds

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

The AI surveillance in wild birds is passive and based on birds found dead or diseased and submitted for postmortem examination. The geographical distribution of wild birds examined for AI is shown in Figure 25. Before 2021 the selection of wild bird species included in AI screening was very broad and all species submitted for postmortem examination were eligible to include. As mortality in wild birds was very high during February and March 2021 the policy was changed so that species that are less susceptible for AI, such as small passerine birds and Columbiformes, were excluded from the surveillance program in wild birds. The wild bird surveillance in Sweden, however, still includes a wider list of species compared to the EFSA list of target species for avian influenza surveillance (EFSA, Avian influenza overview September–November 2017).

Humans

Every year, 1500–2000 samples are collected in Sweden from sentinel patients with influenza-like illnesses during the influenza surveillance season. In addition, in 2021 professionals working in the two largest outbreaks in Kalmar Region were recommended to contact health care and be tested if they developed influenza-like symptoms. Samples are analysed for influenza A and B and since spring 2020 also for SARS-CoV-2. If influenza A is detected, further subtyping is performed by rRT-PCR for H1 (A(H1N1)pdm09) and H3 (A(H3N2)). If samples positive for influenza A cannot be subtyped, sequencing is performed to rule out zoonotic influenza A. Assessment of susceptibility to antivirals is achieved by screening genotypic markers. A further 200–300 of the influenza positive samples from the diagnostic laboratories are subtyped or characterised. The Public Health Agency of Sweden performs acute rRT-PCR of human samples including a subtype-specific rRT-PCR for H5 and H7 when avian influenza is suspected.

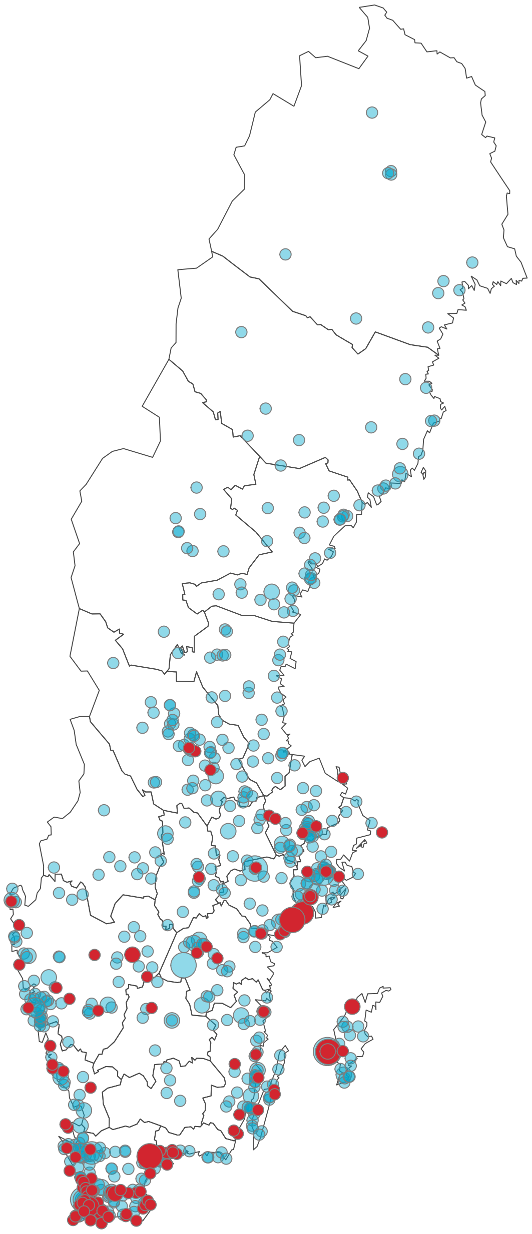


Figure 25: Geographical location of the wild birds analysed for avian influenza in 2021. Point sizes are scaled by the number of birds sampled at a given location. In total, 141 out of 803 wild birds sampled in 2021 were found positive for HPAI.

Table 9: Number of holdings of different poultry categories sampled in the surveillance for avian influenza 2011–2021.

	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021
Laying hens	52	44	58	68	62	68	65	73	63	57
Free range laying hens	27	16	23	23	30	43	49	67	52	47
Turkeys	19	26	16	18	18	16	16	18	18	14
Ducks	3	1	3	3	4	1	2	3	1	5
Geese	20	13	9	9	7	5	6	3	1	2
Broilers[A]	34	26	12	22	33	23	33	22	14	3
Ratites	3	2	3	3	3	2	2	5	3	7
Breeding hens (parents)	36	36	32	31	34	35	30	34	35	28
Breeding turkeys (parents)	3	3	2	3	3	3	3	3	3	3
Game birds (mallards)	7	7	5	6	7	2	5	5	6	10
Game birds (pheasants)	16	16	12	13	9	13	12	8	10	8
Backyard flocks (geese, ducks)	0	0	0	0	0	0	0	0	0	0

[A] Small-scale production.

Table 10: Confirmed HPAI in poultry and other captive birds during 2021.

Date of confirmation	Virus subtype	County	Type of establishment	Number of susceptible animals
2021-01-03	H5N8	Skåne	Chicken breeding	84 864
2021-01-14	H5N8	Skåne	Fattening turkeys	2350
2021-01-18	H5N5	Kalmar	Layers	1 242 250
2021-02-01	H5N5	Kalmar	Pullets (layers)	735 000
2021-02-15	H5N8	Skåne	Fattening turkeys	3500
2021-02-17	H5N8	Västra Götaland	Hobby	46
2021-02-24	H5N8	Östergötland	Chickens	14 300
2021-02-24	H5N8	Skåne	Phesants	470
2021-02-28	H5N5	Skåne	Hobby	11
2021-03-01	H5N8	Halland	Rare breed breeding	263
2021-03-01	H5N8	Skåne	Zoo	38
2021-03-03	H5N5	Skåne	Layer	18 000
2021-03-08	H5N8	Östergötland	Layer	24 000
2021-03-11	H5N5	Skåne	Hobby	33
2021-03-13	H5N8	Östergötland	Layer	33 000
2021-03-13	H5N8	Skåne	Chickens breeding	53 200
2021-03-14	H5N8	Östergötland	Layer	22 700
2021-03-14	H5N8	Östergötland	Layer	26 400
2021-03-15	H5N8	Skåne	Fattening turkeys	30 000
2021-03-21	H5N8	Skåne	Hobby	63
2021-03-23	H5N5	Stockholm	Hobby	14
2021-04-20	H5N8	Skåne	Layer	17 819
2021-12-01	H5N1	Skåne	Hobby	44
2021-12-13	H5N1	Skåne	Fattening turkeys	6100
2021-12-17	H5N1	Skåne	Hobby	29
2021-12-17	H5N1	Skåne	Chicken breeding (rearing)	20 000
2021-12-27	H5N1	Skåne	Fattening turkeys	15 939
2021-12-30	H5N1	Södermanland	Hobby	44

RESULTS

Poultry

In 2021, 1925 blood samples were collected from 184 holdings. Three flocks with game birds (mallards) had single serologically positive H5 results with haemagglutination inhibition tests. These flocks were investigated with oropharyngeal and cloacal swabs with PCR and found negative for Influenza A H5 and H7. In addition, there were positive ELISA results in 12 holdings, which were then found negative using haemagglutination inhibition tests. All other serological samples were found negative for AIV subtypes H5 and H7. Table 9 gives an overview of the number of poultry holdings sampled from 2012 to 2021 (Table 9).

HPAI was detected in 28 holdings during 2021 (Table 10). In total AI was investigated in 81 poultry holdings during 2021 of which 77 were investigated because of clinical suspicions, three because of follow up from serological surveillance, one following postmortem findings and one as part of contact tracing. The clinical suspicions were raised because of increased mortality and in some cases combined with a range of clinical signs such as depression, unresponsiveness, drooping of the wings, incoordination, respiratory distress or diarrhoea.

Wild birds

Within the passive surveillance programme, 141 wild birds were found positive for HPAIV of which 84 were H5N8, 31 H5N1, 19 H5N5, two H5N4 and five H5NX. In total 803 birds of 93 different species were sampled of which 352 were birds of prey, 275 water- or shorebirds and 67 corvids. The geographical location of sampled and wild birds including positive findings are available in Figure 25.

Humans

No cases of zoonotic avian influenza were identified among the samples characterised during 2021 in Sweden. No human cases were associated with the outbreaks in commercial poultry in personnel working with the culling of birds and decontamination activities.

DISCUSSION

During the period covered by this report, the spread of HPAI has been confirmed in more than 50 countries, in Asia, Africa, and Europe. The global spread of the virus is threatening not only animal and human health and welfare but also the economic stability and food security in the affected countries. Since the first detection of HPAI with HA Clade 2.3.4.4.b viruses at the Ubsu-Nur Lake in May 2016, closely related viruses have continued to affect poultry and wild bird populations worldwide. Extensive cocirculation of high and low pathogenic influenza A viruses in the period covered by this report, among wild and domestic birds in Europe has resulted in an exceptional genetic variation among detected viruses.

In 2021, Sweden reported 28 outbreaks of HPAI H5NX in domestic poultry and 141 cases of HPAI in wild birds. These outbreaks were caused by H5NX HPAI clade 2.3.4.4 viruses of the Gs/Gd lineage. Several distinct genotypes from this clade were involved in these outbreaks. The detection of HPAI in Sweden 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 2021 and in several European countries in the winter of 2020/2021. 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. The continuous global threat of HPAI viruses further emphasizes the need for awareness and improved biosecurity in poultry holdings to prevent the introduction of the virus from wild birds.

Detections of H5 and H9 continue to increase in humans and may reflect infections in poultry, considering that H5 and H9N2 viruses are enzootic in Asia. It may also reflect the increase in testing efforts for respiratory infections and diagnostic capacity as a consequence of the COVID-19 pandemic. Controlling the disease in domestic animals is the first step in decreasing the risk to humans.

REFERENCES

European Commission, ADNS

EFSA (European Food Safety Authority), ECDC (European Centre for Disease Prevention and Control), EURL (European Reference Laboratory on Avian Influenza), Brown I, Kuiken T, Mulatti P, Smietanka K, Staubach C, Stroud D, Therkildsen OR, Willeberg P, Baldinelli F, Verdonck F and Adlhoch C, 2017. Scientific report: Avian influenza overview September - November 2017. EFSA Journal 2017;15(12):5141, 70 pp. doi:10.2903/j.efsa.2017.5141

OIE - WAHID database.

WHO 2015 https://www.who.int/influenza/gisrs_laboratory/h5_nomenclature_clade2344/en/

WHO Feb. 2018 https://www.who.int/influenza/vaccines/virus/201802_zoonotic_vaccinevirusupdate.pdf?ua=1

Oliver I, Roberts J, Brown C, Byrne A, Mellon D, Hansen R, et al. A case of avian influenza A(H5N1) in England. Eurosurveillance. 3 Feb 2022. 27;5 https://www.eurosurveillance.org/docserver/fulltext/eurosurveillance/27/5/eurosurv-27-5-1.pdf?expires=1646140238&id=id&accname=guest&checksum=5045AC487CE132037838BD69AAFFDC50

ProMed: PRO/AH/EDR> Avian influenza, human (09): China (JS) H10N3, 1st rep; Archive Number: 20210602.8416833 https://promedmail.org/promed-post/?id=20210602.8416833

WHO; Avian Influenza Weekly Update Number 835 March 2022

ECDC Avian influenza overview September – December 2021

ADIS – Animal disease information system (European Commission)

Swine influenza

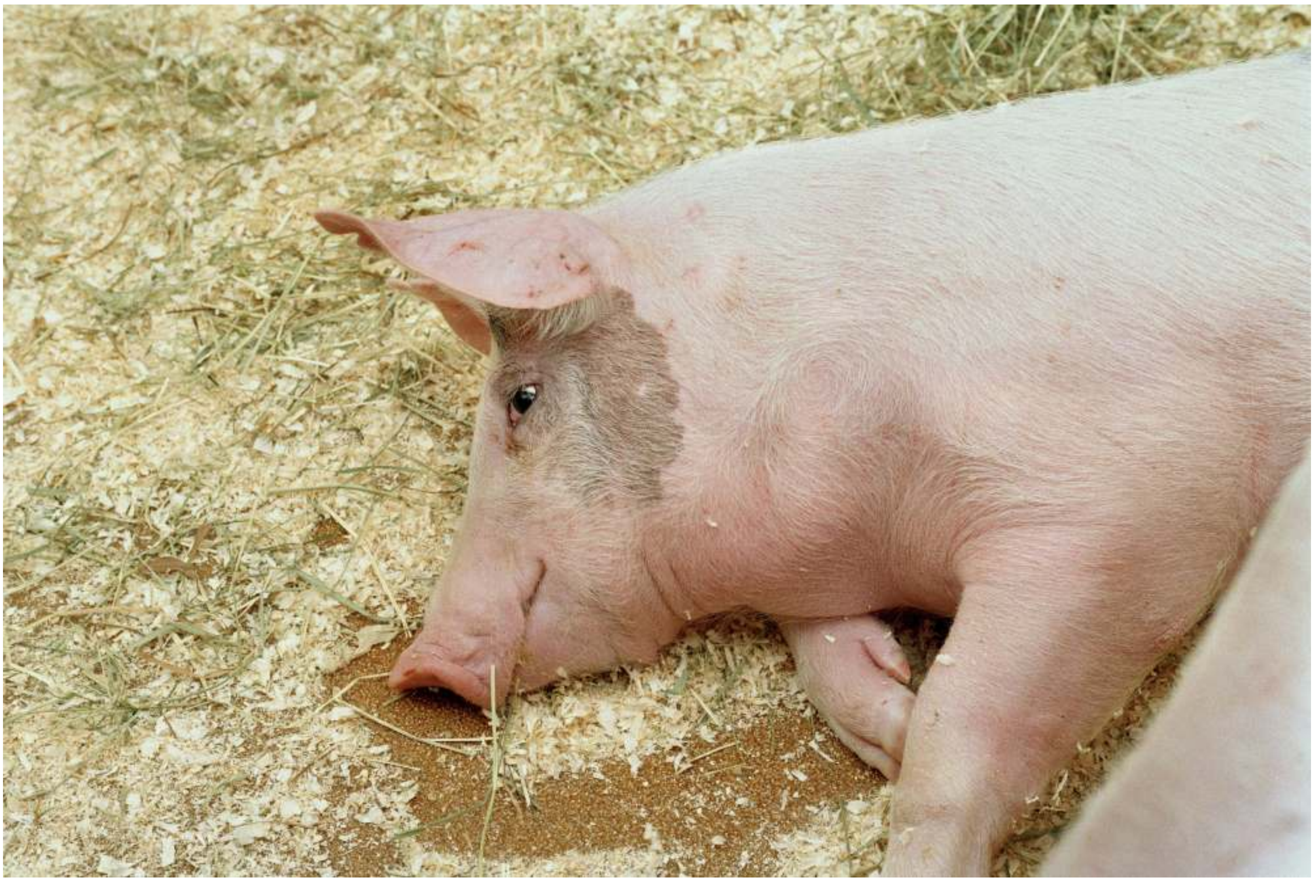


Figure 26: In 2021, samples from 70 pig herds were analysed for swine influenza. Photo: Bengt Ekberg/SVA.

BACKGROUND

Swine influenza (SI), caused by several subtypes of influenza A viruses, has a worldwide distribution and causes an acute upper respiratory disease characterised by fever, lethargy, anorexia, weight loss and laboured breathing in pigs. The 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. 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.

DISEASE

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 pigs in early May 2009 in Canada, H1N1pdm09 has been isolated from pigs throughout the world including several European countries such as 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 an 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 adapted to humans. Although the pH1N2 subtype influenza A virus was exclusively prevalent in the Swedish pig population in 2014, the clinical signs of disease were minor, as later also seen in other countries.

There has not been a regular active 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.

Humans

Influenza A viruses that infect humans but are genetically similar to viruses circulating in swine are called “variant viruses” and depicted with the letter “v” to distinguish them from viruses that normally infect humans. People who have been infected with the 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.

For 2021 ECDC reports 37 cases of swine influenza variant virus infections globally. Five of the cases were reported from countries within the EU/EEA; Austria, Denmark, Germany and France. A human case of A(H1N1)v that was identified in Denmark at the end of November 2021 was in a slaughterhouse worker who needed hospital care. Twenty-four cases of H1N1v were reported, from Canada, China, Denmark, Germany and the US. Ten cases of H1N2v were reported, from Austria, Canada, China, France and the US. Four cases of H3N2v were reported from Canada and the US. Since 2010, 434 human cases of A(H3N2)v, 30 human cases of A(H1N2)v and 18 human cases of A(H1N1)v have been detected in the US. The US-CDC estimated that approximately 90% of human infections with swine influenza were associated with agricultural fairs, where people are in close contact with potentially infected swine populations, and have given recommendations to prevent transmission of swine influenza at such events. The number of human cases infected with swine influenza has decreased over the last few years in the US.

LEGISLATION

Animals

All laboratory confirmed cases of infection in pigs with influenza virus are notifiable as described in SJFS 2021:10s.

Humans

All laboratory confirmed cases of infection with influenza are notifiable according to the Communicable Disease Act (SFS 2004:168 with amendments).

Table 11: Passive and active surveillance for swine influenza in Swedish pig herds from 2014 to 2021.

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	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	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	
2021 – passive	70	7 herds (7 animals)	single animal per herd	1	6	-

SURVEILLANCE

Animals

Passive surveillance

Every year, a number of suspicions of swine influenza in pig herds with respiratory signs consistent with influenza are reported to the National Veterinary Institute (SVA). Serological and virological samples are sent to SVA for laboratory analyses. From each affected herd, 5–10 nasal swab samples are collected and analysed first for the presence of swine influenza A and if positive, samples are further analysed for pandemic influenza A(H1N1)pdm09. (Table 11). Serum samples are screened for the presence of anti-influenza A antibodies using a commercially available ELISA (ID Screen Influenza A antibody competition ELISA kit, Innovative Diagnostics, Grabels, France).

Active surveillance

No active surveillance was performed in 2021. In 2022, active surveillance is scheduled to be performed on sera randomly selected from the porcine reproductive and respiratory syndrome control programme.

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 by rRT-PCR for H1 and H3. 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 by full genome sequencing. The influenza season 2020–2021 was unusual and few influenza infections were detected due to the recommendations to control the spread of SARS-CoV-2.

RESULTS

Animals

Passive surveillance

A total of 136 nasal swab samples from 70 herds with respiratory signs were analysed with rRT-PCR for swine influenza virus in 2021. Seven influenza virus infected herds were identified.

467 serum samples from 36 herds were examined. Of those, 128 (28%) samples tested positive for antibodies against influenza A virus.

Active surveillance

No active surveillance was performed in 2021.

Humans

No cases of zoonotic influenza were identified among the characterised samples during 2021 in Sweden.

DISCUSSION

The results of the passive surveillance indicate the presence, but no large impact, of swine influenza in the Swedish pig population. In the last decade, two new influenza A virus subtypes were detected in the Swedish pig population. Both of these virus types 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) are continuously induced. This could enable the virus to be more transmissible among humans. The veterinary importance and the potential public health significance of the 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 human infections caused by these viruses is critically important to assess their pandemic potential.

REFERENCES

Centers for Disease Control and Prevention (CDC) 2022. Novel Influenza A Virus Infections. Available from: https://gis.cdc.gov/grasp/fluview/Novel_Influenza.html

European Commission, ADNS

OIE - WAHID database.

WHO 2015 https://www.who.int/influenza/gisrs_laboratory/h5_nomenclature_clade2344/en/

WHO Feb. 2018 https://www.who.int/influenza/vaccines/virus/201802_zoonotic_vaccinevirusupdate.pdf?ua=1

Kiss, I., A. Bálint, G. Metrevelli, E. Emmoth, F. Widén, S. Bélak and P. Wallgren (2010). Swine influenza isolated in 1983, 2002 and 2009 in Sweden exemplify different lineages. Acta Vet Scand. 52:65.

Wallgren, P, Paulsson, M. Gerth Löfstedt, M. (2009). Ny influensastam, H1N2, påvisad hos gris i Sverige (Influenza H1N2 demonstrated in Swedish pigs). Svensk VetTidn. 61 (14) 11–17.

World Health Organization (WHO). Influenza at the human-animal interface. Summary and assessment, from January to March 2022. Geneva: WHO; 2022. Available from: https://www.who.int/publications/m/item/influenza-at-the-human-animal-interface-summary-and-assessment-1-march-2022

Leptospirosis

BACKGROUND

Several species of the spirochetal 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.

An even lower prevalence to the indigenous strain of *L.* Sejroe in cattle has 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.

Leptospira may be transmitted directly between animals or environmentally (i.e., indirectly). The bacteria do not multiply outside the host but may survive for long periods in the environment.

DISEASE

Animals

Leptospira 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 2021:10), in all animal species concerned. Reporting is not serovar specific i.e., to which serovar or serovars antibodies are detected is not reported.

In the new updated legislation that came into force 2021 (SJVFS 2021:10), the basis for reporting has changed, and therefore the number of reported positive analysis for this reporting period cannot be compared with previous years.

Humans

Leptospirosis in humans is notifiable according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2022:217).

SURVEILLANCE

Animals

Active surveillance in cattle and pigs is at present performed every third year. The surveillance is designed 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 (SVA). The diagnostic test used for *L.* Hardjo is an indirect ELISA (PrioCHECK® *L.* Hardjo, Antibody detection ELISA, Thermo Fisher Scientific, Lelystad, Netherlands) 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 23) 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 carried out by Farm & Animal Health for porcine reproductive and respiratory syndrome (PRRS). See chapter on PRRS (page 67) 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 number of samples and herds needed is calculated yearly taking the outcome of the surveillance in previous years into account.

In species other than pigs and cattle the surveillance is purely passive.

Serum samples submitted to SVA for MAT-testing are currently routinely tested for *L.* Icterohaemorrhagiae, *L.* Canicola, *L.* Grippotyphosa, *L.* Bratislava, *L.* Saxkoebing, *L.* Sejroe, *L.* Autumnalis.

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 2021. See previous reports for surveillance results from 2019 and earlier. Furthermore, no positive samples originating from sampling other than the active surveillance were reported, and no positive sample results from such sampling from either cattle or pigs were recorded at SVA during 2021.

In dogs, in total 15 Leptospira-positive laboratory analyses were reported, which is lower than previous years due to the updated legislation, with a changed basis for reporting, entering into force during 2021. Hence the number of reported analyses cannot be compared to previous years. In 2020 in total 48 Leptospira-positive laboratory analyses were reported. Most (85%, n=41) were analysed by SVA. In comparison, the total number of positive samples analysed at SVA during 2021 was 35, of which only approximately a third (34% n=12) were reported according to the updated legislation.

One positive sample was reported from one imported horse. No other positive samples were reported, and no positive sample results from horses were recorded at SVA during 2021.

Humans

In 2021, no case of leptospirosis was reported. In previous years the majority of cases reported have been acquired abroad, and the absence of cases in 2021 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. Seropositvity 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.

An even lower prevalence to the indigenous strain of *L.* Sejroe in cattle has 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.Seropositivity to leptospiral serovars in Swedish dogs has for several years been thought to be underreported. The changes in basis for reporting during 2021 lowered the number of reported cases further. One additional challenge is the fact that the acute nature of illness, and high mortality rates in many canine cases where leptospiros is the most likely cause of acute illness makes it difficult for the veterinarians to collect relevant samples for analyses, including samples both for PCR- and serology analyses. Several reports to the SVA describe the death of dogs either prior to sampling, or shortly after. In the latter case prior to seroconversion and development of the distinct rise in titres required for diagnosis. Few cases of human infections are reported each year and the majority are travel-associated. The primary diagnosis for human cases is mainly based on serology.

REFERENCES

Lindahl E, Boqvist S, Artursson K, Magnusson U (2011) A field-study on Leptospira seroprevalence in dairy cows in four geographical areas in Sweden. Acta Vet Scand 53:53

Boqvist S, Eliasson-Selling L, Bergström K, Magnusson U (2012) The association between rainfall and seropositivity to *Leptospira* in outdoor reared pigs. The Veterinary Journal 193:135–9

Schuller S, Francey T, Hartmann K, Hugonnard M, Kohn B, Nally J.E., Sykes J. (2015) European consensus statement on leptospirosis in dogs and cats. *Journal of Small Animal Practice* 56, 159–179

Strand TM, Löhmus M, Persson Vinnersten T, Råsbäck T, Sundström K, Bergström T and Lundkvist Å (2015) Highly Pathogenic *Leptospira* Found in Urban Brown Rats (*Rattus norvegicus*) in the Largest Cities of Sweden. Vector Borne Zoonotic Dis 15:779–81

Båverud V, Gunnarsson A, Olsson Engvall E, Franzén P and Egenvall A (2009) *Leptospira* seroprevalence and associations between seropositivity, clinical disease and host factors in horses. Acta Vet Scand 51:15

Listeriosis

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 and semi-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 70–120 human cases have been reported annually. Outbreaks have been associated with vacuum-packaged fish, with semi-soft cheese, 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.

Figure 27: Soft and semi-soft cheeses are common sources of human listeriosis infection. Photo: Drbouz/iStock.

LEGISLATION

Animals

Listeriosis is a notifiable disease in animals according to SJVFS 2021:10.

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 2022:217).

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 2021, listeriosis was reported in 23 sheep, 12 cattle, five goats, two fallow deer, one roe deer, one dog, one horse and in one cat.

Food

In 2021, 364 samples from different types of food taken by national and local authorities were analysed for presence of *L. monocytogenes* in qualitative analysis (presence or no presence). *L. monocytogenes* was detected in thirteen samples (Table 12). In addition, 12 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.

Humans

During 2021 the incidence of listeriosis increased slightly compared to 2020 and the overall picture shows an increasing trend of listeriosis cases in Sweden (Figure 28). In total, 107 cases were reported compared to 88 cases in 2020 (incidence 1.0 cases per 100 000 inhabitants) (Figure 28). The majority of the cases reported with listeriosis belong to the older age groups. The median age was 78 years and as in previous years, most cases were reported in the age group over 80 years (Figure 29). Fifty-eight cases were males and 49 were females. In total, 21 cases (20 percent of reported cases) died within one month from diagnosis. Listeriosis is most often a domestic infection and for 90 percent of the reported cases in 2021 Sweden was noted as the country of infection. In 2021 all but seven (90 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=64), IVb (n=22) and IIb (n=12) while only two cases of IIc were reported. In addition to serotype, sequence type (ST) is also identified by WGS. During 2021 the most common STs were ST8 (n=12) and ST1 (n=11). A more in-depth cluster analysis showed that the proportion of isolates belonging to a cluster was at the same level as in 2020 (33 percent) which was lower compared with the average value for 2017–2019 (52 percent). In total, 13 different clusters were identified of which 10 contained identical or closely related isolates identified already before 2021. One of the clusters with a rare strain of *L. monocytogenes* in Sweden, ST1593, included 10 cases from 2021 and eight cases from 2019. All cases were notified during the Autumn period and the source of infection could not be identified.

Investigations of outbreaks and single cases of listeriosis

In 2021, five cases of *L. monocytogenes* ST14 could be linked to a cluster of 14 cases in Belgium. The cases in Belgium were reported between 2014–2021 and the outbreak strain was also detected in salmon from Norway. For the Swedish cases, salted non-heat-treated salmon was the suspected source of infection.

The source of a local outbreak with two cases of listeriosis with a rare strain of *L. monocytogenes* in Sweden, ST759, was traced to a meat production establishment. One of the cases had eaten a locally produced sausage and samples of food, equipment and premises at the manufacturing establishment were taken by the competent authority. *L. monocytogenes* could not be found in any sample of sausage or other meat products, but the outbreak strain was found in samples from equipment and processing areas.

In addition, one case of listeriosis (ST 18) was 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 cheese and environmental samples from the dairy showed that premises were contaminated by the outbreak strain and that the strain could be isolated from a washed rind cheese and a semi-hard cheese.

DISCUSSION

During 2021 the incidence of listeriosis increased compared to the year before and the overall picture shows an increasing trend of listeriosis. (Figure 28). 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.

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 detection of outbreak clusters of *L. monocytogenes* and for identifying possible links between human cases and food products, subtyping of isolates using WGS is essential.

REFERENCES

EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2018. Scientific Opinion on the Listeria monocytogenes contamination of ready-to-eat foods and the risk for human health in the EU. EFSA Journal 2018;16(1):5134, 173 pp.

Table 12: Results of analyses in 2021 for presence of *L. monocytogenes* in food samples taken by authorities.

