

SURVEILLANCE OF INFECTIOUS DISEASES IN ANIMALS AND HUMANS IN SWEDEN 2019



Editor: Karl Ståhl

Department of Disease Control and Epidemiology, National Veterinary Institute (SVA), SE-751 89 Uppsala, Sweden.

Authors: Charlotte Axén, Mia Brytting, Ioana Bujila, Erika Chenais, Rikard Dryselius, Helena Eriksson, Pernille Etterlin, Eva Forsgren, Malin Grant, Gittan Gröndahl, Gunilla Hallgren, Anette Hansen, Gete Hestvik, Marika Hjertqvist, Mia Holmberg, Cecilia Hultén, Helena Höök, Cecilia Jernberg, Jerker Jonsson, Ulrika König, Elina Lahti, Emelie Larsdotter, Mats Lindblad, Anna Lundén, Emma Löf, Hans-Olof Nilsson, Oskar Nilsson, Maria Nöremark, Anna Ohlson, Ylva Persson, Karin Persson-Waller, Thomas Rosendal, Karl Ståhl, Robert Söderlund, Kaisa Sörén, Magnus Thelander, Karin Troell, Anders Wallensten, Per Wallgren, Stefan Widgren, Ulrika Windahl, Beth Young, Nabil Yousef, Siamak Zohari, Erik Ågren, Estelle Ågren, Elina Åsbjer

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

Layout: The production of this report continues to be accomplished using a primarily open-source toolset. The method allows the source text, produced by authors, to be edited independently of the template for the layout which can be modified and reused for future reports. Specifically, the chapter texts, tables and captions are authored in Microsoft Word and then converted using pandoc and R to the LaTeX typesetting language. Most figures and maps are produced using the R software for statistical computing. Development for 2019 has further improved the importing of content from Word to LaTeX. The method can now import text, tables and figure captions from Word, as well as the newly designed 'IN FOCUS' sections of some chapters. The tool is available as an R-package at GitHub (<https://github.com/SVA-SE/mill/>). This year the report was also built with a continuous integration pipeline on Microsoft's Azure DevOps platform, allowing every committed change to the content to be built and tested automatically. The report generation R-package and process was designed by Thomas Rosendal and Stefan Widgren. In 2019, figures and the final typesetting were done by Wiktor Gustafsson and Thomas Rosendal with contributions from the report authors.

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Photo: Karin Bernodt.

Introduction

Surveillance of infectious diseases in animals and humans 2019 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 private industry with surveillance mandates along the entire food chain, from farm to fork.

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, a lot of surveillance activities are in place primarily to ensure safe trade and movement of animals, thereby facilitating trade and giving access to foreign markets. This is also where the major costs appear in case of outbreaks of regulated diseases; by the restrictions put in place to maintain trust between trading partners. To reinstate a favourable status, it is necessary to provide evidence in the form of high quality surveillance data that disease is once again absent from the country, region or sector, or at least under control.

This report is subject to constant improvement and development, some more obvious than others. As last year, particular focus for this year has been on improving the animal-public health cross-domain analysis, with the ambition to provide a more integrated description of how the surveillance activities in the different sectors serve to inform one another - all in a true One Health spirit. As a result of this work a new process has been established to strengthen the collaboration between the sectors involved in zoonoses surveillance. In several of the chapters on zoonoses of high importance, specific events have been described more in detail in “In focus” sections that were introduced last year. This initiative was supported by the One Health European Joint Programme (onehealthjp.eu) in a project aimed at improving the interoperability of animal and public health surveillance systems. Swedish partners in the programme are the National Veterinary Institute, the Swedish Food Agency and the Public Health Agency of Sweden.

From the perspective of this report, 2019 was dominated by disease events and surveillance activities at the

interface between wildlife, domestic animals and humans. The first three cases of Chronic Wasting Disease (CWD) in the country were detected during the year, all in older moose in northern Sweden. In accordance with EU legislation these first cases prompted an intensified and logistically complex surveillance effort in the area, which involved different species and categories of animals, and required engagement of voluntary forces as well as actors that are not commonly involved in animal health surveillance. Within the EU and globally, African swine fever (ASF) continued to spread among wild boar and domestic pigs during the year, and to extend its geographical distribution with vast economic consequences. In Sweden, efforts to raise awareness among the general public and engage the hunting community to strengthen the surveillance for this disease resulted in an almost 100% increase in submissions of wild boar found dead compared to previous years. However, the numbers were still small and further measures are needed to ensure sufficient capacity for early detection. During the summer months, the country experienced the largest outbreak of human tularaemia in over 50 years. The significant increase in human cases coincided with unusually high numbers of reports of dead hares as well as hares diagnosed with tularaemia. Moreover, a spatiotemporal correlation between human cases and cases in hares could be assumed demonstrating the value of a One Health surveillance approach for better understanding of disease dynamics at the animal-human interface.

A lot of the information in this report is of key importance to demonstrate the good health and welfare of Swedish animals to the benefit of safe trade and access to foreign markets. As an EU member state, Sweden shares the implications and consequences of exotic disease introduction with many other European countries. We are part of a pan-European surveillance system, where our efforts contribute, directly and indirectly, to the understanding of risks that emerging diseases pose to other EU countries. Openness, transparency and pro-activeness are key for effective early warning and control, and it is important for trust and for joint European preparedness to which we actively contribute. In line with this, our understanding of the Swedish disease situation in 2019 is provided in this report.

Overview of active surveillance 2009-2019

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), 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 2019 can be found by consulting that year's annual surveillance report, which can be found at www.sva.se.

Table 1: Historical overview of active surveillance activities 2009–2019. Filled circles (●) indicate that active surveillance was carried out.

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

Livestock populations and trade in live animals

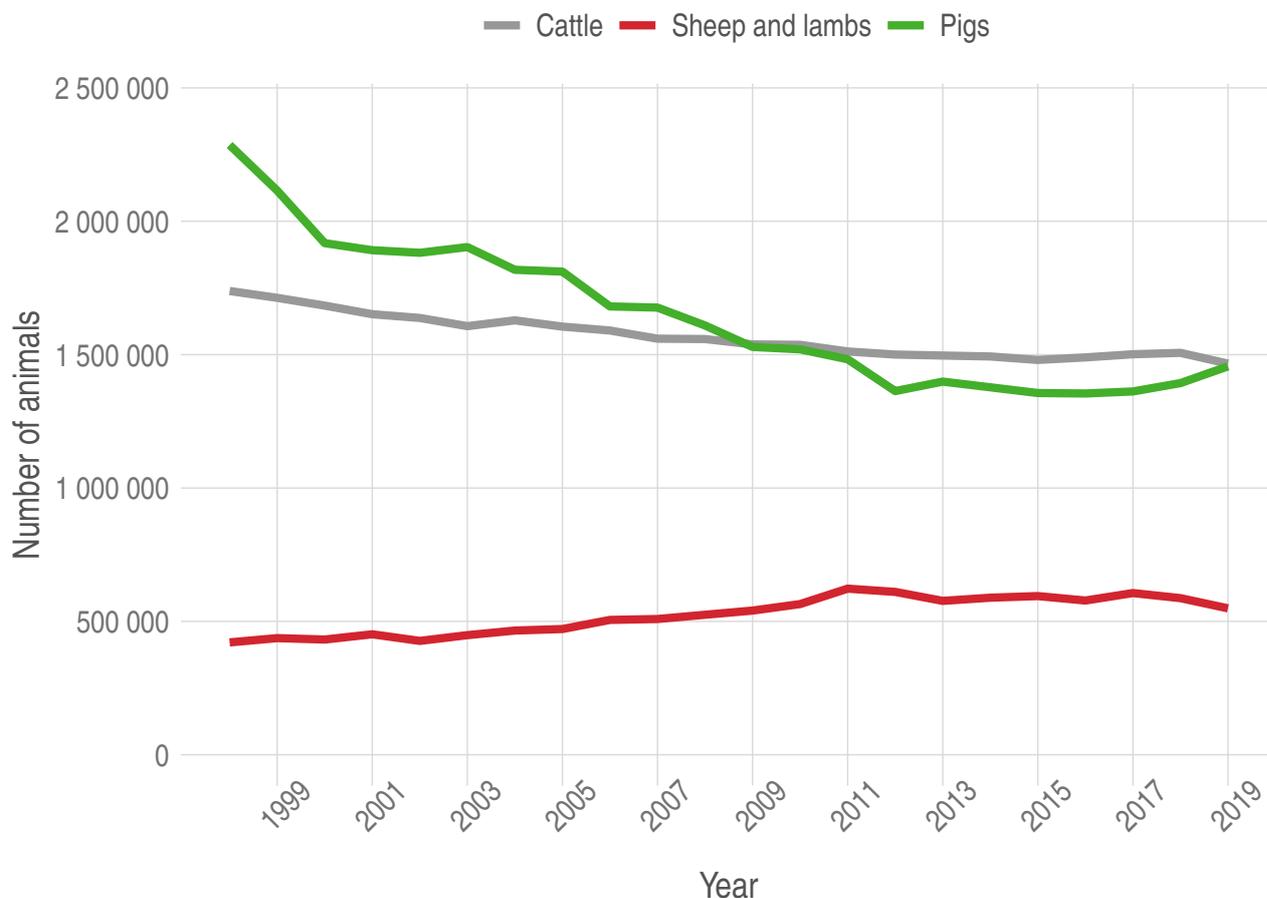


Figure 1: Number of Swedish livestock 1998–2019.

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

Figures 1, 2, 3 and 4 give an overview of the livestock population in Sweden 2019.

The numbers presented reflect 2019, if not otherwise stated.

CATTLE

There are approximately 15 900 holdings with a total of 1.5 million cattle (dairy cows, beef cows, heifers, bulls, steers and calves younger than one year) in Sweden (Figure 2).

The number of holdings with dairy cows, as well as the number of dairy cows, has decreased consistently over a long period. There were approximately 306 000 dairy cows in 3250 holdings, with an average of 94 cows per herd. Nine percent of holdings have 200 or more dairy cows. The number of beef cows has been increasing consistently since the

1980s, but in 2019 the number decreased and was 210 086, with an average herd size of 20 cows.

In total, approximately 418 000 adult cattle and 14 900 calves were slaughtered. The total milk delivered was 2704 million kg. This represents an 8% decrease compared to 2015 and is the lowest production since 1995.

PIGS

The total number of pigs was 1 456 000 (Figure 3). For many years the number was decreasing, but more recently this trend has been reversed and the population is now increasing. However, the number of holdings with pigs is decreasing and was 1086 in 2019, of which 896 held fattening pigs and 670 held breeding pigs.

About 2 573 000 pigs were slaughtered.

SHEEP

There were 8474 sheep holdings with a total of 279 888 ewes and rams (Figure 4). Sheep holdings in Sweden are usually small-scale enterprises with an average herd size of 33 adult sheep.

During 2019, approximately 251 950 sheep were slaughtered, of which 213 600 were lambs.

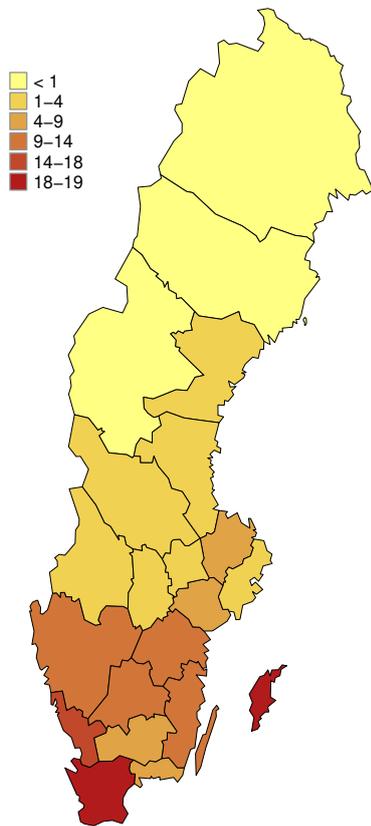


Figure 2: Number of cattle per km² in 21 Swedish counties as of June 2019.

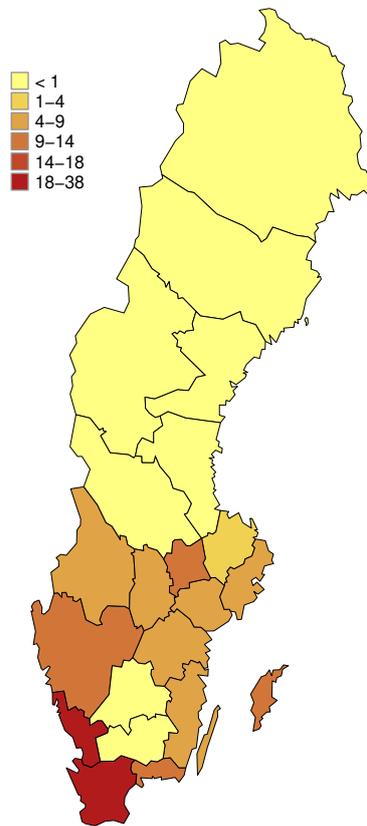


Figure 3: Number of pigs per km² in 21 Swedish counties as of June 2019.

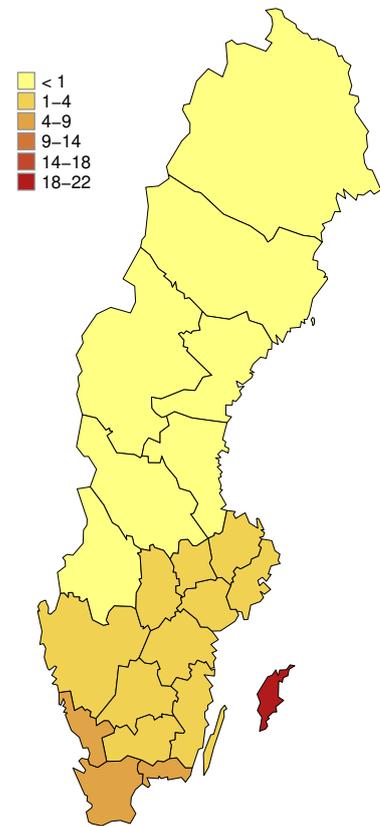


Figure 4: Number of sheep per km² in 21 Swedish counties as of June 2019.

GOATS

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

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

POULTRY

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

Poultry numbers have increased continuously during the last two decades.

In 2019, there were 8.9 million hens over 20 weeks of age in 2400 commercial holdings, which represents an increase in population but a decrease in number of holdings compared to the previous year.

Eggs delivered to wholesalers amounted to 129.3 million kg during 2019.

The number of holdings with broiler production in June 2019 was 202 and approximately 106 million chickens were sent for slaughter during the year. During 2019, 507 000 turkeys were sent for slaughter.

The production of geese and ducks is very small. In 2019, 16 626 geese, 9806 ducks and no guineafowl were slaughtered.

FISH AND SHELLFISH

Rainbow trout is the most common farmed fish in Sweden, followed by arctic char, brown trout, eel and salmon, where salmon and sea trout are mainly farmed for restocking of wild populations. Swedish shellfish production is dominated by cultivated blue mussels, of which 1986 tonnes were produced in 2018. All mussel production and 30% of the production of rainbow trout is situated in the coastal district (marine culture) on the west and east coast respectively. The production of arctic char, eel and other food fish is freshwater based. The most common aquaculture production system is cage culture, both in fresh and saltwater.

In 2018, there were 59 holdings producing food fish, 53 holdings with fish for restocking, three with crayfish for consumption and four with crayfish for restocking. There were ten holdings with production of blue mussels and one with oyster production.

The production was 9400 tonnes of food fish which, when converted to round fresh weight, is the equivalent of

11 108 tonnes, of which 97% was produced in northern Sweden. Production has decreased the last years due to closing of small holdings. Rainbow trout represented the largest production, with 86% of the total production of fish for consumption.

The total production of fish for restocking was estimated to be 731 tonnes. The most common species produced for restocking was also rainbow trout.

REINDEER

In 2019, there were 241 013 reindeer in Sweden, including 56 164 calves, with an average of 52 reindeer per owner. During the 2018/2019 season, 547 557 reindeer were slaughtered, a decrease with 10% compared to 2017/18. There are no wild reindeer in Sweden, only semi-domesticated, and there is cross-border reindeer husbandry between Sweden and Norway.

HORSES

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

Approximately 1840 horses were slaughtered in Sweden in 2019.

BEEES

In 2019, the number of apiaries in Sweden was 16 946 and the number of colonies was 75 859, figures approximated by bee inspectors. Over the last ten years, these numbers have increased by 44 and 11 percent respectively.

TRADE IN LIVE ANIMALS (LIVESTOCK)

The trade of livestock into and out of Sweden is very limited. In 2019, 120 pigs from Norway, 114 from Denmark, three from Germany and one pig from Finland were brought into Sweden as well as 23 cattle and one goat from Denmark and 50 cattle from Finland. Five alpacas were brought into Sweden, of which three came from Norway and one each from Denmark and Germany. Additionally, 3150 reindeer were brought from Finland.

Approximately 500 000 grandparent and parent animals (*Gallus domesticus*) and 8250 turkeys (*Meleagris gallopavo*) entered Sweden as day-old chicks from the Netherlands, Great Britain, Spain and Germany. In addition, 5200 ducks were brought from Denmark, of which 2700 as day-old chicks. Hatching eggs were brought to Sweden from Germany, Estonia and Latvia (*Gallus gallus*), Denmark (*Anas spp*, *Phasianidae*) and France and Poland (*Phasianidae*). There are no data on the numbers.