Reason for sampling	No. of samples	No. of positive samples	Food in which *L. monocytogenes* was detected
Survey	89	3	1 Meat from bovine animals
Routine control	198	7	6 Fish and fish products
Suspected food poisoning or complaint	43	3	3 Cheese
Other or not reported	34	0	-
Total	**366**	**13**	

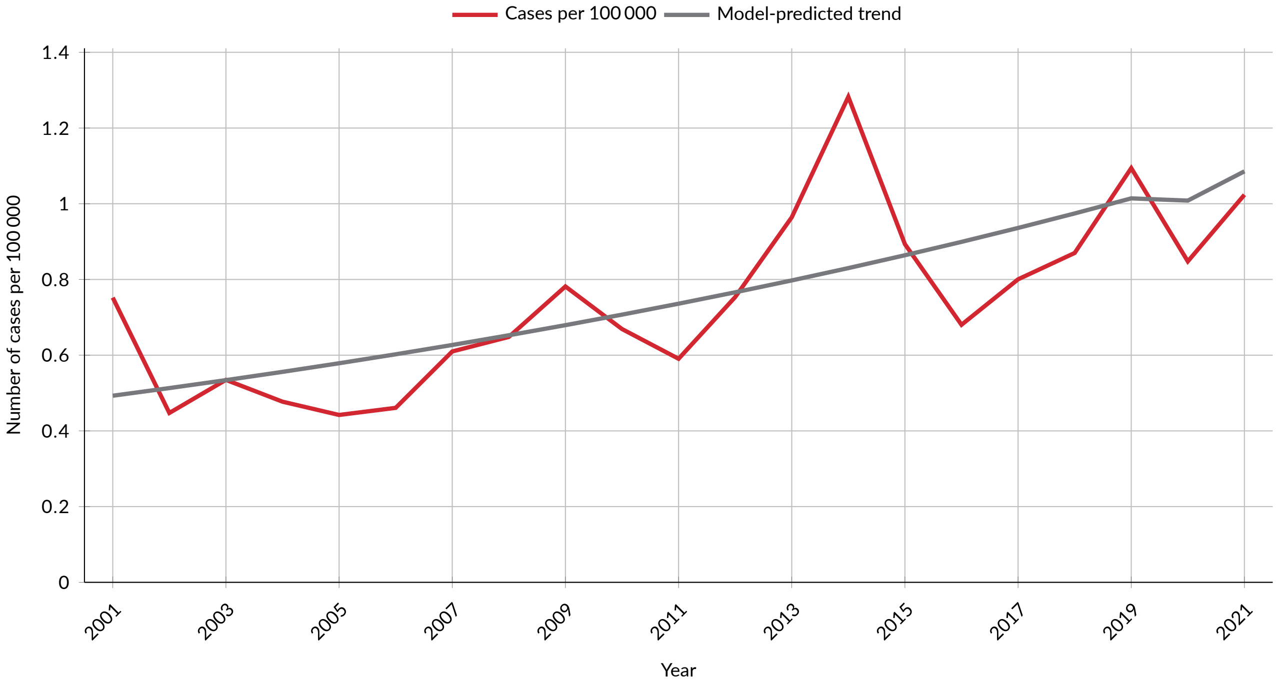


Figure 28: Notified incidence per 100 000 inhabitants of human cases of listeriosis in Sweden 2001–2021 and a model-predicted trend (negative binomial regression). The higher incidence in 2013–2014 is due to two larger outbreaks with in total 49 and 28 cases, respectively.

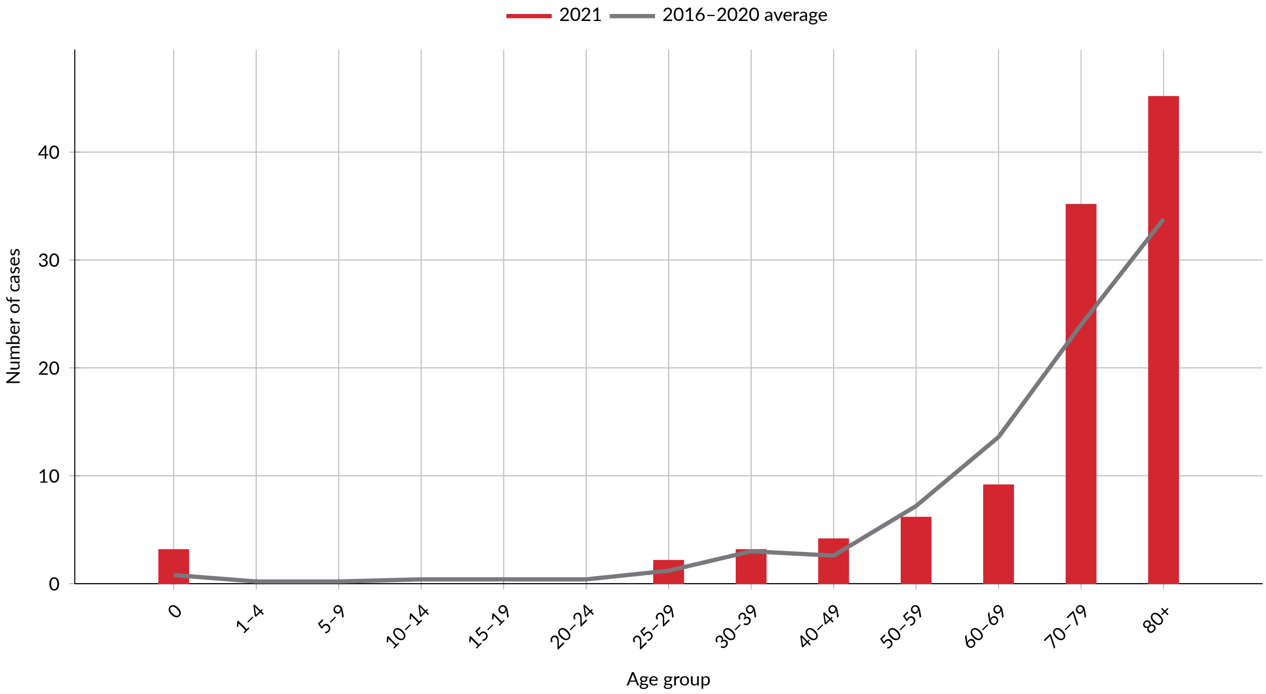


Figure 29: Number of notified human cases of listeriosis per age group in 2021 and annual average for 2016–2020.

Nephropathia epidemica

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 31). 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 30: 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: monap/iStock.

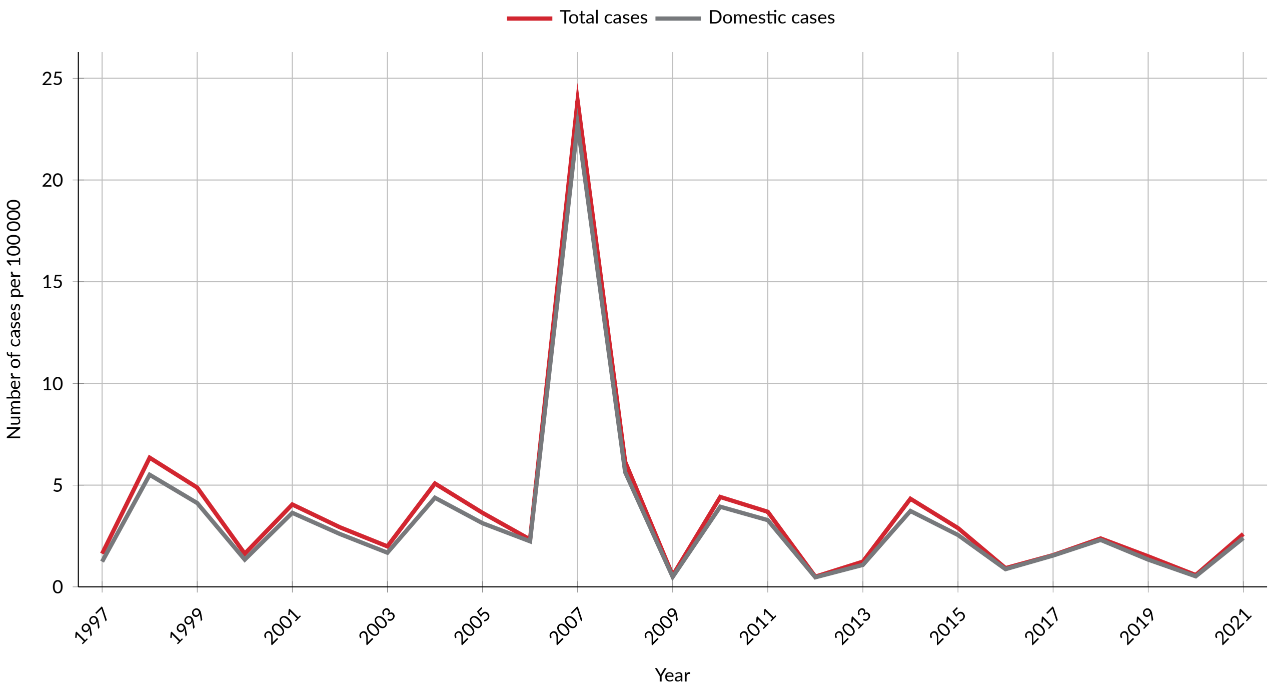


Figure 31: Notified incidence per 100 000 inhabitants of human Nephropathia epidemica in Sweden 1997–2021.

Humans

Nephropathia epidemica has been notifiable since 1989 according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2022:217).

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 2021, 278 cases of NE were reported, which was an increase in comparison to the previous year (Figure 31). The median age among all cases was 57 (range in age from 3 to 91 years) and 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 (60%) 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 2021, almost all cases, for whom the country of infection had been stated, had been infected in Sweden. Two cases stated Finland as their country of infection and one case Romania. For 28 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 counties of Västerbotten and Västernorrland (both with 34 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, as it is very unusual to acquire the infection so far south in the country, one case was suspected to have been infected in the county of Blekinge.

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.

REFERENCES

Evander M, Ahlm C (2009) Milder winters in northern Scandinavia may contribute to larger outbreaks of haemorrhagic fever virus. Global Health Action 2:10.3402/gha.v2i0.2020

Paratuberculosis

BACKGROUND

Paratuberculosis, caused by *Mycobacterium avium* subsp. *paratuberculosis* (MAP), is a common disease of ruminants in most parts of the world. Until today, detected outbreaks in Sweden have been managed through 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.

The limited number of outbreaks of paratuberculosis that have been detected in Sweden have all been directly or indirectly linked to imported beef cattle. The latest case of paratuberculosis 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.

Figure 32: Paratuberculosis has never been detected in Swedish dairy cattle. Photo: Bengt Ekberg/SVA (mirrored).

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. Paratuberculosis is a listed disease (category E) in the Animal Health Law, (EU) 2016/429. SJVFS 2021:23 (K28) complements AHL with provisions as regards measures to prevent spread of Paratuberculosis in Swedish cattle establishments.

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 postmortem 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 post mortem.

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 paratuberculosis. Samples are taken from the ileal wall, ileal contents and ileocaecal lymph nodes and submitted to the National Veterinary Institute (SVA). Most of examined animals have been 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 2021, the voluntary programme for bovine paratuberculosis encompassed 464 herds, of which 428 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, the test method was changed during 2021 from individual faecal samples annually for three years to individual blood samples which are collected annually for two consecutive years from all cattle over two years of age. Serological positive samples are followed up with individual faecal samples from all cattle over two years of age and retested serologically the following year. Herds affiliated to the programme are only allowed to trade with herds of the same status or higher to maintain their level within the programme. After two years of negative test results, the blood sampling is replaced by post mortem examination 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 cattle population, to also include the dairy cattle, it was decided in 2019 to implement annual bulk milk testing. This surveillance component was designed to demonstrate, with a 99% probability and a detection level of 5%, that the Swedish cattle population is free from paratuberculosis, considering an annual 0.1% probability of introduction. To reach this goal, the aim was to randomly collect and test bulk milk samples from 285 dairy herds.

Table 13: Cattle sampled for paratuberculosis in 2021.

Surveillance in cattle	No. of sampled animals	No. of herds
Beef herd surveillance programme	835	35
Cattle sampled at post mortem examinations	224	48
Cattle sampled for export	5	2

Table 14: Exotic ruminants sampled for paratuberculosis in 2021.

Surveillance in exotic ruminants	No. of sampled animals	No. of herds
Exotic and wild kept ruminants sampled at post mortem examination[A]	5	5
Exotic and wild kept ruminants sampled for export	5	2

[A] 1 alpaca, 1 red deer, 1 wisent, 1 moose and 1 reindeer

Table 15: Sheep and goats sampled for paratuberculosis in 2021.

Surveillance in sheep and goats	No. of sampled animals	No. of herds
Sheep sampled in cattle herds within the beef herd surveillance programme	17	3
Sheep sampled at post mortem examinations	58	53
Goats sampled at post mortem examinations	9	8

Abattoir testing

In parallel to the bulk milk testing, a surveillance component designed to demonstrate an equivalent confidence of freedom from paratuberculosis in beef cattle herds was implemented in 2020. This is based on testing of serum samples collected at slaughter.

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

Blood from the voluntary programme, the abattoir testing and the bulk milk samples and are analysed with the ID Screen Paratuberculosis Indirect commercial ELISA kit (Innovative Diagnostics, Grabels, France) on an automated ELISA system (Tecan, Männedorf, Switzerland). Positive reactions in the screening test are confirmed using the IDEXX Paratuberculosis Verification Ab Test (IDEXX Laboratories, Westbrook, Maine, United States), also an indirect commercial ELISA kit but with improved specificity by using individual negative control samples. Any positive serological reactions are followed up with faecal samples for pathogen detection with PCR.

In addition, samples collected from clinical suspicions are analysed with direct PCR. Real-time PCR is performed using a commercial kit.

Tissue samples and faecal samples from post mortem surveillance is cultured for four months (cattle) or six months (sheep and goat). Direct PCR on a new preparation from the stored samples are performed on cultures with mould overgrowth.

All diagnostic analyses are performed at SVA.

RESULTS

Passive surveillance

In 2021, two suspicions of paratuberculosis, in and dairy cow and one alpaca, were raised due to clinical signs of the disease. Both animals were sampled and tested negative for MAP with PCR and the suspicions were ruled out.

Active surveillance

Bulk milk samples from 288 dairy herds were tested, all with negative results. In the abattoir serum sampling, 2182 analyses of samples from 911 herds were conducted. Three samples from three herds had a positive serological test result. In the herds of origin of the test positive cows, individual faecal samples from all cattle over two years of age were collected and analysed with PCR with negative results and MAP were excluded. Moreover, 835 cattle samples from 35 herds, and 17 sampled sheep or goat from 3 herds, were analysed and tested negative within the programme in beef herds. For export reasons, nine cattle were tested. 296 were sampled at post mortem examination: 224 cattle, 58 sheep, 9 goats, 1 red deer (*Cervus elaphus*), 1 alpaca, 1 reindeer (R*angifer tarandus*), 1 wisent (Bison bonasus) and 1 moose (*Alces alces*). No cases of MAP were detected in the examinations completed in 2021 (Tables 13, 14 and 15). Based on surveillance from present and previous years the Swedish cattle population can be considered free from paratuberculosis with a probability of >95%.

DISCUSSION

If present at all, the prevalence of paratuberculosis in Swedish ruminants remains at a very low level. However, a previous evaluation of the paratuberculosis surveillance programme indicated that the surveillance sensitivity in the last years has decreased. In order to improve the surveillance sensitivity in the dairy cattle population and beef cattle herds not affiliated to the voluntary programme, testing of bulk milk samples and abattoir serum samples were added to the surveillance programme during 2019 and 2020.

Adding these surveillance components, will enable us to reach the desired level of freedom from paratuberculosis at 99% in Swedish cattle within the next couple of years. The risk of introduction of paratuberculosis to Swedish herds is assessed to be very low (1% annually), due to the low number of animals brought in from other countries. The 3 positive serological samples in the surveillance during 2021 were considered to be false positives because of the detailed follow-up investigations. The test specificity for the serological test was previously estimated to >99.5%. The testing applied to Swedish cattle herds during the period 2020–2021 indicate that the specificity of the test is higher. During this period, 4105 samples were tested with 5 samples positive which were considered false positives after confirmatory testing and one herd is still under investigation. This indicated that the specificity of the serological screening test may be as high as 99.85%.

The risk of introduction of paratuberculosis to Swedish herds is assessed to be very low, due to 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 introduction of MAP into 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.

REFERENCES

Frössling J, Wahlström H, Ågren E, Cameron A, Lindberg A, Sternberg-Lewerin S (2013) Surveillance system sensitivities and probability of freedom from *Mycobacterium avium* subsp *paratuberculosis* infection in Swedish cattle. Prev Vet Med 108:47–62.

Rockström U (2011) Slutrapport; Undersökning avseende paratuberkulos i nötkreatursbesättningar som varit sista besättning till djur, vilka importerats till Sverige under 1990 till 2005. Jordbruksverkets diarienr 33–4861/11.

Sternberg Lewerin S, Ågren E, Frössling J, Bölske G, Holmström A, Lindberg A, Szanto E, Viske D (2007) Control of paratuberculosis in Sweden. In the proceedings of: 9th ICP, Japan, Nov 2007.

Porcine reproductive and respiratory syndrome

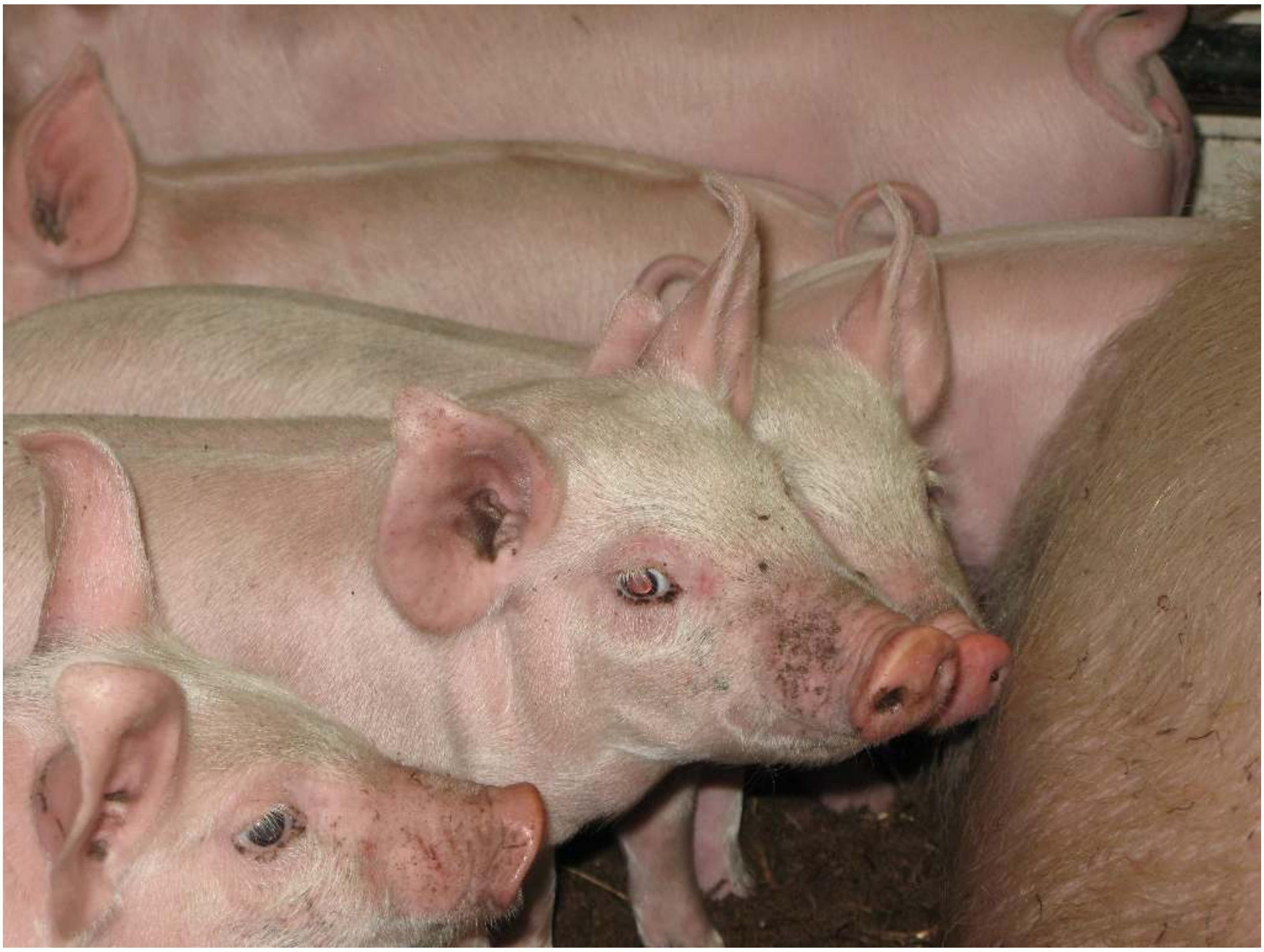


Figure 33: After the successful eradication of porcine reproductive and respiratory syndrome virus (PRRSV) following an outbreak in 2007, annual surveillance shows that Sweden has remained free from the PRRSV since 2008. Photo: Marie Sjölund.

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 (SVA). 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 factors such as virulence of the particular strain of PRRS virus, age of the infected animals, presence of other disease agents in the herd and herd management practices. The incubation period is 2–7 days and, in adult pigs, the clinical signs are often mild, consisting of fever, lethargy and inappetence, although certain strains of PRRSV can cause severe disease, including high mortality, in adult animals. The most obvious clinical signs of PRRSV infection in this category of animal are typically reproductive problems including abortion, mummified foetuses, small litters, weak-born piglets, high piglet mortality 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.

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. PRRS is a listed disease (categories D and E) in the Animal Health Law, (EU) 2016/429. SJVFS 2021:24 (K29) complements the AHL with provisions as regards measures to prevent the spread of PRRS in Swedish pig establishments.

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 SVA. To detect antibodies against PRRSV, a commercial ELISA method (IDEXX PRRS X3 Ab Test, IDEXX Laboratories, Westbrook, Maine, United States) 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 135).

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. Eight samples per herd are collected 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 2021, the calculated number of samples required was 2400 from the abattoir sampling in addition to the field sampling described above.

RESULTS

Passive surveillance

Three investigations following clinical suspicions of PRRS were conducted in 2021. In all three herds, reproductive problems such as abortion, weak-born piglets and increased piglet mortality were the primary clinical signs. In one herd, increased mortality in weaned pigs was also noted. 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, 16 foetuses from 12 herds were examined for the presence of PRRSV genome and all samples were negative.

Active surveillance

In 2021, 626 samples from 41 nucleus herds, multiplying herds and sow pools were analysed. In the abattoir sampling, 2175 samples originating from 433 herds on 726 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 2021’s active surveillance, 3 samples from 3 different herds were serologically positive by both ELISA and IPMA testing. Two of these positive samples were collected in sow herds and one sample was collected at an abattoir. Herd investigations were conducted in all 3 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

Table 16: Number of samples and herds tested in the active surveillance for porcine reproductive and respiratory syndrome 2009–2021 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
2021	626	41	2175	726	433	2801	1190

[A] Jordbruksverket statistikdatabas (statistik.sjv.se/pxweb).
[B] Some herds were sampled more than once.

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 >95%.

Also in 2021, one herd investigation was initiated after a serum sample taken from a group of animals prior to export tested positive for PRRS antibodies by both ELISA and IPMA analysis. No clinical signs indicative of PRRS were observed in the group and follow-up samples taken from the animals 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.

REFERENCES

Carlsson U, Wallgren P, Renström LH, Lindberg A, Eriksson H, Thorén P, Eliasson-Selling L, Lundeheim N, Nörregard E, Thörn C, Elvander M (2009) Emergence of Porcine Reproductive and Respiratory Syndrome in Detection, Response and Eradication. Transboundary and Emerging diseases 56:121–131

Frössling J, Ågren ECC, Eliasson-Selling L, Sternberg-Lewerin S (2009) Probability of freedom from disease after the first detection and eradication of PRRS in Sweden: Scenario-tree modelling of the surveillance system. Prev Vet Med 91:137–45

Hultén C, 2012. Översyn av den aktiva övervakningen av porcine reproductive and respiratory syndrome (PRRS) i Sverige. SVA D-nr 2012/50 (In Swedish)

Kleiboeker AB, Schommer SK, Lee AM, Watkins S, Chittick W, Polson D (2005) Simultaneous detection of North American and European porcine reproductive and respiratory syndrome virus using real-time reverse transcriptase-PCR. J Vet Diagn Invest 17(2):165–170

Lindberg A, 2008. PRRS-översyn av övervakningsprogrammet. SVA D-nr 2008/429 (In Swedish)

Psittacosis

Figure 34: Contact with faeces from wild birds, for example when cleaning bird feeders, is considered a major risk of human psittacosis infection. Photo: Tunatura/iStock.

BACKGROUND

Psittacosis is caused by *Chlamydia psittaci*, an intracellular bacterium. In 1879, psittacosis was described for the first time in humans when an outbreak of pneumonia associated with exposure to tropical pet birds was diagnosed 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. Between birds the infection is transmitted via contact, by ectoparasites or contaminated equipment. *C. psittaci* may persist in dry faecal material for months.

In some countries, infections caused by *C. psittaci* have been described in mammals, such as cattle, sheep and horses.

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 usually recover from the infection, but mortality can reach 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 birds according to SJVFS 2021:10.

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 2022:217).

SURVEILLANCE

Animals

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

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 2021, *C. psittaci* was detected in one of ten pet birds tested at SVA. In addition, one wild pigeon and one chicken were tested, with negative results.

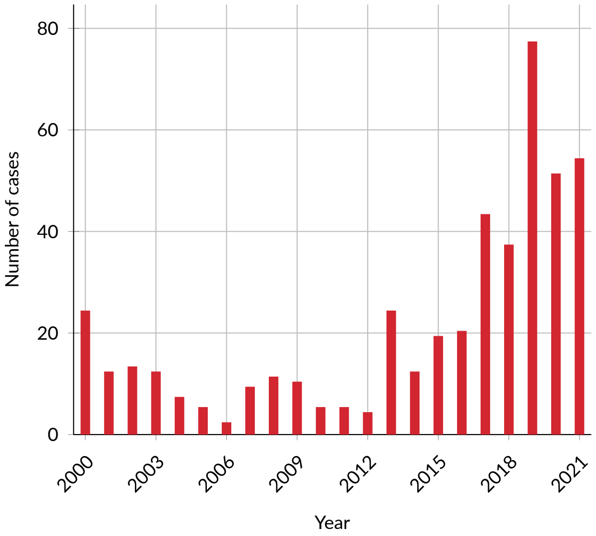


Figure 35: Number of notified human cases of psittacosis in Sweden 2000–2021.

Humans

In 2021, 54 cases of psittacosis were reported which is about the same number as the year before (Figure 35). In Sweden, psittacosis is mainly a domestic infection and during this year none of the cases were reported to have been infected abroad. The highest number of cases were reported from the Region of Västra Götaland (n=10), followed by Stockholm (n=7) and Kalmar (n=6). Of the cases 43 (80%) were male and 48 (89%) over 50 years old. Contact with birds and bird droppings were considered an important route of transmission. For 21 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 2021, 37 (69%) of the cases were reported in January-February and December.

DISCUSSION

During the recent four years, there has been a marked increase in the number of notified cases of psittacosis in humans. 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. Exposure to infected pet birds and poultry species can lead to zoonotic transmission.

C. psittaci has been detected in a variety of wild bird species, most often in seabirds, doves and parids. 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. No screening has so far been done among hobby poultry.

REFERENCES

Rehn M, Ringberg H, Runehagen A, Herrmann B, Olsen B, Petersson AC, Hjertqvist M, Kühlmann-Berenzon S, Wallensten A (2013) Unusual increase of psittacosis in southern Sweden linked to wild bird exposure, January to April 2013. Euro Surveill 18:20478.

Blomqvist M, Christerson L, Waldenström J, Herrmann B, Olsen B (2012) *Chlamydia psittaci* in Swedish wetland birds: a risk to zoonotic infection? Avian Dis 56:737–40.

Blomqvist M, Christerson L, Waldenström J, Lindberg P, Helander B, Gunnarsson G, Herrmann B, Olsen B (2012) *Chlamydia psittaci* in birds of prey, Sweden. Infect Ecol Epidemiol 2:10.3402/iee.v2i0.8435.

Chereau F, Rehn M, Pini A, Kühlmann-Berenzon S, Ydring E, Ringberg H, Runehagen A, Ockborn G, Dotevall L, Wallensten A (2018). Wild and domestic bird faces likely source of psittacosis transmission – a case-control study in Sweden, 2014–2016. Zoonoses Public Health 65(7):790–797. doi: 10.1111/zph.12492.

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.

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. 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.

Figure 36: 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: Bengt Ekberg/SVA.

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 37). 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.

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.