In total, 57 consignments of honeybees (*Apis mellifera*) were brought to Sweden, mainly for breeding purposes, from Denmark, Finland, France, Great Britain, Italy, Malta, Norway, Romania, Slovenia, Austria and Germany. Furthermore, 97 consignments of bumblebees (*Bombus spp*) were brought for crop pollination to Sweden from the Netherlands and Belgium.

The number of animals that left Sweden for intra-Union trade during 2019 were: 502 cattle, 2202 pigs, 52 sheep, 15 goats, 32 alpacas, 13 llamas, three domestic yaks, one

muskoos and one bison. In addition, two muskoos were exported to Norway and 1918 reindeer were sent from Sweden for slaughter.

Six million day-old chicks (*Gallus gallus*) for breeding purposes and 630 000 live poultry (*Gallus domesticus*) also left Sweden for intra-union trade in 2019.

Hatching eggs (*Gallus gallus*) were sent to Finland, Hungary, Norway, Estonia, Germany, the Netherlands, Denmark, Belgium and Russia from Sweden. There are no data available on the amount.

A total of 24 consignments of honeybees (*Apis mellifera*) left Sweden for intra-union trade to destinations in Malta, Spain, Germany, the Netherlands, Poland, Lithuania, Romania and Finland.

REFERENCES

TRACES (**TR**ade **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 (2020). "Lantbruksdjur efter län/riket och djurslag. År 1981–2019." [Data accessed 2020-03-11 using pxweb R package 0.9.1], <https://statistik.sjv.se/PXWeb>

Swedish Board of Agriculture (2020). "Lantbruksdjur efter län/riket och djurslag. År 1981–2019." (available 2020-03-23 at <https://nya.jordbruksverket.se/e-tjanster-och-databaser/sok-i-vara-databaser>)

Bitillsyn 2019, Swedish Board of Agriculture, (available 2020-03-26 at: <https://www.jordbruksverket.se/download/18.48b2d7e314c2713c21e2aa1e/1582619711714/Statistik%20fr%C3%A5n%20bitillsynen.pdf>) (statistics on honeybees)

Aquaculture in Sweden in 2016, JO 60 SM 1901, SBA (available 2020-03-24 at: <https://www.jordbruksverket.se/webdav/files/SJV/Amnesomraden/Statistik,%20fakta/Vattenbruk/JO60SM1901%20ny%20version/JO60SM1901a.pdf>)

Goats 2018; statistic report 2019:01, SBA (available 2020-03-23 at: https://www.jordbruksverket.se/webdav/files/SJV/Amnesomraden/Statistik,%20fakta/Husdjur/Statistikrapport_201901/201901._ikortadrag.htm)

Livsmedelsverket, Tillförda otjänligförklarade godkända 2019, (available 2020-03-24 by Henrik Sundström, Livsmedelsverket) (statistics on poultry slaughter)

Sametinget (available 2020-03-24 at: <https://www.sametinget.se/renstatistik>) (statistics on reindeer)

Bitillsyn 2018 (available 2019-03-28 at: <https://www.jordbruksverket.se>)

Animal registers and data sources used in surveillance

THE CENTRAL REGISTER OF HOLDINGS

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

THE CENTRAL DATABASE OF PIG, SHEEP AND GOAT MOVEMENTS

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

THE CENTRAL DATABASE FOR BOVINE ANIMALS

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

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

THE SLAUGHTER REGISTER

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

THE DATABASE OF DAIRY HERDS

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

THE ANIMAL HEALTH DATABASE

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

CENTRAL AQUACULTURE REGISTER

All aquaculture premises authorised by the County Administrative Boards are registered in the Central Aquaculture Register. The register is administered by the Swedish Board of Agriculture. The data encompasses name and coordinates of

the premise as well as type of production and species kept. It also contains results from official controls, information on the farms' water supply and discharge as well as date information on health status. The establishment of the register is regulated through European and Swedish legislation.

THE POULTRY REGISTER

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

site and more. The establishment of the register is regulated through European and Swedish legislation.

SVALA

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

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

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

Institutions, organisations and laboratories involved in surveillance

SWEDISH BOARD OF AGRICULTURE

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

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

NATIONAL VETERINARY INSTITUTE

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

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

THE PUBLIC HEALTH AGENCY OF SWEDEN

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

Concerning communicable diseases, the agency has the overall national responsibility and coordinates communicable disease control on a national level. Some of the

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

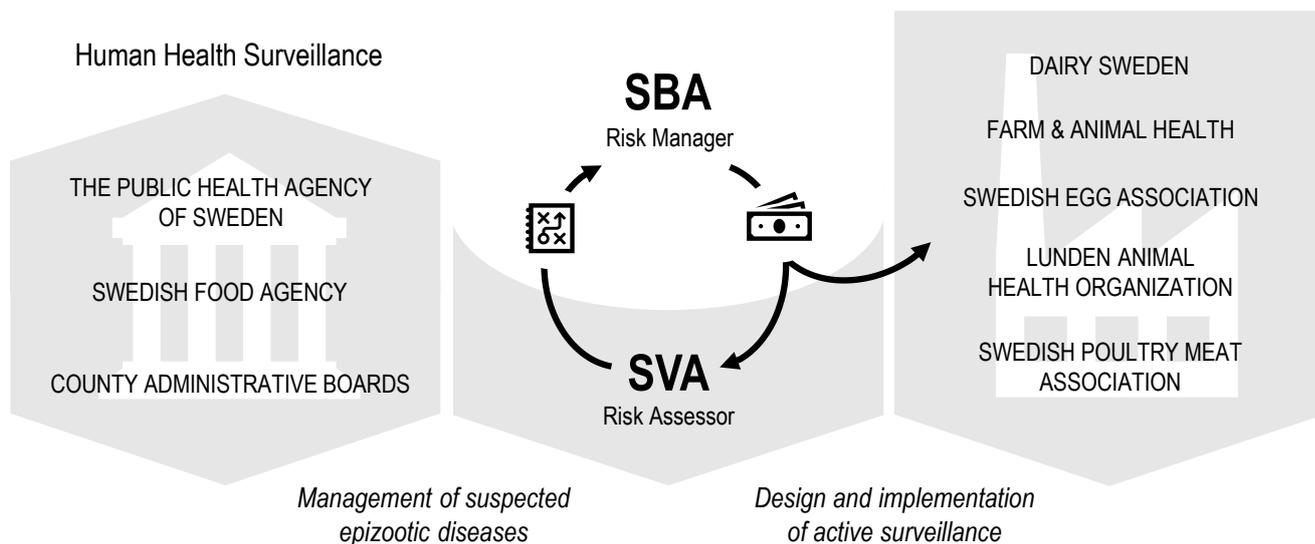
The agency also performs microbiological laboratory analyses, including diagnostics, and supports quality and method development at laboratories engaged in diagnostics of communicable disease pathogens. High containment laboratories have round-the-clock preparedness every day of the year to conduct microbiological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

SWEDISH FOOD AGENCY

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

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.



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.

VÄXA SVERIGE

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

FARM & ANIMAL HEALTH

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

Activities are performed with a clear national focus and the consulting services are available to all farmers. A large part of the activities and services are based on officially approved animal health programmes for pigs, cattle and

sheep. In addition, Farm & Animal Health is assigned by the Swedish Board of Agriculture to implement specific disease control and surveillance programmes. Examples of such programmes are surveillance of porcine reproductive and respiratory syndrome virus in pigs, the control of maedi-visna in sheep and Johne's disease in cattle, monitoring of antimicrobial resistance in disease-causing bacteria and the national post mortem programme of livestock animals.

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

LUNDEN ANIMAL HEALTH ORGANISATION

Lunden Animal Health Organisation is a veterinary consulting company working with pig health and welfare. Its objective is to gather, develop and communicate knowledge on pig issues. The organisation is involved in national surveillance programmes for pig diseases and is assigned by the Swedish Board of Agriculture to perform health controls as well as to implement the on-farm national biosecurity programme for pigs.

SWEDISH POULTRY MEAT ASSOCIATION

The Swedish Poultry Meat Association (SPMA) represents 99% of the chicken meat production and 95–97% of the

turkey meat production in Sweden, with members from the entire production chain. Members are obligated to participate in the animal welfare and health programmes administered by SPMA, such as controls for *Salmonella*, *Campylobacter*, coccidiosis and clostridiosis, to meet high standards for food hygiene and safety.

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

THE SWEDISH EGG ASSOCIATION

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

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

SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES

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

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

These activities also include bee health and how this is affected by pathogens, environmental factors, pesticides and beekeeping practices. Also located in the Ecology Centre on SLU's main campus is the National Reference Laboratory for Bee Health, whose activities are carried out in close cooperation with relevant authorities and beekeepers.

BEE INSPECTORS

Bee inspectors (bitillsynsmän) are experienced beekeepers that are specifically trained to examine honeybee colonies

for disease. The main duties of the bee inspectors are to examine bee colonies and hive material for signs of disease, both when disease is suspected or with requests to move bee colonies out of designated disease protection or surveillance zones. Bee inspectors also issue transit-permits, implement or order specific control measures for certain diseases and inform beekeepers about suitable treatments for certain diseases and parasites. Seven of the Swedish CABs have a regional responsibility for bee health. They set the borders for inspection districts and are responsible for appointing bee inspectors in all counties. Sweden is divided into around 400 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.

REFERENCES

Nabil Yousef, Swedish Food Agency (www.slv.se)

Pernilla Stridh, County Administration Östergötland (<https://www.lansstyrelsen.se/>) (County Administrative Boards)

Märta North, Swedish Board of Agriculture

Andrea Holmström, Växa Sverige (www.vxa.se/)

Ebba Schwan, Farm & Animal Health (www.gardochdjurhalsan.se/)

Anders Wallensten, Folkhälsomyndigheten (www.folkhalsomyndigheten.se/)

Maria Donis, Swedish Poultry Meat Association (www.svenskfagel.se/)

Anna-Maria Erixon, The Swedish Egg Association (www.svenskaagg.se/)

Erik Lindahl, Lunden animal health organisation (www.lundens.com/)

Ingrid Karlsson, Swedish Board of Agriculture (bee inspectors)

Eva Forsgren, Swedish University of Agricultural Sciences

Disease Surveillance 2019

Atrophic rhinitis

BACKGROUND

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

DISEASE

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

LEGISLATION

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

SURVEILLANCE

The purpose of the control programme is to declare herds selling breeding stock free from infection with toxigenic *P. multocida*, and thereby decrease the incidence of AR in all herds. Nucleus and multiplying herds are actively tested for the presence of toxigenic *P. multocida* at least once a year including a total of 20 animals per herd. These 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.

Table 2: The total number of samples and the outcome of nasal swabs analysed for *P. multocida* 2005–2019 at SVA. The samples have been collected in all nucleus and multiplying herds, as well as in production herds suspected for AR. When individual samples in a herd are positive, the herd is further scrutinised and either considered confirmed as affected, or declared free from AR.

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

RESULTS AND DISCUSSION

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

Aujeszky's disease



In 2019, 2548 samples from 507 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: Neil Burton/Shutterstock.

BACKGROUND

Aujeszky's disease (AD) is caused by a herpes virus that has the capacity to infect many species, but pigs are the natural hosts. The disease is of importance for pig production worldwide, although it has been eradicated from the domestic pig population in many countries. AD is widespread in European wild boar populations, which may act as reservoirs, but their role in transmitting the disease is not well known. In both 2018 and 2019, 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 estrus, 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

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

SURVEILLANCE

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

Passive surveillance

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

Active surveillance

In 2019, all samples collected in the abattoir sampling component of the surveillance for porcine respiratory and reproductive syndrome (PRRS) virus, carried out by Farm & Animal Health (see chapter on PRRS for details), 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 2019, 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 on *Infectious diseases in wild boars*), with the exception of 2018 when testing was not undertaken due to a redistribution of funding.

RESULTS

Passive surveillance

In 2019, two clinical suspicions of AD were investigated. In one herd, late-term abortion was the main clinical manifestation. During this investigation, blood samples from sows were analysed for the presence of antibodies to AD. In the other herd, neurological signs and high mortality in newborn piglets were the primary clinical signs. In this investigation, tissue samples from affected piglets were analysed for the presence of the virus causing AD. All samples tested during the course of the investigations were negative, and both herds were subsequently declared free from AD.

Table 3: Number of finisher pigs and herds sampled at the abattoir in the active surveillance of Aujeszky's disease each year 2009–2019.

Year	Number of pigs sampled	Number of herds sampled
2009	2712	-
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

Active surveillance

In 2019, 2548 samples from pigs from 507 herds taken on 851 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.

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 2019, 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



After being declared free from bluetongue virus (BTV)-8 in 2010, surveillance has been carried out annually on cattle that are exposed to the vector during the summer months on pasture. Photo: Mia Holmberg.

BACKGROUND

Bluetongue is a vector borne disease of ruminants and camelids caused by any of 27 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. A vaccination campaign and intensive surveillance activities were initiated nationally, with focus on the southern part of the country. Following the detection of infected animals in new areas, the zones were adjusted accordingly. Vaccination and surveillance activities continued in 2009. In the first quarter of 2009 transplacental infection was detected in three newborn calves, all three cases originating from infections of their dams in autumn 2008.

In December 2010, after extensive surveillance, Sweden was declared free from BTV-8. After that, surveillance according to Commission Regulation (EC) No 1266/2007, with amendments, has been carried out annually.

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

DISEASE

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

LEGISLATION

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

SURVEILLANCE

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

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 2019 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, from December 2019 until January 2020. Samples were analysed with the milk ELISA routinely used.

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

RESULTS

Bulk milk samples from 188 holdings were tested in the field surveillance, all with negative results. Two clinically suspect cases were investigated and tested during 2019 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 2019, 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-8 circulation in direct neighbouring countries. However, in 2015, France reported that BTV-8, of the Northern European strain from 2007, had re-emerged in the country. Since September 2015, several thousand cases (defined as animal found positive for BTV with real-time PCR) have been reported by France. Most of these cases are animals found positive within active surveillance activities; few are animals with clinical signs of disease. From December 2018 an increase in trans-placental 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 each reported some cases of BTV-8 (using the same definition) found during routine surveillance and tests for export/import. The United Kingdom reported single cases of BTV-8 in cattle imported from France in 2018.

During 2019, as in all previous years, several BTV serotypes were circulating in sheep and cattle in the countries around the Mediterranean.

The detection of BTV-8 in France in 2015 after several years of silence, and the numerous cases detected in France since then, as well as limited number of cases in Germany, Switzerland and Belgium in 2019, again demonstrate that BTV8 may spread and become established in livestock populations in northern Europe. Moreover, as the prevalence of seropositive animals decline, the population will again become 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

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

In 1996, the disease became a public health concern, after the detection of a new variant of Creutzfeldt-Jacob Disease in humans (vCJD), likely to be linked to classical BSE in cattle. This resulted in actions taken to prevent transmission to humans through removal of specified risk material (such as brain and spinal cord) from cattle at slaughter, restrictions related to feed to avoid recycling of infectious material to ruminants through infected MBM and an intensified surveillance which started in 2001 after rapid diagnostic tests became available.

Atypical strains of BSE, which show diagnostic and epidemiological dissimilarities with classical BSE, have been described. These atypical BSE cases probably occur spontaneously and possible links to classical BSE and potential zoonotic aspects are subject to debate within the scientific community.

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

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

DISEASE

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

LEGISLATION

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

SURVEILLANCE

Feed

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

Animals

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

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

Passive surveillance

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

with Bio-Rad TeSeE Western Blot.

Clinical suspects are a category of animals that should be included in the surveillance, but since the control measures have been effective and the European epidemic of classical BSE has declined, it is a challenge to keep farmers and veterinarians alert and report symptoms. Substantial efforts have been made starting 2018 and continuing 2019 to find animals that display symptoms which could be compatible with BSE and to include these in the surveillance programme.

Active surveillance

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

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

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

RESULTS

Feed

In 2019, 22 feed samples were taken at feed mills; 19 of these were from feed (13 were cattle feed) and three from raw materials for feed production. All of these samples were negative for PAP, except one feed which contained fish particles, but it was a feed for pigs which included fish meal in the recipe.

Animals

Passive surveillance

In 2019, 18 bovines were examined due to clinical suspicion, all with negative results.

Active surveillance

In 2019, 8423 samples were examined for BSE. All samples were negative. Of these samples 8226 were from fallen stock, 26 samples were from animals with remarks at antemortem inspection before slaughter and 152 samples were from emergency slaughtered animals.

DISCUSSION

No positive BSE cases were detected in Sweden in 2019. Preventive measures have been in place for many years and

the fact that no cases were detected supports that these measures have been effective. 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. There has previously been a long trend of decreasing number of clinical suspicions compared to the years during the peaks of the BSE crisis, which can be explained by to a lower degree of awareness among farmers and veterinarians when there is less reporting about the disease.

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

On OIE and European union level, a revision of the current surveillance of animals is being discussed, and a revision is welcomed. Spending large resources on sampling animals is not the most efficient way to prevent a new BSE crisis. But keeping bans and controls in place to avoid recirculation is still relevant to avoid a new BSE crisis.

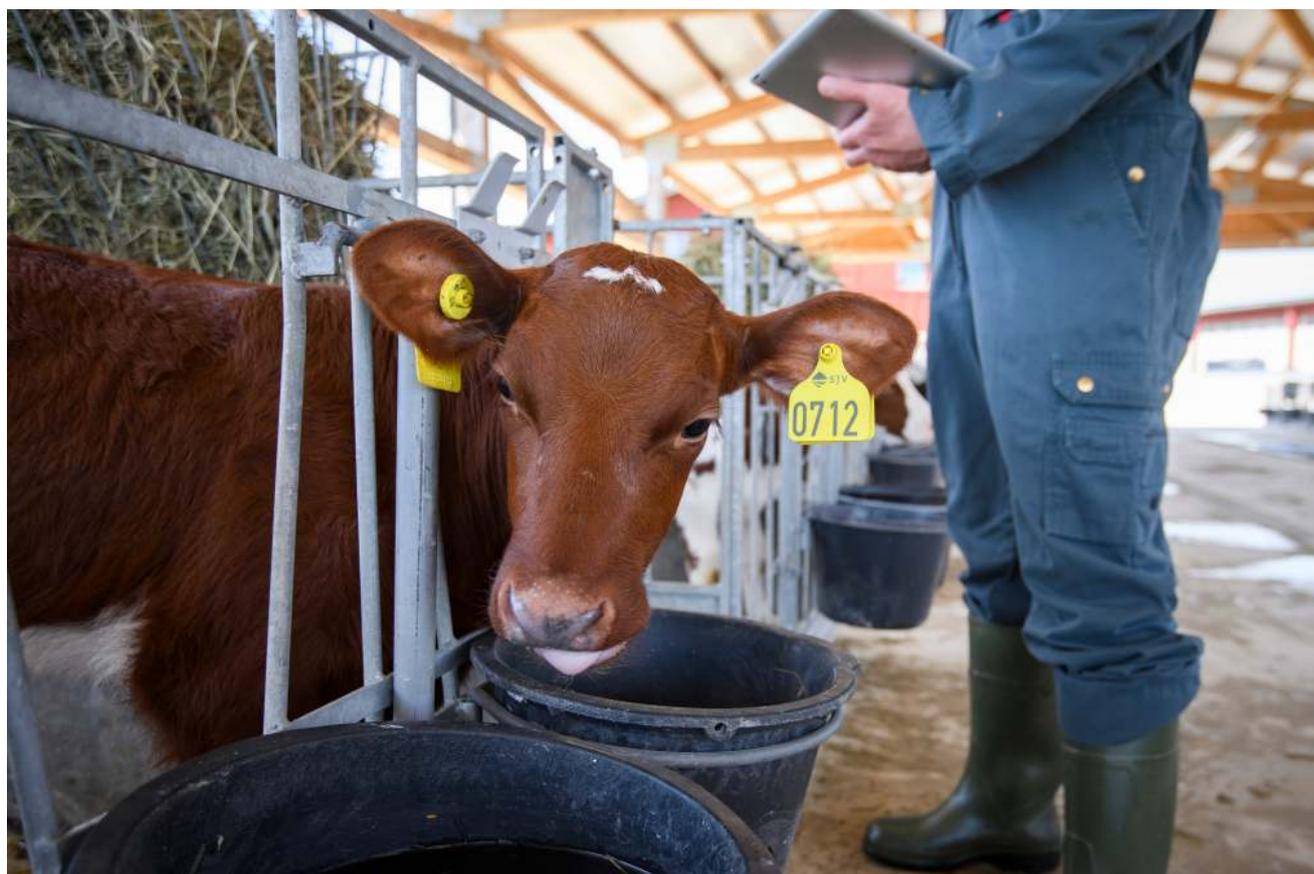
REFERENCES

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>

Bovine viral diarrhoea



Sweden has been considered free from BVD since 2014, which is very important for the animal health in both beef and dairy herds. Photo: Magnus Aronson.

BACKGROUND

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

DISEASE

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

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

LEGISLATION

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

SURVEILLANCE

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.

Surveillance of dairy herds is performed by sampling bulk milk in conjunction with milk quality testing. The laboratory gets an order from Växa Sverige (the former Swedish Dairy Association) about which herds to sample. All samples are marked using bar code labels. Surveillance of beef herds is performed by blood sampling at slaughter. Field testing can also be carried out as a backup component if herds to be tested cannot be accessed through the abattoir or through sampling of bulk milk. 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 2019 are given in Tables 5 and 6.

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

RESULTS

The outcome of antibody testing of bulk milk, slaughter, and field samples tested in 2019 is given in Table 5. As shown in Table 5, two blood samples from beef-cattle herds and two bulk milk samples 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. Younger animals in these herds were tested negative. The two dairy herds were retested with negative result. In 2019, 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 2019. At the end of the year, no herd was diagnosed as having an ongoing BVDV-infection. A newly infected herd has not been detected since 2011, and the last virus positive animal was born in an infected dairy herd in 2012. Since 2014, Sweden is considered free from BVDV. Continued surveillance is necessary to maintain confidence in freedom from the disease.

REFERENCES

Växa Sverige, Statistics for 2019.

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.

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

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

Table 5: Total numbers of samples with different contents of BVDV antibodies tested in 2019.

Sample type	Class/Finding	Herds	Animals
Bulk milk	0–1 ^A	2639	-
Bulk milk	2–3 ^A	2	-
Blood sample at slaughter	Negative	-	6922
Blood sample at slaughter	Positive	-	2
Field sample	Negative	-	0
Field sample	Positive	-	0

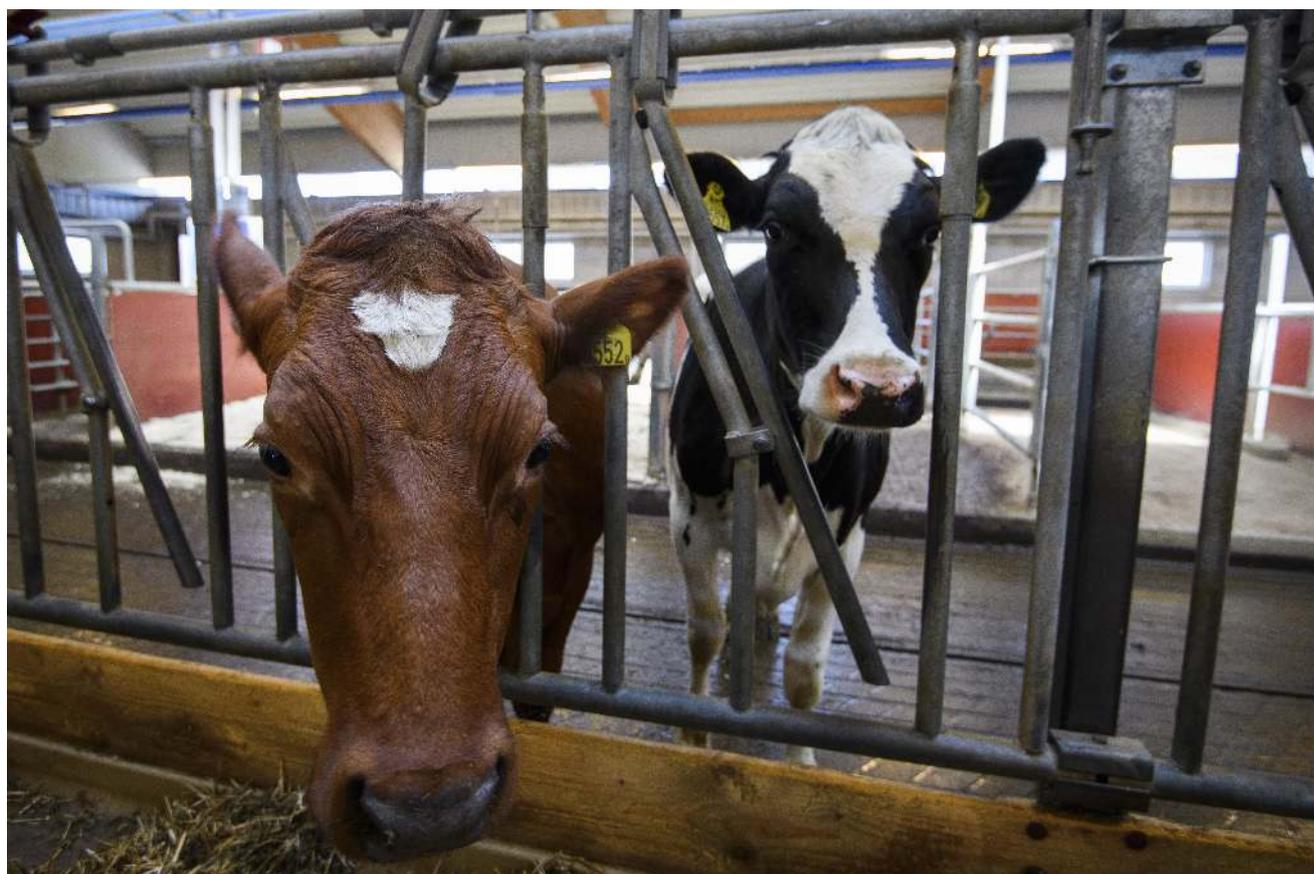
^A Class 0–1 = no or very low levels of antibodies; Class 2–3 = moderate or high levels of antibodies. (Based on Niskanen, 1993)

Table 6: Dairy and beef herd results from testing of BVDV antibodies in bulk milk or blood samples in 2019 divided by herd level risk.

Herd level risk ^A	Herd numbers (N)	Production type	
		Dairy	Beef
<i>Low risk</i>	N of herds	2344	7691
	N of herds tested	1105	1267
	N positive	2	0
<i>Medium risk</i>	N of herds	1284	2034
	N of herds tested	922	759
	N positive	0	2
<i>High risk</i>	N of herds	256	497
	N of herds tested	198	199
	N positive	0	0

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

Brucellosis



The last case of bovine brucellosis in Sweden was recorded in 1957 and Sweden is officially free from *Brucella abortus* and *Brucella melitensis*. Photo: Magnus Aronson.

BACKGROUND

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

Since 2010 there has been approximately one domestic case reported annually. Predominantly these cases have, or were suspected to have, consumed unpasteurised milk products from endemic countries.

DISEASE

Animals

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

Humans

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

LEGISLATION

Animals

Brucellosis in food-producing animals is included in the Swedish Act of Epizootic diseases (SFS 1999:657 with amendments). Vaccination is prohibited and notification of suspect cases is mandatory. Sweden's bovine brucellosis free status has been officially stated in EU legislation since 1994, Decision 2003/467/EC. Ovine brucellosis is covered by Directive 91/68/EEC. Sweden was declared officially free from brucellosis in sheep and goats in 1995, stated in Decision 2001/292/EC.

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

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

Humans

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

SURVEILLANCE

Animals

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

Diagnostic tests for animals with clinical signs suggesting brucellosis or animals that are to be exported/imported will often be tested with the same diagnostic tests as used in the surveillance programme. Samples from animals (foetuses) included in the enhanced passive surveillance of aborted foetuses 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 PCR, serology and culture. Positive colonies are investigated by microscopy, MALDI-TOF, repeated PCR and commonly tested for antibiotic resistance.

Passive surveillance

Animals

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

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.

Ongoing 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

This sampling is since 2010 conducted every third year and was performed in 2019. 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.

The bovine brucellosis surveillance of 2019 was designed with a between-herd design prevalence of 0.2%, a within-herd prevalence of 40%, a surveillance sensitivity of 88%, and a risk of introduction of 1 in 50 years. 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 were tested for antibodies against *B. melitensis*. The sheep serum samples were collected within the surveillance programme for Maedi/Visna and the goat serum

samples were collected within the Caprine Arthritis Encephalitis programme. The samples were 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 2019 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 2019. Serum samples were collected within the surveillance programmes for Porcine reproductive and respiratory syndrome and Aujeszky's disease. The samples were selected by systematic random sample by collecting the first sample submitted from each herd in this surveillance programme.

The porcine brucellosis surveillance of 2019 was designed with a between-herd design prevalence of 0.5%, 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 99% at the end of the year. To reach this target, 750 samples from 750 herds are required.

RESULTS

Passive surveillance

Animals

During 2019, one clinical suspicion was reported in a pig herd with increased abortion rate. The suspicion was ruled out after investigation in the herd and examination of three aborted fetuses. No clinical suspicions of brucellosis were seen in any other food-producing animal species.

Within the surveillance of aborted fetuses, 21 bovine, 12 ovine, three caprine, and 31 pig fetuses were examined for *Brucella* spp. All samples were negative.

Humans

In 2019, 14 cases were reported, which is within the same range observed during the last ten years. Seven of the cases were travel-associated mainly from regions of the Middle East and the Horn of Africa regions. Three of the cases were

reported as domestic infections. Seven cases had consumed unpasteurised milk products, where three had consumed the products in Iraq and one of the cases with domestic infection had consumed unpasteurised cheese purchased in Iraq. The two additional cases of domestic infections had unknown routes for infection. The majority of cases were diagnosed by PCR and subsequent cultivation. For these cases *Brucella melitensis* was identified. For one of the cases the infection was diagnosed based on antibodies. All retrieved isolates were susceptible to relevant antibiotics for treatment.

Active surveillance

Animals

During 2019, 3700 bovine samples (2299 serum samples and 1401 bulk milk samples) from 3700 individual holdings were analysed for *B. abortus*, 1977 ovine and caprine serum samples from 359 individual holdings were analysed for *B. melitensis* and 742 porcine serum samples from 484 individual holdings were analysed for *B. suis*. All these samples were negative, assuring sustained freedom from *B. abortus* with a probability of >99% in the dairy cattle population, 98.8% in the beef cattle population, 95% probability of freedom from *B. melitensis* in the ovine and caprine population and 98% probability of freedom from *B. suis* in the pig 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 2019. The long standing and extensive serological screenings performed without finding any infection accompanied by the additional enhanced passive surveillance in aborted fetuses 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 eight years, six 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



In 2019, the prevalence of *Campylobacter* in chicken slaughter batches was lower than in previous years which was accompanied by a lower domestic incidence of campylobacteriosis in humans. Photo: Bengt Ekberg/SVA.

BACKGROUND

Thermophilic *Campylobacter* species (spp.) are the most common cause 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, although *Campylobacter* can colonise the intestinal tract of many other animals. The bacterium is excreted in faeces. *Campylobacter* spp. are fragile organisms but can survive in fresh-water for longer periods. The infectious dose for humans is low. Most European countries have a seasonal peak of *Campylobacter* prevalence 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 the last two decades, the incidence of human campylobacteriosis has varied between 67 and 110 cases per 100 000 inhabitants (Figure 5). Most cases are infected abroad, but in 2014–2018 the proportion of domestic infections increased due to several major outbreaks caused by domestically produced chicken meat.

DISEASE

Animals

Asymptomatic carriage of thermophilic *Campylobacter* is common in several animal species, including poultry, 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 2012:24. In addition, *Campylobacter fetus* subsp. *venerealis*, which causes bovine genital campylobacteriosis, is notifiable.

Food

Detection of *Campylobacter* spp. in food is not notifiable. From 2018 and onwards, food business operators at slaughterhouses are obliged to sample neck skins of broilers for 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 are taken from June through September.

Humans

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

SURVEILLANCE

Animals

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

The programme covers more than 99% of the broilers slaughtered in Sweden. Since 2006, sampling is performed by collecting intact caeca from 10 birds per sampled slaughter batch at the major slaughterhouses. In 2019,

seven slaughterhouses delivered samples. When the flock is slaughtered at more than one time point and the time interval between the slaughter batches is longer than four days, samples are taken from both batches, otherwise only from one of the batches. The caeca are pooled into one composite sample per batch and analysed according to ISO-10272 part 1.

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

Food

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

Since 1 January 2018, slaughterhouses are obliged to sample neck skins from poultry carcasses for *Campylobacter* analyses using a culture-based method (ISO 10272-2 or alternative methods), according to regulation (EC) No. 2073/2005. A limit of 1000 CFU/g applies to a set of 50 pooled samples derived from 10 consecutive sampling sessions. In 2019, the regulation allowed up to 40% of the samples to exceed the limit.

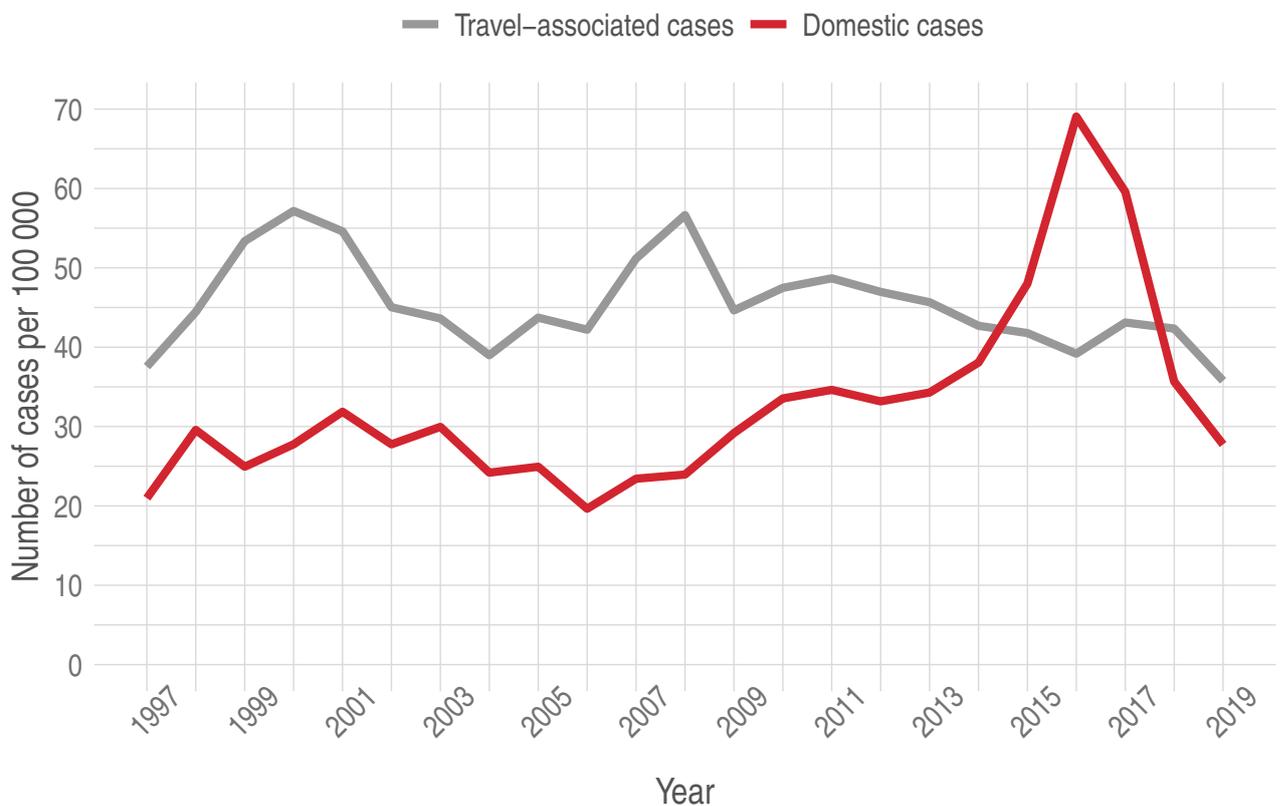


Figure 5: Incidence (per 100 000 inhabitants) of notified human cases of campylobacteriosis in Sweden, 1997–2019. Travel-associated cases are those where the patient has reported travel to another country during the incubation period prior to clinical presentation. Domestic cases are patients that have not recently travelled outside Sweden.