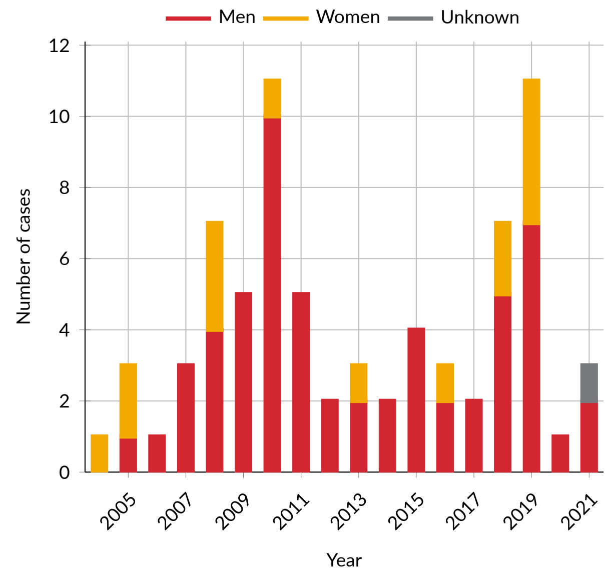


Figure 37: Number of human cases of Q fever by sex 2004–2021.

LEGISLATION

Animals

Q fever is a notifiable disease (SJVFS 2021:10). 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 2022:217).

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 2021 on sheep, cattle and water buffaloes, mainly for export reasons. Blood samples from 98 sheep, 5 cattle and 8 water buffaloes 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. All samples that were submitted for testing were negative.

Humans

In 2021, three cases of Q fever were reported, which is at a comparable level to the last ten years, with the exception of 2018–2019 (Figure 37). Two of the cases were men and for the third case the sex was unknown. All of them were older than 50 years of age. Two cases had acquired their infections in Ethiopia and Spain respectively, while the country of infection was unknown for the third one. For one case, unpasteurized camel milk was mentioned as a probable source of infection.

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.

REFERENCES

ECDC. Technical report: Risk assessment on Q fever. [46 pp] doi:10.2900/28860. Available online: https://www.ecdc.europa.eu/en/publications/Publications/1005_TER_Risk_Assessment_Qfever.pdf

EFSA Panel on Animal Health and Welfare (AHAW); Scientific Opinion on Q Fever. EFSA Journal 2010; 8(5):1595. [114 pp.]. doi:10.2903/j.efsa.2010.1595. Available online: https://www.efsa.europa.eu

Rabies

Figure 38: Illegally imported dogs from endemic countries are probably the greatest threat to the rabies-free status of Sweden. Photo: GoodLifeStudio/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 a listed disease (category B, D and E) in the Animal Health Law, (EU) 2016/429. Sweden is officially free from the disease in accordance with (EU) 2021/620. Rabies is notifiable on clinical suspicion as described in SJVFS 2021/10 (K12).

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.

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 2021, six dogs were examined for rabies due to clinical suspicion. In addition, three dogs originating from outside of Sweden were examined for rabies on request by the County Medical Officers due to human exposure through bites. Four dogs with foreign origin displaying unspecific clinical signs (not specific to rabies) were also examined for rabies to rule out the diagnosis.

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

In addition, 40 illegally introduced euthanized dogs 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 2021 tested negative.

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.

This scenario can be exemplified by a case reported in Germany 2021. A dog was adopted from Turkey in September 2021 by the owner during a vacation, and illegally imported to Germany. After eight days, the dog had developed non-specific clinical signs and was taken to a private veterinarian. During the clinical examination, the dog died and was sent to the regional veterinary laboratory for necropsy where it was confirmed to be infected by rabies virus. Sequence analysis showed that the rabies virus was closely related to a virus isolated in a fox in Turkey 2001. There was no further secondary transmission to other animals and all contact persons received post-exposure vaccination.

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. In 2021, cases have only been reported in Romania and Poland. In Romania, the situation has improved in recent years, while in Poland there was a resurgence of fox rabies in a previously freed area close to the eastern border to Belarus and Ukraine. Vaccination campaigns of wild and domestic animals, and other control measures have been put in place by Polish authorities. 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, Belarus, Ukraine, Moldova and Turkey are considered high-risk countries with several 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 developed 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 2021, as in 2020, the COVID-19 pandemic has resulted in both a very low incidence of salmonellosis and a very 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 and pigs 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 with amendments, SJVFS 2022:3) 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 2022:217). 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 (SVA) for confirmation and serotyping. 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, flock or the companion animal, findings of *Salmonella* at postmortem 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 further 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 a subset of isolates of all serovars from food and animal sources is characterized by whole genome sequencing (WGS).

All isolates of *Salmonella* from domestic human cases are sent to the Public Health Agency of Sweden for typing using 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.

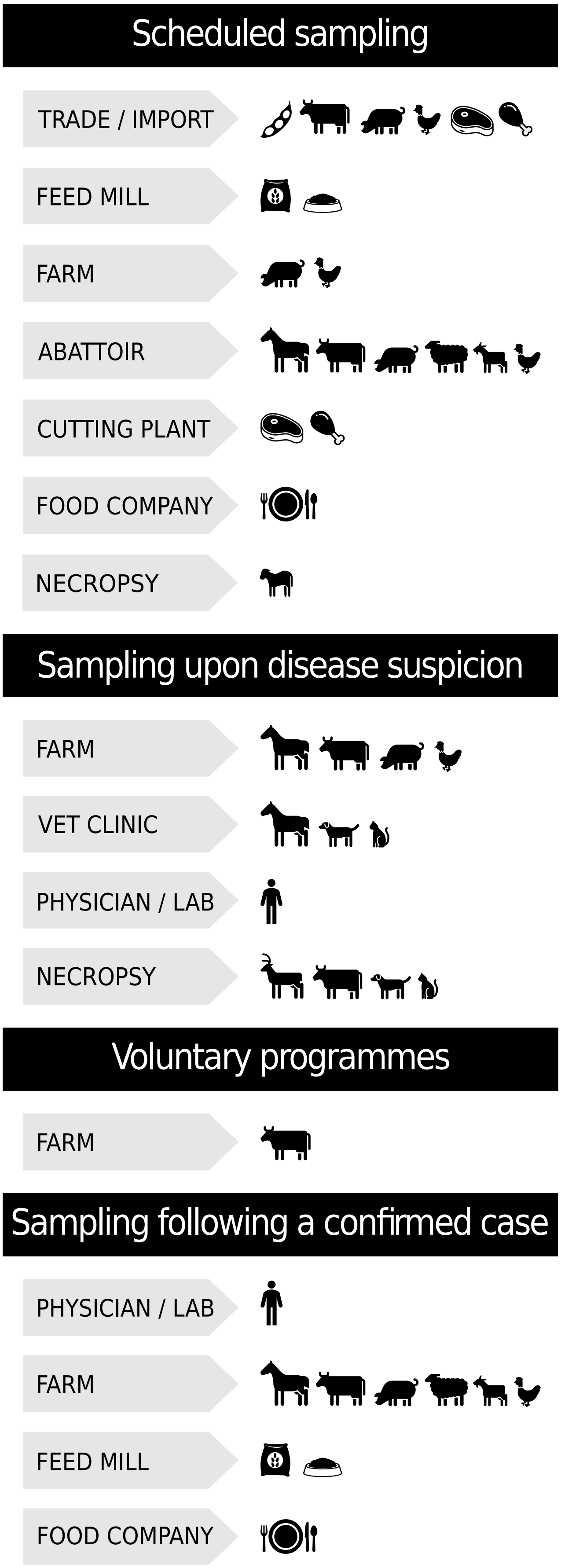


Figure 39: An illustration of the Swedish surveillance of *Salmonella* in feed, food, animals and humans. Infographic by Arianna Comin.

IN FOCUS: Re-emergence of *Salmonella* Choleraesuis

Salmonella Choleraesuis is a host-adapted serovar most often associated with pigs and wild boar, but which may also cause disease in humans and occasionally in other mammalian species. This serovar, like the other host adapted serovars, is more often a cause of systemic disease and septicaemia than the more universal ones.

Prior to the detection of *S*. Choleraesuis in a pig herd, one of its contact herds, and a small game enclosure of wild boar in the autumn of 2020, the serovar had not been found in pigs or other Swedish animals since 1979. Following these detections of *S*. Choleraesuis, a surveillance in free-living wild boar was initiated. All wild boars found dead and submitted to the National Veterinary Institute were tested for *Salmonella*. In addition, a subset of hunted wild boars was tested, beginning first in the vicinity of the initial detection site in pigs in Skåne and the game enclosure in Södermanland. The survey was expanded during 2021 to include all counties with an established wild boar population. This sampling continued throughout 2021, with the aim of estimating the occurrence of *S*. Choleraesuis in wild boar in other counties.

Prior to the detection of *S*. Choleraesuis, *Salmonella* surveillance in wild boar was passive. Wild boars were tested for *Salmonella* within the wild animal surveillance programme only upon clinical suspicion. After detection of *S*. Choleraesuis, isolates of this serovar from wild boar found dead and tested through wild animal surveillance were sequenced, with one isolate from June 2020 shown to be closely related to the isolates from domestic pigs. The only other recent wild boar isolate, recovered in 2018, was found to be unrelated to all other sequenced isolates. In addition, there was one human case from 2019 which was closely related to the strain found in wild boar and pigs in 2020.

By the end of 2021, a total of 546 wild boar have been sampled. In the counties of Skåne and Södermanland/Stockholm, a high proportion of samples were positive for *S*. Choleraesuis (Table 17). Outside these regions, there was only one finding of the specific serovar in a wild boar found dead in the county of Halland. In addition, the surveillance resulted in sporadic findings of several other serovars (see under Results/Other animals).

During 2021, *S*. Choleraesuis was confirmed in three additional pig herds. One of these herds was detected after the finding of this serovar in a lymph node at slaughter, another through contact tracing of this herd and the third herd was detected after traceback of a human case of *S*. Choleraesuis. These three herds had no other known direct or indirect connections to the pig herd in which *S*. Choleraesuis was originally detected in 2020, other than being located in the same county with findings in wild boar.

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.

In addition, within the scheduled sampling of the control programme during 2021, *S*. Choleraesuis was detected in a lymph node from one slaughter pig, in a lymph node from cattle and in one cattle carcass sample. *S*. Choleraesuis was not detected in the two herds at trace-back from lymph nodes.

So far, all isolates with an antigenic formula of O6,7:-:1,5 or O6,7:c:1,5 from wild boar submitted for sequencing have been verified as *S*. Choleraesuis.

Sequenced isolates from pigs and wild boar show minor genomic variation consistent with area county of origin but are overall very similar to each other and to the two human cases. This indicates a comparatively recent common source of the infection. In an international comparison, the Swedish outbreak isolates most closely resemble previously sequenced isolates from Poland, the Czech Republic and Germany. The isolates have been tested for antimicrobial resistance and found to be fully susceptible to all tested antimicrobial substances.

The re-emergence of *S*. Choleraesuis in Sweden and the presence of this pathogen in the wild boar population pose a threat to the pig production and calls for strengthened biosecurity measures in pig farms directed towards avoiding introduction of pathogens from the environment. As *Salmonella* may be present in wild boar, measures to avoid contamination of the meat include using only apparently healthy game for food, applying thorough hygiene measures when dressing and butchering, as well as when preparing wild boar meat in the kitchen. To determine the distribution and spread of *S*. Choleraesuis a continuous surveillance in the wild boar population would be needed. Further investigations, including sampling of feed and at feeding stations could be added to the surveillance, to assess the possibility of managing and reducing the presence of *S*. Choleraesuis in the wild boar population.

Table 17: Results of surveillance of *S*. Choleraesuis in wild boar found dead and in apparently healthy hunted wild boar from October 1st 2020 to December 31st 2021.

County/Area	Category	Number sampled	*S*. Choleraesuis	Other *Salmonella*
Stockholm and Södermanland	Hunted	112	23 (20.5%)	5 (4.5%)
	Found dead	30	11 (36.7%)	1[A]
Skåne	Hunted	184	19 (10.3%)	7 (3.8%)
	Found dead	7	4 (57.1%)	0
Other counties	Hunted	174	0	8 (4.6%)
	Found dead	39	1[B]	2[A]

[A] Percentage is not reported when the number of animals is low.

[B] One fallen boar with *S*. Choleraesuis was found in the County of Halland.

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 39).

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 SVA (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 (Thermo Fisher Scientific, Lelystad, Netherlands).

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 39).

Compulsory programme

All breeding flocks with more than 250 birds are tested (Table 18). 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 18). 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 the 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

Table 18: 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

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 39).

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 nucleus and gilt-multiplying herds and biannual sampling from sow pools. In cattle, *Salmonella* testing is performed in all calves <15 months of age that are submitted for necropsy. In both cattle and pigs, *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 “FriskKo (Healthy Cow)” 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 2021, regional bulk milk screenings were performed on the islands of Gotland and Öland in June and October. Gotland and Öland were the counties with the highest proportion of test positive herds in the national screening in 2019. All samples were analysed with PrioCHECK® Salmonella Ab bovine ELISA (O antigens 1, 4, 5, 12 and 1, 9, 12; Thermo Fisher Scientific, Lelystad, Netherlands). Samples with a PP-value higher than twenty (PP>20) in this first test were also analysed with PrioCHECK® Salmonella Ab bovine Dublin ELISA (Thermo Fisher Scientific, Lelystad, Netherlands; 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 39). Wild animals necropsied at SVA are also tested for *Salmonella* on suspicion (see chapter ”Post mortem examinations in wildlife” on page 140).

Surveillance of *Salmonella* in wild boar was initiated during 2020 following the detection of *Salmonella* 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 SVA from all of Sweden and a subset of apparently healthy shot wild boar from all counties with a wild boar population were analysed for *Salmonella* according to ISO 6579:1. Suspected isolates of *S.* Choleraesuis were whole genome sequenced for confirmation and further typing. The surveillance activity is ongoing (see “In focus”).

Food

Control of *Salmonella* is an important part of in-house quality control programmes in many food enterprises in Sweden (Figure 39). 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 SVA.

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 to be reported to EFSA, but they 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 39). 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, 7412 samples were analysed for *Salmonella;* 17 of these samples (0.23 %) were positive. Nine serovars were detected; *S.* Typhimurium was the most common (n=6) (Table 19).

In addition, *Salmonella* was detected in 7 out of 1949 analysed batches from feed materials of vegetable origin. The most common serovars were *S.* Senftenberg, *S.* Tennessee and *S.* Typhimurium (n=2). No *Salmonella* was detected during the year in feed materials of animal origin and from pet food out of 1146 analysed batches.

Animals

Poultry

Salmonella was detected in 11 of the 4077 broiler flocks tested in routine sampling before slaughter (Table 20 and Figure 40). *Salmonella* was detected in three of the 891 layer flocks tested (Figure 41). One of these layer flocks tested positive for *Salmonella* was detected after a cluster of foodborne infections.

Salmonella was not detected in any breeding flocks. Parent flocks of chicken from one breeding company were euthanised due to the outbreak of Avian Influenza which led to a shortage of production animals. Therefore, the Swedish Board of Agriculture permitted the industry to import hatching eggs from another EU MS. After the import, *S.* Enteritidis, of an indistinguishable genotype, was detected in altogether nine chicken flocks delivered by the same hatchery. In addition, *S.* Enteritidis of an unrelated genotype, was detected in a layer flock.

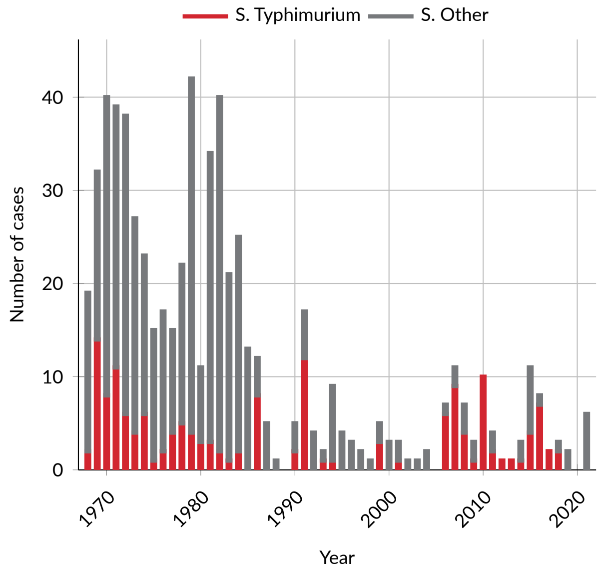


Figure 40: Annual notifications of *Salmonella* in broiler holdings during 1968–2021, breeding flocks included.

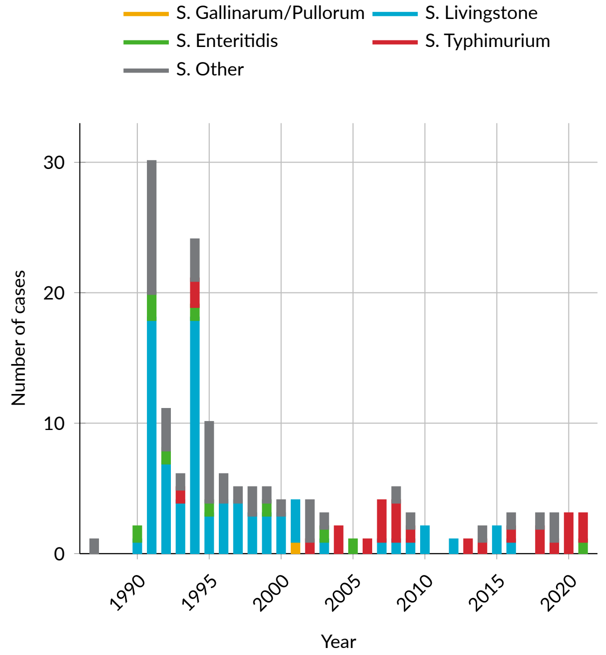


Figure 41: Annual notifications of *Salmonella* in layer holdings during 1987–2021.

Table 19: Serovars of *Salmonella* isolated in feed control in 2021.

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. Enteritidis	-	-	-	-	-	1	-
S. Infantis	-	-	-	-	-	1	-
S. London	-	-	1	-	-	1	-
S. Mbandaka	-	-	-	-	-	4	-
S. Molade	-	-	1	-	-	-	-
Monophasic *S.* Typhimurium	-	-	-	-	-	1	-
S. Senftenberg	-	-	2	-	-	-	-
S. Tennessee	-	-	2	-	-	1	-
S. Typhimurium	-	-	2	-	-	6	-
S. Welikade	-	-	-	-	-	1	-
S. Yoruba	-	-	-	-	-	1	-
Total	**0**	**0**	**7**[D]	**0**	**0**	**17**	**0**
Number of samples	1030	116	1340	550	59	7412	749

[A] Meat and bone meal, animal fat, fish meal, greaves, protein meal, meat meal, poultry offal meal, tallow balls and animal by-products.

[B] Derived from palm kernel, rape seed, soya bean, linseed, peanut and sunflower seed.

[C] Peas, algae, beans, herbs (dried), and berries.

[D] In one of the units positive for *Salmonella* two other serotypes were found.

Table 20: Results from the *Salmonella* control programme in poultry flocks in 2021. 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
Gallus gallus	Meat production	Adult Grand Parent	0	0	-	-
Gallus gallus	Meat production	Adult Parent	0	0	-	-
Gallus gallus	Meat production	Production	4077	11	0.27%	*S.* Enteritidis (n=9), *S.* Tennessee (n=2)
Gallus gallus	Egg production	Adult Parent	0	0	-	-
Gallus gallus	Egg production	Production	891	3	0.11%	*S.* Enteritidis (n=1), *S.* Typhimurium (n=2)
Turkeys	Meat production	Adult Parent	0	0	-	-
Turkeys	Meat production	Production	175	0	0.00%	-
Geese	Meat production	Production	0	0	-	-
Ducks	Meat production	Production	14	1	7.14%	*S.* Typhimurium

Salmonella was detected in one flock of geese but not in any flocks with commercially raised flocks of turkeys, ducks, quails, or ostriches. 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.

Cattle

In total, *Salmonella* was detected in eight new herds in 2021 (Figure 42). *Salmonella* was isolated from three (0.08%) of 3776 mesenteric lymph nodes from cattle at slaughter (Table 21 and Figure 44). The serovar *S.* Choleraesuis was detected in samples of mesenteric lymph nodes from one cattle and from one carcass swab.

In the regional bulk milk screenings in Gotland, 6.4% of the tested herds were positive in June (8/125) and 26.2% in October (32/122), of which non were positive in the Dublin ELISA. This was a at the same level as in October 2019 when 22% (30/139) of the herds in Gotland had positive test results, but more than in the regional screenings 2020 and in April 2021. Results in Öland were 18% (22/122) and 26% (28/108) test positive herds in June and October respectively, of which most were also positive in the Dublin ELISA. This confirms a continued endemic situation of *Salmonella* Dublin in Öland. 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 six pig herds (Figure 43) and in five (0.15%) of 3417 lymph node samples taken from adult pigs and from five (0.16%) of 3146 lymph node samples from fattening pigs (Table 21, Figures 45 and 46). In one case, after detection of salmonella in a pooled sample of lymph nodes, samples from four individual lymph nodes from the pool were also found positive. As these four lymph nodes originated from animals from different herds but still had identical resistance profiles, a failure either at the abattoir or at the laboratory analysing the primary samples is strongly suspected. Thus, when summarising the results this finding is counted as one (not four).

One of the pig herds in which *Salmonella* was detected in 2021 was the hub of a large sow pool where *S.* Derby was isolated from samples taken within the compulsory biannual faecal sampling of sow pools. There were over 2000 sows in the sow pool, which consisted of the hub herd, three internal satellite herds and five external satellite herds. Subsequent sampling indicated that all the satellite herds were also infected with *S.* Derby. Because of the continuous movement of sows between the hub and the satellites, all herds in the pool have been treated as one epidemiological unit during the management of the outbreak.

In 2020, the serovar *S.* Choleraesuis was detected in a breeding herd and one of its contact herds. These were the first detections of *S.* Choleraesuis in domestic pigs in Sweden in over 40 years. During 2021, *S.* Choleraesuis was detected in an additional three pig herds (see “In focus”)

Other animals

Salmonella was detected in two horse stables. Index cases of *Salmonella* infection were detected in 42 cats, 7 dogs, 5 wild birds and two hedgehogs (Table 22).

Salmonella was detected in wild boar in 21 municipalities in eight counties (Halland, Kalmar, Kronoberg, Skåne, Stockholm, Södermanland, Västra Götaland and Östergötland) and 23 index isolates were notified from these municipalities (Table 22). In total during 2021, *S.* Choleraesuis was detected in 13 out of 61 wild boar found dead and in 22 out of 318 shot wild boar (See In focus). In addition, other serovars were found in one wild boar found dead and in 14 shot wild boar. Serotypes other than S. Choleraesuis isolated from wild boar were S. Diarizonae (9), S. Typhimurium (4), S. Newport (2) S. Hessarek (1, by sequencing), S. Duesseldorf, S. Enteriditis, S. Coeln, four belonging to the O6,8-group and one belonging to the O4-group (no further typing available).

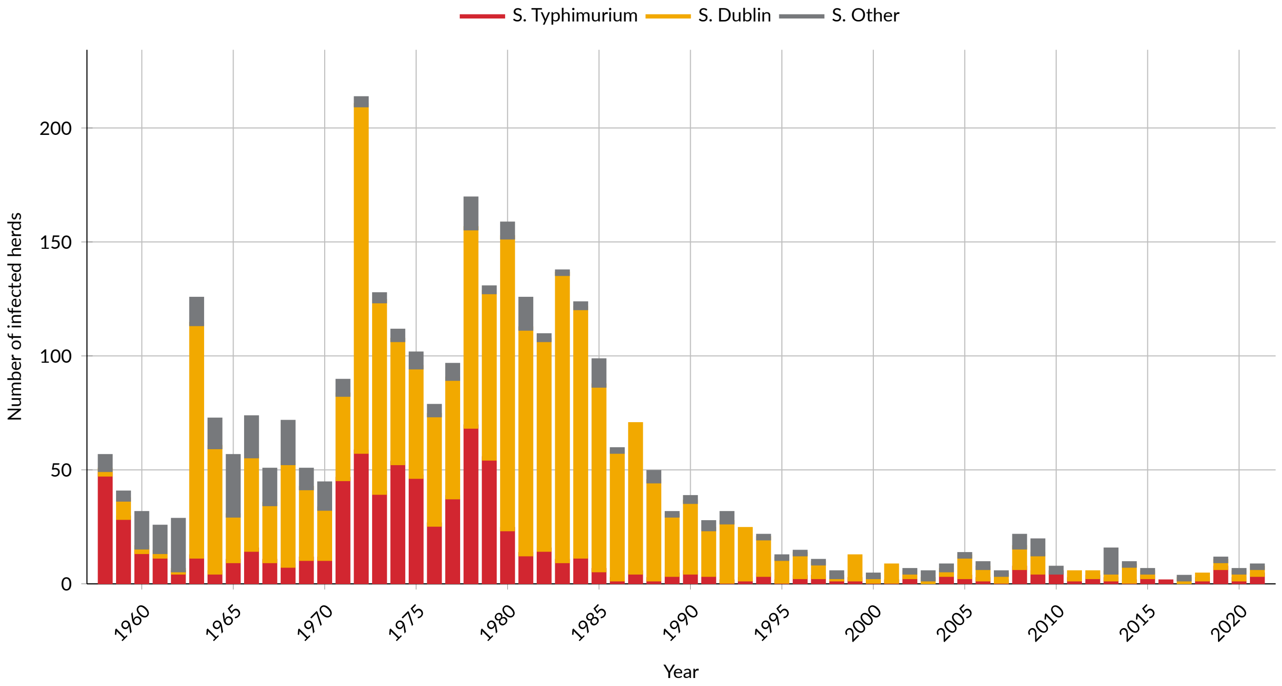


Figure 42: Annual notifications of *Salmonella* in Swedish cattle herds during 1958–2021. Data from 1958 through 1967 is extracted from a graph presented by J.Å. Robertsson (1985).

Table 21: Results from the *Salmonella* control programme at abattoirs and cutting plants in 2021.

Animal species	Sample type	No. samples	No. positive	Percentage	Serovar
Cattle	Lymph node	3776	3	0.08%	*S.* Choleraesuis (n=1), *S.* Typhimurium (n=2)
	Carcass swab	3831	2	0.05%	*S.* Choleraesuis (n=1), *S.* Typhimurium (n=1)
Adult pigs	Lymph node	3417	5	0.15%	*S.* Choleraesuis (n=1), *S.* Typhimurium (n=4)
	Carcass swab	3336	1	0.03%	*S.* Typhimurium
Fattening pigs	Lymph node	3146	5	0.16%	*S.* Choleraesuis (n=1), *S.* Typhimurium (n=4)
	Carcass swab	3090	0	0.00%	-
Cattle and pigs	Meat trimmings	4921	0	0.00%	-
Poultry	Neck skin	2940	0	0.00%	-
	Meat trimmings	1205	0	0.00%	-

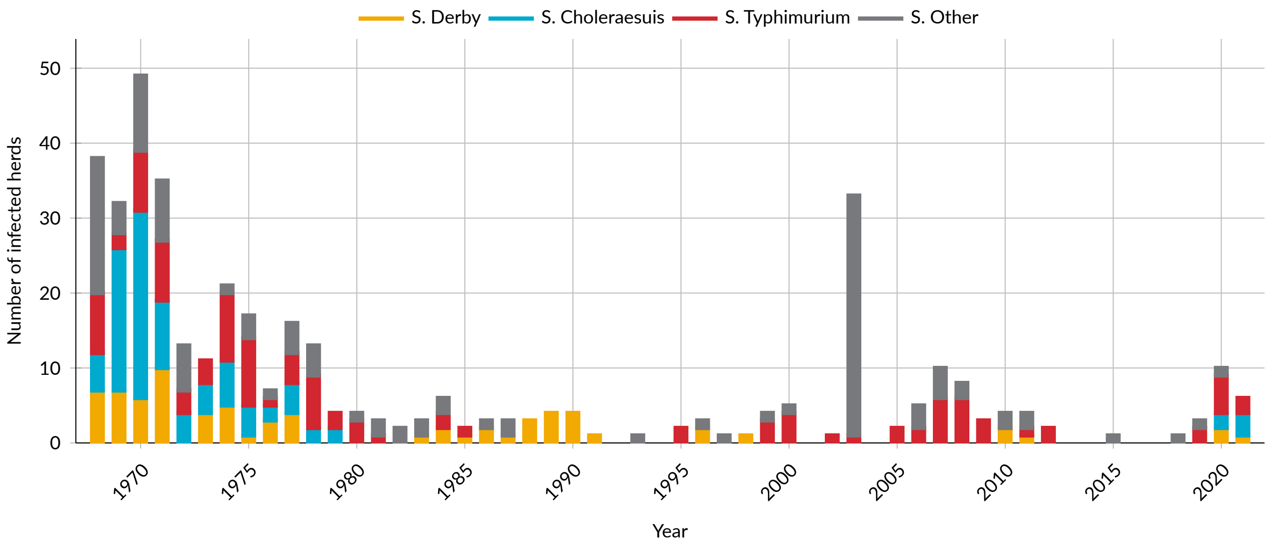


Figure 43: Annual notifications of *Salmonella* in swine herds during 1968–2021. In 2003, a feed borne outbreak of *S.* Cubana occurred in Sweden. In 2016 and 2017, *Salmonella* was not detected in any herd.