IN FOCUS: Comparing human and retail chicken isolates using whole genome sequencing reveals high degree of clustering

In 2017 when the Public Health Agency of Sweden began its microbial surveillance programme for *Campylobacter* spp, there was a large ongoing outbreak in Sweden caused by domestically produced chicken meat. In conjunction with this, the Swedish Food Agency began to sample and analyse chicken retail meat to investigate occurrence and levels of *Campylobacter* spp. in meat from different slaughterhouses and to compare meat isolates to isolates from humans using WGS. After the outbreak, retail sampling as well as comparison of isolates from humans and chicken meat was repeated each August (high season) three years in a row (2017–2019). The aim was to understand the frequency and distribution of clustering isolates from humans and chicken meat in a non-outbreak situation. In total, 302 human and 167 chicken retail isolates were sequenced. The human isolates showed a high degree of clustering where 40 to 54% clustered with one or more isolate collected during the same time period (Table 7). Almost all clusters identified included human isolates from more than one county, indicating geographically dispersed sources of infection. Some isolates also clustered between the sampling years, indicating a reoccurring source of infection. Approximately one third of the human isolates clustered with chicken meat isolates. This pattern was observed in all three sampling periods. The majority of the chicken meat isolates that clustered with human cases originated from the largest poultry slaughterhouse in Sweden. A limited number were from other conventional Swedish, organic or foreign slaughterhouses.

These findings show that campylobacteriosis is not foremost a sporadic disease during high season but constitutes clusters with cases geographically distributed across the country. The clustering strains are often continuously replaced with new, however a few remain over the years. Overall, the comparison of human and retail chicken isolates indicates that if a reduction of *Campylobacter* in the chicken production is achieved, this will have a direct effect on the number of people who become infected by *Campylobacter*.

Table 7: Number of human and chicken meat isolates sequenced in August 2017, 2018 and 2019 as well as the proportions of human isolates clustering with other human isolates or chicken meat isolates.

	August 2017	August 2018	August 2019
Number of human isolates sequenced	92	98	112
Proportion of human isolates clustering with other human isolates	40%	44%	54%
Proportion of human isolates clustering with chicken meat isolates	33%	30%	33%
Number of chicken meat isolates sequenced	54	64	49

Humans

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

Since 2017, the Public Health Agency of Sweden requests isolates from all domestic cases reported during week 11 (low season) and week 34 (high season) for whole genome sequencing analysis. The periods for collection were chosen to reflect the diversity in different seasons. 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.

In 2017–2019, the analysis of human isolates collected during high season has been preceded by analysis of *Campylobacter* in chicken meat from retail. Results from comparative investigations of human and chicken meat isolates are summarised in “In Focus”.

RESULTS

Animals

In 2019, thermophilic *Campylobacter* spp. were detected in 230 (5.3%) of the 4363 broiler chicken batches tested at slaughter (Figure 6), which is less than in previous years. Among the slaughter batches at the four largest slaughterhouses, which cover 97.2% of the slaughtered chicken, *Campylobacter* spp, was detected in 4.3% of them. The monthly prevalence of *Campylobacter* in chicken slaughter batches varied between 0.3% and 13% with the highest prevalence in July. The prevalence of *Campylobacter* in incoming batches varied between slaughterhouses.

Food

In August 2019, a survey was performed by the Swedish Food Agency in which 100 samples of fresh chicken meat were collected at retail and analysed for *Campylobacter*. In the survey, *Campylobacter* was detected in 51% of the samples. *Campylobacter* levels exceeded 10 CFU/g in 13% of the samples.

In addition, 98 samples were taken by national and local authorities from different types of food. No sample was

positive. 51 of the 98 samples were taken from meat from broilers within the framework of a control project.

Food business operators at five slaughterhouses collected 419 pooled neck skin samples according to regulation (EC) No. 2073/2005. Test results at all slaughterhouses were satisfactory according to the legislation, and only seven (1.7%) of the 419 samples exceeded the limit of 1000 CFU/g.

Humans

A total of 6693 cases of campylobacteriosis were reported in 2019. Of the reported cases, 44% (2865 cases) were domestic. The incidence in domestic cases decreased by 22% from the year before to 27.4 per 100 000 inhabitants. Hence, the domestic incidence is back at the same level as in the first decade of the 2000s and well below the levels in 2014–2018 when several large outbreaks related to consumption of domestically produced chicken affected the incidence (Figure 5).

For the domestic cases in 2019, the median age was 47 years with a spread from 0 to 97 years. Like previous years, the domestic incidence was higher among adults than children and more men (56%) than women were reported with campylobacteriosis.

In the microbial surveillance programme at the Public Health Agency of Sweden, isolates from domestic cases were collected one week during low season (week 11) and one in high season (week 34). Of the 137 isolates, all but one was *C. jejuni*. Twelve clusters were identified that together contained 47% of the isolates. In August, isolates from the microbial surveillance programme and isolates from the survey performed by the Swedish Food Agency were compared by WGS. One third (33%) of the human isolates clustered with isolates from fresh chicken meat, mainly originating from large scale domestic production.

Human campylobacteriosis cases versus positive chicken slaughter batches

A comparison was made between the number of human domestic cases and the proportion of *Campylobacter* positive chicken slaughter batches during 2019. The comparison shows a clear covariation over the year with the highest number/largest proportion in the summer and the lowest number/smallest proportion in winter and spring (Figure 7).

DISCUSSION

The domestic incidence of campylobacteriosis was lower in 2019 compared with recent years. Most campylobacteriosis cases have been considered sporadic, but cluster analysis of isolates typed with WGS indicates that a large part of the cases could indeed be part of outbreaks. Many of these outbreaks appear genetically linked to isolates from retail poultry meat.

In 2019, the annual prevalence of *Campylobacter* in chicken slaughter batches was lower than in previous years (Figure 6). However, the high detection rate of *Campylobacter* in the survey of retail meat warrants stringent preventive measures. The correlation between human cases of campylobacteriosis and *Campylobacter*-positive broiler batches further underscores the need for preventive measures.

Campylobacter prevalence varies considerably between slaughterhouses, with only a few findings at some and higher prevalence at others. During the last ten-year period, the Swedish chicken production has increased by approximately 30% and the share of fresh chicken meat has increased compared to frozen meat. This has led to a higher amount of potentially contaminated chicken meat at the market, because *Campylobacter* are sensitive to freezing and therefore more common in fresh than in frozen meat.

Sampling of the neck skin for analysis of *Campylobacter* according to regulation (EC) No. 2073/2005 functioned well in most of the slaughterhouses concerned. The results show that no slaughterhouse in Sweden had any difficulties in meeting the criterion in the regulation, which is set at a level that reflects the much higher prevalence of *Campylobacter* in broilers in many other EU member states.

Reducing *Campylobacter* prevalence at the farm level decreases the risk of human infection. 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 lead to an increase in human illnesses and illustrated the importance of biosecurity measures, not only at farm level but in the whole production chain. In 2019, no such failures were reported.

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/>
- Hansson I, Vågsholm I, Svensson L, Olsson Engvall E (2007) Correlations between *Campylobacter* spp. prevalence in the environment and broiler flocks. *J Appl Microbiol* 103:640–9
- Lindqvist R, Lindblad M (2008) Quantitative risk assessment of thermophilic *Campylobacter* spp. and cross-contamination during handling of raw broiler chickens evaluating strategies at the producer level to reduce human campylobacteriosis in Sweden. *Int J Food Microbiol* 121:41–52
- 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

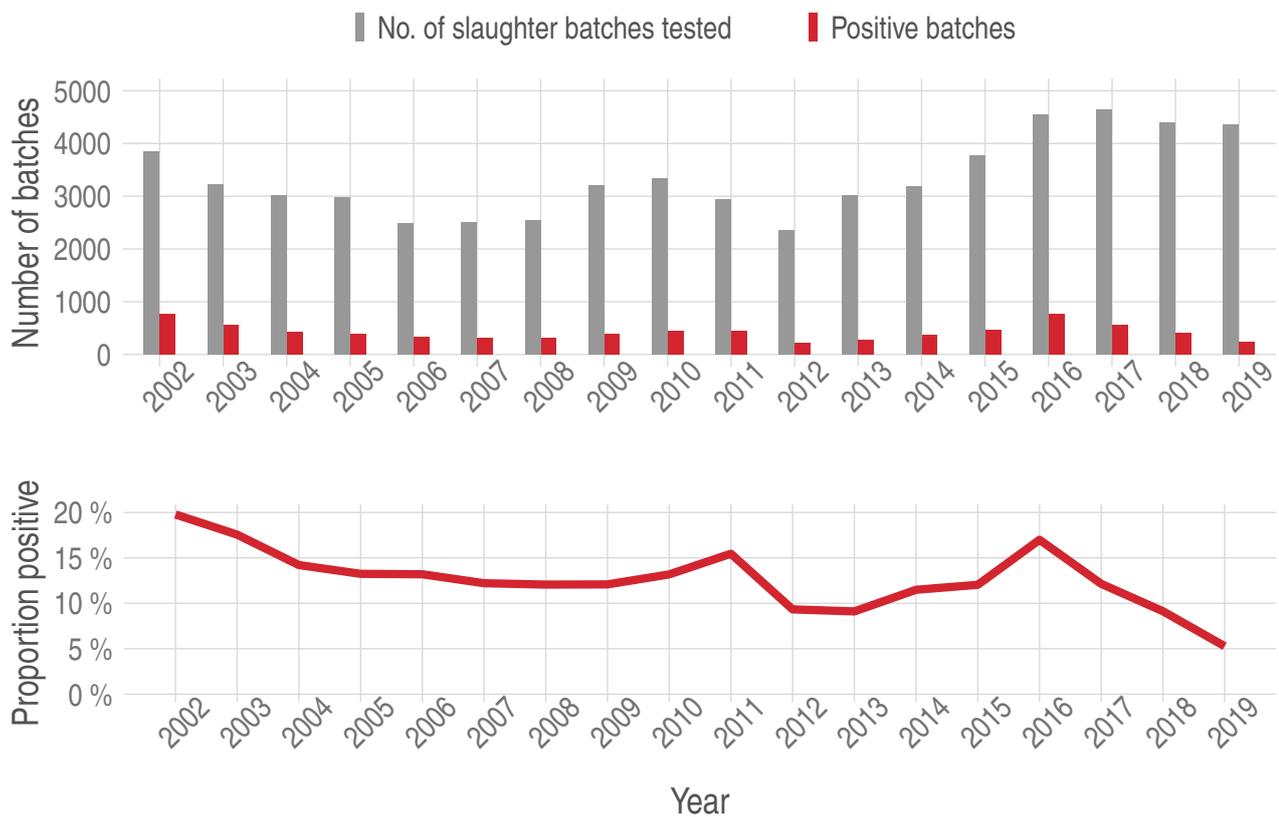


Figure 6: Prevalence of *Campylobacter* in slaughter batches of broiler chicken in 2002–2019.

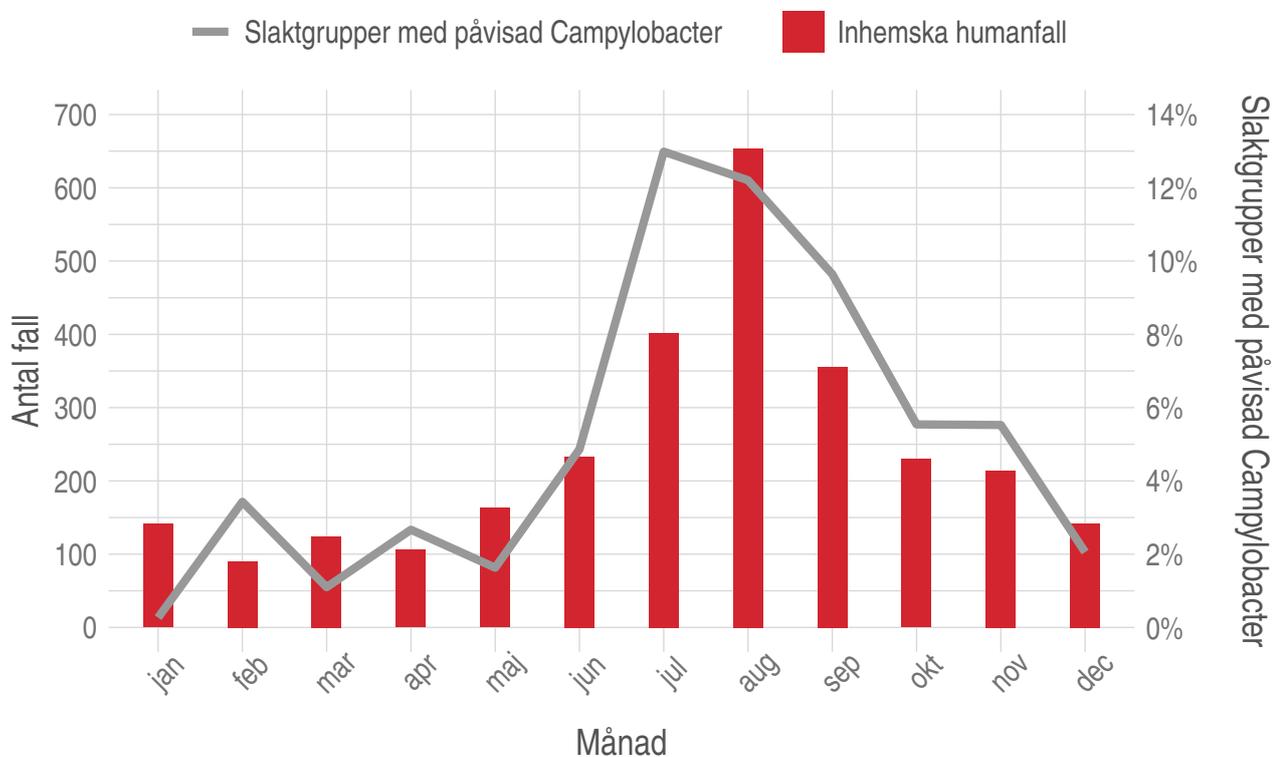


Figure 7: Number of notified domestic cases of human campylobacteriosis, along with the proportion of *Campylobacter*-positive broiler batches, broken down per month in 2019.

Chronic wasting disease



In 2019, 1965 reindeer were tested for chronic wasting disease (CWD), most of them within the intensified sampling in the county of Norrbotten and all with negative results. Photo: Jellis Vaes/Shutterstock.

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 24 states in the USA, and in two Canadian provinces (CDC, 2020). Through export of live cervids, CWD has also spread to South Korea.

Before 2016, CWD had not been reported in Europe. In spring of 2016, the first case in Europe was detected in wild reindeer (*Rangifer tarandus tarandus*) in the region of Nordfjella in Norway (Benestad et al., 2016). As a consequence of the finding, surveillance in Norway was intensified and this has so far (April 2020) resulted in the detection of the disease in six moose (*Alces alces*) (three in Selbu and one each in Lierne, Flesberg and Sigdal), one red deer (*Cervus elaphus*) (in Gjemnes) and detection of 18 further cases in the reindeer flock of Nordfjella. The cases in reindeer show similarities with the cases found in North America (although not identical) whilst the cases in moose and red deer have been shown to differ from the cases in reindeer. It is still unknown what this means in terms of differences in e.g. the disease transmission pattern, but it has been hypothesised that these “atypical” cases may be spontaneously occurring

in older animals (Pirisinu et al., 2018).

Due to the detection of CWD in Norway, surveillance for CWD is currently mandatory in several EU member states (see Legislation and Surveillance).

In March 2018, the first case of CWD in Finland was reported. It was a fifteen-year-old moose that was found dead in Kuhmo in the eastern parts of Finland. The case showed similarities with the cases in moose and red deer in Norway (Ruokavirasto, 2020).

The first Swedish cases, in elderly moose, were detected in 2019 (see Results).