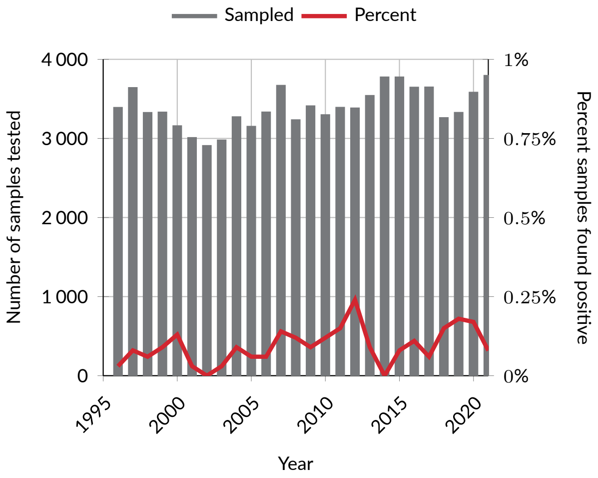


Figure 44: Samples tested (bars — left axis) and percentage of *Salmonella* found (line — right axis) in lymph node samples from **cattle.**

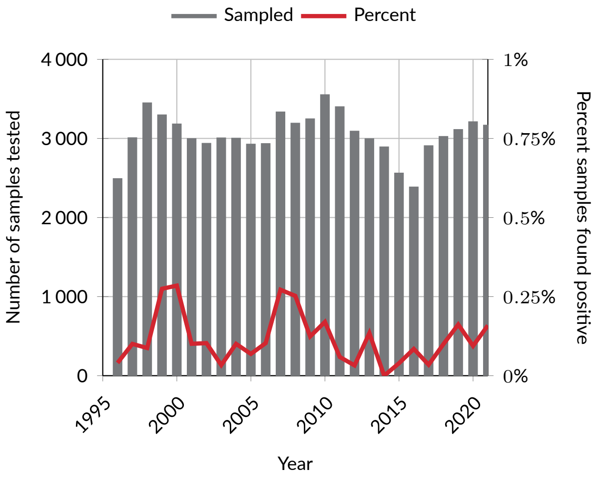


Figure 46: Samples tested (bars — left axis) and percentage of *Salmonella* found (line — right axis) in lymph node samples **fattening pigs** sampled at abattoirs.

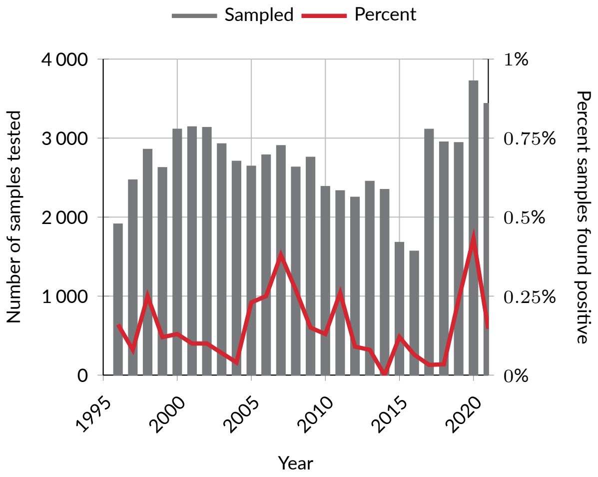


Figure 45: Samples tested (bars — left axis) and percentage of *Salmonella* found (line — right axis) in lymph node samples from **sows and boars**.

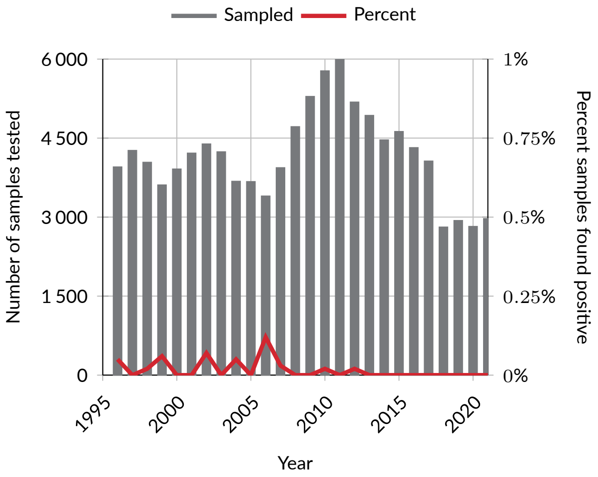


Figure 47: Samples tested (bars — left axis) and percentage of *Salmonella* found (line — right axis) in neck skin samples from poultry at major abattoirs.

Table 22: Notified index isolates of *Salmonella* in cats, dogs, horses, wild birds and wild mammals in 2021. 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, 21 of the notified index isolates were index cases.

Serovar	Cats	Dogs	Horses	Wild birds	Wild boar	Other wild animals
S. Agona	0	1	0	0	0	0
S. Choleraesuis	0	0	0	0	12	0
S. Coeln	0	1	0	0	0	0
S. Derby	0	1	0	0	0	0
S. Duesseldorf	1	0	0	0	1	0
S. Enteritidis	0	0	0	0	0	2[A]
S. Fulica	0	0	0	1	1	0
S. Hessarek	0	0	0	2	0	0
S. Infantis	0	2	0	0	0	0
S. Typhimurium	26	2	2	2	2	0
Salmonella enterica sp *diarizonae*	1	0	0	0	6	0
Salmonella, O:4	14	0	0	0	0	0
Total	**42**	**7**	**2**	**5**	**22**	**2**
Number of samples[B]	2210	152	60	57	22	20

[A] Hedgehogs.

[B] Number of samples tested per household (pets), stable (horses) or municipality or location (wild animals).

Food

Within the Swedish *Salmonella* control programme, swab samples were taken from 6426 pig carcasses and 3831 cattle carcasses. Neck skin samples were taken from 2940 poultry carcasses. *Salmonella* was detected in swab samples from one adult pig carcass and two cattle carcasses (Table 21). At cutting plants, *Salmonella* was not detected in any of the 4921 red meat or 1205 poultry meat samples taken. (Table 21 and Figure 47).

In addition to the sampling performed within the control programme, 533 samples were taken by national and local authorities. *Salmonella* was detected in 24 samples. (Table 23).

At the EU-level, Sweden notified ten findings of *Salmonella* in food during 2021. All these concerned intra-community traded or imported batches within the food categories meat, spices, nuts and seeds, bakery products and egg products. In total, data from serotyped isolates from 621 batches of food or carcasses sampled at retail, slaughterhouses, or other food enterprises between 2010 and 2021 is available. Of these, 363 were from imported food batches, 146 of domestic origin (48 food batches and 128 carcasses) and 82 from food batches of mixed or unknown origin. The distribution of serovars differ between the major food categories (Figure 48). *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.

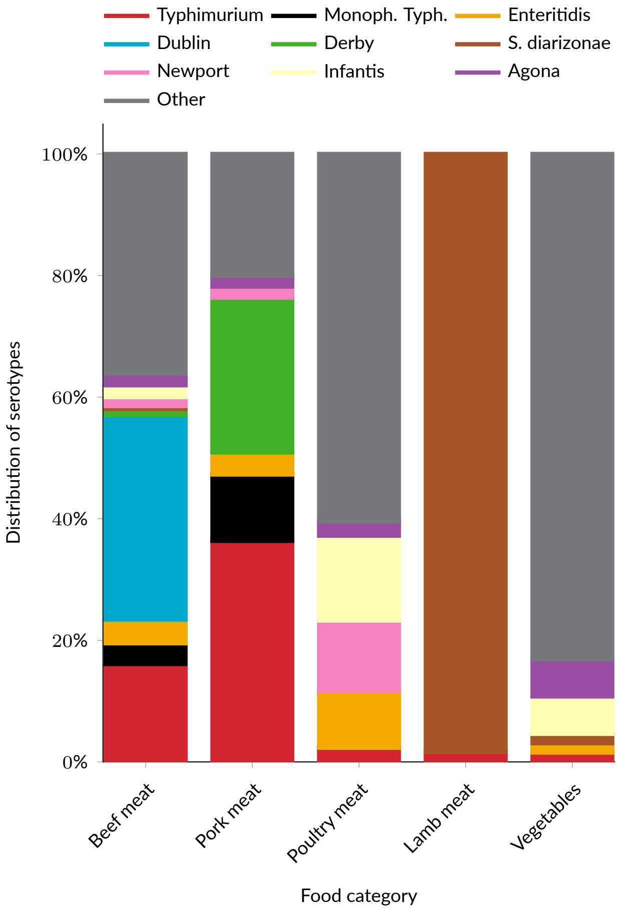


Figure 48: Distribution of *Salmonella* serovars in different food categories. Results of serotyping of isolates from samples taken at retail, slaughterhouses or other food enterprises by authorities or food business operators 2010 – 2021. In total, samples are from 489 batches of food or carcasses (beef meat 205, pork meat 55, poultry meat 43, lamb meat 121, vegetables 65). Food categories with isolates from samples of less than 20 batches of food are not included.

Table 23: Results of *Salmonella* analyses of food samples taken by the authorities in 2021.

Reason for sampling	Total no. of samples	No. of positive samples
Survey	15	2 Tahini
Routine control	89	6 Halva
Suspected food poisoning or complaint	311	2 Chocolate
Border control	70	1 Seeds
Other or not reported	48	0

Humans

In 2021, a total of 946 cases of salmonellosis were reported, compared to 826 cases in 2020 and 1993 cases in 2019 (Figure 49). Domestic cases increased by 71% from 422 cases in 2020 to 722 cases in 2021, resulting in an incidence of 6.9 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 until the start of the COVID-19 pandemic. The clear increase compared to 2020 is reflected by a number of major outbreaks in 2021 (see below).

A total of 20% of the cases (n=187) 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 2021, the proportion of travel-associated cases decreased by 85 percent from 11.8 (n=1215) to 1.8 cases per 100 000 inhabitants. Half of the travel-associated cases in 2021 (n=93) reported Europe as region of infection and 10% (n=18) had Spain as reported country of infection.

Among the domestic cases, the median age was 38 years (0–100 years) and the incidence was highest for children younger than 5 years of age with 17.3 cases per 100 000 inhabitants followed by the age group of persons over 80 years with an incidence of 11.4 per 100 000 inhabitants.

Of the isolates from domestic cases, 87% were serotyped and the most common serovars among these were *S.* Enteritidis (23%), monophasic *S.* Typhimurium (12%) and *S.* Typhimurium (10%). An additional 60 different serovars were identified in domestic cases during 2021. Of the cases infected in other countries, 23% were serotyped and *S.* Enteritidis was the most common serovar (41% of the isolates that were typed).

For domestic salmonellosis a clear seasonality is usually observed, with most cases occurring during late summer and early autumn. In 2021, the number of domestic cases followed normal seasonal levels. Travel-related cases showed a similar seasonal pattern but at levels far below normal, especially during the first half of the year when particularly severe travel restrictions prevailed (Figure 50).

Outbreaks

In 2021, eleven outbreaks involving ten or more cases were identified, a clear increase compared to 2020 when only two such outbreaks occurred. Together, these outbreaks accounted for 41% (293/722) of the total number of reported domestic infections. For some, cases of illness occurred over longer time periods, while others led to a larger number of illnesses in a short time, for example in February, April-May and September-October (see Figure 50).

Outbreak of S. *Enteritidis, chocolate wafers*

Beginning in February, an outbreak of *S.* Enteritidis was investigated where 19 of a total of 34 reported cases were younger than ten years old. Early in the investigation, a connection was established to purchases at a major retail chain and that many of the cases had eaten wafers and other sweets. Information about two friends who had met and consumed such products just once, shortly before both fell ill directed suspicions at a specific brand of chocolate wafers. However, repeated sampling and analyses of products from stores did not lead to any findings of *Salmonella*. It was not until products from cases' homes were analysed that the outbreak strain of *Salmonella* was detected, but only in two of a total of 22 analysed subsamples. Neither the company that produced the chocolate wafers nor the responsible control authority could identify any salmonella in the production line or the product.

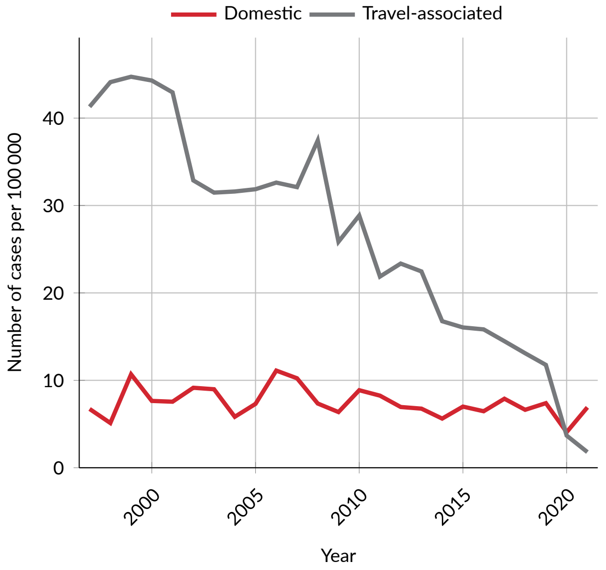


Figure 49: Incidence (per 100 000) of notified human cases of salmonellosis in Sweden, 1997–2021. Travel-associated cases are those where the patient has reported travel to another country during the incubation period prior to clinical presentation. Domestic cases are patients that have not travelled outside Sweden.

Outbreak of S. *Braenderup, melons*

In early May 2021, Denmark informed about an outbreak involving thirteen people with clustering isolates of *S.* Braenderup. Outbreak cases were noted in several different countries in both Europe and North America, including seven cases in Sweden, and an international investigation coordinated by ECDC was initiated. In Denmark, early suspicions were directed at melons, mainly Galia melons. Based on epidemiological evidence, the suspicions were strengthened and expanded against additional types of melons that, based on harvest time, seemed to originate from South and Central America. In early June, a large analysis campaign in UK led to a couple of positive *Salmonella* findings in Galia melons originating from Honduras. By this time, melon exports had ceased for the season and the number of reported illnesses had begun to decline. Backtracking and extensive sampling at production sites yielded no results. In November 2021, Food Safety News reported about a finding of the outbreak strain on the surface of a washing tank in a Honduran packing facility for Galia melons. In total, more than 350 cases were reported from 16 countries. Sweden had 48 outbreak cases of which 40 were female.

Outbreak related to sesame seed products

In April 2021, the Public Health Agency of Sweden informed in EpiPulse about two clusters with *S.* Mbandaka and *S.* Havana, respectively. Several of the cases were small children. Germany announced that they had had an outbreak with the same strain of *S.* Havana in 2019 and also had cases with the same strain of *S.* Mbandaka in 2020. In addition, Germany informed about a previous RASFF notification mentioning that the two outbreak strains along with three additional serotypes had been identified in tahini originating from Syria. Also, US reported related food isolates including additional serotypes of *Salmonella*, not only in tahini but also halwa produced in Syria. Following collection and analysis of tahini and halwa products of the suspected brand, the Swedish Food Agency identified several different serotypes of salmonella in tahini and halwa products available on the market. An additional RASFF notification was published and products were removed from the market. From the summer of 2021, further findings of *Salmonella* have been done in products of the same brand in several European and North American countries, after which a large number of disease cases with clustering isolates have been identified. In Sweden, 42 outbreak cases have been linked to six serotypes and eight different strains of Salmonella.

Outbreak of S. *Coeln, sprouts*

In mid-September 2021, a rapidly growing cluster of *Salmonella* Coeln was identified by the microbial surveillance programme at the Public Health Agency of Sweden. In the previous week, the infection control unit at the Region of Örebro County had observed several salmonella cases among children and via epidemiological investigation found a possible connection to sprouts served at two schools. In the further investigation, suspicions against sprouts were strengthened, both through individual interviews of cases and through a case/case-study. Backtracing led to a company that had received a batch of seeds earlier in the summer and since over 80% of the cases were reported to have fallen ill within two weeks, it was thought that one contaminated batch had been released on the market. Unpasteurized and pasteurized seeds were sampled and analysed both before and after germination but without salmonella being detected. Identification of new outbreak cases ceased quickly and the outbreak eventually came to include 53 people.

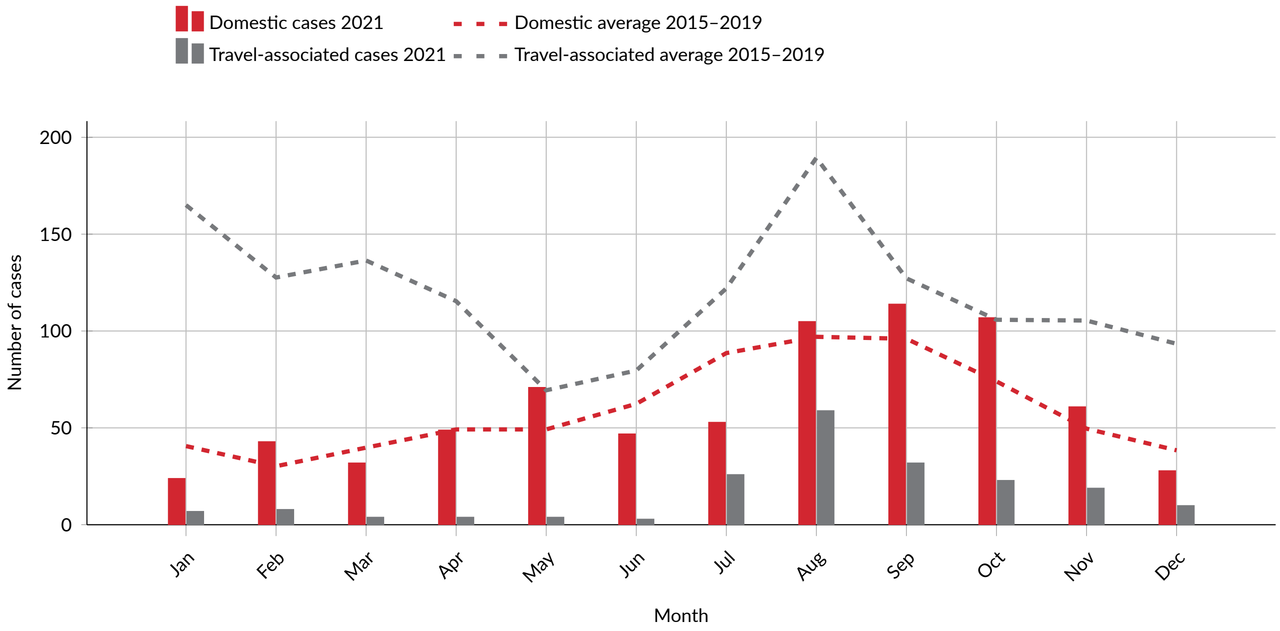


Figure 50: Monthly notifications of domestic and travel-associated human cases of salmonellosis in 2021 and a monthly average for domestic and travel-associated notifications in 2015–2019.

Outbreak of S. *Dublin, unclear transmission route from cattle*

Between September 2019 and the end of 2021, 22 human cases with clustering isolates of *S.* Dublin have been identified across 10 counties. In most of these cases, the bacterium was isolated from blood, which indicates a high degree of invasiveness. In April 2020, the same strain was isolated from a cattle lymph node sampled at an abattoir and traced to a large dairy herd located in Östergötland. During 2021, the outbreak strain was detected in three more cattle herds, all of which were located in Östergötland. This particular strain had been identified previously in 2018 in another cattle herd from the same region, which indicates that the strain may be endemic in that area. Since the start of the outbreak, this subtype of *S.* Dublin has been identified in two samples of Swedish beef products but investigations so far have not identified the source of the contamination. The epidemiological investigations indicated that some of the infected people had consumed cheese produced by a dairy located in Östergötland. The dairy was inspected twice and samples were taken both from the premises and products produced by the dairy. *Salmonella* was not detected in any of the samples. During the first inspection, it was determined that the dairy receives all its milk from a single, large dairy herd located in Östergötland, which led to an investigation in that dairy herd. Faecal samples collected from the herd were positive for *S.* Dublin. The transmission route for this isolate of *S.* Dublin between cattle and humans remains unclear.

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. However, in 2020 and 2021 the number of reported *Salmonella* cases have halved compared with pre-pandemic numbers and, in addition, the proportion of domestically infected has become the majority (51 and 76 percent of cases in 2020 and 2021, respectively). These changes are probably due to restrictions and changed behaviour during the pandemic, where travel restrictions in particular can be assumed to have played a major role.

In the feed sector, in 2021 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=6). 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*.

Salmonella was detected in six pig herds during 2021. Most of these herds were geographically concentrated in one region in the south of Sweden. The size and production structure of several of the herds, including a large sow pool made the control and eradication challenging and very costly. The detection of *S.* Choleraesuis in a breeding herd and one of its contact herds in 2020 and in another three herds in 2021 has called for measures to avoid a re-establishment of this serovar in the Swedish domestic pig population. Sequences of *S.* Choleraesuis isolates from wild boar and domestic pigs were very similar to the sequence of a human isolate from 2019 and one from 2021. The findings so far, with high similarity between isolates from wild boar, domestic pigs and the human cases indicate a common source and a recent introduction. The surveillance in wild boar is ongoing and includes all counties with a wild boar population.

In 2021, regional bulk milk screenings were used to follow up areas 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. However, the programme is costly and could be modernised. During 2021 the Swedish Board of Agriculture and the National Veterinary Institute (SVA) received a joint government assignment to review the control program and make suggestions for a revision. The review will be finalized during 2022.

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.

REFERENCES

European Centre for Disease Prevention and Control, European Food Safety Authority, 2021. Multi-country outbreak of *Salmonella* Braenderup ST22, presumed to be linked to imported melons - 20 July 2021. Stockholm: ECDC/EFSA; 2021.

European Centre for Disease Prevention and Control, European Food Safety Authority, 2021. Multi-country outbreak of multiple *Salmonella enterica* serotypes linked to imported sesame-based products – 14 October 2021. Stockholm: ECDC/EFSA; 2021.

Söderlund R, Jernberg C, Trönnberg L, Pääjärvi A, Ågren E, Lahti E (2019) Linked seasonal outbreaks of *Salmonella* Typhimurium among passerine birds, domestic cats and humans, Sweden, 2009 to 2016. Euro Surveill 24 (34) pii=1900074. https://doi.org/10.2807/1560-7917.ES.2019.24.34.1900074.

Sörén K, Lindblad M, Jernberg C, Eriksson E, Melin L, Wahlström H, Lundh M (2015) Changes in the risk management of *Salmonella enterica* subspecies *diarizonae* serovar 61:(k):1, 5, (7) in Swedish sheep herds and sheep meat due to the results of a prevalence study 2012. Acta Vet Scand 57:6

SARS-CoV-2

BACKGROUND

Severe Acute Respiratory Syndrome Coronavirus 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 525 million confirmed human cases worldwide and over 6 million deaths to date (mid-May 2022).

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 (MERS, 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.

During fall 2020 SARS-CoV-2 was detected in Swedish mink in 13 farms. Moreover, a serological screening, which covered the majority of mink fur farms active at the time, suggested that most of them had been exposed to the virus. Given the extensive spread of SARS-CoV-2 among Swedish mink, with possible spillover 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. In January 2021, the Swedish mink population consisted of approximately 90 000 breeding animals in 28 mink farms.

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 most people, COVID-19 manifests as a respiratory tract infection, and many different symptoms may be present.

Most people get mild symptoms and can recover at home without professional medical care. Some people get a severe form of the illness, with breathing difficulties and pneumonia.

LEGISLATION

Animals

Infection with SARS-CoV-2 in animals is notifiable as an emerging infection in animals (SJVFS 2013:23). Since 12th May 2021, surveillance of SARS-CoV-2 in mink is carried out in accordance with Implementing Decision (EU) 2021/788.

Humans

During 2021, COVID-19 in humans was notifiable according to the Communicable Disease Act (SFS 2004:168 with amendments, SFS 2013:634).

SURVEILLANCE

Animals

A surveillance scheme based on enhanced passive surveillance has been in place in Sweden since fall 2020, which foresees that all fur farms submit animals found dead, or throat swabs from animals found dead, to the National Veterinary Institute (SVA) for SARS-CoV-2 testing using qRT-PCR. Positive cases are further analysed through whole genome sequencing. The scheme was initially run on voluntary basis, but is since 12th May 2021 compulsory in accordance with Implementing Decision (EU) 2021/788.

To have a better overview of the situation, the surveillances scheme described above was complemented with a serological screening targeting each of the active farms. From each farm, 30 mink blood samples collected on filter papers were submitted to SVA for the detection of SARS-CoV-2 specific antibodies using a commercially available ELISA (IDvet, ID Screen SARS-CoV-2 Double Antigen Multi-species ELISA, Innovative Diagnostics, Grabels, France).

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 2020. This surveillance program continued during spring 2021. 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.

RESULTS

Animals

During 2021, 406 samples from 16 farms were received at SVA and analysed for presence of SARS-CoV-2, with positive results from one farm. The farm in question, with 11 000 breeding animals at the time, was located in Skara municipality in the south-west of Sweden. No increased morbidity or mortality had been observed on the farm. At the time of the outbreak, all people associated with the farm had either had the infection (COVID-19 confirmed in farm workers in November 2020) or been vaccinated, or both. Moreover, a serological screening carried out in December 2020 demonstrated that also the mink on the farm had been exposed to SARS-CoV-2 although virus could not be detected at the time. Despite this, SARS CoV-2 was again introduced to the farm, most likely through one of the farm workers, although this was never confirmed.

Whole genome sequencing of the virus demonstrated that the virus belonged to sub-lineage B.1.1.464 of SARS CoV-2. None of the amino acid mutations described on the spike protein and considered associated with adaptation to mink were present in the sequence. At the time, matching sequences from sub-lineage B.1.1.464 had previously been described from at least 14 countries globally in samples originating from people. Moreover, this sub-lineage had also been detected in mink in two other countries. B.1.1.464 had not been detected previously in Sweden.

From the serological screening, 30 samples per farm were received from 25 out of the 28 active mink farms. Specific SARS-CoV-2 antibodies were detected in samples from 12 farms, eleven of which were positive also during the previous screening conducted during fall 2020. In these eleven farms, the proportion of positive samples were lower (in ten farms) or equal in this screening compared to the previous screening. In one farm, which was negative in the screening in 2020, 16 out of 30 samples tested positive suggesting that the animals on the farm had been exposed to the virus during this reporting period. No increased morbidity or mortality had been observed on the farm.

Humans

During 2021 a total of 74 people from 17 farms were registered in the program. The 1162 samples that were taken and analysed for ongoing viral infection within the surveillance program resulted in 4 positive people. No association between the human cases and cases in mink could be found.

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 in 2020 demonstrated 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 spillover to people associated to the farms and to human communities close to the farms. Also, extensive spread within and between farms occurred in Sweden in 2020 in spite of implemented biosecurity measures. 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. During 2021, the SARS-CoV-2 situation in Swedish mink farms was different as shown by the surveillance results, and virus detection was limited to one farm, with no further spread. The ban on mink breeding in place during the entire season 2021 can be assumed to have contributed to reduced risk of SARS-CoV-2 infection associated with Swedish mink and to the improved situation observed. Given that no breeding took place, there was no need for guest workers during periods of the season that normally require extra labour. Additionally, the remaining mink population was limited in size and had to a large extent been exposed previously to SARS-CoV-2 and thus assumed to have had some level of herd immunity, albeit with limited duration. The successive roll-out of the COVID-19 vaccination in the Swedish society can also be assumed to have contributed to the improved situation compared to 2020, and was also the decisive factor that led to the decision from The Swedish Board of Agriculture to allow mink breeding again in 2022.

REFERENCES

European Food Safety Authority and European Centre for Disease Prevention and Control, Boklund A, Gortazar C, Pasquali P, Roberts H, Nielsen SS, Ståhl K, Stegeman A, Baldinelli F, Broglia A, Van Der Stede Y, Adlhoch C, Alm E, Melidou A and Mirinaviciute G. 2021. Scientific Opinion on the monitoring of SARS-CoV-2 infection in mustelids. EFSA Journal 2021;19(3):6459, 68 pp. https://doi.org/10.2903/j.efsa.2021.6459ISSN:

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 bovine spongiform encephalopathy (BSE) in cattle became a disease of public health concern (see chapter on BSE, page 20), and the existence of BSE in small ruminants was suspected, both surveillance and control of TSE in small ruminants was intensified within the European Union in 2002. Since the start of this intensified 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 a 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.

Figure 51: 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: Bengt Ekberg/SVA.

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 subsequent skin lesions. The disease is progressive and always fatal. All routes of transmission of classical scrapie have not been established, but transmission occurs horizontally within flocks and especially at lambing, as foetal fluid and the placenta may contain large amounts of prions. Prions may remain on contaminated pastures for long periods of time. Scrapie has, based on epidemiological data, not been considered a zoonotic disease. Still 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.

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. 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 (SVA), which is appointed the National Reference Laboratory (Regulation (EC) 999/2001). Samples are analysed at SVA. A majority of the samples are collected at rendering and hence there is a close collaboration with Svensk Lantbrukstjänst and Konvex, two companies that collect and render carcasses.

Passive surveillance

All clinical 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 contact with disease experts. If scrapie still cannot be excluded, the animal is euthanized. Brainstem samples from animals with a clinical suspicion of scrapie are examined with the TeSeE™ SAP Combi kit (short assay protocol; Bio-Rad Laboratories, Hercules, California, United States). If the results are positive or inconclusive, the TeSeE™ Western Blot kit (Bio-Rad Laboratories, Hercules, California, United States) is used for confirmation.

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 in Sweden is 1500 fallen sheep and 100 fallen goats above the age of 18 months. The samples should be representative for the population. 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.

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, a sufficient number of animals 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%.

It is mandatory to send fallen animals for rendering, except for in the northern parts of Sweden, where animal density is low (less than 10% of the sheep population is in this area). 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 that are sent for postmortem examinations are sampled by veterinarians or veterinary assistants.

The samples from active surveillance are examined with Bio-Rad TeSeE ™ SAP Combi Kit (short assay protocol) at SVA in accordance with Regulation (EC) 999/2001. If results are positive or inconclusive the Bio-Rad TeSeE ™ Western Blot kit is used for confirmation.

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

RESULTS

Passive surveillance

In 2021, one sheep (a mouflon sheep) was tested due to clinical suspicion of scrapie with a negative result.

Active surveillance

Sheep

In 2021, SVA examined 1689 sheep from fallen stock. All samples were negative for classical scrapie and atypical scrapie/Nor98. The northern part of the country is underrepresented in the sampling and due to problems with rapid decomposition of carcasses during the summertime, sampling is not evenly distributed throughout the year. Apart from this, sampling seems representative.

Goats

In 2021, SVA examined 169 goats from fallen stock for scrapie. All were negative both for classical scrapie and for atypical scrapie/Nor98.

DISCUSSION

Classical scrapie

Classical scrapie is a challenging disease both to detect and to 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 an introduction of the disease could potentially have negative consequences for the sheep industry. The import of sheep and goats to Sweden has 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 the 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 the number of 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 detected. Out of these, two were detected through passive surveillance and the rest through active surveillance. 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 a contagious disease normally is distributed in the population and supports the hypothesis that atypical scrapie is spontaneously 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.

As a measure to further the knowledge of atypical scrapie/Nor98, farms with confirmed cases were for a number of years obligated to carry out increased surveillance in the herd for two years (Regulation (EC) 999/2001). In 2021 EFSA published a report on the analysis of this intensified surveillance which reached similar conclusions as the two previous publications. The increased surveillance was discontinued in 2021 (Commission Regulation (EU) 2021/1176).

REFERENCES

Fediaevsky A, Maurella C, Nöremark M, Ingravalle F, Thorgeirsdottir S, Orge L, Poizat R, Hautaniemi M, Liam B, Calavas D, Ru G, Hopp P (2010) The prevalence of atypical scrapie in sheep from positive flocks is not higher than in the general sheep population in 11 European countries. BMC Vet Res. 6:9

Fediaevsky A, Tongue SC, Nöremark M, Calavas D, Ru G, Hopp P (2008) A descriptive study of the prevalence of atypical and classical scrapie in sheep in 20 European countries. BMC Vet Res 4:19

European Food Safety Authority (EFSA), Arnold M, Ru G, Simmons M, Vidal-Diez A, Ortiz-Pelaez A, Stella P. (2021) Scientific report on the analysis of the 2-year compulsory intensified monitoring of atypical scrapie. EFSA J. 2021 Jul 8;19(7)

Elvander M, Engvall A, Klingeborn B (1988) Scrapie in sheep in Sweden. Acta Vet Scand 29:509–10

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 2021, 146 cases with STEC were reported to develop HUS (n=146/4483, 3.2%). When analysing which serotypes and stx profiles that have been associated with HUS during 2015 to 2021 the most prevalent serotype was the domestic serotype O157:H7 clade 8 with 49 (35%) cases, followed by O26 with 21 (15%) cases, O157:H7 with 8 cases (5,6%) and O121 with 7 cases (4,9%). (Table 24). 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 as described in SJVFS 2021:10.

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 2022:217). 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 last study was performed during 2020–2021. In these conducted studies, STEC O157 has predominantly been isolated from cattle originating from southern Sweden and 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 24: Serotypes and shigatoxin (stx) profiles for reported cases with haemorrhagic uremic syndrome (HUS), 2015–2021.

Serotype	*stx1*	*stx1+stx2*	*stx1a*	*stx1a+stx2a*	*stx1c+stx2b*	*stx2*	*stx2a*	*stx2a+stx2c*	*stx2a+stx2d*	*stx2b*	*stx2b+stx2d*	*stx2c*	*Unknown/other stx*	Total
Untyped	-	-	-	-	-	3	-	-	-	-	-	-	34	37
O145:H28	-	-	-	-	-	-	2	-	-	-	-	-	-	2
O113:H4	-	-	-	-	3	-	-	-	-	-	-	-	-	3
O157:H7	-	-	-	2	-	-	5	1	-	-	-	-	-	8
O121:H19	-	-	-	-	-	-	7	-	-	-	-	-	-	7
O26	-	1	3	8	-	-	9	-	-	-	-	-	-	21
O157:H7, clade 8	-	-	-	-	-	-	8	41	-	-	-	-	-	49
Other[A]	2	-	2	2	-	1	4	1	1	2	1	1	2	19
Total	**2**	**1**	**5**	**12**	**3**	**4**	**35**	**42**	**1**	**2**	**1**	**1**	**36**	**146**

[A] ONT:H2, ONT:H6, ONT:H29, O77:H41, O103, O112ac:H19, O113:H21, O117:H7, O130:H11, O146:H21, O153, O156, O165:H25, O175:H21, O182:H25.

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, 1239 samples were collected from 12 abattoirs. STEC O157 was detected in 35 samples (2.8%) of which 5 samples belonged to the serotype O157:H7, clade 8. STEC O26 was detected in 5 samples (0.7%).

Food

In 2021, 20 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.

Humans

In 2021, 653 human cases were reported of which 530 were domestically acquired (81%). The domestic incidence in 2021 was 5.1 (cases per 100 000 inhabitants), and over a longer period of time an increasing trend is seen (Figure 52). As in previous years, the incidence was highest in children.

STEC-associated HUS was reported in 24 cases of which 23 were domestically acquired infections. 16 of the HUS cases were children under the age of 10. Isolates could be retrieved and serotyped from 21 of the HUS cases. Seven of the domestic HUS cases belonged to serotype O157:H7, clade 8 (Table 25).

An isolate could be retrieved and thereby serotyped from 59% of the domestically acquired STEC cases. However, for the travel-associated cases only 39% were typed (Table 26). 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 80 different serotypes were identified, but for 12 of these the O type could not be identified. The most common serotypes were O157:H7, O103:H2 and O26:H11. 41 cases were diagnosed with the domestic clade 8 of O157:H7, stx2a and stx2c alternatively only stx2a. Seven of these cases developed HUS. The second most common serotype in Sweden, O103:H2, normally carries stx1a and gives milder symptoms. In 2021 six cases were infected with the more potentially virulent variant carrying both stx1a and stx2a. In total, five percent (n= 25) of all O103 isolates have been identified with this type in Sweden since 2012.

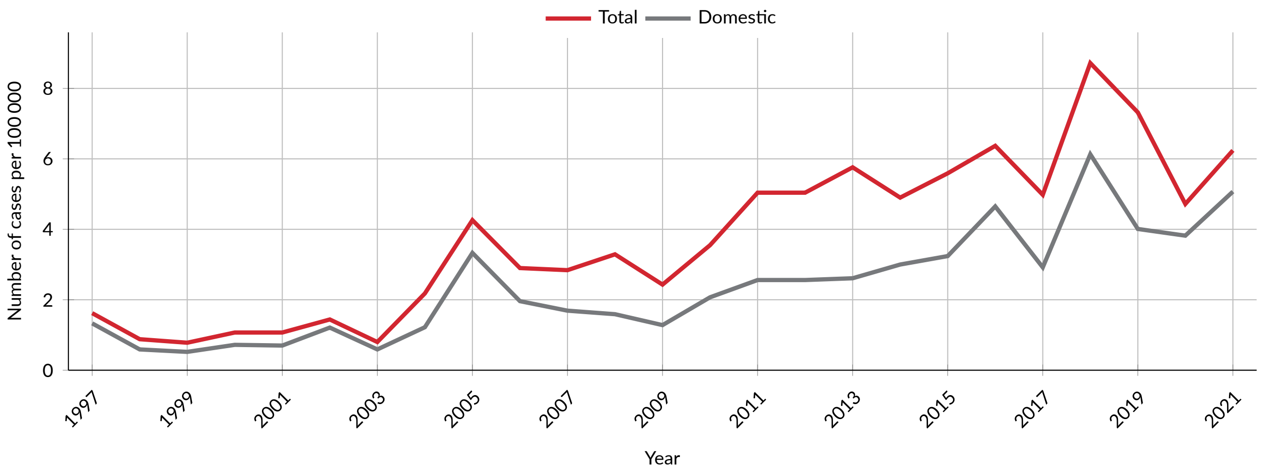


Figure 52: Incidence (per 100 000 inhabitants) of notified human shigatoxin producing *Escherichia coli* (STEC) cases in Sweden, 1997–2021. Prior to 2005, only O157 was required to be reported. In 2005, all serogroups of STEC including PCR findings became subject for notification. In 2005, 2016 and 2018, the number of cases increased due to one or more domestic outbreaks.

Table 25: Distribution of serotypes and shigatoxin-subtypes in haemorrhagic uremic syndrome (HUS) cases in 2021.

HUS serotypes 2021	Stx unknown	stx1a, stx2a	stx2	stx2a	stx2a, stx2c	stx2e	stx2f	Total
Untyped	1	-	2	-	-	-	-	3
:H16	-	-	-	-	-	-	1	1
O111:H8	-	1	-	-	-	-	-	1
O145:H28	-	-	-	1	-	-	-	1
O157:H7	-	1	-	4	-	-	-	5
O157:H7, clade 8	-	-	-	3	4	-	-	7
O26:H11	-	3	-	2	-	-	-	5
O8:H19	-	-	-	-	-	1	-	1
Total	**1**	**5**	**2**	**10**	**4**	**1**	**1**	**24**

Table 26: Number of reported human cases of shigatoxin producing *Escherichia coli* (STEC) in comparison to number of cases where an isolate could be retrieved 2021.

Origin of infection	Number of reported cases	Number of isolates typed (%)
Domestically acquired infection	530	315 (59%)
Travel associated infection	97	38 (39%)
Unknown country of infection	26	7 (27%)
Total	**653**	**360 (55%)**

Investigations of outbreaks and single cases of infection of STEC

In 2021, four joint farm investigations were carried out after human cases were detected with suspicion of connection to farm animals. Within these investigations, five animal herds were sampled. One of the farms was positive for STEC and the isolate matched the one that was detected in current human cases. It was a farm with cattle where STEC O157: H7 clade 8 stx2a, stx2c, eae + was identified. Other farms were examined for STEC O157, STEC O121 and STEC O26 but were negative during sampling. In addition to the cases of suspected farm connection, three national outbreaks were investigated with cases spread across the country where the source of infection is suspected to have been food, but no source could be identified. It was STEC O103, O157 and O157 clade 8.

The most common cause of HUS cases in Sweden remains the O157:H7 variant known as clade 8, which is endemic in the southeast.

DISCUSSION

The long-term trend for human cases of STEC infection in Sweden is rising. One known factor contributing to the higher incidence of notified cases in some regions in Sweden is an increased use of multiplex PCR panels, where a higher number of faecal samples are screened for STEC. Thereby, more STEC cases are identified. It is important to type identified cases. Without characterization of isolates, it is challenging to perform outbreak investigations, identify highly pathogenic types and compare animal, food, and environmental isolates.

REFERENCES

Tamminen LM. Transmission and dynamics of VTEC O157:H7 - a story about the complex associations between pathogen, host and environment (2020). Acta Universitatis Agriculturae Sueciae, 1652-6880; 2020:16 (Doctoral thesis)

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. Lentiviruses persists in the animal for life despite the presence of neutralising antibodies.

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 caprine arthritis-encephalitis (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 (at the time called Svenska Djurhälsovården) 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, a progressive viral pneumonia, is occurring in Swedish sheep flocks. The visna form, a central nervous system disease characterised by chronic wasting, is not, as far as we know, manifested in Swedish sheep. 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.

Figure 53: The purpose of the control programme is to eradicate maedi-visna (MV) and caprine arthritis-encephalitis (CAE) from Swedish sheep and goat flocks and to prevent introduction into free flocks. Photo: Ylva Persson.

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 2021:10). The control programme is regulated through SJVFS 2015:17 (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 individual serological testing of sheep and goats 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-/CAE-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. In case of MVV/CAEV infection, 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. In the beginning of October 2021, the screening ELISA test was changed to an ELISA test with higher sensitivity; from IDEXX CAEV/MVV Total Ab (IDEXX Laboratories, Westbrook, Maine, United States) to ID Screen MVV/CAEV indirect (Innovative Diagnostics, Grabels, France). 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 agar gel immunodiffusion (Maeditect AGID, Alpha Scientific, Slough, United Kingdom).

Post mortem examinations and histopathology are additional important tools to detect MV. Diagnostic testing is performed at the National Veterinary Institute (SVA). Serum samples collected in the MV-programme are also used for other active surveillance activities in sheep (e.g., Brucellosis).

RESULTS

During 2021, approximately 8000 samples from sheep and goats were analysed in the MV/CAE control programme for antibodies against MV/CAE- virus.

At the end of 2021, 3418 sheep flocks with 121 844 sheep and 250 goat flocks with 2655 goats were enrolled in the programme. This corresponds to about 45% of the Swedish sheep population, and about 13% of the goat population. Most of the flocks have achieved M3/C3 or MV/CAE free status. The rest of the flocks are somewhere in the process from unknown to free, which normally takes five years and four sampling occasions.

In 2021, 25 animals in five different flocks were considered MV/CAE positive. The positive herds consisted of 1 sheep flock, 2 goat flocks and 2 flocks with both sheep and goats.

DISCUSSION

It is now more than 25 years since the MV programme was launched. A series of measures have been taken to enrol the majority of Swedish sheep flocks as one of the main purposes of the programme is to reach freedom from disease. This has been hard to achieve despite of campaigns and economic support. A revision of the MV programme was made during 2013 by Farm & Animal Health and SVA. 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. The programme was evaluated during 2020 for more cost-effective sampling, diagnostics, and control measures. Implementation of the recommended updates are in progress.

After a successful programme, Norway has declared most herds free from CAE, showing that it is possible to eradicate the disease.

REFERENCES

Kampen AH, Åkerstedt J, Rømo G, Mork J, Nordstoga A, Klevar S. The surveillance programme for small ruminant lentivirus infections in sheep and goats in Norway 2019. Annual report 2019. Oslo: Norwegian Veterinary Institute 2020

Lindqvist Å. Kontrollprogram hos maedi-visna hos får. Svensk veterinärtidning 1993, 11, 463–5

Persson, Y.; Andersson, E.; Frössling, J.; Wensman, J.J. Occurrence of CAE and CLA in Swedish Dairy Goats and Comparison of Serum and Milk as Sampling Material. Dairy 2022, 3, 190–198. https://doi.org/10.3390/dairy3010015

Tine/Helsetjenesten for geit. 2016. Sluttrapport, prosjekt friskere geiter, 2001–2015

Underlag till Gård & Djurhälsans översyn av kontrollprogrammet för MV, Dnr SVA 2021/44

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. In April 2022, a new vaccine against strangles in horses was launched in Sweden.

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 animal disease in Sweden (SJVFS 2021:10). It is notifiable both on clinical suspicion and when it is confirmed.

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 54 illustrates the number of notified cases per year.

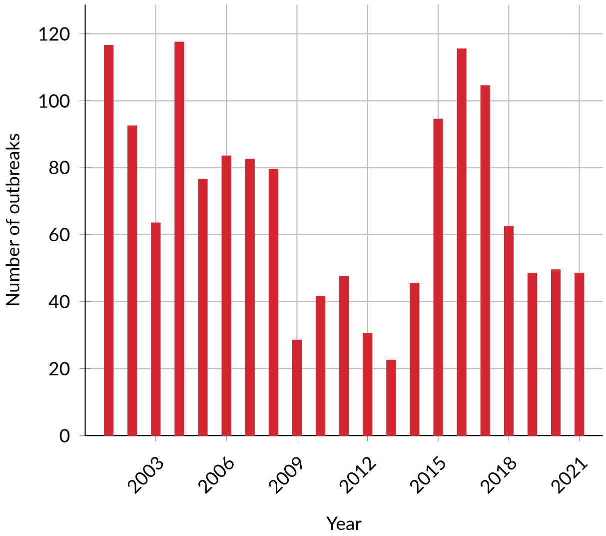


Figure 54: Reported index cases (farm outbreaks) of *Streptococcus equi* infections in horses in Sweden during years 2001–2021. Data source: Swedish Board of Agriculture.

RESULTS

In 2021, there were 48 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 54).

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 in regard to finding infected horses. However, antibodies induced from vaccination with the new vaccine are not interfering with the serology test.

REFERENCES

Swedish Board of Agriculture, Statistics of index cases of notifiable animal diseases, https://www.jordbruksverket.se

Swine dysentery

BACKGROUND

Swine dysentery (SD) caused by *Brachyspira hyodysenteriae* (*B. hyodysenteriae*) is a severe disease affecting the large intestine of pigs. Clinical signs of SD include mucohaemorrhagic diarrhoea occasionally being blood-tinged, ill-thrift, inappetence and weight loss. Mortality can be significant, but the largest economical losses are induced by a reduced weight gain and treatment costs.

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, SD was more frequently diagnosed. Since then, improvements in management and biosecurity have contributed to a reduction in the occurrence of SD in the population. More recently, a voluntary programme for certifying the SD status of nucleus and multiplying herds has also contributed to a reduction in the occurrence and spread of SD. The pig health organisations organise and operate the programme. In addition, SD has also successfully been eradicated from affected herds following special sanitation protocols involving removal, medication, cleaning and disinfection. Despite this, SD is still diagnosed in a few herds annually. 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 them of their existing SD status, rendering further spread possible.

Tiamulin has been the drug of choice for controlling SD. However, in 2016, tiamulin-resistant SD was identified for the first time in Sweden. This is particularly worrisome as few antibiotics are available for treatment of SD. Fortunately, the tiamulin resistant strain of SD was successfully eradicated, but this incident awakened a general interest in eradicating SD at a national level.

LEGISLATION

SD is not a regulated or notifiable disease.

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 includes the pig producers' organisation, abattoirs, pig health organisations and the National Veterinary Institute (SVA). The work is coordinated 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 clinical signs make SD a differential diagnosis, are tested by culturing from rectal swabs at SVA. All information on positive herds is shared with the network.

In herds that were previously diagnosed with SD and not yet declared free from the infection on the 1st of January 2020, measures on transports agreed within the network were implemented to reduce the risk for infecting other herds. Similarly, from then on, these measures have been applied to all herds that test positive for SD until they have been declared free from the infection. Results and discussion

During 2016–2020, SD was diagnosed in 30 herds, whereof nine still had not been declared free by the 31st of December 2020.

In 2021, a total number of 158 herds were tested for SD (Table 27). Of these, 45 were nucleus or multiplying herds tested within the programme. All these herds tested negative. Another 95 herds were tested due to clinical signs indicative of SD. SD was detected in three of these 95 herds, one farrow-to-finish herd that previously had been positive for SD, and two specialized fattening herds. SD could not be detected in the supplying piglet producing herds. By the 31st of December, SD had been confirmed in 12 herds, where eradication programmes were active in nine of these herds.

Table 27: Herds monitored for swine dysentery (SD) in Sweden during 2021.

Reason for testing	Sampled herds	Positive herds
Certification testing of breeding stock herds	45	0
First clinical suspicion	95	3
Previous positive result	18	6

The overarching goal of the programme and the network is to eradicate SD from the Swedish pig population. By the end of 2021, there were 12 herds positive for SD compared to nine herds one year earlier (Table 28). Despite the increased number of positive herds at the end of 2021, the Swedish situation on SD has improved by an increased certainty of the disease status with increased testing of the population. The number of positive herds is expected to decrease in 2022 with enforced efforts in controlling SD.

Table 28: Number of herds positive for swine dysentery (SD) at end of 2021.

Herds with SD on 2021-01-01	9
New herds diagnosed during 2021	3
Herds declared free from SD during 2021	0
Herds with SD on 2021-12-31	**12**

REFERENCES

Wallgren, P. (1988) Svindysenteri: förekomst, klinik och sanering. (Swine dysentery: presence, clinical symptoms and combatting). Komp. Allm. Vet. Möt. 1988: 305–315.

Wallgren, P., Molander, B. and Ehlorsson, C.J. (2019) Eradication of Tiamulin-resistant swine dysentery in a 500-sow herd selling fatteners to 5 herds. Proc. ECPHM 11: BBD-PP-04.

Wallgren, P. (2020) Swine dysentery - a control program at national level initiated in Sweden. Proc IPVS. ISSN-412X: 303.

Tick-borne encephalitis

Figure 55: The tick-borne encephalitis virus is spread by ixodid ticks. The most common tick species in Sweden is the *Ixodes ricinus*. The photo shows an adult, female, *I. ricinus*. Photo: Ladislav Kubeš/iStock.

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 ixodid ticks, *Ixodes ricinus* and *I. persulcatus*, which become infected when they suck blood from infected wild 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 European, Siberian and Far eastern subtypes. So far, only the European subtype has been identified in Sweden.

The first human 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 200–400 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, sheep and cattle 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 (e.g., moose and deer), and grazing domestic animals, as well as analysing colostrum from goat, sheep and cattle, 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 for infection with the European subtype, 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 2022:217).

SURVEILLANCE

Animals

The veterinary aspects of this zoonotic disease are little noticed since animals rarely show any clinical signs.

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 2021.

Humans

In 2021, 533 cases of TBE were reported. This is the highest number of TBE cases ever reported in Sweden and a doubling from 2020 (n=268, (Figure 56).

More men (61%) 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 2 to 97 years of age. Normally, there are few young children reported with TBE and this was the case also in 2021 with only six cases among children below the age of 5, despite the high total number of cases.

All but nine cases had acquired their infections in Sweden. Five people were infected in Finland, the others were infected in Estonia, Slovakia, France and Ukraine, respectively. The first TBE case became ill in January and the last in December. Most cases were reported in September. Nowadays cases are reported from Gävle to Skåne and the distribution of TBE cases have spread to the west, which corresponds to the pattern in the rest of Europe. (Figure 57). The large increase of TBE cases during 2021 is probably due to several factors, including for example a large rodent population in 2020, favourable weather for ticks and more people hiking outside due to the pandemic.

DISCUSSION

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 peak in reported cases during 2021, and 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. Climate change causes increased average temperature with milder winters and less snow cover and extended

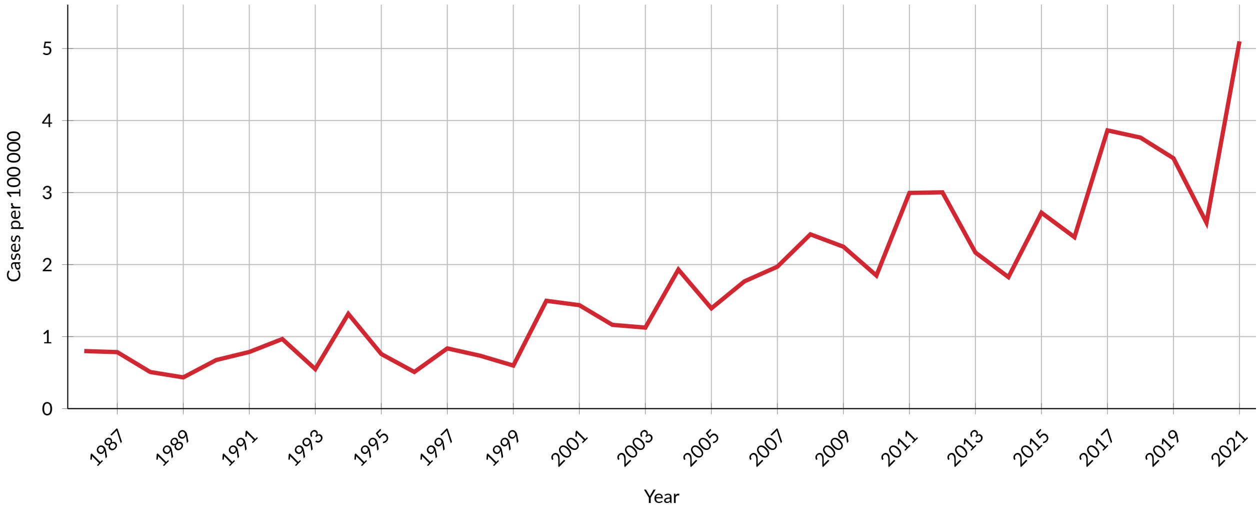


Figure 56: Incidence (per 100 000 inhabitants) of notified cases of tick-borne encephalitis in humans 1986–2021.

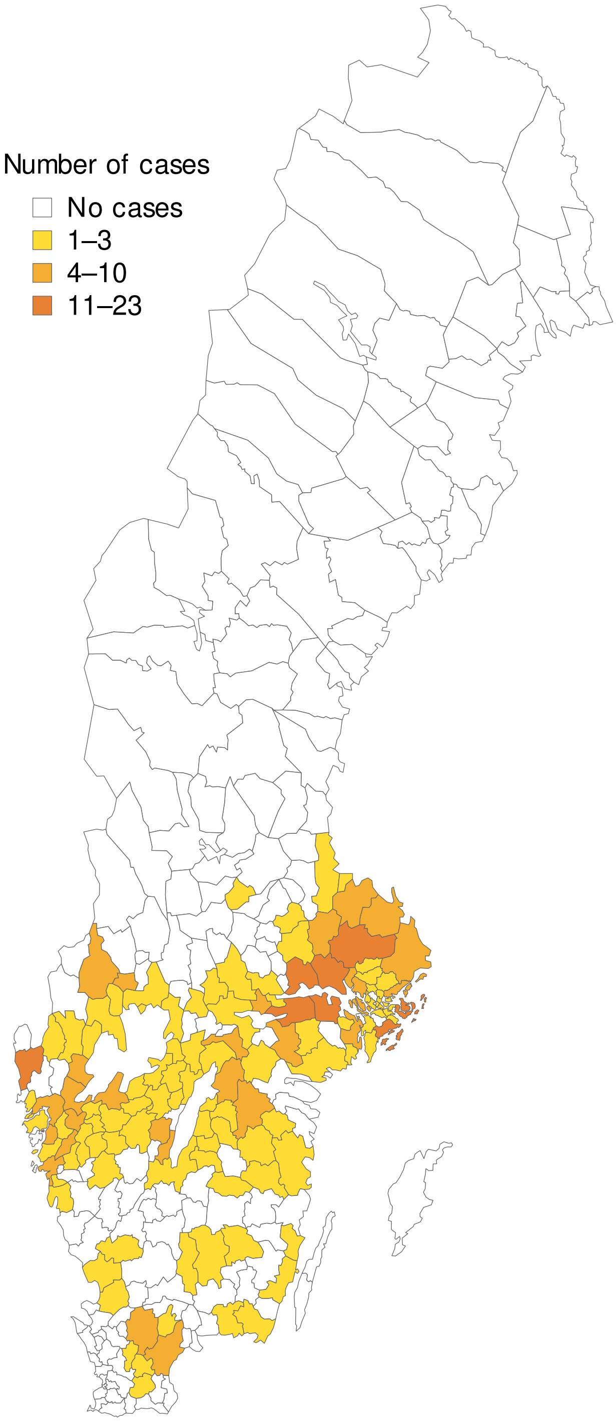


Figure 57: Geographical distribution of notified cases of tick-borne encephalitis in humans in 2021, based on the municipality of infection.

growing season in Sweden leads to better conditions for tick survival and reproduction and plays a potential role in the long term, enabling ticks to spread to new areas.

I. ricinus can transmit the European TBEV whereas *I. persulcatus* can harbour also Siberian and Far-Eastern subtypes of TBEV that are associated with much more severe forms of the disease. At present, the two latter subtypes have not yet been identified in Swedish ticks. However, the risk of their appearance (likely to be followed by severe human cases of TBE) in the northern parts of the country now or in the near future has become real considering the ongoing spread of *I. persulcatus* along the northern coastline.

REFERENCES

Andersson E, Kendall A, Url A, Auer A, Leschnik M (2020) The first RT-qPCR confirmed case of tick-borne encephalitis in a dog in Scandinavia. Acta Vet Scand, 62:51, https://doi.org/10.1186/s13028-020-00550-2.

Blomqvist G, Näslund K, Svensson L, Beck C, Valarcher JF (2021) Mapping geographical areas at risk for tick-borne encephalitis (TBE) by analysing bulk tank milk from Swedish dairy cattle herds for the presence of TBE virus-specific antibodies. Acta Vet Scand, 63:16, https://doi.org/10.1186/s13028-021-00580-4.