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

Due to similarities with BSE, which is linked to variant Creutzfeldt-Jakob disease in humans, and the known

fact that many TSEs experimentally can be transmitted between several different species, there has been a suspicion that CWD may be a zoonotic disease. Currently, there is not enough data to exclude that CWD could be zoonotic, however the risk is deemed to be very low (VKM 2016 and 2017, Waddell 2018). In areas where CWD is endemic, people are recommended not to consume animals displaying clinical signs consistent with CWD or animals with positive test results for CWD.

HISTORY

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

DISEASE

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

The currently accepted theory of TSEs, or prion-diseases, is that they are transmitted through small proteins, prions with abnormal structural conformation. These prions induce a structural transformation of normal prion-proteins in the body of the recipient. Thus, the disease is not caused by parasites, bacteria, fungi or viruses, but by proteins. 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 CJD in humans).

As mentioned, it has been hypothesised that the cases in older moose may have of spontaneous rather than contagious origin. This has not yet been confirmed, but so far it is clear that the cases in elderly moose detected in the Nordic countries clearly differ from what is previously known as CWD in North America.

LEGISLATION

CWD is a notifiable disease under the Swedish Act of Epizootic diseases (SFS 1999:657, with amendments) and there is a scheme to compensate farmers for losses due to eradication measures. CWD is also regulated through the Regulation (EC) No 999/2001 of the European Parliament and

of the Council on TSEs. The surveillance programme is regulated in the Commission Regulation (EU) 2017/1972 amending Annexes I and II to Regulation (EC) No 999/2001.

SURVEILLANCE

In response to the detection of CWD in Norway, general sampling of all adult cervids sent for postmortem to the National Veterinary Institute started in summer 2016. As a consequence of the additional finding of a CWD-positive moose in Norway close to the Swedish border, a limited active surveillance was conducted in the county of Jämtland during the fall of 2017, where samples were collected from hunter-harvested moose.

The EU-regulated surveillance programme, mentioned under “Legislation” above, started in January 2018. For the member states concerned, a minimum of 6000 animals are to be tested between the years 2018 and 2020. Samples shall be collected from wild, semi-domesticated and farmed/captive cervids. In Sweden, moose, red deer, roe deer and reindeer are included in the surveillance programme. Samples from wild cervids (moose, red deer, roe deer) are collected from fifty primary sampling units (PSU) covering the whole country. Samples from farmed cervids (red deer) and semi-domesticated cervids (reindeer) are collected from all red deer farms (n=117) and all Sami villages (n=51), the latter being the administrative unit for reindeer herding as well as a geographically defined area. All animals sampled must be over twelve months of age and preferably from a risk category, i.e. cervids found dead or diseased and road/train killed cervids (assumed to have higher probability of infection).

The CWD surveillance programme is run in collaboration between the National Veterinary Institute and the Swedish Board of Agriculture and is financed by the latter. Samples are analysed at the National Veterinary Institute, Uppsala, which is the National Reference Laboratory (Regulation (EC) 999/2001) for TSEs.

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

Results of the testing are reported to the European Food Safety Authority by the Swedish Board of Agriculture, based on data provided by the National Veterinary Institute.

In 2019, in accordance with EU legislation, an intensified sampling was carried out in the area where the first two Swedish CWD cases (see Results) were detected. The purpose was to investigate if the disease was spread in the area and present in more age groups, but also to contribute to the understanding of the epidemiology of CWD in moose. The sampling was done during the moose hunt and reindeer slaughter period in the autumn of 2019 and winter of 2020. 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. The area for sampling was decided to be “Älgförvaltningsområde 3” (a moose population

management area) in the county of Norrbotten. This area was chosen based on knowledge about animal populations and migratory patterns in the area.

Sampling was performed on as many as possible of hunted moose ≥ 1 year of age and on slaughtered reindeer ≥ 1 year of age from the ten Sami villages in the area. Sampling was performed by hunters, slaughterhouse personnel and reindeer owners. In addition to brainstem and lymph node samples, parts of lower jaw with teeth for determination of age of the sampled animals were sent to the National Veterinary Institute.

In other parts of Sweden, samples were as during 2018 primarily taken from cervids found dead or diseased and road/train killed cervids.

RESULTS

The number of samples tested from 2016 to 2019 is detailed in Table 8.

In 2019, 31 cervids were sampled due to clinical suspicion of CWD (29 moose, 2 fallow deer). In total, 854 moose, 31 red deer, 73 roe deer, 5 fallow deer and 1965 reindeer were examined for CWD at the National Veterinary Institute during 2019. Most of the moose and reindeer analysed were part of the intensified sampling in the county of Norrbotten performed during the hunting and slaughter season, autumn 2019 to winter 2020. During 2019, 661 moose and 1747 reindeer (and one hunted roe deer) were investigated within the intensified sampling. Age determination of sampled animals was in 2019 only performed for detected cases of CWD.

In total, three cases of CWD were detected during 2019; the cases are described in detail below.

In March 2019, CWD was detected in Sweden for the first time. The disease was confirmed in a sixteen-year-old female moose in the municipality of Arjeplog, county of Norrbotten. The moose was euthanised after being observed emaciated, staggering, walking in circles and apparently blind. Samples from the moose were analysed at the National Veterinary Institute within the ongoing CWD surveillance programme. Brainstem and retropharyngeal lymph nodes were screened with a TSE rapid test. Samples from brainstem were positive in the screening test and confirmed positive for transmissible spongiform encephalopathy with Western Blot. Samples from lymph nodes were negative in the screening test. The case showed similar features with cases of “atypical” CWD previously detected in Norwegian moose and described by Pirisinu et al (2018), in that it was an older moose and only brainstem was positive.

In May 2019, a second case of CWD was reported in the county of Norrbotten, this time in the municipality of Arvidsjaur. It was again a sixteen-year-old female moose, euthanised after being observed emaciated, weak and with behavioural changes. Like the first case, samples from brainstem were confirmed positive for transmissible spongiform encephalopathy, but samples from lymph nodes were negative.

A third case of CWD in moose was detected during the intensified sampling in September 2019, the second case in

the municipality of Arjeplog. The moose was shot during the hunting season and did not display any signs of disease at that time but was sampled within the intensified surveillance in the area. The age of the moose was determined to be at least ten years. Again, only brainstem samples, but not lymph nodes, were confirmed positive.

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

Table 8: The number of animals tested for CWD per year in Sweden 2016–2019.

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 ^A	5	1965 ^A

^A 661, 1 and 1747 of the moose, roe deer and reindeer, respectively, were tested within the intensified sampling in the county of Norrbotten.

DISCUSSION

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

However, the number of samples received from the nationwide sampling during 2018 and 2019, the first two years of the surveillance programme, 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 (preferred animals due to the assumed higher probability of infection) is relatively small. The number of road-killed animals is quite high, but divergent interpretations of legislation related to work environment and taxation (related to minor compensation for sampling) has delayed sampling of this group of cervids.

Much effort was put into the implementation of the intensified sampling in the county of Norrbotten. Out of 907 reported hunted moose ≥ 1 year of age, 661 were sampled, reaching the target for the increased surveillance. The target number of reindeer to be sampled during the slaughter season was 1480. Although this number was reached, the plan is to continue sampling during the slaughter season of 2020/2021, since the aim is to sample in total at least 4400 reindeer in the area for intensified sampling. The number of reindeer sampled in different Sami villages varied greatly, and not all Sami villages reached the number of samples set to be taken during the slaughter season of 2019/2020.

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 been detected in the brain and not in lymph nodes. Further studies are ongoing to characterize these strains and to understand more about

the epidemiology. As mentioned, it has been hypothesised that the CWD cases in older moose may not be contagious, but rather a spontaneous variant of CWD occurring in old animals (Pirisinu et al., 2018).

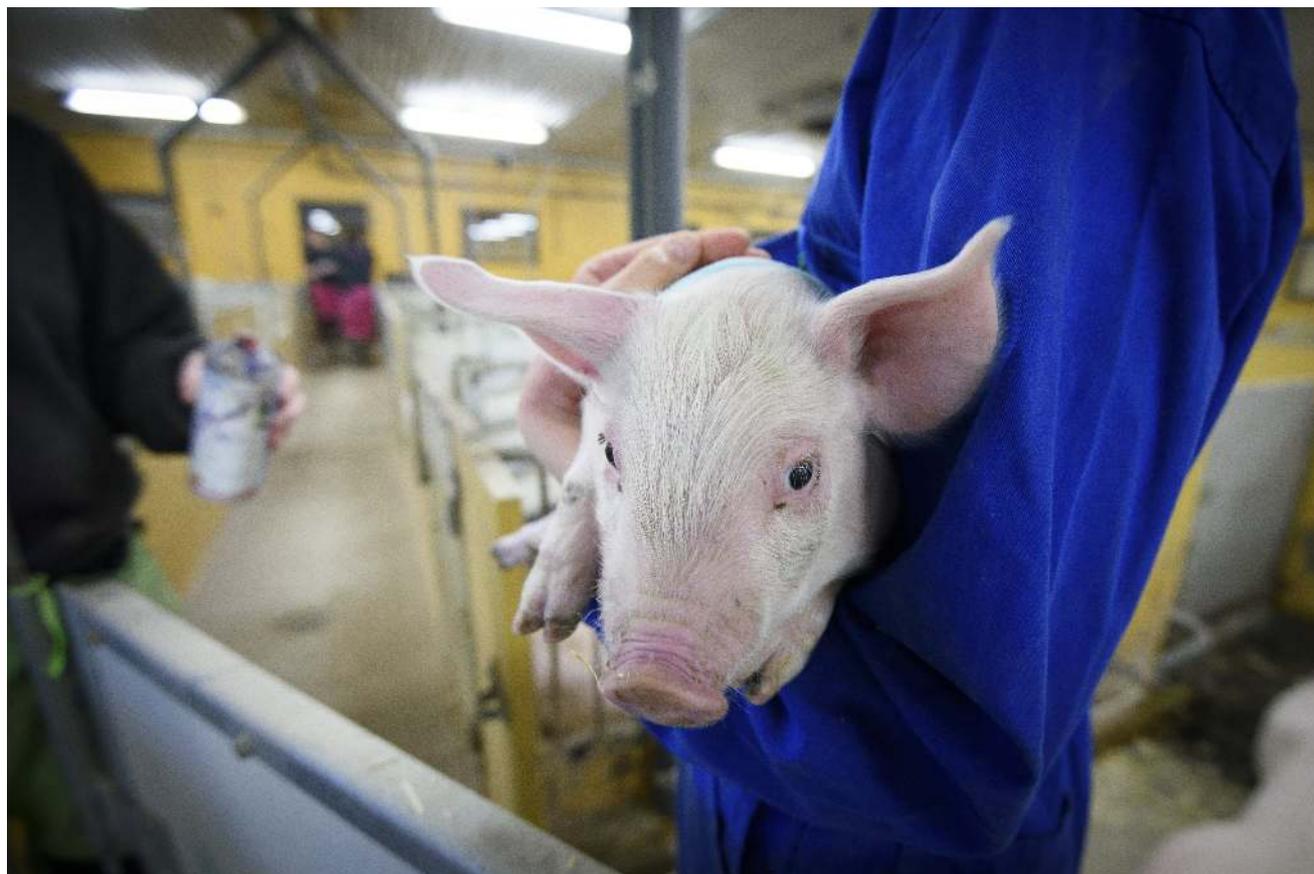
Consequently, the detection of three cases of CWD in moose in a limited geographical area in Sweden (detected prevalence 0.4%) does not necessarily mean that a contagious variant of the disease is present in the region. The fact that cases were only found in relatively old animals and that prions were only detected in brain in screening tests, while not in lymph nodes, still fits the hypothesis of spontaneous cases in old animals. The region where all three Swedish cases were found 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 than females). The ongoing determination of the age of sampled moose in the area for intensified sampling will contribute to further understanding of the situation.

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 strain of CWD with the characteristics of “classical” CWD would be present or introduced into Sweden, it would have large negative consequences for reindeer, wild cervid populations and farmed cervids. Consequently, the disease could also have large consequences for people making their living from, or being involved in activities related to, these species. However, if the cases found in older moose in Norway, Finland and Sweden would in fact have a spontaneous origin, the disease could be expected to occur sporadically in all cervid populations, without leading to the same severe consequences as “classical” CWD. Further studies are crucial to increase the understanding of the epidemiology of the different CWD-strains.

REFERENCES

- Centers for Disease Control and Prevention, <https://www.cdc.gov/prions/cwd/occurrence.html> (accessed 2020-03-10)
- 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
- 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

Classical swine fever



The purpose of the surveillance programme for Classical swine fever (CSF) in Sweden is to document freedom from CSF in the pig population and to contribute to the maintenance of this situation by early detection of an introduction. In 2019, 2000 pigs were tested and found negative for the disease. Photo: Magnus Aronson.

BACKGROUND

Classical swine fever (CSF) is a disease of pigs caused by a pestivirus closely related to bovine viral diarrhoea virus and border disease virus. CSF is endemic in many parts of the world and is one of the most important diseases affecting pig production globally. The disease is endemic in parts of Asia, South America, Africa and on some Caribbean islands. In Europe, several large outbreaks of CSF occurred in the 1980's and '90's, 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 wild boar in the eastern parts of the EU, including Lithuania (2009, 2011) and Latvia (2012–2015). The last reported case of CSF in the EU was in 2015. Sweden, where CSF has not been diagnosed since 1944, was issued official status as a historically CSF-free country by the OIE in February 2015.

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

caused by direct or indirect contact with wild boar. Feeding pigs swill contaminated with CSFV has also resulted in the spread of the disease to new areas. Because of this, swill feeding of pigs is prohibited in the European Union.

DISEASE

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

LEGISLATION

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

SURVEILLANCE

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

Passive surveillance

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

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

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 2019, 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*”), were used for the active surveillance of CSF in domestic pigs. Two to three samples per herd tested for PRRS were also analysed for CSF.

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

RESULTS

Passive surveillance

Four investigations following clinical suspicions of CSF in domestic pigs were carried out during 2019. In two herds, the primary clinical sign was the sudden, unexplained death of multiple animals within a short period of time. In the other two herds, the main clinical manifestations included sows with fever, weak-born litters and piglets with neurological signs and high mortality. Following the investigations, which included sampling and analysis for CSF (and ASF), all the herds were declared negative for CSF.

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

Active surveillance

Serum samples from 2000 domestic pigs were analysed for the presence of antibodies for CSF in 2019. All samples were negative. Taking the surveillance outcome from previous years into account, the probability of freedom from CSF during 2019 was >99%.

DISCUSSION

The results from the active and passive surveillance for CSF in Sweden in 2019 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

Coccidiosis and clostridiosis

BACKGROUND

Coccidiosis and clostridiosis are intestinal diseases that commonly affect broiler chickens worldwide. Both diseases are major causes of economic losses and reduced welfare. To prevent these diseases a combined coccidiosis and clostridiosis surveillance programme was initiated in 1998 by the Swedish Board of Agriculture.

DISEASE

Coccidiosis is caused by microscopic parasites (genus *Eimeria*) that invade the intestinal epithelium. *Eimeria spp.* are ubiquitous, resilient and host specific parasites that are easily transmitted between birds by the faecal-oral route, especially when birds are kept on litter at a high stocking density. The severity of the intestinal lesions is influenced by parasite and host factors, such as parasite species, infectious dose, host age and level of immunity. Generally, young broiler chickens are highly susceptible.

Clostridiosis is a multifactorial disease and the pathogenesis is not well understood. The disease is associated with proliferation of the bacterium *Clostridium perfringens* type A, which together with management factors and loss of mucosal integrity cause lesions in the intestines (necrotic enteritis: NE) and liver (cholangiohepatitis).

Clinical signs of coccidiosis and clostridiosis range from clinical disease with significantly increased mortality rates to mild or subclinical forms, which are associated with reduced weight gain and impaired feed conversion. Clostridiosis is also a cause of condemnation at slaughter due to liver lesions. Both diseases may be prevented by in-feed ionophorous anticoccidials.

LEGISLATION

The health control programme for coccidiosis and clostridiosis in broilers is regulated in the Swedish legislation (SJVFS 2015:17, K152) and is administered by the Swedish Poultry Meat Association. These regulations apply to producers who breed more than 500 broilers annually.

SURVEILLANCE

The purpose of the surveillance is to document that the anticoccidials efficiently protect broilers from disease. The long-term goal is to replace anticoccidials by other preventive measures such as vaccines.

Intestinal lesion scoring

Field control of anticoccidial efficacy is performed by a lesion scoring method in broiler chickens from 20 randomly selected farms originating from regions served by different feed mills. The flock selection is performed by the Swedish Poultry Meat Association. From each selected farm, intestinal lesion scoring (scale 0–4) is conducted on 5 birds on two occasions during the year when the birds are between 22–24

days of age. If the mean total lesion score of an individual flock exceeds a certain level (2.5), an on-farm disease investigation is supposed to be carried out.

On-farm investigation of disease outbreaks in flocks

In flocks with lesion scores exceeding 2.5 and in flocks with acute outbreaks of suspected coccidiosis/clostridiosis an on-farm disease investigation may be carried out. Housing environment, hygiene and disease monitoring routines, feed composition (including analysis of concentration of anticoccidials) and mortality rate is assessed by the farm veterinarian in collaboration with the herd owner, the feed mill company and the control section of the Swedish Poultry Meat Association.

Histological examination of tissue lesions

Samples of tissues with representative pathological lesions collected during on-farm investigations are submitted for histological evaluation to the National Veterinary Institute (SVA). In addition, liver samples from herds with a high (>2%) presence of liver lesions registered at the abattoir are occasionally also sent to SVA for histological evaluation.

RESULTS

In 2019, 37 broiler flocks were investigated for lesion scoring, and a mean total lesion score (MTLS) of 0.34 was registered. In none of the flocks the lesion score exceeded 2.5, indicating low clinical disease occurrence and sufficient efficiency of anticoccidials in the examined flocks.

Sixteen samples of condemned livers from abattoirs belonging to 5 different broiler flocks and 59 samples of different tissues (livers, intestines, bursa fabricii, spleen, heart) from 9 different broilers flocks experiencing acute outbreaks of suspected coccidiosis/clostridiosis were submitted to SVA for histological evaluation. Indications of coccidiosis/clostridiosis (i.e. cholangiohepatitis, coccidiosis and/ or necrotic enteritis) were recognised in 11 of these 14 cases.

DISCUSSION

Approximately 103 million broilers were slaughtered in Sweden in 2019.

In conclusion, histological sampling and flock investigations were relatively few but recognised some farms with coccidiosis and/or clostridiosis/NE, and on these farms no convincing indications of long-term trends toward reduced anticoccidial efficacy were observed. Detailed information on the field situation regarding coccidiosis and NE is however not available.

REFERENCES

Johnson J, Reid WM (1970) Anticoccidial drugs: lesion scoring techniques in battery and floor-pen experiments with chickens. *Exp. Parasitol* 28:30–36

Cryptosporidiosis

BACKGROUND

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

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

Cryptosporidium was first described in animals and was not officially recognised as a significant human pathogen until the early 1980's. 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 sixth most important foodborne parasite globally, and as number five 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



In 2019, kale was identified as the probable source of three local foodborne outbreaks with *Cryptosporidium parvum*. Photo: Alicja Neumiler/Shutterstock.

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 also be affected by infections in 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.



Figure 8: Number of notified human cases per 100 000 inhabitants from 2009 to 2019.

IN FOCUS: National increase in the number of reported cases of cryptosporidiosis in humans Oct-Dec 2019

There was a national increase in the number of reported cases of cryptosporidiosis in the autumn of 2019. 58 percent (n=450/771) of annual domestic cases were reported from 1 October-31 December. Reported cases peaked during three weeks in November (Figure 9). An outbreak investigation was initiated and 300 isolates from cases were typed as part of that investigation. Five foodborne outbreaks were identified during this period, all attributed to infection with *C. parvum* (n=285). Dominating subtypes were IIdA22G1c (n=122) and IIdA24G1 (n= 65). Both these subtypes have been detected both earlier in 2019 and in the previous years. During the outbreak period, 122 cases in ten different regions were caused by subtype IIdA22G1c. The county of Stockholm had the most cases (n=58) followed by Västra Götaland (n=16) and Halland (n=16) counties. The median age of the cases was 39 years (2–83 years) with no significant gender difference (52% women, 48% men). Using surveys in collaboration with other authorities, unpasteurised juice with spinach was identified as the source of infection with subtype IIdA22G1c.

During the same period, cryptosporidiosis in 65 cases in twelve different regions were caused by *C. parvum* subtype IIdA24G1. The county of Västra Götaland had the most cases (n=13) followed by Stockholm (n=12), Östergötland (n=12) and Jönköping (n=11) counties. More women (62%) than men (38%) were infected and the median age was 40 years (11–79 years). No source of infection was identified for subtype IIdA24G1. Other common outbreak subtypes were IIdA20G1e (n=23) and IIdA21G1* (n= 20). These subtypes were also found in cases that had visited different Christmas buffets in December where fresh kale from four kale producers in the southern parts of Sweden was identified as the probable source of infection.

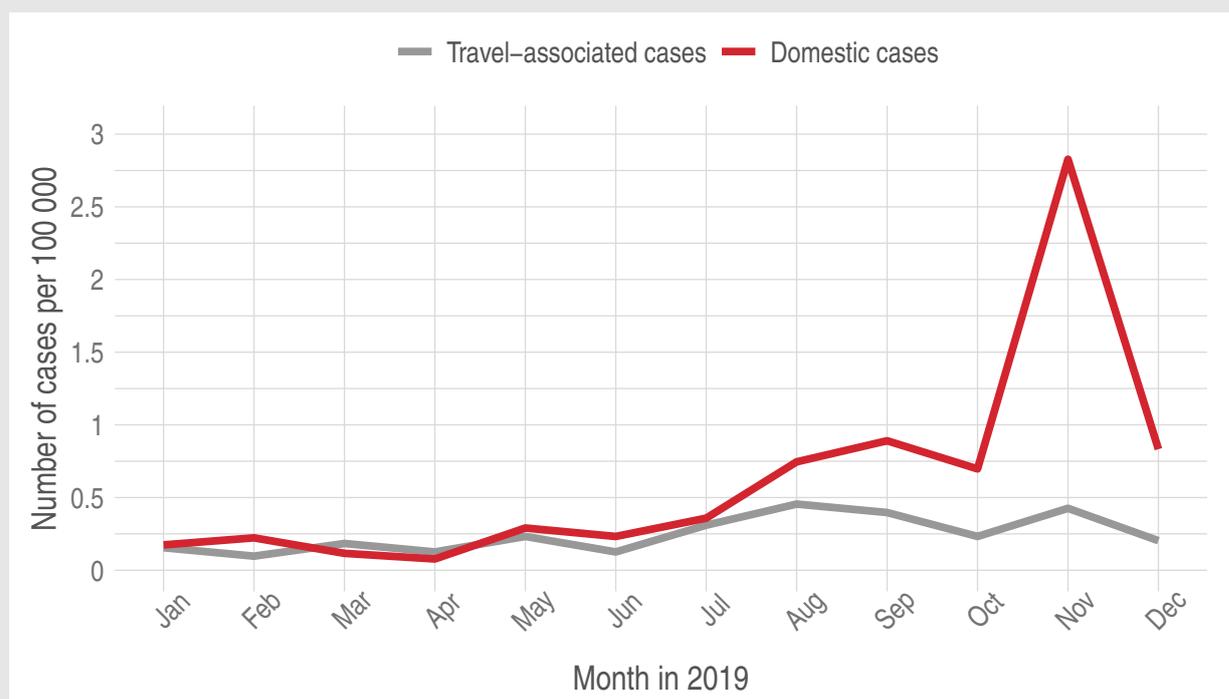


Figure 9: Number of notified human cases of cryptosporidiosis during 2019.

Humans

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

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 a microbiological surveillance programme with the aim of determining species and subtypes of all domestic cryptosporidiosis cases in order to better understand the national epidemiology.

LEGISLATION

Animals

Detection of *Cryptosporidium* spp. in animals is notifiable.

Humans

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

RESULTS

Humans

In 2019, a total of 1088 cases of cryptosporidiosis were reported corresponding to an incidence of 10.5 cases per 100 000 inhabitants. This is the highest incidence reported since 2004 when cryptosporidiosis became a notifiable disease. (Figure 8). Among reported cases the median age was 34 years (0–87 years) and 54 percent were women (n=585/1088); 771 cases were reported as domestic, 304 cases as travel-associated and for 13 cases there were no information regarding place of infection. Most of the travel-associated cases were reported from Portugal (n=36) followed by Spain (n=33) and Turkey (n=16). The incidence varies between different counties most likely depending on what type of diagnostic method is used, when patients are sampled and what analyses are requested.

In the autumn of 2019 (Oct-Dec), there was a substantial increase in the number of domestic reported cases of cryptosporidiosis and five foodborne outbreaks of *C. parvum* were identified through typing and surveys (see In Focus Box).

Up until the start of the investigation initiated by the increase of reported cases, 299 samples were analysed as part of the microbiological surveillance programme. The majority of samples, 80 percent were *C. parvum* (n=239) and 9.2 percent were *Cryptosporidium hominis* (n=22), where the most common *C. hominis* subtype was IbA10G2 (n=14). The most common *C. parvum* subtypes were IIaA16G1R1b (n=40), IIaA24G1 (n= 26) and IIaA22G1c (n=23). The latter two subtypes were also the two dominating subtypes

in the autumn of 2019 (see In Focus Box). The following species were also detected in 2019: *Cryptosporidium* chipmunk genotype I (n=12), *Cryptosporidium cuniculus* (n=3), *Cryptosporidium erinacei* (n=2), *Cryptosporidium felis* (n=1) and *Cryptosporidium* horse genotype (n=1).

In May, one patient sought care for abdominal symptoms in Jönköping county. The patient had been attending a confirmation reception where 11–12 others also were reported to have abdominal symptoms. Four samples were analysed and they were all positive for *C. parvum* subtype IIaA22G1. Through surveys, green salad was identified as the probable cause of infection. A smaller outbreak of *Cryptosporidium* chipmunk genotype I was detected at a pre-school in Stockholm in the end of September. The suspected source of infection was a culture of peas in the yard of the pre-school where red squirrels had been spotted. Three samples from cases were typed and they were all *Cryptosporidium* chipmunk genotype I, but the source of infection could not be confirmed. Attempts were made to collect environmental samples and squirrel faeces on site but none of the samples could be confirmed to originate from squirrels.

DISCUSSION

The incidence of reported human cases of cryptosporidiosis during 2019 was the highest number reported since the disease became notifiable in 2004. The large waterborne outbreaks in 2010 and 2011 caused considerably more illness than in 2019 but most of these cases were not diagnosed or reported.

The increase in incidence of human cryptosporidiosis was mainly due to several national as well as local foodborne outbreaks in the autumn of 2019 (Oct-Dec). Vegetables as vehicles for *Cryptosporidium* spp. warrants further investigation. This route of transmission is complex as it may involve animals, irrigation water, contaminated water and natural fertilizers. Not seldom are these outbreaks widespread, as the distribution of vegetables can be nationwide and require national coordination and collaboration between various agencies and regional disease prevention offices.

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

During 2019, *C. parvum* was the most common species causing human cryptosporidiosis in Sweden and *C. hominis* was the second most common cause. Human infection with *Cryptosporidium* chipmunk genotype I was the third leading cause of cryptosporidiosis both in 2018 and 2019 in Sweden.

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, and no case of alveolar echinococcosis had been reported in Sweden. As a response to the finding of *E. multilocularis* in foxes in Denmark, an active monitoring programme of red foxes (*Vulpes vulpes*) was implemented in Sweden in 2000. From 2000 to 2009, a total of 2962 red foxes, 68 raccoon dogs (*Nyctereutes procyonoides*) and 35 wolves (*Canis lupus*) were examined for *E. multilocularis*, all with negative results. Samples from the majority of foxes ($n=2675$) were examined by ELISA (CoproAntigen ELISA) at the Institute for Parasitology, Zurich University, for the presence of the *E. multilocularis* coproantigen. The remaining samples and those that were ELISA positive, were examined using the sedimentation and counting technique (SCT) ($n=726$). All samples from raccoon dogs and wolves were examined by SCT.

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

During the spring of 2011, a national surveillance programme was implemented where 2985 hunter-shot foxes were analysed with the segmental sedimentation and counting technique (SSCT). Three foxes were found positive: one in Västra Götaland, one in Södermanland and one in the

county of Dalarna. In addition, 119 faecal samples from hunting dogs collected in the region of the first positive finding were analysed with egg PCR and all were negative. In the same area 236 rodents were necropsied and all potential lesions examined by an in-house PCR without any positive finding.

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

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

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

Within the Emiro research project (finalized in 2016) and the FoMA Zoonosis monitoring programme (www.slu.se/en/environment) at the Swedish University of Agricultural Sciences (SLU), the parasite was found for the first time in intermediate hosts; voles caught in the county of Södermanland in 2013 (Gnesta/Nyköping). One out of 187 field voles (*Microtus agrestis*) and eight out of 439 water voles (*Arvicola amphibius*) had 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.; $n=285$). Within this project, a new infected area was identified in 2014 near the town Väckjö in the county of Kronoberg.

In 2012, alveolar echinococcosis was diagnosed in humans in Sweden for the first time. There were two human cases with clinical symptoms, and both were considered to have been infected abroad. No human cases were diagnosed in 2013 to 2015. In 2016 one case was reported and there were four cases in 2017.

Disease

Animals

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

Humans

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

Legislation

Animals

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

Humans

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

Surveillance

Animals

As *E. multilocularis* does not cause clinical signs in the definitive host, surveillance in these species must either be active or enhanced passive for example by collection of materials from animals submitted for other reasons. In 2019, all free-living wolves submitted to necropsy at the National Veterinary Institute were tested with MC-PCR or SSCT.

Humans

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

Results

Animals

During 2019, 22 wolves (*Canis lupus lupus*), two red foxes and one dog were tested with the MC-PCR (except one of the wolves that was tested with SSCT) and all were negative.

Humans

In 2019, there were two cases of alveolar echinococcosis reported. It cannot be ruled out that they had been infected in Sweden, but they could also have acquired the infection while travelling abroad.

Discussion

E. multilocularis occurs sporadically in Sweden. It is not known how and when the parasite was introduced into the country. The national screening finalised in 2014 can be used as a baseline estimate of the national prevalence, against which the future trend can be assessed. It is well known from other countries that the prevalence of this parasite varies geographically. Regional screenings have previously shown a prevalence of more than 1% in a part of the county of Södermanland, and within the Emiro research project and FoMA Zoonosis monitoring programme 18 of 80 (20%) fox scats were found to be positive in one of four investigated small areas. However, the true geographical distribution is unknown. 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 one of these areas shows that the parasite is still present in this location. Since it is now more than five years since the last national screening it is time for a follow-up investigation to assess the present prevalence in foxes.

E. multilocularis was found for the first time in an intermediate host 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 was suggested that the absence of *Microtus arvalis* in Sweden may be a contributing factor to the low prevalence of the parasite. However, in small restricted areas, prevalence has been reported to be higher and more research is needed to clarify which intermediate host(s) are most important.

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

CYSTIC ECHINOCOCCOSIS

Background

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

History

Echinococcosis was quite common in reindeer in the northern parts of Scandinavia in the first half of the 20th century. In the 1990's, single cases of *E. granulosus* s.l. were detected in moose and reindeer in Sweden.

Disease

Animals

In animals, the infection is usually asymptomatic.

Humans

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

Legislation

Animals

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

Humans

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

Surveillance

Animals

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

Humans

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

Results

Animals

E. granulosus s.l. was not detected in any animal in 2019.

Humans

In 2019, 17 cases of cystic echinococcosis were reported. Annually around 15–30 cases are reported in Sweden. In 2019, the reported cases ranged in age from 6 to 65 years

(median 40 years). Six cases were women and 11 were men. They were all considered to have been infected abroad in areas where the parasite is endemic. The most frequently specified countries of infection were Syria (6 cases) and Iraq (5 cases).

Discussion

E. granulosus s.l. has not been detected in animals in Sweden since the late 1990s, when it was reported in two reindeer in the northernmost regions of Sweden, bordering to Norway and Finland. In Finland, the parasite is present at a low prevalence in wildlife (wolves, moose and reindeer) and has been genotyped as *E. canadensis*. This species is considered as less pathogenic, and possibly with a lower zoonotic potential, than *E. granulosus* sensu stricto that is prevalent in other parts of Europe and identified mainly in a cycle between dogs and farm animals.

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

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 was declared officially free from EBL by the European Union (EU) in January 2001 (former Decision 2001/28/EC, currently Decision 2003/467/EC last amended by Decision 2005/764/EC). Before this, a voluntary control programme had started in 1990 and a mandatory eradication programme had been running since the autumn of 1995.

DISEASE

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

LEGISLATION

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

SURVEILLANCE

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

From 2010 onwards, surveillance in dairy herds has been performed by random sampling. The between-herd design prevalence is 0.2% and the within-herd design prevalence 15%, with a 99% confidence, given known freedom of infection the previous year. To achieve this, approximately 1500 herds need to be randomly sampled per year. Bulk milk samples are collected within the quality control programmes of

the dairies. The surveillance in beef herds is performed with an aim to randomly sample 1–3 animals per herd in 2000 herds every year. Serum is collected from slaughtered cattle above 2 years of age originating from sampled herds. Details on numbers of herds and animals tested in 2019 are given in Table 9.

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

RESULTS

Six bulk milk samples were tested antibody positive in 2019. After investigation and field sampling the conclusion was that these were false positive results.

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.

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

Växa Sverige, Statistics for 2019.

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

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

Table 9: Total numbers of herds and animals tested for BLV antibodies in 2019.

Herd type (sample type)	Herds	Animals
Dairy herds (one bulk milk sample per herd)	2367	-
Beef herds (blood from 1–3 animals per herd)	2099	6131
Beef herds with at least three animals tested	708	-
Beef herds with two tested animals	947	-
Beef herds with one tested animal	444	-

Footrot



Footrot is one of the major causes of lameness in sheep. Photo: Bengt Ekberg/SVA.

BACKGROUND

Footrot is a globally distributed contagious disease in sheep and goats. The causative agent is *Dichelobacter nodosus* (*D. nodosus*). The disease is characterised by interdigital dermatitis, and 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 study on the prevalence in slaughter lambs was performed in 2009 and a voluntary control programme for footrot (“Klövkontrollen”) was established by Farm & Animal Health in 2009. Within the programme, the definition of footrot is when virulent strains of *D. nodosus* are detected with or without clinical lesions or when benign strains are detected together with clinical lesions.

DISEASE

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

LEGISLATION

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

SURVEILLANCE

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

Flocks in which no clinical signs of footrot or virulent strains of *D. nodosus* are detected in any of the adult sheep are certified as free (F-status). If signs of footrot (virulent strains with or without clinical lesions or benign strains with clinical lesions) are detected, measures to eliminate footrot are undertaken, including: foot baths, 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.

368 (out of a total of 8 500) sheep flocks are affiliated to the control programme. Almost all pedigree flocks in Sweden are affiliated to the programme.