Omazic A, Bylund H, Boqvist S, Högberg A, Björkman C, Tryland M, Evengård B, Koch A, Berggren C, Malogolovkin A, Kolbasov D, Pavelko N, Thierfelder T, Albihn A (2019) Identifying climate-sensitive infectious diseases in animals and humans in Northern regions. Acta Vet Scand, 61:53, https://actavetscand.biomedcentral.com/articles/10.1186/s13028-019-0490-0.

Wallenhammar A, Lindqvist R, Asghar N, Gunaltay S, Fredlund H, Davidsson Å, Andersson S, Överby A K., Johansson M (2020) Revealing new tick-borne encephalitis virus foci by screening antibodies in sheep milk. Parasites Vectors, 13:185, https://doi.org/10.1186/s13071-020-04030-4.

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 foodborne outbreaks and thus the reported numbers of cases fluctuate between years, but without any significant increase or decrease during the period 2016–2020. 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 2020 positive pigs were reported from Romania, Bulgaria, Greece, Croatia, France, Spain and Italy. 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 dominating 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.

Figure 58: Testing for *Trichinella* is part of routine meat inspection for animal species that can become infected, including wild boar. In 2021, the parasite was found in 3 out of 130 826 tested boars. Photo: SVA.

DISEASE

Animals

Animals rarely develop a clinical infection, although both pigs and rodents can exhibit clinical signs.

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 2021:10. 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 2022:217).

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 2015/1375). The risk of Trichinella infection in pigs from such production sites is considered as negligible and only certain categories of pigs are required 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 (ISO 18743:2015) 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 five laboratories during 2021.

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 2021, the number of tested pigs from controlled housing conditions were 35 351 breeding sows, 468 boars and 1 746 698 fattening pigs. In addition, 470 293 slaughtered pigs (all categories) from uncontrolled housing conditions were tested. The number of slaughtered and tested horses was 1108. *Trichinella* was not detected in domestic pigs or horses.

Trichinella spp. was detected in 3 out of a total of 130 826 (0.002%) wild boar samples and also in 6 lynx, 1 red fox and 1 wolf, see Table 29. These figures are based on results from examination of samples from animals submitted to wild game establishments (16569 wild boars and 89 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 (SVA) within the general surveillance programme for wildlife diseases.

Humans

No human case of trichinellosis was reported in 2021.

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 in 2021.

Animal species	No. samples	No. positives	Percentage (%)	*T. britovi*	*T. nativa*	*T. pseudospiralis*	*T. spiralis*	*Trichinella* sp.
Badgers	9	0	0.00%	-	-	-	-	-
Bears	325	0	0.00%	-	-	-	-	-
Beavers	6	0	0.00%	-	-	-	-	-
Lion	2	0	0.00%	-	-	-	-	-
Lynx	111	6	5.41%	2	4	-	-	-
Red fox	41	1	2.44%	-	-	1	-	-
Seals	4	0	0.00%	-	-	-	-	-
Wild boars	130 826	3	0.002%	-	-	1	1	1
Wolverine	3	0	0.00%	-	-	-	-	-
Wolves	42	1	2.38%	-	1	-	-	-
Total	-	11	-	2	5	2	1	1

Tuberculosis

Figure 59: Due to successful eradication efforts, the probability that Swedish farmed deer are free from tuberculosis (TB) is high. There have been no confirmed cases since 1997. Photo: SVA.

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 3.5 per 100 000 inhabitants, which is among the lowest in the world. Almost 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 0.5 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

Infection by mycobacteria included in the *M. tuberculosis* complex (here defined as *M. bovis, M. caprae* or *M. tuberculosis*) is a listed disease (category B, D and E in cattle and other bovine animals, and D and E in goats, sheep, deer, camelids and other cloven-hoofed mammals) in the Animal Health Law, (EU) 2016/429. Sweden is officially free from the disease in bovine animals in accordance with (EU) 2021/620, and surveillance to demonstrate freedom is implemented in accordance with (EU) 2020/689. Tuberculosis caused by infection with *M. bovis* or *M. tuberculosis* is included in the Swedish Act of Epizootic diseases (SFS 1999:657 with amendments) and notifiable as described in SJVFS 2021/10 (K12). Infections caused by other members of the *M. tuberculosis* complex are not covered by the Swedish Act of Epizootic diseases but are still notifiable.

Humans

Tuberculosis in humans is a notifiable disease according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2022:217). 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 (SVA) for histology and PCR, as described above. For tissue from macroscopic lesions indicating TB, histology and PCR for *M. tuberculosis* and *M. avium*-complex are performed. Samples positive for M tuberculosis-complex at PCR are cultured on solid media (Löwenstein-Jensen and Stonebrink's) at SVA 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 subtyped.

Skin fold tuberculin tests are performed according to (EU) 2020/689. 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 post mortem 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, 22 animals whereof 19 pigs, 1 cattle, 1 horse and 1 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 5 pigs. No other slaughterhouse samples yielded any mycobacteria.

Due to clinical suspicions, macroscopic lesions, or findings of acid-fast bacteria, samples from three cats, one horse, one antelope, two wild boars and two alpacas (from two different herds) were investigated. From these samples NTM (Non-tuberculous mycobacteria), from the *Mycobacterium avium/intracellulare*-complex were isolated from one cat. No other sample yielded any mycobacteria.

During 2021, 9 alpacas, 4 camels and 2 llamas were tested serologically in relation to export or import, and within the voluntary control program 291 alpacas from 21 herds were tested, all with negative final results.

In 2021, there were approximately 350 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 2021.

Humans

The total number of detected cases of tuberculosis in humans in 2021 was 365. Out of these, four cases were caused by *M. bovis*, one case which presented with pulmonary TB and three cases with extrapulmonary TB. All four were most probably infected in their respective country of origin: Eritrea, Morocco, Somalia and Rwanda. All four 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 2021. The officially free status for bovine TB in cattle has been maintained during 2021. Although the surveillance is mainly dependent on inspections of slaughtered animals, this has been considered sufficient. However, the number of submissions of lesions from slaughtered ruminants has decreased over the years and work has been initiated in 2019 to increase submissions. During the end of 2021 SVA started to use 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. This aim together with the implementation of the Animal Health Law, (EU) 2020/688, imply that a review of TB surveillance in farmed deer is needed. 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.

REFERENCES

Alvarez J, Bezos J, de Juan L, Vordermeier M, Rodriguez S, Fernandez-de-Mera IG, Mateos A, Domínguez L. Diagnosis of tuberculosis in camelids: old problems, current solutions and future challenges. Transbound Emerg Dis. 2012 Feb;59(1):1–10. doi: 10.1111/j.1865-1682.2011.01233.x. Epub 2011 Jun 2

Rhodes S, Holder T, Clifford D, Dexter I, Brewer J, Smith N, Waring L, Crawshaw T, Gillgan S, Lyashchenko K, Lawrence J, Clarke J, de la Rua-Domenech R, Vordermeier M. Evaluation of gamma interferon and antibody tuberculosis tests in alpacas. Clin Vaccine Immunol. 2012 Oct;19(10):1677–83. Epub 2012 Aug 22.

Wahlström H, Frössling J, Sternberg Lewerin S, Ljung A, Cedersmyg M, Cameron A (2010) Demonstrating freedom from infection with Mycobacterium bovis in Swedish farmed deer using non-survey data sources. Prev Vet Med 94:108–118

Tularaemia

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.

Figure 60: Dead hare diagnosed with tularaemia. In 2021, *Francisella tularensis* was detected in 16 European brown hares and 4 mountain hares. Photo: Henrik Uhlhorn.

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 2021:10).

Humans

Tularaemia has been a notifiable disease since 1970 according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2022:217).

SURVEILLANCE

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 2021, 54 European brown hares, 12 mountain hares, one common shrew, one guinea pig, two domestic rabbits and 11 dogs were investigated. The number of reported dead hares and the number submitted for examination was lower than in the outbreak year 2019. *F. tularensis* subsp. *holarctica* was detected in 16 European brown hares and 4 mountain hares. Tularaemic hares were evenly distributed over the year and over several counties. In the counties where tularaemia was found (Stockholm, Uppsala, Västra Götaland, Västmanland, Örebro, Västerbotten, Värmland and Södermanland), the number of cases ranged from one to five. Four investigated dogs were serologically positive for tularaemia.

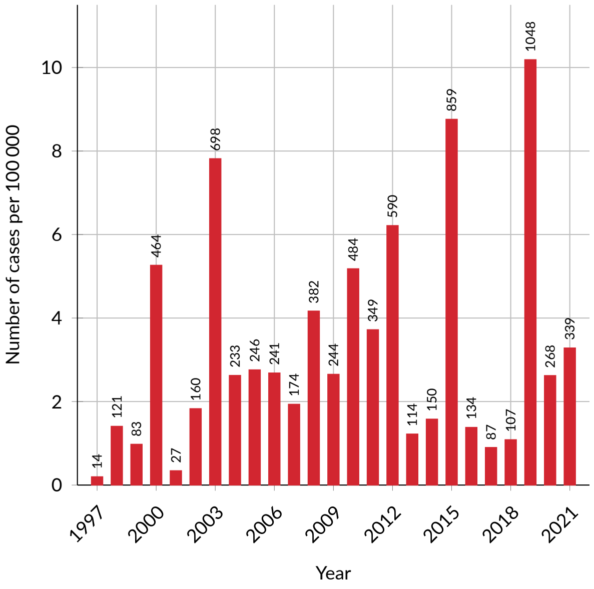


Figure 61: Incidence of notified human cases of tularaemia in Sweden 1997–2021. Bars indicate the incidence per 100 000 inhabitants and adjacent numbers the total number of cases reported.

Humans

In 2021, 339 human cases of tularaemia were reported, which is an average number of cases as seen over the last three decades (Figure 61). Of the cases for which the country of infection was known, all were reported as infected in Sweden. For the population as a whole, the incidence was 3.2 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 62). During 2021, the incidence was highest in the County of Värmland with 16 cases per 100 000 inhabitants, followed by the County of Örebro with 13 cases per 100 000 inhabitants. The reasons behind the annual and regional fluctuations observed are not known.

More men (62%) than women were reported to be infected in 2021, 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.

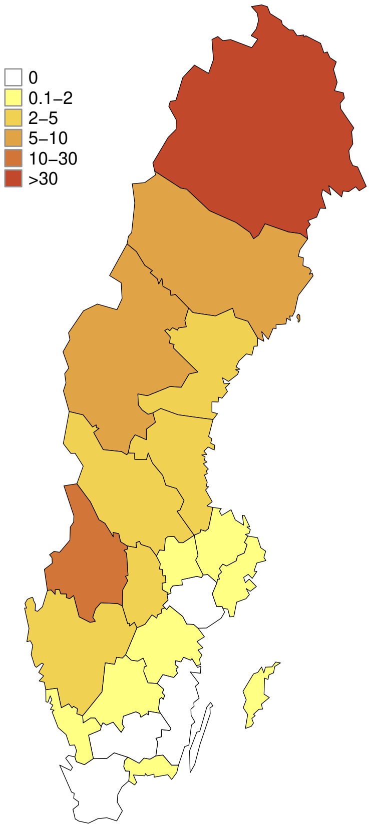


Figure 62: Incidence of reported human tularaemia cases by county in Sweden 2021. The colour scale represents the number of cases per 100 000 inhabitants.

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.

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.

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.

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 most recent available information, from 2014–2015, indicates that the prevalence of *Y. enterocolitica* in the Swedish domestic pig population (30.5% of herds) is similar to that of other pig producing countries in Europe. Human yersiniosis is primarily a domestic infection with about three quarters of the cases 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 septicaemia 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 2022:217). Diagnosis of yersiniosis by serology is not notifiable.

SURVEILLANCE

Animals

Active surveillance for *Yersinia* was not conducted during 2021, 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 authorities 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 2021, *Y. pseudotuberculosis* was isolated at the National Veterinary Institute (SVA) from 10 wild hares and four pet and zoo animals animals. *Y. enterocolitica* was isolated from three zoo animals. *Y. intermedia* was isolated from a porpoise. A total of 49 animals were investigated at SVA for *Yersinia* spp during 2021.

Food

In 2021, no samples taken by national and local authorities were analysed for *Yersinia*.

Humans

During 2021, 313 cases were reported (3.0 cases per 100 000 inhabitants). This is a clear increase compared to 2020 and more in line with levels in the 2010s. The proportion reported as infected in Sweden was 90% while travel-associated infections were a record low, 5% of the cases (Figure 63).

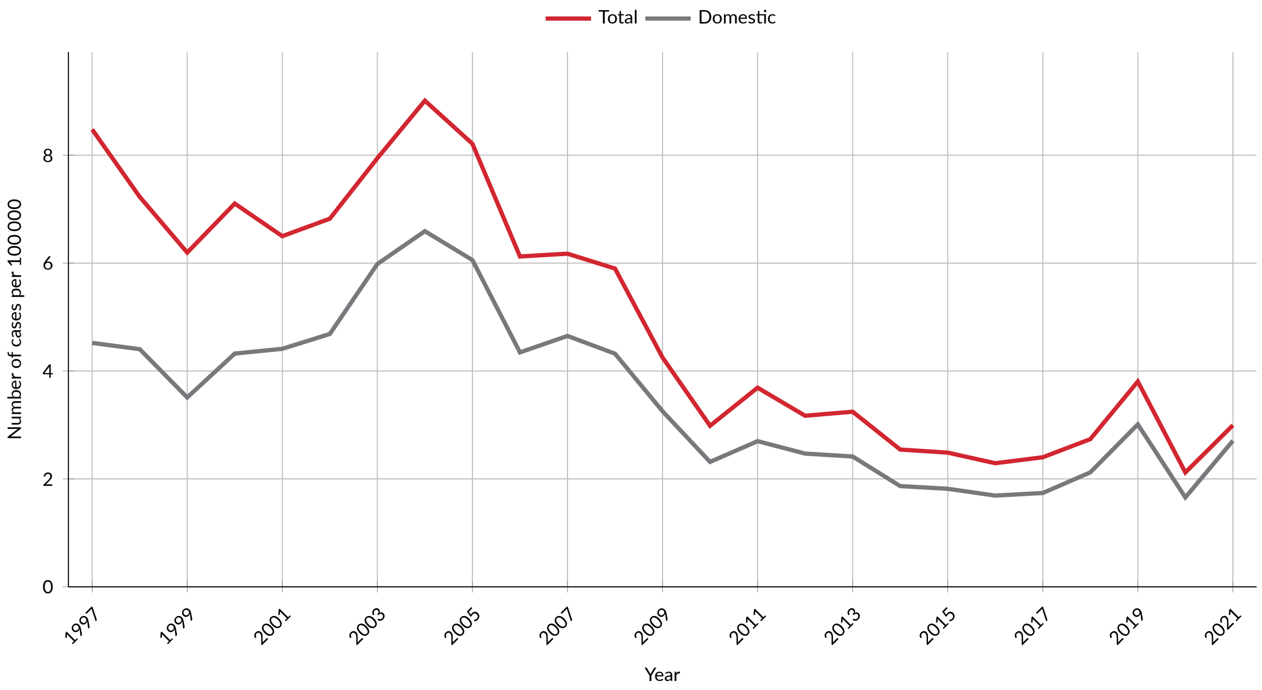


Figure 63: Notified incidence (per 100 000 inhabitants) of human cases of yersiniosis in Sweden, 1997–2021.

Like previous years, the incidence was high among children younger than five years of age. The incidence was 9.6 cases per 100 000 inhabitants for infants and 6.6 for children 1–4 years old, compared to 3.0 for all cases. In 2021, the incidence was also higher than average among cases 10–29 years old (4.9).

Yersiniosis follows a minor seasonal variation with the highest number of cases infected during the summer. In 2021, a large proportion of the cases were reported during the first months, partly due to a large outbreak (see below). During the rest of the year, the seasonal variation was more similar to normal (Figure 64). For the majority of cases, species was reported, with 211 being *Y. enterocolitica* and 29 *Y. pseudotuberculosis*. For *Y. pseudotuberculosis*, this is a sharp increase compared to 2019 and 2020 when 8 and 12 cases, respectively, were reported.

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

In mid-January, a clear increase in the number of yersiniosis cases was observed compared with the same period in previous years. The majority of cases were aged 10–39 years and about two thirds were female. Isolates were collected for sequencing from clinical microbiological laboratories in the regions with the largest number of cases. A cluster of 16 cases with Y. enterocolitica serotype O:3 was identified. Interviews and a subsequent case/case study indicated that the outbreak cases had visited the same restaurant chain to a much greater extent than non-outbreak cases. In follow-up interviews about what the outbreak cases had eaten at the restaurant chain, it emerged that iceberg lettuce was the common denominator. The fact that the collection of isolates was directed to a limited number of laboratories means that the actual number of persons affected was probably significantly higher than the 16 confirmed cases. During the investigation, comparisons were also made against isolates collected and sequenced in outbreak investigations in the spring of 2019. Interestingly, the outbreak strain was similar to a small cluster of isolates of four cases who fell ill in May 2019, which may indicate a recurring source of infection.

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 and the subsequent increase in 2021 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. 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 by the outbreak in January 2021 as well as in a Swedish-Danish outbreak in 2019 (Espenhain et al., 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

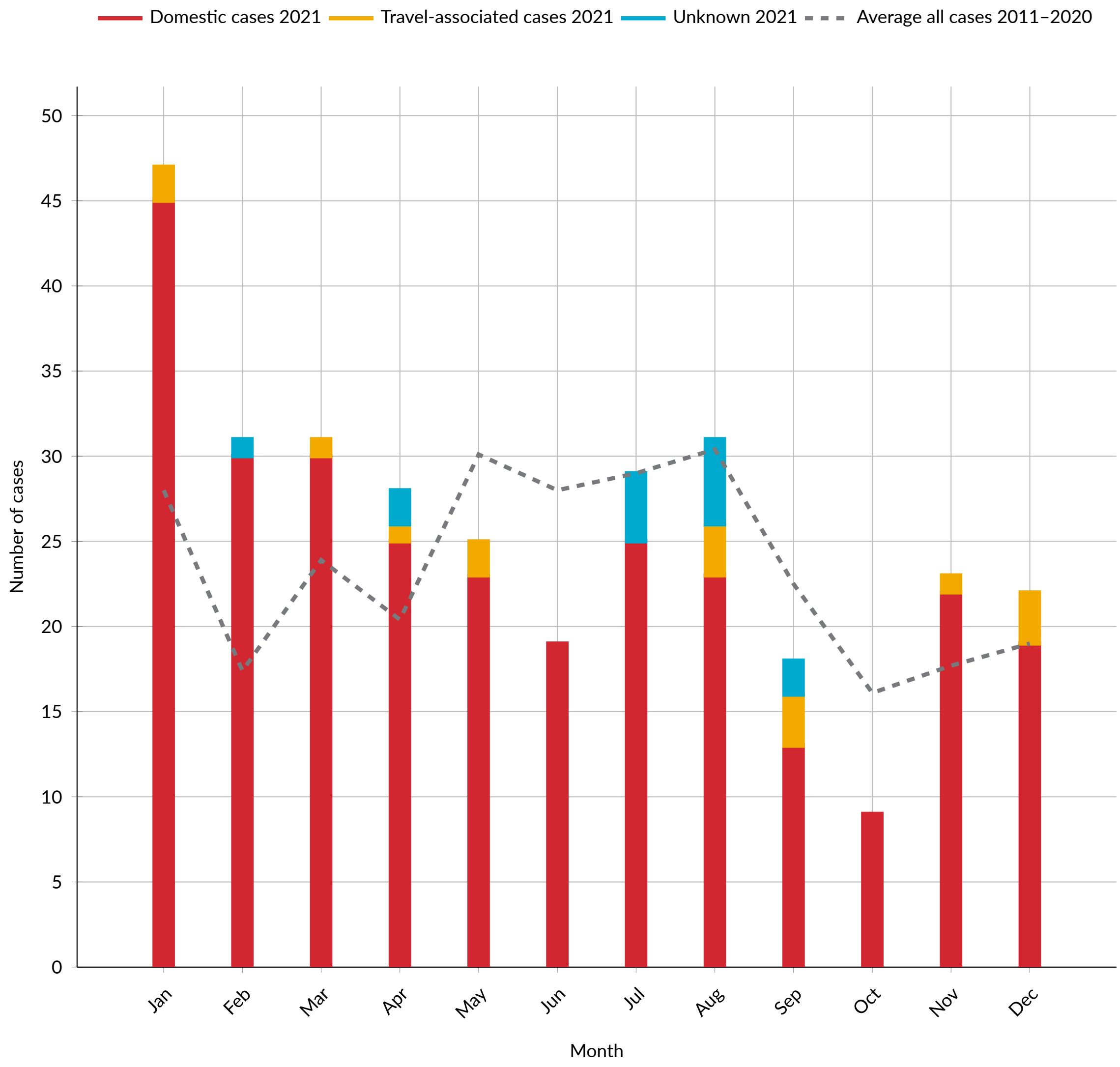


Figure 64: The monthly number of notified cases of yersiniosis of domestic, travel-associated and unknown country of origin in 2021 and the mean monthly number of all cases in 2011–2020.

of *Yersinia*.

REFERENCES

EFSA and ECDC (European Food Safety Authority and European Centre for Disease Prevention and Control), 2021. The European Union One Health 2019 Zoonoses Report. EFSA Journal 2021;19(2):6406, 286 pp. https://doi.org/10.2903/j.efsa.2021.6406

Espenhain L, Riess M, Müller L, Colombe S, Ethelberg S, Litrup E, Jernberg C, Kühlmann-Berenzon S, Lindblad M, Hove NK, Torpdahl M, Mörk MJ (2019) Cross-border outbreak of Yersinia enterocolitica O3 associated with imported fresh spinach, Sweden and Denmark, March 2019. Eurosurveillance 24:24

European Centre for Disease Prevention and Control. Yersiniosis. In: ECDC. Annual epidemiological report for 2019. Stockholm: ECDC; 2021.

Fredriksson-Ahomaa, M., & Korkeala, H. (2003). Low occurrence of pathogenic Yersinia enterocolitica in clinical, food, and environmental samples: a methodological problem. *Clinical microbiology reviews*, *16*(2), 220–229. https://doi.org/10.1128/cmr.16.2.220-229.2003

Hallanvuo, S., Herranen, M., Jaakkonen, A., Nummela, M., Ranta, J., Botteldoorn, N., … & Interlaboratory study group. (2019). Validation of EN ISO method 10273-Detection of pathogenic *Yersinia enterocolitica* in foods. *International journal of food microbiology*, *288*, 66–74. https://doi.org/10.1016/j.ijfoodmicro.2018.01.009

Tan, L. K., Ooi, P. T., Carniel, E., & Thong, K. L. (2014). Evaluation of a modified cefsulodin-irgasan-novobiocin agar for isolation of *Yersinia* spp. *PloS one*, *9*(8), e106329. https://doi.org/10.1371/journal.pone.0106329

Additional Surveillance 2021

Clinical surveillance

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 despite 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 and in 2021 it reached the Americas as both the Dominican Republic and Haiti reported outbreaks. 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, 21 outbreaks of ND have occurred in Sweden, all of which have been successfully eradicated. Sweden has status of ND free without vaccination (Commission implementing regulation (EU) 2021/620).

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 (SVA) 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 (Regulation (EU) 2016/429 and the supplements Commission Delegated Regulation (EU) 2020/689 and Commission Delegated Regulation (EU) 2020/687). 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 SVA. 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 SVA 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 SVA for laboratory analyses. Due to clinical similarity, samples from domestic pigs collected for ASF are in general also analysed for classical swine fever (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 boar, page 121). 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 SVA 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.

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 SVA 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 SVA 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 119).

RESULTS

The suspicions of epizootic diseases that were reported and further investigated based on sampling of sick or dead animals between 2014–2021are compiled in Table 30.

In 2021, three clinical suspicions of ASF in domestic pigs and two in wild boar were investigated, with negative results. Samples from the suspicions in domestic pigs were also analysed for CSF, and one for *Salmonella* Choleraesuis, all with negative results. In addition, 57 samples from wild boar found dead were analysed for ASF, as part of the enhanced passive surveillance, all with negative results.

Twelve clinical suspicions of anthrax in cattle, one in sheep, one in a horse were reported and investigated during 2021. In addition, one elk 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.

No clinical suspicions of FMD were investigated during 2021.

24 clinical suspicions of ND were investigated of which one was positive for Newcastle disease virus (avian paramyxovirus-1). 23 of the suspicions were concurrently investigated for avian influenza in connection with the ongoing outbreak during 2021 (see page 49).

Table 30: Suspicions of epizootic diseases reported and further investigated between 2014–2021, based on sampling of sick or dead animals.

	Investigated[A] (Confirmed)								
Disease	2013	2014	2015	2016	2017	2018	2019	2020	2021
African swine fever[B]	17 (0)	6 (0)	17 (0)	20 (0)	18 (0)	18 (0)	38 (0)	80 (0)	63(0)
Anthrax[C]	18 (1)	18 (0)	11 (0)	74 (15)	34 (0)	16 (0)	15 (0)	10 (0)	15(0)
Aujesky's disease	2 (0)	2 (0)	1 (0)	2 (0)	0 (0)	1 (0)	2 (0)	1 (0)	1 (0)
Avian influenza[D]	12 (1)	16 (0)	15 (0)	17 (2)	28 (4)	9 (1)	9 (0)	8 (2)	81(28)
Bluetongue	2 (0)	2 (0)	2 (0)	2 (0)	2 (0)	2 (0)	2 (0)	4 (0)	3 (0)
Brucellosis	5 (0)	2 (0)	1 (0)	0 (0)	0 (0)	1 (0)	1 (0)	0 (0)	4 (0)
BSE[E]	4 (0)	3 (0)	1 (0)	2 (0)	2 (0)	42 (0)	18 (0)	10 (0)	13 (0)
CWD[F]	0 (0)	0 (0)	0 (0)	0 (0)	1 (0)	17(0)	31 (2)	27 (1)	17 (0)
Classical swine fever	4 (0)	5 (0)	3 (0)	5 (0)	3 (0)	4 (0)	5 (0)	8 (0)	4 (0)
FMD	2 (0)	1 (0)	1 (0)	1 (0)	0 (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)	1 (0)
Lumpy skin disease	0 (0)	0 (0)	1 (0)	1 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Newcastle disease	15 (0)	25 (3)	15 (0)	17 (1)	29 (3)	8 (1)	11 (0)	9 (1)	24 (1)
Paratuberculosis	4 (0)	7 (0)	3 (0)	5 (0)	5 (0)	1 (0)	4 (0)	4 (0)	2 (0)
PRRS	9 (0)	4 (0)	5 (0)	5 (0)	2 (0)	2 (0)	12 (0)	5 (0)	7 (0)
Rabies	8 (0)	5 (0)	10 (0)	3 (0)	6 (0)	9 (0)	5 (0)	12 (0)	13 (0)
Tuberculosis[G]	8 (0)	14 (0)	8 (0)	6 (0)	9 (0)	7(0)	15 (0)	20 (0)	14 (0)
West Nile fever	2 (0)	1 (0)	2 (0)	1 (0)	2 (0)	0 (0)	5 (0)	4 (0)	0 (0)

[A] In many cases clinical suspicions were investigated for several diseases with similar clinical picture (e.g., ASF/CSF/PRRS, AI/ND).

[B] Includes wild boar found dead, also described in the specific chapter on infectious diseases in wild boar (page 121).

[C] Includes animals from the intensified surveillance in the two areas with outbreaks in 2008 and 2011 respectively.

[D] Does not include surveillance of, or cases in, wild birds.

[E] The 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.

[F] Does not include surveillance of, or cases, in the intensified sampling.

[G] Reported as cases per herd or owner, surveillance at slaughter included.

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 in the enhanced passive surveillance increased substantially during 2019 and 2020, followed by a small decrease in 2021. The rise of submitted wild boar in 2019 and 2020 was 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 300 000–400 000) and the expected number of wild boars that would die from other causes than hunting and road kills, and thus constitute the potential sampling frame for the surveillance, the number is not adequate. Further measures are therefore being taken to increase the numbers.

REFERENCES

EFSA AHAW Panel (EFSA Panel on Animal Health and Welfare), 2015. Scientific opinion on African swine fever. EFSA Journal 2015;13(7):4163, 92 pp. doi:10.2903/j.efsa.2015.4163

DG(SANCO) 2013–6780. Report from an audit carried out in Sweden on Animal health - disease contingency plans; protection during depopulation for disease control, pp 14–17. https://ec.europa.eu/food/audits-analysis/act_getPDF.cfm?PDF_ID=11146

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 are notifiable according to provisions issued by the Swedish Board of Agriculture (SJVFS 2021:10). The diseases included in the programme during 2021 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 foetuses 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. Infection with both biovars are included in the Swedish zoonosis legislation (SJVFS 2004:2) and are listed diseases (categories D and E) in the Animal Health Law, Regulation (EU) 2016/429. 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. *Mycoplasma gallisepticum* and *M. meleagridis* are listed diseases (categories D and E) in the Animal Health Law (EU) 2016/429. 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. *Mycoplasma gallisepticum* and *M. synoviae* are present in the backyard poultry population in Sweden and in 2016, 2017 and 2019 antibodies to *M. synoviae* were detected in chicken breeding flocks. In 2020, antibodies to *M. meleagridis* were detected in a turkey breeding flock in the Poultry Health Control Programme for the first time.