RESULTS

In 2019, footrot was confirmed in four new flocks; two within the control programme and two outside the programme (Figure 10). In 2 of the 4 flocks, virulent strains of *D. nodosus* were detected. In the programme, 366 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.

DISCUSSION

The control programme demands quarantine before new animals can enter the herd, and hence the awareness of biosecurity and disease control in general has been enhanced in the sheep farming community. Since most pedigree flocks are affiliated, the impact of the programme is significant although they represent a minority of sheep flocks in Sweden. Their 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 in the future to limit mandatory notification to virulent strains of footrot.

REFERENCES

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, Slette-meås 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

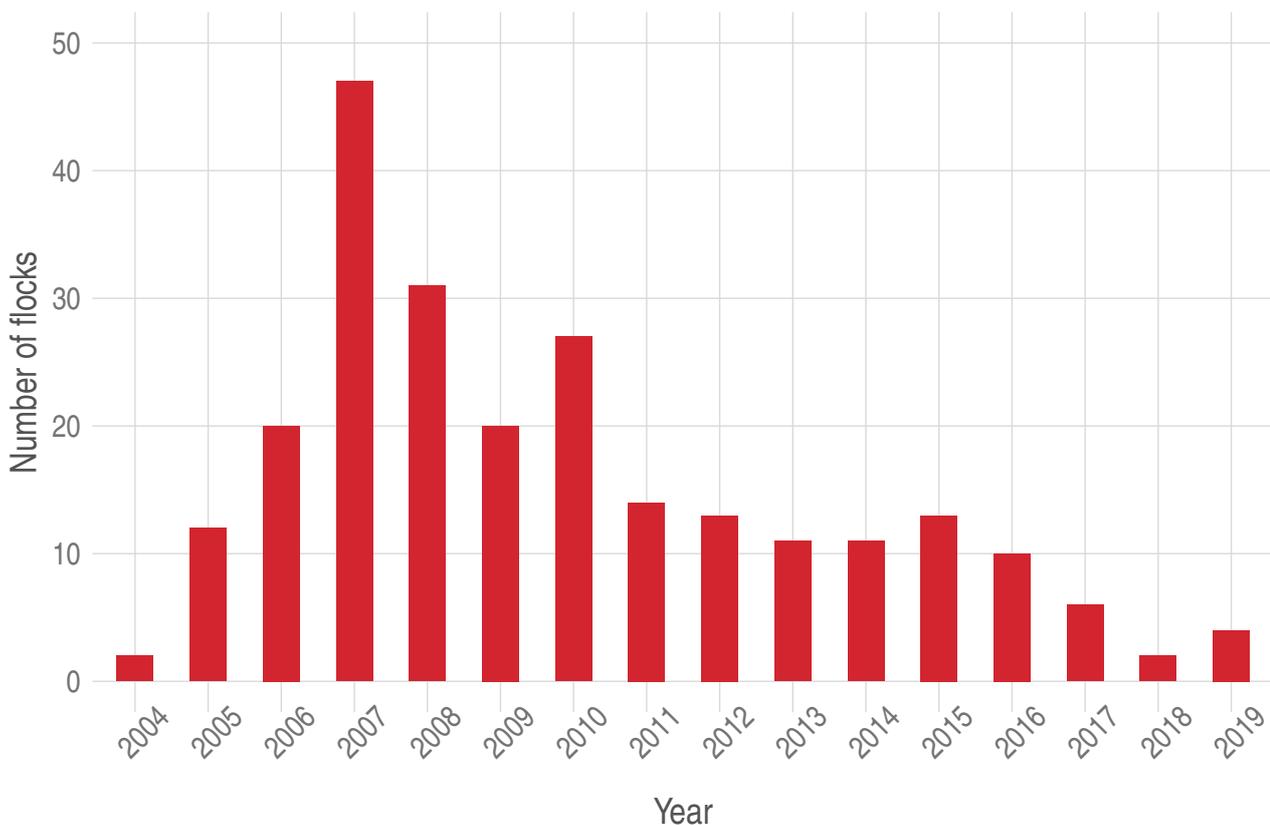


Figure 10: Number of sheep flocks detected with footrot within the programme, 2004–2019.

Infectious bovine rhinotracheitis

BACKGROUND

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

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

DISEASE

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

LEGISLATION

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

SURVEILLANCE

All diagnostic testing was performed at the National Veterinary Institute. Milk and sera were analysed for the presence of antibodies using a blocking-ELISA (IBR/BHV-1 gB Ab ELISA kit, IDEXX) and a virus neutralisation test (in accordance with the OIE manual) was used for confirmatory testing. Semen and organ samples were tested with a real-time PCR (Wang et al., 2007). A positive case is defined as an animal with a positive PCR result or a confirmed positive serological reaction for IBR.

Passive surveillance

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

Active surveillance

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

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

RESULTS

Within the active surveillance, 3729 bulk milk samples and 7049 serum samples from beef cattle were examined. In addition, 228 cattle, 9 alpaca, 1 llama, 2 water buffalo and 1 camel were tested as part of health schemes or prior to export. All samples were negative.

One herd was investigated due to clinical suspicion of IBR, with negative results.

DISCUSSION

In summary, no herd or individual animal was diagnosed with IBR infection during 2019. 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

BACKGROUND

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

Influenza type A is a viral disease affecting both birds and mammals, including humans. The causative agent is an RNA virus with a marked ability to change over time. New strains are created both through accumulation of point mutations (antigenic drift) and through genetic reassortment (antigenic shift). Influenza type A viruses are classified into different subtypes based on the surface glycoproteins: haemagglutinin (H) and neuraminidase (N). Currently, there are 18 haemagglutinin (H1-H18) and eleven known neuraminidase (N1-N11) subtypes.

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

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

AVIAN INFLUENZA

Background

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

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

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

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

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

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

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

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

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

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

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

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

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

^B Small-scale production.

Disease

Animals

The case fatality rate in birds infected with HPAIV may be as high as 100%, but this depends on the species affected, co-infections, virulence of the virus and other factors. In general, gallinaceous birds, including turkeys and chickens, suffer a more severe disease than waterfowl such as ducks and geese, which may exhibit only minor or no clinical disease. LPAIV infections most often cause asymptomatic infections or mild respiratory disease. HPAIV infections cause variable clinical signs such as cyanosis, respiratory distress, diarrhoea, nervous signs, depression, decreased food and water intake and decreased egg production with altered egg quality. Sometimes the only clinical sign is the sudden death of a large numbers of birds.

Humans

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

Legislation

Animals

HPAI of all subtypes, as well as LPAI of H5 and H7 subtypes, are included in the Swedish Act of Epizootic diseases (SFS 1999:657 with amendments) and cases are notifiable upon suspicion. If AI is suspected or confirmed on a farm, measures will be taken to combat the disease and to prevent further spread according to Council Directive 2005/94/EC.

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

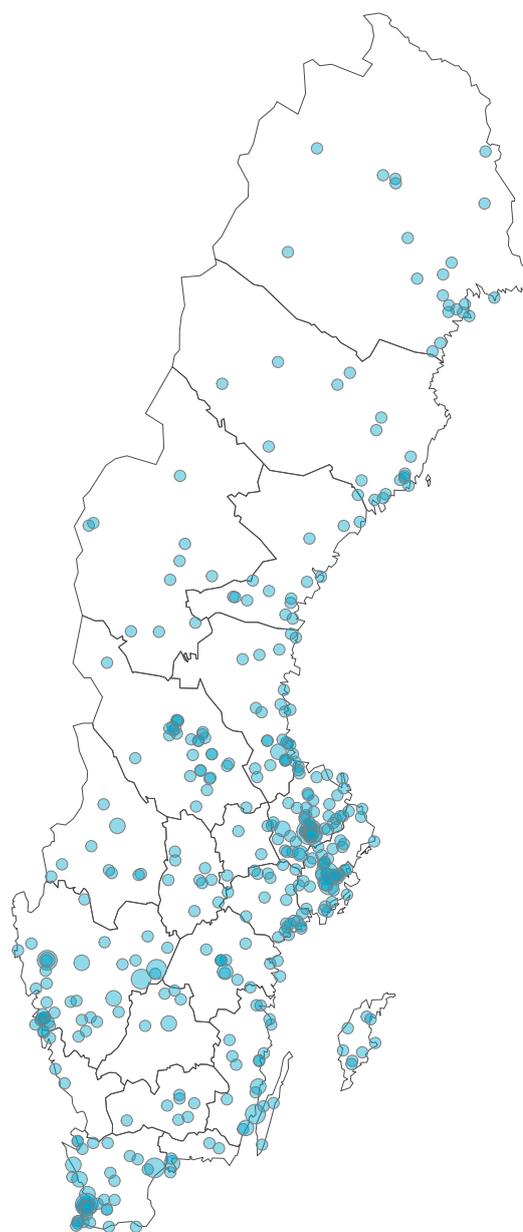


Figure 11: Geographical location of the wild birds analysed for avian influenza in 2019. Point sizes are scaled by the number of birds sampled at a given location. All 456 wild birds sampled in 2019 were found negative for avian influenza. ©EuroGeographics for the administrative boundaries.

Humans

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

Surveillance

Surveillance programmes have been carried out annually in all EU member states since 2002 to monitor the AIV situation in poultry and wild birds, with a focus on early detection/early warning of in particular the subtypes H5 and H7.

Poultry

The surveillance programme in poultry for 2019 included kept game birds (mallard ducks and pheasants), layers, breeders, small-scale broiler production, turkeys, geese, ducks and ratites. Ten blood samples from each holding were collected except for holdings with geese, ducks or mallards where 20 samples from each flock were collected. In flocks with fewer individuals than the abovementioned sample size, all individuals were sampled. In addition to the surveillance programme, samples were taken on clinical suspicion. On clinical suspicion of AI or Newcastle disease, laboratory analyses for both diseases are generally performed.

The surveillance programme for 2019 was based on representative sampling and the serological analyses were performed at the National Veterinary Institute. All poultry samples were collected at slaughter, except breeders and game birds. Blood samples from these categories of birds were collected at their holdings. Breeders were sampled late in their production period. Samples were analysed using an ELISA (IDEXX Influenza A Ab Test). Positive results were confirmed with haemagglutination inhibition tests (for subtypes H5, H7 and H5N8) in accordance with the OIE guidelines.

Wild birds

Autumn migrations of wild birds have been implicated in the incursion of HPAIV into Europe in 2005, 2014, 2016 and in December 2019. Wild birds play a key role in the long-distance spread, introduction into new areas or countries and further local amplification and spread of HPAIV.

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

Humans

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

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

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

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

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

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

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

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

Results

Poultry

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

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

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

Wild birds

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

Humans

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

Discussion

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

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

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

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

SWINE INFLUENZA

Background

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

Animals

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

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

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

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

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

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

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

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

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

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

Humans

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

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

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

Legislation

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

Surveillance

Animals

Enhanced passive surveillance

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

Active surveillance

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

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

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

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

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

No active surveillance was performed in 2019.

Humans

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

Results

Animals

Passive surveillance

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

Active surveillance

No active surveillance was performed in 2019.

Humans

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

Discussion

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

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

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

REFERENCES

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. Bélaç 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.

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. Ictero-haemorrhagiae*, *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

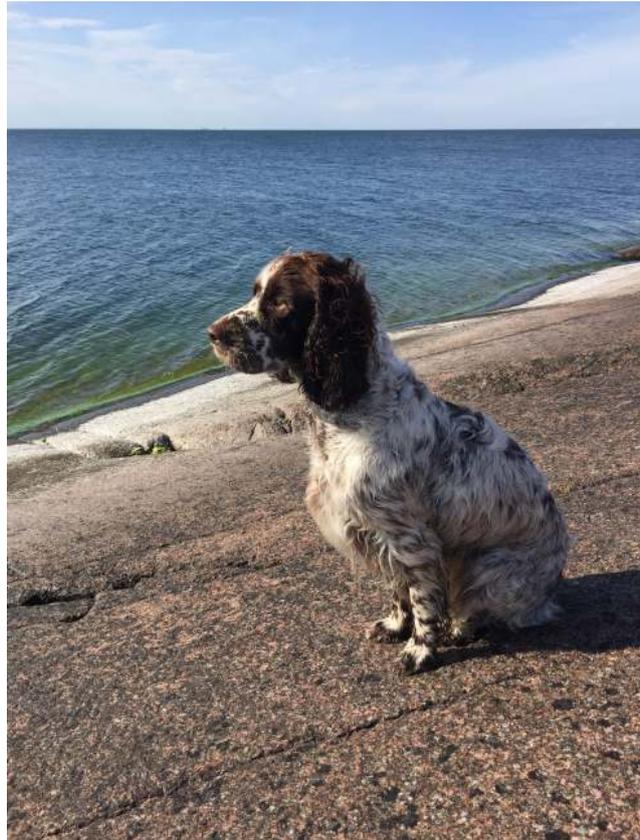
Animals

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

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

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

The clinical presentations in dogs infected with *Leptospira* range from subclinical to severe clinical illness and death; liver and/or kidney affection as well as varying degrees of vasculitis is typical. A peracute pulmonary form



Several *Leptospira* serovars known to be pathogenic for humans as well as other animal species have been shown to be present in both healthy and severely ill Swedish dogs. Seropositivity is however currently underreported and prevalence of clinical disease and death in Swedish dogs due to leptospiral infection is currently not readily available. Photo: Mia Holmberg.

with high mortality rate is not uncommon.

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

Humans

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

LEGISLATION

Animals

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

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

Humans

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

SURVEILLANCE

Animals

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

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

The surveillance in cattle is based on serum and bulk milk samples selected by systematic random sampling from the surveillance programme for bovine viral diarrhoea virus (BVDV) and evenly distributed throughout the sampling period. See chapter on BVDV 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 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. For 2019, the calculated number of samples required for the active surveillance of *L. Hardjo* in cattle was 450 bulk milk samples and 1100 serum samples and for *L. Pomona* in pigs 405 serum samples.

Passive surveillance in animals including dogs and horses consists of mandatory reporting of positive results from onsite tests detecting antibodies used at veterinary clinics, PCR-positive samples, and seropositivity confirmed at laboratories, including titers as low as 1:100 regardless of serovar. Furthermore, all positive results are reported regardless of whether clinical suspicion of disease is present or if previous vaccination might be the cause of the detected antibodies. Serum samples submitted to the National

Veterinary Institute for MAT-testing are currently tested for *L. Icterohaemorrhagiae*, *L. Canicola*, *L. Grippotyphosa*, *L. Bratislava*, *L. Saxkoebing*, *L. Sejroe*, *L. Autumnalis* and sometimes *L. Australis*.

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

During 2019, 1089 serum samples and 471 bulk milk samples were analysed in cattle and 390 serum samples in pigs. All cattle samples were negative for *L. Hardjo* antibodies and all pig samples were negative for antibodies to *L. Pomona*. With these results it is concluded that the active surveillance in cattle and pigs in 2019 fulfilled the purpose to demonstrate freedom from disease at the specified level.

In dogs, thirty leptospira-positive laboratory analyses were reported of which twenty (60%) from the National Veterinary Institute. The National Veterinary Institute reported thirteen seropositive and seven PCR positive analyses. Methods used in the remaining 26% of reported results, including whether a validated test-method was used or not, is unknown. The reasons for samples being submitted to the National Veterinary institute include clinical suspicion of acute disease as well as sampling of clinically healthy dogs and horses due to export requirements or suspected leptospirosis in other animals in the household.

Furthermore, a serologically positive sample was reported from one cat and one pig, respectively. The pig was sampled as part of an investigation of reproductive failure and had a positive serological reaction to *L. Icterohaemorrhagiae*. After further investigation in the herd including paired serological samples with no increase in titers to *L. Icterohaemorrhagiae* it could be concluded that the reproductive failure was not caused by infection with *Leptospira*.

One seropositive horse was reported during 2019, which equals the average yearly number of reported cases since 2014: one horse yearly.

Humans

In 2019, seven cases of leptospirosis were reported. The median age was 34 (range 23–49 years) and five of the cases were male. Two of the cases were reported to have acquired their infections in Sweden. Five cases were noted as infected abroad, three in Asia one in Central America and one in Africa. One of the cases of domestic leptospirosis was identified during the summer 2019. The case had been bitten by a rat two weeks before symptom onset and suffered from kidney failure and jaundice and was admitted to hospital. Serum samples were analysed with one week between sampling dates. The first sample was positive in PCR but negative in ELISA. The second sample was positive in ELISA

but negative in PCR illustrating the development of the disease. The case was diagnosed with Weil's disease, the severe form of leptospirosis, and was treated with relevant antibiotics and was fully recovered. The incident is regarded as a very rare event in Sweden.

DISCUSSION

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

The commercial cattle and pig populations in Sweden are considered free from *L. Hardjo* and *L. Pomona* based on only negative results from the surveillance system since 1994. Seropositivity to *Leptospira* spp other than *L. Pomona* are occasionally confirmed in Swedish pigs, mostly to an indigenous serovar of *L. Sejroe*, *L. Bratislava* and *L. Icterohaemorrhagiae*. An even lower prevalence to the indigenous strain of *L. Sejroe* in cattle has been recorded. Since 2006, the surveillance programme in cattle and pigs is no longer performed on a yearly basis as the probability of introduction is very low and the serological screening of *Leptospira* is considered of less importance compared to screening programmes of other contagious animal diseases.

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

Currently, all positive MAT results in dogs are reported without knowledge of vaccination status, travel history and whether clinical disease is suspected or not. Furthermore, in clinical cases paired samples (sometimes three samples) are needed for diagnosis as the immune response providing specific antibodies to the causing serovar often is delayed. A negative result is common during the acute phase of illness, as is cross reactions leaving the causative serovar unidentified.