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-one outbreaks of Newcastle disease have occurred in Sweden. The disease is listed (categories A, D and E) in the in the Animal Health Law, (EU) 2016/429. Since all outbreaks have been successfully eradicated, Sweden has a status of Newcastle disease free country without vaccination according to Commission Implementing Regulation (EU) 2021/620.

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 (SVA) and financed by the Swedish Board of Agriculture and the participating companies. In 2021, six breeding companies participated in the programme: four broiler, two 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

Table 31: Sampling schedule for chicken grandparent and parent flocks. Number of blood samples tested at different weeks of age.

	Age in weeks						
Agent	16	24	36	48	60	72	84
S. Pullorum / *S.* Gallinarum	-	60	-	-	-	-	-
Mycoplasma gallisepticum	60	60	60	60	60	60	60
Mycoplasma synoviae	60	60	60	60	60	60	60
Paramyxovirus type 1	-	-	-	60	-	-	-
Egg drop syndrome virus	-	30	-	-	-	-	-

the official veterinarian. In the remaining flocks the official veterinarian takes the samples. The blood samples were sent by mail to SVA where serological tests were performed. The sampling and testing schemes are presented in tables 31 and 32.

RESULTS

Table 33 gives an overview of all samples taken in breeding flocks of chickens and turkeys, and the laboratory methods used, during 2021. All analysed samples tested negative for *Salmonella* Gallinarum/*Salmonella* Pullorum and paramyxovirus type 1.

Serological reactions to *M. synoviae* were detected in ten chicken parent flocks. All ten flocks were considered free from *M. synoviae* based on clinical status and testing of new samples.

Table 32: Sampling schedule for turkey parent flocks. Number of blood samples tested at different weeks of age.

	Age in weeks			
Agent	20	32	44	56
S. Pullorum / *S.* Gallinarum	-	60	-	-
Mycoplasma gallisepticum	60	60	60	60
Mycoplasma meleagridis	60	60	60	60
Mycoplasma synoviae	60	60	60	60
Paramyxovirus type 1	-	-	-	60

Two chicken parent flocks and one turkey parent flock 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, one turkey parent flock investigated due to a few positive samples for *M. meleagridis* and one chicken grandparent flock and four chicken parent flocks 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 previous years, antibodies have been detected to both *M. synoviae* (chicken breeding flocks in 2016, 2017 and 2019) and *M. meleagridis* (one turkey breeding flock in 2020) within the Poultry Health Control Programme. In 2021, the results from the serological screening supports the status of freedom from these diseases as well as several other important infectious diseases in the Swedish breeding poultry population. In addition to the serological screening, 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 2021.

	No. of sampling occasions			No. of samples			
	Chickens		Turkeys	Chickens		Turkeys	
Agent	GP	P	P	GP	P	P	Method
S. Pullorum / *S.* Gallinarum	10	104	4	600	6240	240	Serum plate agglutination test, antigen, Ceva Biovac
Mycoplasma gallisepticum / *Mycoplasma synoviae*	50	430	17	3000	25 800	1020	*Mycoplasma gallisepticum/synoviae* Antibody Test Kit, BioChek
Mycoplasma meleagridis	0	0	17	0	0	1020	Serum plate agglutination test, antigen, Ceva Biovac
Paramyxovirus type 1	10	81	4	600	4860	240	NDV screen competition ELISA, ID.Vet
Egg drop syndrome virus	10	104	0	300	3120	0	Antibody haemagglutination inhibition test, antigen, GD Animal Health

Infectious diseases in wild boar

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 2021, cases of the disease were reported in the wild boar population of 10 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 boars 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 boars, 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 (SVA) 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. Since late 2020, wild boars submitted to SVA are also examined for the presence of Salmonella by tissue culture (see chapter "Salmonellosis" (page 76).

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 SVA for analysis for the presence of antibodies to infectious agents that are of importance to domestic pig production. In 2021, the samples were used for the active surveillance of AD, CSF and *Brucella suis*. The samples were tested for antibodies against AD and CSF using ELISA kits (SVANOVIR® PRV-gB-Ab ELISA, Svanova, Uppsala, Sweden and IDEXX HerdChek® CSFV Ab Test Kit, IDEXX Laboratories, Westbrook, Maine, United States, respectively) and for antibodies against *Brucella suis* with the Rose-Bengal test. 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.

Since late 2020, hunters have also had the opportunity to submit tissue and faecal samples from hunted wild boars for *Salmonella* culturing. More information about this surveillance can be found in the chapter "Salmonellosis" (page 76).

RESULTS

Passive surveillance

Samples from 57 wild boars that were found sick or dead were submitted by members of the public for examination for the presence of ASF virus genome in 2021. The number of wild boars submitted annually over the last two years represents an approximate doubling in the number of animals submitted for analysis as compared to previous years. 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 recent finding of *Salmonella* Choleraesuis in populations of wild boar in some areas of the country (see chapter "Salmonellosis", page 76) has likely also increased public interest in submitting dead wild boars for post mortem examination.

The geographic distribution of the sampled dead wild boars is shown in Figure 65. 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 140) in this report. The results of the *Salmonella* surveillance in wild boar are reported in the chapter "Salmonellosis" (page 76).

During 2021, several clinical suspicions of diseases included in the Swedish Act of Epizootic Diseases were investigated in free-living wild boars. One suspicion of brucellosis arose after an apparently healthy, hunted wild boar was found to have enlarged testicles. Samples were taken and cultured for Brucella with negative results. One suspicion of tuberculosis was investigated after nodular lesions were found in multiple organs from a hunted wild boar. Organ samples were analysed for *Mycobacterium tuberculosis* complex by PCR and found negative while *Mycobacterium avium* was identified. Two suspicions of ASF arose after multiple dead wild boar were found at the same time in the same place. In both cases, organ samples from the dead animals were analysed for the presence of ASF virus by PCR and found negative.

Active surveillance

In 2021, 112 blood samples were collected from hunted wild boars and analysed for the presence of antibodies against AD and CSF. Additionally, 102 samples were analysed for the presence of antibodies against *B. suis*. All samples were negative. The geographical distribution of sampled wild boars was roughly correlated to the distribution and density of the Swedish wild boar population (Figure 65) (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 2021 is sufficient to indicate that the prevalence of AD, CSF and *Brucella* 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 denser, 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 post-mortem and ASF testing are currently being investigated.

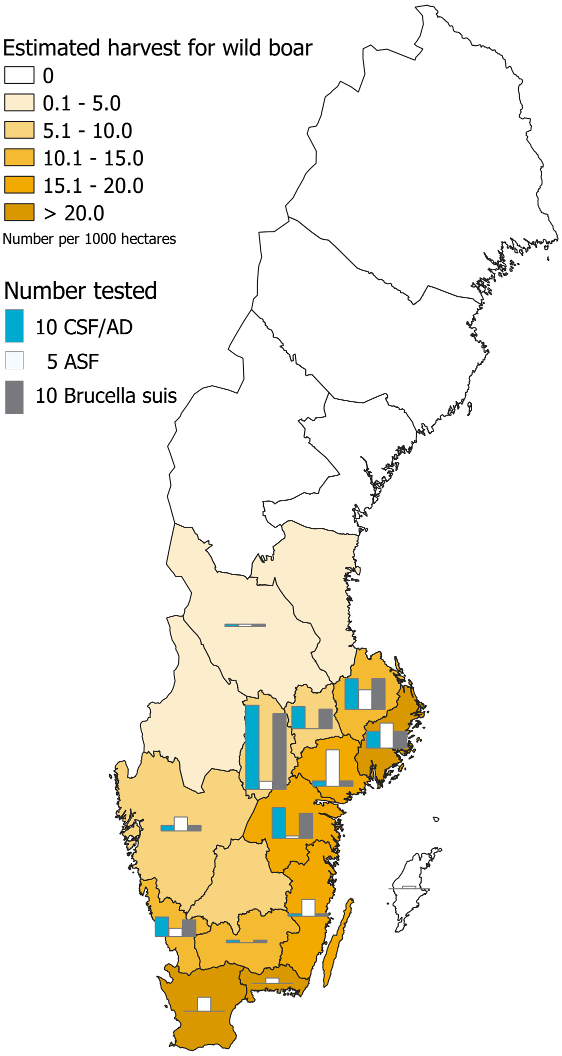


Figure 65: Geographical distribution by county of origin of wild boar samples included in the surveillance. Note that in some cases, the coordinates for the site at which a wild boar was sampled were not provided and those animals are not included on the map. The number of hunted wild boar sampled and tested for antibodies against Aujeszky's Disease (AD) and Classical Swine Fever (CSF) in 2021) are indicated by the blue bars (total 80), while those tested for antibodies against *Brucella suis* are indicated by the grey bars (total 73). The white bars indicate the number of wild boar found dead and tested for ASF (total 57). The background colours indicate wild boar density based on hunting statistics from 2020–2021 (Swedish Association for Hunting and Wildlife Management, game monitoring).

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 to date 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, who are appointed and given the responsibility over local inspection districts by seven of the CABs. Sweden was in 2021 divided in 315 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 bee inspectors, veterinarians and 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 2021:10). 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.

Figure 66: A honeybee foraging on a clover. The health situation for Swedish honeybees is good. Photo: Apinordica AB.

Bee inspectors can send samples of diseased brood, larvae, pupae or adult bees to the National Reference Laboratory (NRL) for bee health 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 listed disease (category D and E) in the Animal Health Law, (EU) 2016/429. 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.

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 it is spreading and there were reports of findings of the mite in hitherto free areas during 2021. Varroa is a listed disease (category C, D and E) in the Animal Health Law, (EU) 2016/429.

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. Tropilaelaps mite infestation is a listed disease (category D and E) in the Animal Health Law, (EU) 2016/429.

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. Small hive beetle infestation in honeybees is a listed disease (category D and E) in the Animal Health Law, (EU) 2016/429.

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 in Sweden is done through diagnostics related to disease outbreaks, and the 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 67.

Active surveillance

In 2016, a baseline study of the prevalence of Varroa mites, the viruses DWV, ABPV, the bacteria *Melissococcus plutonius* and *Paenibacillus larvae* was initiated by the national reference laboratory (NRL) for bee health and conducted in collaboration with the National Veterinary Institute (SVA). According to the national surveillance plan (NÖP), follow up studies should be done at 5-year intervals and was therefore carried out during 2021.

Table 34: Number of samples from the Swedish honeybee population analysed at the national reference laboratory for bee health during 2021. 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	286	67	39	3295	349	88
EFB	19	2	2	27	6	6
A. woodi	2	0	0	6	0	0
V. destructor	59	57	14	170	164	16
Tropilaelaps spp.	0	0	0	1	0	0
A. tumida	2	0	0	2	0	0

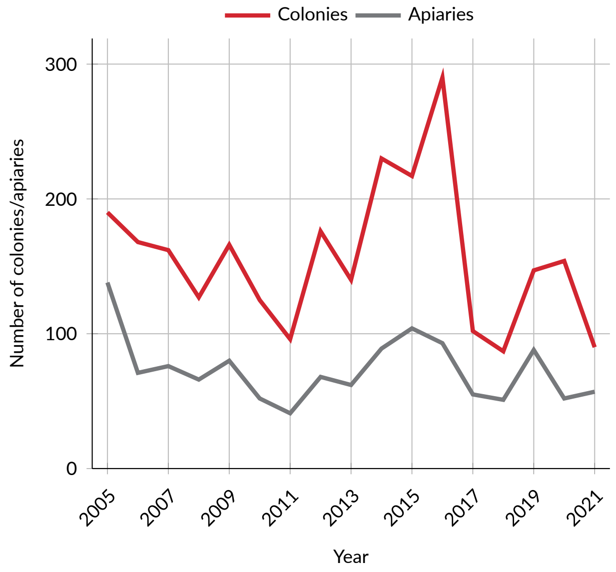


Figure 67: Number of new cases of American foulbrood in 2005–2021 in bee colonies and apiaries, based on reports from bee inspectors to the County Administrative Boards. A total of 3888 colonies in 1025 apiaries were inspected in 2021.

RESULTS

Passive surveillance

Samples from a total of 3295 bee colonies in 286 beekeeping operations were analysed by the NRL for bee health in 2021. The results are shown in (Table 34). American foulbrood was detected in 349 colonies in 67 beekeeping operations. European foulbrood was detected in 6 colonies from 2 beekeeping operations.

The national bee inspectors performed visual inspection of disease symptoms in 3888 colonies in 1025 apiaries and reported symptoms of AFB in 90 colonies in 57 apiaries. See Figure 67.

Active surveillance

Samples of adult bees were collected from honeybee colonies in 397 randomly selected apiaries (≤5 colonies per apiary) distributed throughout the country. Samples were collected during the beekeeping season 2021 and sent to the NRL at the Swedish University of Agricultural Sciences, SLU, for analysis. Samples from individual honeybee colonies were examined macroscopically for Varroa mites, and pooled apiary samples analysed by molecular methods (RT-qPCR for ABPV and CBPV; PCR for *M. plutonius* and *A. woodi*) and by microbial culturing (*P. larvae*).

Paenibacillus larvae, the causative agent of AFB, was detected in 2% of all sampled apiaries (Figure 68).

Melissococcus plutonius, the causative agent of EFB was detected in 2% of all sampled apiaries (Figure 69).

Varroa mites were detected in 63% of the sampled colonies and in all counties except Jämtland (Figure 70) which reinforces earlier observations and reports from bee inspectors. DWV was detected in 92% of the investigated apiaries and present in all counties (Figure 71). ABPV was detected in one county in the south (Skåne; Figure 72).

The tracheal mite, *Acarapis woodi,* was not detected.

DISCUSSION

The reporting of AFB incidence is based on the information that the bee inspectors report to the CABs and is based on visual observation of clinical signs (Figure 67). However, since January 2019, the bee inspectors can also send samples of adult bees to the NRL for the detection of *Paenibacillus larvae* in connection with a disease outbreak and tracking, which has resulted in a substantial increase in the number of honeybee colonies analysed yearly for the presence of the bacterium (Table 34). This complement to visual inspection of honeybee colonies in connection with outbreaks of AFB have proven to be a useful tool for the bee inspectors to track symptomatic colonies.

In the 2016 baseline study, *Paenibacillus larvae* was detected in 6% of the investigated apiaries, whereas the total prevalence in 2021 was 2% 68. Based on these two observations and the reports from the bee inspectors, the AFB incidence in the country is still low and seems to be relatively stable. Future follow up studies and disease monitoring are needed to confirm this observation.

The causative agent of EFB, *Melissococcus plutonius*, was detected in only two apiaries in the county of Östergötland in the 2016 baseline study, whereas it was detected in 2% of the investigated apiaries in four counties in the 2021 follow up study (Figure 69). 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 in the early 90s, 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 2021 baseline survey reinforcing earlier observations and reports from bee inspectors (Figure 70). Although the results from the 2021 study shows that the total Varroa prevalence is higher than 2016, we still have areas where the mite seems to be absent. In the 2021 baseline survey, DWV was detected in all counties, however with lower prevalence in the northern counties (Figure 71). The spread of DWV coincides with the presence of Varroa and follows the spread of the mite. The other virus associated with Varroa, ABPV, was detected in one county only and the incidence seems to be stable compared to the 2016 baseline study (Figure 72). A possible explanation for the sparse occurrence of ABPV is that the virus is highly virulent and kills its host (honeybee larvae) 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 county where ABPV is detected, Skåne, is one of 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 honeybee tracheal mite *Acarapis woodi* has, to date, not been detected in Swedish apiaries and is therefore regulated in national legislation. Earlier surveys of the occurrence of the mite have been performed by SLU on behalf of the SBA in 1993 and 2010/11. There have been discussions among beekeepers about the validity of the national legislation on tracheal mites and the claimed absence in the country. The 2021 baseline study reinforces this absence and provides a valuable argument for continued legislation and surveillance.

The lack of a national bee register makes it difficult to organize sampling of honeybees. As part of the new EU legislation on animal health, Regulation (EU) 2016/429 (the Animal Health Law), registers of all animals kept in husbandry for food production will be mandatory, and a register for honeybee operations will be in place shortly. 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.

REFERENCES

Surveillance of infectious diseases in animals and humans in Sweden 2017, National Veterinary Institute (SVA), Uppsala, Sweden. SVA:s rapportserie 52 ISSN 1654–7098. (www.sva.se)

Silva de Oliveira V H, Nilsson A, Kim H, Hallgren G, Frössling J, Fabricius Kristiansen L, Forsgren E (2021). Honeybee pathogens and parasites in Swedish apiaries – a baseline study. Accepted Feb 21 for publication in Journal of Apicultural Research. DOI: 10.1080/00218839.2021.1902679

Nordström S, Forsgren E, Fries I (2002). Comparative diagnosis of American foulbrood using samples of adult honeybees and honey. Journal of Apicultural Science 46, 5–13

Locke B, Low M, Forsgren E (2019). An integrated management strategy to prevent outbreaks and eliminate infection pressure of American foulbrood disease in a commercial beekeeping operation. Preventive Veterinary Medicine 67, 48–52. DOI: 10.1016/j.prevetmed.2019.03.023

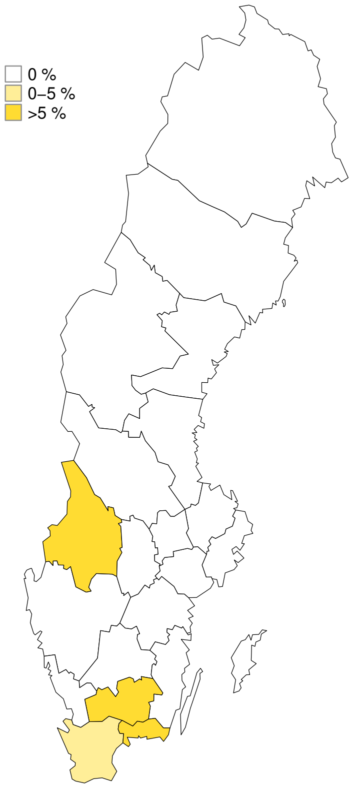


Figure 68: Proportion of apiaries positive for *P. larvae* in 2021.

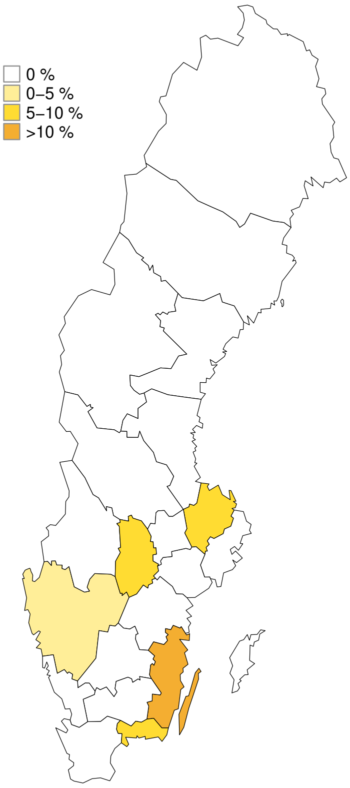


Figure 69: Proportion of apiaries positive for *M. plutonius* in 2021.

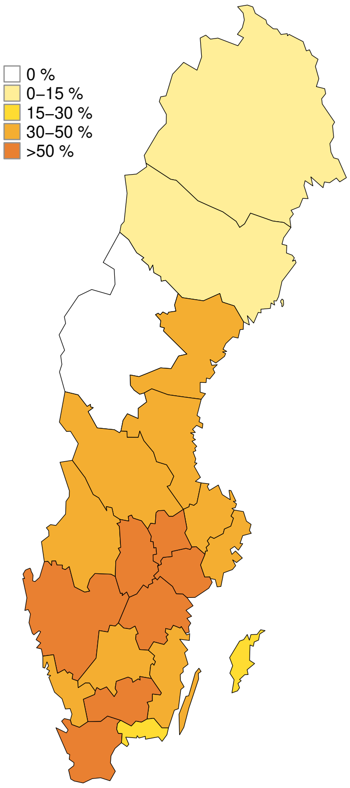


Figure 70: Proportion of **colonies** positive for *Varroa destructor* in 2021.

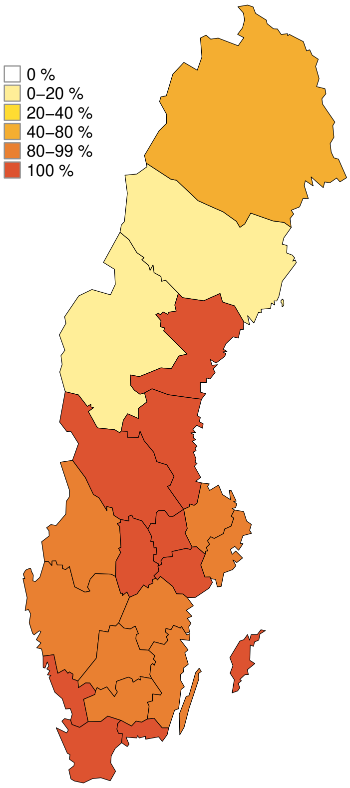


Figure 71: Proportion of apiaries positive for DWV in 2021.

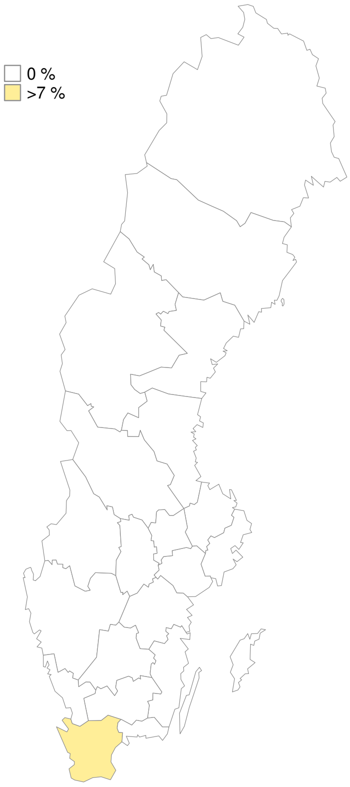


Figure 72: Proportion of apiaries positive for ABPV in 2021.

Infectious diseases in fish, crustaceans and molluscs

BACKGROUND

All registered aquaculture farms are obligated to participate in the Official Health Control Programme, regulated in accordance with the Animal Health Law, (EU) 2016/429 and its implementing regulation (EU) 2018/1882. Sweden has a 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. During 2021, when the new Animal health law (EU 2016/429) was implemented, legislation for disease surveillance and methodology was also changed. Previously the Commission Implementing Decision (EU) 2015/1554 was followed regarding both surveillance and diagnostics. Currently, surveillance is regulated by the Commission Implementing Regulation (EU) 2018/1882 and diagnostic manuals have been removed and are now the responsibility of the European Union Reference Laboratory for Fish and Crustacean diseases, Denmark and the European Union Reference Laboratory for Molluscs diseases (Ifremer), France. Sweden is officially free from Viral haemorrhagic septicaemia (VHS) and Infectious haematopoietic necrosis (IHN) in accordance with (EU) 2021/620. Sweden is considered free from SVC, and has approved national measures in accordance with (EU) 2021/620. Sweden is considered free from Infectious Pancreatic Necrosis (IPN) in the inland zone and has approved national measures in accordance with (EU) 2021/260. The inland zone has an eradication programme for Renibacteriosis/bacterial kidney disease (BKD) and the

Figure 73: Blue mussel suffering from marteiliosis. Photo: Anders Alfjorden.

coastal zone for IPN (EU) 2021/620. These diseases are notifiable in accordance with SJVFS 2021:10. Further, IHN, VHS, IPN (other than genogroup 2/serotype ab) 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. Marteiliosis and bonamiosis (shellfish) and crayfish plague and white spot syndrome (crayfish) are actively tested for within SVA's wild crustacean and mollusc surveillance programmes. These diseases are also regulated by the Swedish legislation on notifiable diseases (SJVFS 2021:10). Other notifiable diseases such as furunculosis (*Aeromonas salmonicida* subsp. *salmonicida*, ASS) and yersiniosis/Enteric redmouth disease (ERM), 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 and is a listed disease (category A, D and E) in the Animal Health Law, (EU) 2016/429. Susceptible species present in Sweden are rainbow trout, European/redfin perch, Northern pike and pike-perch. Fish are 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. VHS and IHN are listed diseases (category C, D and E) in the Animal Health Law, (EU) 2016/429. 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. A large outbreak of IHN occurred in Danish rainbow trout farms and associated put and take lakes in the spring and summer of 2021. The disease was spread to Åland (Finland archipelago) rainbow trout farms by sale of live fish. Extra surveillance of wild salmon returning to Swedish river systems was done during the summer because they pass Åland en route, but the virus has not been detected in our wild salmon populations. Further, no rainbow trout had been imported from Denmark during winter and spring 2021. 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 with up to 40% mortality can occur. Infected fish may have reduced growth and secondary bacterial infections such as ASS, which demands antimicrobial treatments, 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. KHV is a listed disease (category E) in the Animal Health Law, (EU) 2016/429. 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. WSS is a listed disease (category A, D and E) in the Animal Health Law, (EU) 2016/429. 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 if introduced, 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 protist parasite (*Marteilia refringens* in oysters and *M. pararefringens* in blue mussels). Marteiliosis is a listed disease (category C, D and E) in the Animal Health Law, (EU) 2016/429. 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 in the Swedish west coast waters.

Bonamiosis

Bonamiosis is a disease in oysters caused by the protistan parasite *Bonamia ostreae*. Bonamiosis is a listed disease (category C, D and E) in the Animal Health Law, (EU) 2016/429. 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.

Perkinsosis

Perkinsosis is a disease in bivalves caused by protists of the genus *Perkinsus*. Perkinsosis is a listed disease (category A, D and E) in the Animal Health Law, (EU) 2016/429. The most relevant species under Swedish conditions is *P. marinus* that infects *Magallana gigas* among other species. *M. gigas* usually do not show any signs of disease. The disease has never been found in Sweden or neighbouring countries.

Mikrocytosis

Mikrocytosis is a disease in oysters that is caused by the protist *Mikrocytos mackini*. Mikrocytosis is a listed disease (category A, D and E) in the Animal Health Law, (EU) 2016/429.

The parasite usually infects connective tissue and muscles. Infected animals often die but subclinical infections occur. The disease has never been found in Sweden or neighbouring countries.

SURVEILLANCE

The aim of the Official Health Control Programme is to document freedom from disease and to contribute to the maintenance of this status.

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 risk classification system is under revision and will expand to nine risk classes and include every third-year sampling. The Board of Agriculture expects that all farms will have been classified in accordance with the new system at the end of 2022. There is also active surveillance in imported quarantined fish (eel - IPN and koi/carp - KHV). Active surveillance is also done when 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.

Since 2020 there is also an active health surveillance of wild fish, crustaceans and molluscs. Within this surveillance samples for different infectious diseases are taken.

Crayfish plague, WSS and porcelain disease (the latter not notifiable) are monitored by passive surveillance and testing is done based on suspicion of disease outbreaks. In 2021, a pilot for active surveillance of crayfish plague using eDNA in water has been performed and is currently under evaluation.

Table 35: Samples taken in the Swedish surveillance programmes for notifiable diseases in fish, crustaceans and molluscs during 2021. One case = one outbreak.

Disease	No. of sampled production sites[A]	No. of infected production sites	No. of tested individuals[A]	No. of tested pools[A]	No. of infected individuals/pools
Fish					
VHS	68/33	0	0/10	450/54	-/0
IHN	68/33	0	0/10	450/54	-/0
IPN	68/33	0	0/10	450/54	-/0
ISA	2/1	0	90/8	-	0/-
SVC	3/1	0	7[B]	15	0/0
KHV	1[C]	0	7	-	0/0
BKD	62/0	4	3402/0	-	not relevant
Crustaceans					
Aphanomyces astaci[E]	8[D]	4[D]	19	-	not relevant
WSSv[E]	8	0	8	-	0/-
Molluscs					
Bonamia sp.[E]	5	0	150	0	0/-
Marteilia (para)refringens[E]	5–10	0	300	0	0/-
Perkinsus sp.[E]	5	0	150	0	0/-
Mikrocytos mackini[E]	5	0	150	0	0/-

[A] Farms/wild fish sampling points

[B] One koi import company tests individual quarantined fish

[C] One koi import company that tests quarantined fish

[D] A total of 8 locations were sampled, representing 7 separate waterways with wild crayfish. Three waterways were positive.

Abbreviations:

EHN	Epizootic haematopoietic necrosis
VHS	Viral haemorrhagic septicemia
IHN	Infectious haematopoietic necrosis
IPN	Infectious pancreatic necrosis
ISA	Infectious salmon anaemia
SVC	Spring viraemia of carp
KHV	Koi herpesvirus
BKD	Bacterial kidney disease

Infectious diseases in shellfish are monitored through sampling of 150 blue mussels and 150 European oysters per year.

Within the wild fish programs, samples are taken based upon suspicion of infectious disease or through short-term prevalence estimating projects.

For details about the different programs included in the wild fish, crustaceans and molluscs surveillance, please see chapter “Wild fish surveillance programme” (page 133).

DIAGNOSTIC PROCEDURES

All diagnostic virus analyses are performed at the Swedish reference laboratory for fish diseases at the National Veterinary Institute in accordance with e manuals published by the EU reference laboratories or the OIE aquatic manual. Pooled organ material (for EHN, VHS, IHN and IPN spleen, kidney, heart/brain, for SVC spleen, kidney, brain and gill) are tested by inoculation on cell cultures. 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 real-time 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, WSSv and *Thelohania contejeani* are detected with real-time PCR. The number of sampled animals varies from case to case.

Bonamia sp. is detected by real-time PCR. *Marteilia refringens*, *Perkinsus* sp. and *Mikrocytos mackini* are preliminary detected by histology and confirmed by real-time PCR.

RESULTS

Official health control programme for fish farms and crustacean surveillance

The number of samples analysed during 2021 and results are shown in Table 35. In summary, the active surveillance detected three cases of BKD (one case = one outbreak). All cases were detected in previously uninfected farms. The first case was in a small rainbow trout farm mostly active as a middle hand for transfer of fish from other farms to put and take lakes. The second and third case were detected in disease tracking for the first farm. These were two separate sites within the same company, selling fish to the first farm.

Voluntary health control programme for fish farms

One case of BKD was detected during voluntary screening of Arctic char brood stock females.

There were four recorded outbreaks of “other” notifiable diseases in fish during 2021. Three concerned furunculosis (ASS) and all three cases were recurrent infection. One of the farms had concurrent BKD infection. Yersiniosis was detected in one farm.

Eleven cases of flavobacteriosis due to *Flavobacterium psychrophilum* were detected. This is similar to the previous two years with five and nine cases respectively, but), fewer than the regular 20–30 cases per year during the past decades until 2018 *Flavobacterium columnare* was detected in nine disease cases during summer and autumn. Infection with *Aeromonas* bacteria other than *A. salmonicida* subsp. *salmonicida* was identified in 13 cases of disease.

OUTBREAKS IN WILD FISH, CRUSTACEANS AND MOLLUSCS

During 2021, suspicions of crayfish plague were investigated in eight outbreaks of mortality in noble crayfish. Crayfish plague was detected in four cases. The cases were also investigated for presence of WSSV and *Thelohania contejeani* (causing porcelain disease). In two cases *Thelohania contejeani* was detected. This was suspected to be the cause of mortality in one case, but in the other case parasite burden was low and detected together with crayfish plague. Thus, the latter was deemed as the cause of death. *Vibrio anguillarum* was detected in cod from two samplings in Hanöbukten on the Swedish Southeast coast and in round goby that had been caught along the East coast (Gävle). *Pseudomonas anguilliseptica* was detected in an eel that was found dead on the West coast.

DISCUSSION

The number of farms that were sampled during 2021 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 2021.

The most problematic disease to control is renibacteriosis/BKD, due to its vertical transmission and variable clinical presentation. In 2021 four cases were detected, all in farms that have not previously been infected in recent years. 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 six 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 potentially be improved by adding a modified sampling method to allow *in vivo* sampling of brood stock in commercial farms. Also, rapid slaughter in infected net pen farms to avoid manifestation of the bacterium in wild fish is imperative to avoid reinfection at re-stocking and secondary bacterial diseases that require antibiotic treatment. To get a more reliable assessment for health surveillance additional resources invested in risk-based analysis of individual aquaculture farms would be needed.

Wild fish surveillance programme

Figure 74: Noble crayfish (*Astacus astacus*) which has been sent to the National Veterinary Institute (SVA) for inspection, due to suspicion of crayfish plague. Photo: Anna Aspán.

BACKGROUND

In 2020, a general surveillance programme for wild fish, crustacean and mollusc health was launched, organised by the National Veterinary Institute (SVA) by commission from the Swedish Agency for Marine and Water Management. Previously, wild fish had only been investigated through short term projects or in cases of acute disease, except for eel, that had been monitored since 2018. Crayfish plague has been monitored for several years, and wild molluscs have been included in bonamiosis and marteiliosis projects for farmed molluscs. The surveillance programme 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 currently available results from 2021 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 (rapporterafisk.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 SVA 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 2021, a total of 161 salmon collected by traps, gill nets or in fish ladders were sampled in the summer. Both healthy looking and diseased individuals were sampled. Analysis of viral, histopathological samples, blood smears and thiamine have been performed. Analysis of thyroid status is ongoing. A summary of results will be done once all results are present. 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 30 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 >12 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 2021, a total of 252 eels were sampled. Generally, they were in good condition. Of 167 eels examined for the presence of swim bladder worm, 58 were infected. Eel herpes was the only virus detected and it was found in 44 of 85 organ pools, with each pool containing 2–3 eels.

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 cods and 100 flounders were collected in the first quarter of the year, and in Kattegat 100 cods and a total of 100 flounders 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 2021, a project on pike sarcoma has been running. A total of 50 pikes were to be sampled for pathology, histopathology and microbiology to identify the associated retrovirus. Only 11 pikes were sent to SVA and the project continues 2022 before a summary of results will be performed.

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 *Thelohania contijeani*, are investigated if crayfish plague is ruled out as the cause of mortality. Results for 2021 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 was run to begin active surveillance of crayfish plague and crayfish species using eDNA analysis. Results are currently under evaluation.

MOLLUSCS

Saltwater molluscs

Saltwater molluscs are included in the surveillance from 2021. A total of 150 blue mussels and 150 European/flat oysters (*Ostrea edulis*), from five sites each are investigated for the presence of bonamiosis, marteiliosis, perkinsosis and mikrocytosis. 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.

Examinations 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 137), 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 postmortems 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.

RESULTS

In 2021, a total of 62 foetuses from 46 herds were examined (Table 36). This number represents an increase in submissions over the previous year. However, this number is well below the 140 foetuses that were expected to be examined during the year. All analysed samples were negative for *Brucella*, PRRS and CSF.

Figure 75: Examination of aborted foetuses is an important part of the national surveillance for infectious and emerging diseases. Photo: Ulrika Rockström.

Table 36: The number of foetuses investigated and the number of investigated herds (in parentheses) by species 2011–2021 through the aborted foetus examination programme. The number of investigated herds were not available prior to 2014.

Species	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021
Cattle	21	63	114	32 (27)	29 (23)	34 (23)	20 (18)	34 (28)	21 (20)	22 (20)	22 (18)
Goat	3	5	4	2 (2)	0	2 (2)	2 (1)	5 (3)	3 (2)	2 (2)	0
Sheep	45	79	89	28 (14)	31 (21)	16 (13)	22 (15)	23 (16)	12 (8)	7 (5)	26 (17)
Alpaca	0	0	0	0	2 (1)	1 (1)	0	0	0	0	0
Bison	0	1	0	0	0	1 (1)	0	0	0	0	0
Wisent	2	1	0	0	0	0	0	0	0	0	0
Gnu	0	0	1	0	0	0	0	0	0	0	0
Pig	51	54	46	31 (12)	17 (10)	43 (22)	6 (4)	16 (9)	31 (14)	21 (11)	14 (11)
Water buffalo	0	0	0	0	0	0	1 (1)	0	0	0	0
Total	**122**	**203**	**259**	**93 (55)**	**79 (55)**	**97 (62)**	**51 (39)**	**78 (56)**	**67 (44)**	**52 (38)**	**62 (46)**

DISCUSSION

The post mortem examination and sampling of aborted foetuses is an important part of the national surveillance for infectious and emerging diseases. For example, this was demonstrated in 2012–2013, when the then newly identified Schmallenberg virus (SBV) was detected in Sweden through the surveillance of aborted foetuses.

Since 2008, the number of foetuses of different species submitted for examination has varied from year to year, but for the last eight years, the number of submissions has been less than anticipated across all species (Table 36). The trend is concerning and the reasons for the decrease are not yet well-understood. One possible contributing factor may be the overall decrease in the number of farms in Sweden. A similar drop in the number of food-producing animals submitted for postmortem has also been observed over the years (see chapter “Post mortem examinations in food producing animals”, page 137). 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 foetuses 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 foetuses must be stored on the farm, may discourage producers from sending foetuses 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. In 2021, the number of sheep foetuses sent in for post mortem examination did represent an increase over the previous two years when numbers were particularly low. It was speculated that the low number of sheep submissions during 2019–2020 was a result of the severe drought in 2018 which forced many sheep producers to cull their herds. The increase in sheep foetus submissions in 2021 may be an indication that the sheep industry is recovering.

Post mortem examinations in food producing animals

BACKGROUND

Post mortem examination is an important tool to help veterinarians solve animal health problems at the farm level. International and national experiences show that post mortem examinations also play an important role in infectious disease surveillance and detection of emerging diseases. Early detection of infectious diseases is of utmost importance to prevent negative consequences. For diseases that produce clearly evident clinical signs and/or macroscopic lesions, the first line of defence is the detection of disease by animal owners, field veterinarians and pathologists.

SURVEILLANCE

A specific programme for post mortem 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. 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, 2000–3000 animals are examined within the programme. Transportation of carcasses to the post mortem facilities is arranged and financed by the animal owner. Transportation 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 the facility is large.

Post mortem examinations are performed at six different facilities, 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). Since 2019, in the area around Skara, post mortem examinations of animals weighing more than 15kg have been performed on-farm by experienced ambulatory veterinarians as a pilot study in on-farm post mortems.

In 2017, another pilot study was launched to facilitate

Figure 76: The total number of post mortem examinations in 2021 was lower than in recent years, particularly for cattle and pigs. This may be partially explained by the decrease in the number of farms with food producing animals. Photo: Ulrika Rockström.

timely post mortems of large animals in remote areas of Sweden using a Remote Digital Autopsy (RDA) method. The method allowed field veterinarians or animal owners to perform a simple gross post mortem examination on the farm and send digital photographs of key organs and disease history information to a pathologist who made a presumptive diagnosis. Since then, the method has been further developed into a live digital technique where the person in the field is guided through the post mortem and sample taking process by experienced personnel 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 post-mortem of reindeer, but the aim is to increase its use for all large animals when immediate transport to a laboratory is not possible.

Cadavers sent for post mortem examination serve as an important source of sample material for several surveillance programs. 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 foetuses 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 135).

The programme also includes webinar training for both large animal practitioners and reindeer owners. 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

A total of 1904 post mortem examinations were performed within the programme during 2021. The distribution of species examined over the last 17 years is shown in Table 37. In 2021, 95 cases of a notifiable disease were diagnosed through post mortem examination (Table 38). Additionally, 6 investigations into suspicions of diseases included in Swedish Act of Epizootic diseases (SFS 1999:657 with amendments) were launched based on post mortem findings, including 3 suspicions of tuberculosis, 2 suspicions of anthrax and 1 suspicion of African swine fever/classical swine fever. All samples taken and analysed during those investigations were negative.

DISCUSSION

Post mortem examinations are a vital part of the national surveillance for infectious and emerging diseases, as illustrated by the detection of 95 index cases of notifiable disease in 2021. The number of post mortem examinations performed each year varies but has remained at around 2000 per year over the last five years. 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 2021 was lower than in recent years and dropped to below 2000 for the first time in over 15 years. The decrease was caused primarily by a drop in the number of sheep, pig and poultry carcasses submitted for post mortem. Poultry submissions have typically shown large variations from year to year, but the number of cattle examined had previously been relatively stable at around 700 animals per year. Pig submissions during 2021 were also 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. Higher costs for destruction of carcasses after post mortem at certain facilities may also play a role. For the last four years, the number of sheep undergoing post mortem examination has declined, with 2021 seeing the lowest number of submissions since 2005. In addition to the factors mentioned above, one additional explanation for this is the drought of 2018 which forced many sheep producers to reduce the size of or cull their flocks.

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 live digital method has yet to increase the number of large animal post mortem examinations performed. However, these techniques did contribute to the largest number of reindeer post mortems 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 and also contribute to an increase in on-farm post mortems in the rest of the country. 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 2022.

REFERENCES

Wahlström, H. 2003. Sjukdomsövervakning hos animalieproducerande djur - en översyn på uppdrag av Jordbruksverket och Köttböndernas Forskningsprogram.

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, 2005–2021.

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**
2021	373	655	253	20	9	523	15	54	2	**1904**

Table 38: Number of index cases of diseases notifiable according to SJVFS 2021:10 (K12) diagnosed from samples taken at post mortem examination, 2014–2021. Statistics from Farm & Animal Health.

Disease	2014	2015	2016	2017	2018	2019	2020	2021
Anthrax	0	0	1	0	0	0	0	0
Avian rhinotracheitis	0	0	0	0	0	0	0	0
Blackleg	4	19	26	25	24	25	9	26
Bovine Malignant Catarrhal fever	1	1	6	6	2	2	3	2
Duck Viral Enteritis[A]	1	0	0	0	0	0	0	0
Dichelobacter nodosus	-	-	-	-	-	-	2	0
Fowl typhoid (*S.* Gallinarum)	0	0	0	3	0	0	0	0
Gumboro (Very virulent IBDV)	-	-	-	5	4	0	1	0
Infectious Bronchitis	0	0	0	0	0	0	1	0
Infectious laryngotracheitis	35	26	26	17	20	21	16	16
Swine influenza, pigs	1	0	0	1	0	0	0	0
Influenza A typ (H1N1) 2009, pigs	0	0	0	1	0	0	0	3
Listeriosis	31	22	20	22	22	9	14	28
Mycoplasma gallisepticum	4	4	0	1	7	32	15	15
Mycoplasma, poultry (not *gallisepticum*)	0	0	2	0	0	0	0	0
Necrotic haemorrhagic enteritis (*Clostridium perfringens* type C), pigs	0	0	0	0	0	0	0	0
Salmonellosis	3	3	1	2	2	5	6	5
Total	**80**	**75**	**87**	**88**	**83**	**94**	**67**	**95**

[A] This 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 the National Veterinary Institute (SVA). The surveillance programme is financed partly by annual state hunting permit fees, and partly by governmental funding. The aim is to monitor and follow 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 report and when relevant and possible, 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 (*Ursus arctos*), 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 as sets of predetermined tissue samples.

RESULTS

In 2021, whole carcasses or parts of 3212 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 2021 are mentioned below.

Avian influenza surveillance throughout the whole year has dominated the wildlife work in 2021. More than 1500 reports of wild dead birds were received, and 803 birds were sampled, with 141 cases positive for highly pathogenic avian influenza (HPAI; Table 39). Several different variants of influenza viruses have been recorded throughout the year, with findings of H5N8, H5N5, and H5N1 strains, mainly affecting waterfowl and raptors (for details, see chapter on Avian Influenza, page 49). Spillover to scavenging mammals occurred, with two red foxes and one grey seal found positive for HPAI.

Figure 77: An aerial view of the stranded humpback whale on the coast of Öland in the Baltic Sea in April 2021. Sampling of tissues had to be done in shallow water wearing waders, as a full necropsy could not be performed on site. Photo: SVA.

Table 39: Number of cases per wild bird species diagnosed with highly pathogenic avian influenza in 2021.

Species	Number of cases
Barnacle goose	18
Bean goose	2
Black-headed gull	1
Great black-backed gull	2
Buzzard	14
Canada goose	8
Common eider	8
Crow	1
Goldeneye	2
Eurasian eagle owl	10
Greylag goose	7
Herring gull	5
Jackdaw	2
Kestrel	1
Mallard	4
Marsh harrier	1
Mute swan	10
Goshawk	9
Oyster catcher	1
Peregrine falcon	11
Pheasant	6
Tawny owl	2
Whooper swan	8
White-fronted goose	2
White-tailed eagle	6
Total	**141**

Table 40: Reportable infectious diseases in wildlife and number of outbreaks/cases diagnosed at SVA in 2021. Here, individual cases are listed, and may differ from other official numbers of disease outbreaks or number of index cases. Where a disease was diagnosed in several species, the number of cases per species is listed in parentheses.

Disease	Cases	Species
Avian pox	1	Magpie
Echinococcus multilocularis	16	Red fox
European brown hare disease	2	European brown hare
Highly pathogenic avian influenza[A]	3	Grey seal (1), red fox (2)
Listeriosis	3	Fallow deer (2), roe deer (1)
Malignant catarrhal fever	1	Moose
Myxomatosis	5	Wild rabbit (5)
Pasteurellosis	4	Fallow deer (3), moose (1)
Pigeon paramyxovirus	14	Rock pigeon (14)
Plasmodium sp.	1	Blackbird (1)
Pseudotuberculosis	14	European brown hare (13), mountain hare (1)
Rabbit hemorrhagic disease	13	Wild rabbit
Salmonellosis	75	Black-headed gull (1), bullfinch (2), great spotted woodpecker (1), hedgehog (3), jackdaw (4), wild boar (64)
Sarcoptic mange	13	Lynx (8), red fox (4), wild boar (1)
Toxoplasmosis	4	European brown hare
Trichomoniasis	39	Chaffinch (8), dove/pigeon (3), great tit (1), greenfinch (18), hawfinch (2), rock pigeon (3), siskin (3), sparrow hawk (1)
Trichinellosis	11	Lynx (6), red fox (1), wild boar (3), wolf (1)
Total	**178**	

[A] Wild birds diagnosed with HPAI are listed separately in Table 39.

The EU-determined surveillance of chronic wasting disease (CWD, a prion disease of cervids), was finalized in 2021 with 3316 sampled cervids, reaching and exceeding the total target number of 6000 cervids to be sampled from 2018. An intensified surveillance during the moose (*Alces alces*) hunt in 2021 in the area in the county of Västerbotten where the fourth case of CWD was detected in 2020, did not discover any further cases in 382 sampled hunter harvested moose. For more details, see the CWD chapter (page 32).

The enhanced passive surveillance of African swine fever virus in found dead wild boar continues, but so far, the disease has not been found in Sweden. The finding of *Salmonella* Choleraesuis in several areas in Sweden in 2020 has been followed by both general and targeted surveillance in 2021, with continued findings in the previously known two counties, and single positive cases also found in other counties. For details, see the chapter about infectious diseases in wild boar (page 121).

The programme for health and disease surveillance of marine mammals initiated in 2020, continued with increased numbers of necropsied cetaceans and seals in 2021, a work done in collaboration with the Museum of Natural History, financed by the Swedish Agency for Marine and Water Management. A coastal network reporting and handling stranded marine mammals have been vital to find suitable carcasses for necropsy. In all, 44 cetaceans and 18 seals were necropsied and or sampled in 2021, some at SVA and some in the field. Notable cases were one humpback whale stranded on the Öland coast in the Baltic Sea, and a rare finding of a Northern bottlenose whale (*Hyperoodon ampullatus*) on the west coast. Also, the first finding of cetacean brucellosis caused by *Brucella ceti* in Sweden was in a harbour porpoise (*Phocoena phocoena*) necropsied in 2021.

Use of the SVA online form (rapporteravilt.sva.se) to report sick or dead wildlife 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 helping to submit 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 40) show that there are only few serious infectious disease threats to wildlife, but some that may infect domestic animals or humans.

REFERENCES

SVA annual report (Årsredovisning) 2021. SVALA-data on wildlife diagnoses 2021. SVA report: Wildlife disease surveillance in Sweden 2021.

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 of 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 C. *coli,* as well as 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 and turkeys (only 150 samples) or from pigs and cattle are analysed for presence of 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. Furthermore, meat from countries outside EU is sampled at border control posts and analysed for indicator *E. coli* and presence of ESBL/AmpC- and carbapenemase producing *E. coli*.

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 SvarmPat 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 in Figure 78.

LEGISLATION

As mentioned above, parts of the antibiotic resistance monitoring performed in Sweden are regulated by EU legislations (2003/99/EG and 2020/1729/EU, which from 2021 replaced 2013/652/EU). Furthermore, there is also national legislation indirectly affecting the antibiotic resistance monitoring. More precisely, findings of carbapenemase producing Enterobacterales ($\text{ESBL}_{\text{CARBA}}$) 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 MONITORING IN 2021

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 2021, reported sales of antibiotics for animals were 9129 kg, of which 57% were penicillins with narrow spectrum. The corresponding figures for 2012 were 11 385 kg and 53%, respectively. Sales of antibiotics that should be used with special restrictions (fluoroquinolones, third generation cephalosporins and polymyxins) have decreased considerably since 2012 (84–95%). During the whole decade, the proportion of products for treatment of individual animals has been over 90% of the total sales.

Since the withdrawal of growth-promoting antibiotics from the Swedish market in 1986, the total sales of antibiotics corrected for population sizes over time have decreased by more than two thirds. 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 79).

Extended spectrum beta-lactamase (ESBL) producing Enterobacterales (previously Enterobacteriaceae)

ESBL-producing Enterobacterales (previously Enterobacteriaceae) are generally rare among animals in Sweden. Previously, the occurrence in intestinal samples from broilers was high but it has decreased in recent years (Figure 80). In 2021, the occurrence of ESBL-producing *E. coli* in intestinal samples from pigs, cattle under one year, and broilers, as well as samples of pig and bovine meat was investigated with selective methods. Such bacteria were isolated from 1% of the intestinal samples from pigs, 12% of the intestinal samples from cattle under one year, and 1% of the intestinal samples from broilers. The number of samples from cattle under one year is however limited. Furthermore, such bacteria were isolated from <1% of both pig and bovine meat of Swedish origin.

Bacteria that produce $\text{ESBL}_{\text{CARBA}}$ have not been confirmed from domestic animals in Sweden.

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

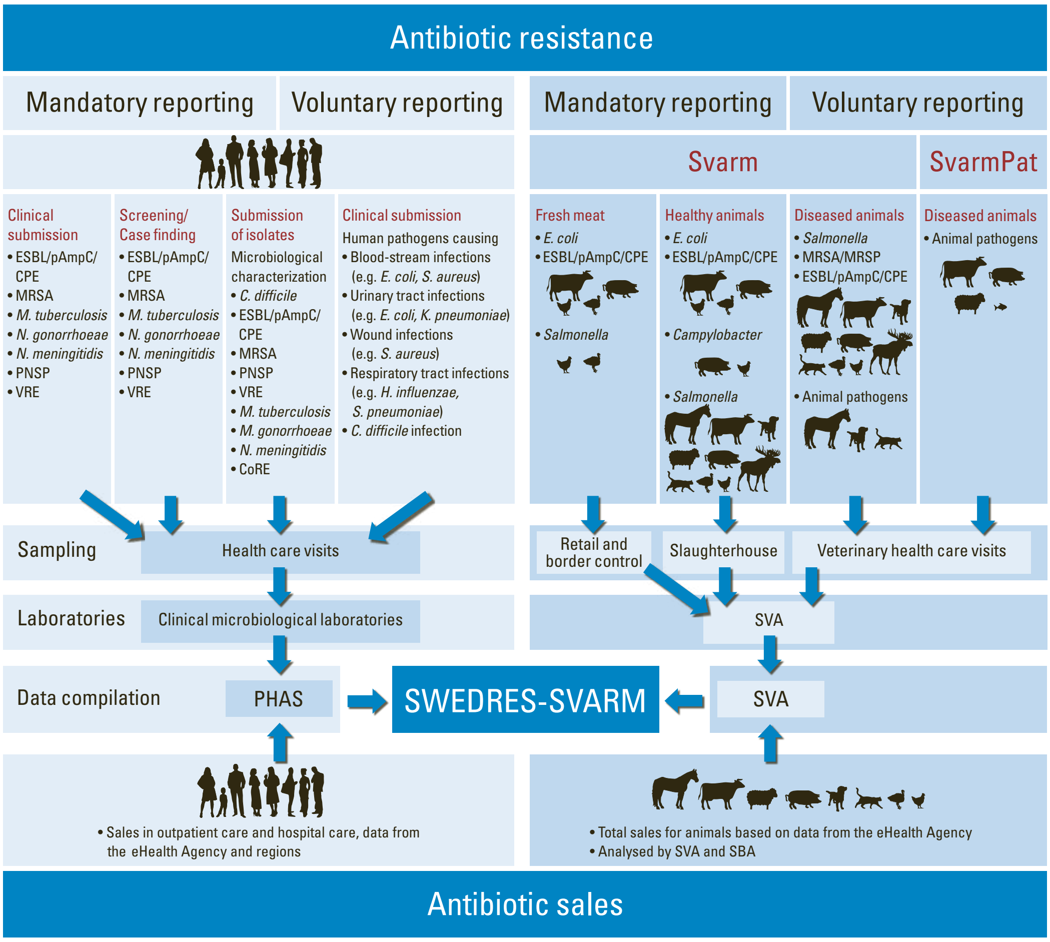


Figure 78: A schematic illustration of data included in the Swedres-Svarm report.

found sporadically in horse, dog, and cat. In horses the number of MRSA cases in 2021 (n=23) was as in 2020 (n=27) higher than in previous years. The previous highest figure was in 2014 (n=9). The increase could partly be explained by an outbreak in an equine hospital with eight cases. The outbreak in horses was caused by a, for horses in Sweden new spa-type, t034, belonging to the livestock-associated MRSA clonal complex 398. In companion animals, the same types of MRSA as in humans dominate, indicating a human source of MRSA in these animals.

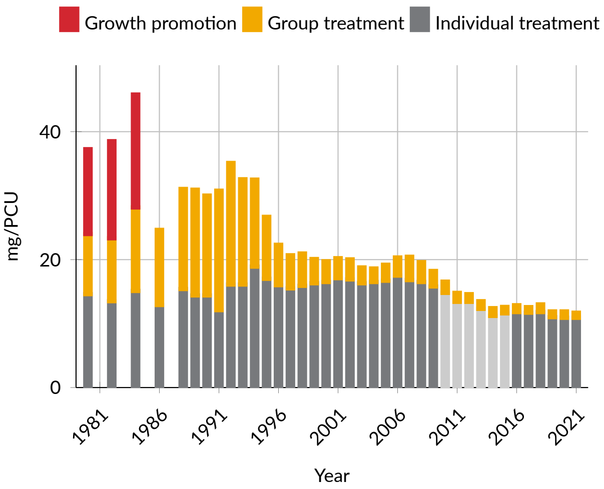


Figure 79: Sales of antibiotics for animals expressed as mg per population correction unit (PCU). Data from 2010–2015 are uncertain because of a lack of completeness mainly affecting injectable products (indicated in a lighter grey). In the present figure, all products (including tablets) are included while in data presented in the European surveillance of veterinary antimicrobial consumption tablets are excluded when calculating mg/PCU.

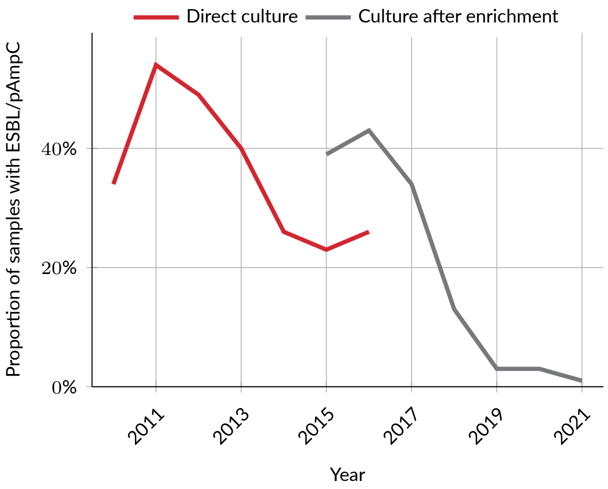


Figure 80: Proportion (%) of samples from broilers positive for *Escherichia coli* with ESBL/pAmpC from 2010 to 2021.

Methicillin-resistant *Staphylococcus pseudintermedius* (MRSP)

In 2021, the number of reported cases of methicillin-resistant *Staphylococcus pseudintermedius* (MRSP) in animals was around the same level as in previous years. In total 43 cases of MRSP were notified to the Swedish Board of Agriculture: 41 from dogs, 1 from a cat and 1 from a horse. All isolates were available for further investigations. When MRSP first occurred among animals in Sweden, the sequence type ST71 dominated. However, since several years the isolates of MRSP are more diverse with several sequence types occurring.

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 bensylpenicillin, but penicillin resistance is common in *Staphylococcus pseudintermedius* from dogs and occurs in *S. aureus* from horses and *S. felis* from cats. However, in *S. schleiferi* from dogs penicillin resistance is uncommon. Resistance to commonly used antibiotics 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. As an example, in the latest investigations of indicator *E. coli* from broilers and pigs, 72 and 64% respectively, were susceptible to all tested substances (Table 41).

Table 41: Proportion of randomly selected indicator *Escherichia coli* from broilers and pigs that are susceptible to all investigated antibiotics.

	Year							
Species	2014	2015	2016	2017	2018	2019	2020	2021
Pigs	–	68	–	71	–	71	–	64
Broilers	75	–	71	–	69	–	72	–

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