As all laboratory diagnostics must be paid for by the dog owner there is a lack of such paired samples. In addition, not all dogs survive the infection and autopsies are rare due to the cost to the owner as well as the emotional aspect. Furthermore, the number of samples sent to laboratories abroad, and to what extent possible positive results are being reported or not by the referring veterinarians, is currently unknown. In 2018 and 2019, the number of samples sent to SVA for PCR analyses instead of MAT analyses increased. In 2019 only a quarter of all samples sent to SVA for *Leptospira*-analyses were for serologic examination. This is reflected in a lowered number of reported positive serological results. PCR is expected to be negative in the majority of cases, including dogs with severe clinical illness.

Furthermore, an onsite ELISA test not distinguishing between different serovars is now available and in use in several

small-animal hospitals and clinics. The number of reported seropositive results from use of such tests during 2019 is one, or at the most six dogs (only one report specifies onsite test as the method used). The number of positive onsite test results retrospectively mentioned during phone calls to the National Veterinary Institute from clinically active small-animal veterinarians far exceeds that number, indicating that underreporting is common. Reliable data on how common underreporting is however lacking.

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

A limited collaborative study (Swedish university of Agricultural Sciences and National Veterinary institute) seroprevalence study is ongoing with so far 300 canine serum samples collected during autumn 2019. Further studies are however warranted, as the number of suspected or confirmed clinical cases is rising, indicating an increase in exposure- but confirmatory data is lacking. There is currently no available system to aid in reporting and evaluating suspicion of Leptospiral infection as the true cause of disease in clinical cases. Information on presence or absence of clinical disease or results from any confirmatory laboratory investigations carried out is currently not included in the data reported.

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

Few cases of human infections are reported each year and the majority are travel-associated. The primary diagnostics of human cases is mainly based on serology. However, with increasing awareness of molecular based techniques for diagnosis could probably lead to an increase in incidence.

REFERENCES

- Lindah 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
- 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 is often found as an environmental contaminant in food producing establishments. However, it is only *L. monocytogenes* that is relevant regarding human health. The main sources of human listeriosis are contaminated food products, such as cold-smoked or gravad vacuum-packaged fish products, meat products and soft cheeses or other ready-to-eat foods with a long shelf-life. *L. monocytogenes* is destroyed by heating (pasteurisation or cooking).

The main sources of listeriosis for animals are feed or environment. To prevent listeriosis in ruminants it is essential to feed animals with a silage of good quality (low pH and without contamination with soil) as the less acidic pH enhances multiplication of *L. monocytogenes*.

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

DISEASE

Animals

L. monocytogenes can infect a wide range of animal species, both domestic and wild. Animals may be asymptomatic carriers and shed the organism but especially sheep may develop clinical disease, such as encephalitis, abortions, mastitis or septicaemia.

Humans

Listeriosis can be manifested either as a milder noninvasive 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.



Over the last ten years, Swedish outbreaks of listeriosis have been associated with vacuum-packaged fish, unpasteurised cheese, cold cuts, frozen corn and convenience meals. Photo: Amarita/Shutterstock.

LEGISLATION

Animals

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

Food

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

Humans

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

SURVEILLANCE

Animals

Surveillance in animals is passive. Suspicions on listeriosis can be raised on clinical signs and/or laboratory analyses. The diagnosis is based on histological findings at post-mortem or by detection of the organism by cultivation methods using enrichment in selective broth followed by culture on selective and non-selective agar or by direct plating. Identification is made by mass spectrometry (MALDI-TOF). The Swedish Board of Agriculture can decide on epidemiological investigations if needed.

Food

No official control programme exists for *L. monocytogenes*. National and local authorities may perform sampling as part of extended official controls or targeted projects. Producers

of ready-to-eat foods are obliged to take samples for analysis of *L. monocytogenes* as part of their self-controls, but the results are not normally reported to the authorities.

Humans

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

RESULTS

Animals

In 2019, listeriosis was reported in 10 sheep, three cattle, one goat, one horse and in one wild and one domesticated bird.

Food

In 2019, 295 samples from different types of food were sampled by national and local authorities and analysed for presence of *L. monocytogenes* in qualitative analysis (i.e. presence or no presence). *L. monocytogenes* was detected in eight samples (Table 13). In addition, 20 samples were analysed in quantitative analysis (i.e. number of colony forming units per gram) only. The levels of *L. monocytogenes* in these samples were <10 cfu/g.

Humans

During 2019 the incidence of listeriosis increased slightly compared to 2018 and the overall picture shows an increasing trend of cases of listeriosis in Sweden (Figure 12). In total, 113 cases were reported compared to 89 cases in 2018 (incidence 1.1 cases per 100 000 inhabitants). (Figure 12). The majority of the cases reported with listeriosis belong to the older age groups. The median age was 75 years and as in previous years, most cases were reported in the age group over 80 years (Figure 13). Sixty-four cases were females and 49 were males. In total, 20 cases (18 percent of reported cases) died within one month from diagnosis. Listeriosis is most often a domestic infection and for 96 percent of the reported cases in 2019 Sweden was noted as the country of infection. In 2019 all but five (96 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=73), IVb (n=18) and IIb (n=16) while only one case of IIc was reported. In addition to serotypes, sequence types (ST) are also identified by WGS. Different STs can belong to the same serotype and during 2019 the most common STs were ST-8 and ST-451 both belonging to serotype IIa. A more in-depth cluster analysis showed that 48 percent of the isolates belonged to a cluster with one or more other isolates from 2019 or previous years. In total, 17

different clusters were identified and the largest contained isolates from 22 cases. The analysis also identified genetically almost identical isolates over a time period of up to ten years, indicating that such strains may be established in production facilities and occasionally contaminate food products causing illness in patients during long time periods.

Investigations of outbreaks and single cases of listeriosis

In total, eight investigations involving a national cross-sectoral approach were conducted in 2019. Two of these were international investigations and six were national. The majority of the investigations pointed towards linkage with historical isolates of *L. monocytogenes*, indicating that the outbreak strains persist in food processing establishments.

One Swedish case was connected to a Norwegian outbreak with rakfisk, a fermented fish product. The results of microbiological analyses of samples of the product showed that levels of *L. monocytogenes* were exceptionally high. The fish to be fermented in Norway was produced in Sweden. The outbreak strain, ST-20, was also found at the Swedish establishment.

A prolonged multi-country outbreak of 22 listeriosis cases in five countries was identified in an international investigation led by the European Centre for Disease Prevention and Control (ECDC) and the European Food Safety Authority (EFSA). The outbreak was caused by a newly identified type of *L. monocytogenes* within clonal complex (CC) 8, named ST-1247. Sweden had in total four historical cases from 2015–2016 linked to this strain. The probable source of infection was cold-smoked or gravad fish from a production establishment in Estonia.

A rare strain of *L. monocytogenes* in Sweden, a ST-91, caused one case of listeriosis. A sample of an unpasteurised French cheese, Brie de Meaux, was collected from the freezer of the case and was found positive for the outbreak strain in microbiological analysis. This led to a notification from Sweden in the Rapid Alert System for Food and Feed (RASFF) and an alert in the Epidemic Intelligence Information System (EPIS). However, no other cases with this strain had been observed in any other country.

Table 13: Results of analyses for presence of *L. monocytogenes* in food samples taken by authorities in 2019.

Reason for sampling	No. of samples	No. of positive samples	Food in which <i>L. monocytogenes</i> was detected
Survey	16	0	-
A routine control or verification sample	21	1	1 fish product
Investigation of a complaint or a suspected food poisoning	33	2	1 minced meat, 1 cow milk cheese
Unknown	225	5	5 cold-smoked fish
Total	295	8	

DISCUSSION

During 2019 the incidence of listeriosis increased compared to the year before and the overall picture shows an increasing trend of listeriosis. (Figure 12). 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. One of the international outbreaks from 2019 where cold-smoked fish produced in Estonia was implicated, is an example of such collaboration where WGS is the tool that connects countries having the same outbreak strain.

In 2019 as in previous years, typing using WGS indicated that many of the linked cases were geographically dispersed and that the sources of infection had persisted for many years. Continued surveillance of *L. monocytogenes* in humans and in food and food processing environments is essential for understanding the sources for human infection and providing tools for prevention. For identification of possible links between human cases and food products, subtyping of isolates is essential.

REFERENCES

- Carrique-Mas J, Hökeberg I, Andersson Y, Arneborn M, Tham W, Danielsson-Tham ML, Osterman B, Leffler M, Steen M, Eriksson E, Hedin G, Giesecke J (2003) Febrile gastroenteritis after eating on-farm manufactured fresh cheese - an outbreak of listeriosis? *Epidemiol Infect* 130:79–86
- 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.
- European Centre for Disease Prevention and Control and European Food Safety Authority. Multi-country outbreak of *Listeria monocytogenes* clonal complex 8 infections linked to consumption of cold-smoked fish products – 4 June 2019. Stockholm and Parma: ECDC/EFSA; 2019.
- Lopez-Valladares G, Tham W, Parihar VS, Helmersson S, Andersson B, Ivarsson S, Johansson C, Ringberg H, Tjernberg I, Henriques-Normark B, Danielsson-Tham ML (2014) Human isolates of *Listeria monocytogenes* in Sweden during half a century (1958–2010). *Epidemiol Infect* 142:2251–60
- Thisted Lambertz S, Ivarsson S, Lopez-Valladares G, Sidstedt M, Lindqvist R (2010) Subtyping of *Listeria monocytogenes* isolates recovered from retail ready-to-eat foods, processing plants and listeriosis patients in Sweden 2010. *Int J Food Microbiol* 166:186–92
- Thisted Lambertz S, Nilsson C, Brådenmark A, Sylvén S, Johansson A, Jansson L-M, Lindblad M (2012) Prevalence and level of *Listeria monocytogenes* in ready-to-eat foods in Sweden 2010. *Int J Food Microbiol* 160:24–31

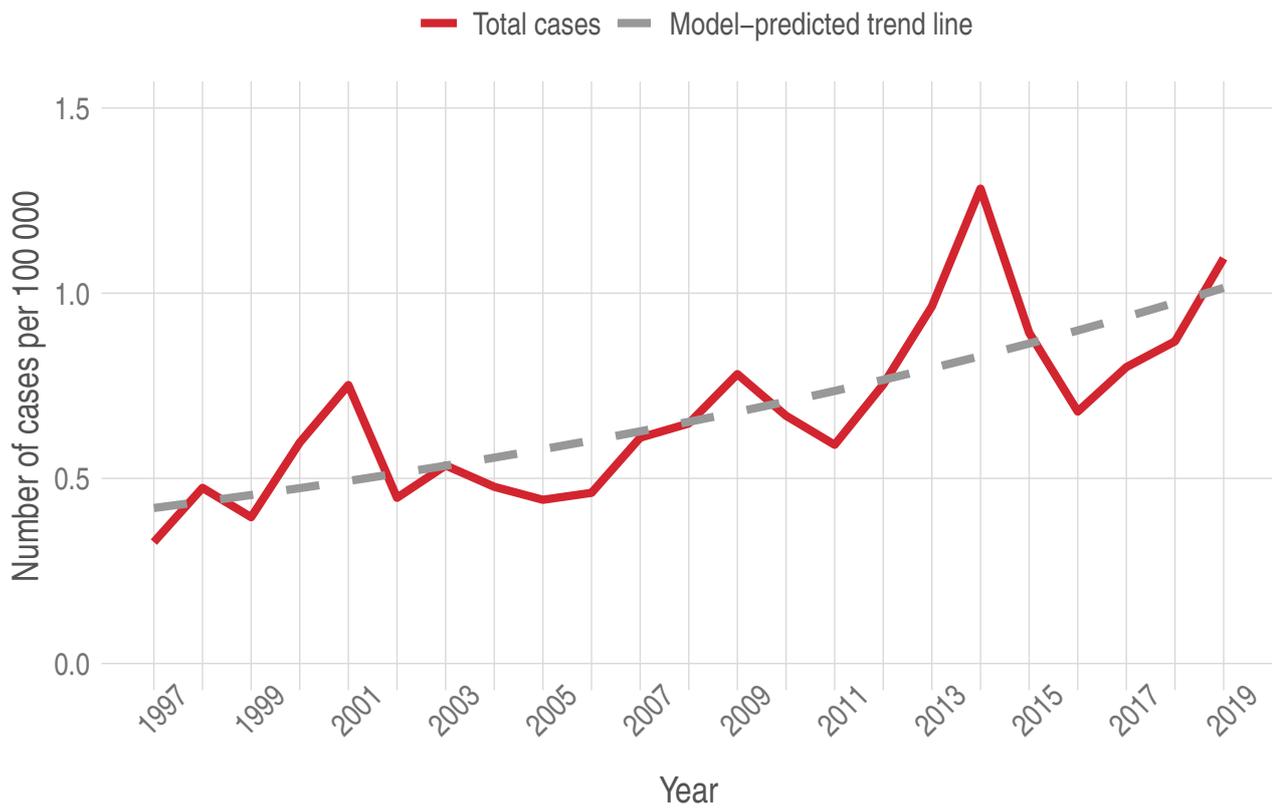


Figure 12: Notified incidence per 100 000 inhabitants of human cases of listeriosis in Sweden 1997–2019 and a model-predicted trend.

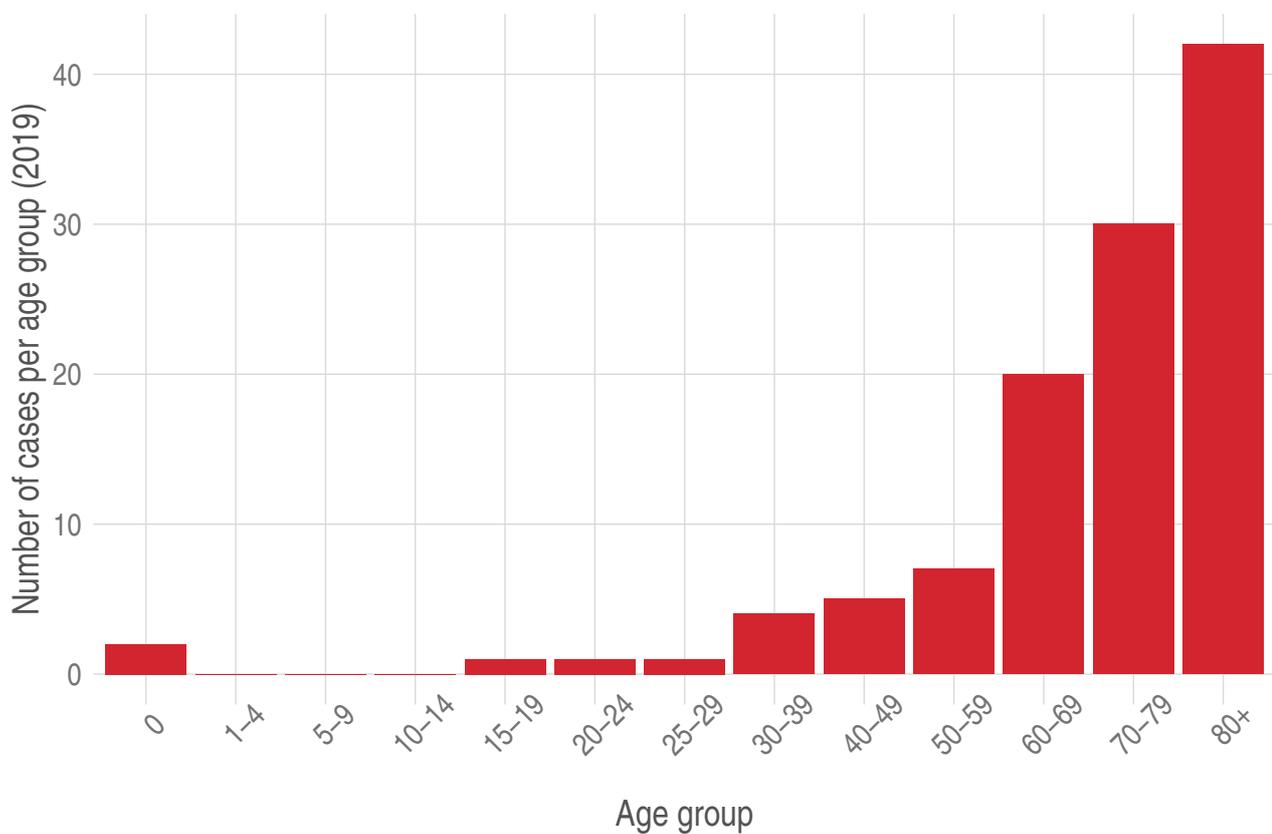


Figure 13: Number of notified human cases of listeriosis per age group in 2019.

Nephropathia epidemica



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

BACKGROUND

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

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

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

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

DISEASE

Animals

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

Humans

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

LEGISLATION

Animals

Hantaviruses are not notifiable in animals.

Humans

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

SURVEILLANCE

Animals

There is no surveillance in animals.

Humans

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

RESULTS

Humans

In 2019, 155 cases of NE were reported, which was a decrease in comparison to the previous year (Figure 14). The median age among all cases was 57 and most reported cases were males in the age category 25 years and older. There were very few cases below the age of 25 years reported, both among men and women. Consistent with previous years, more cases were reported in men (63%) 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 2019, there was only one case who had been infected in Finland as well as fifteen cases with unknown country of infection.

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 County of Norrbotten (24 cases per 100 000 inhabitants) followed by the County of Västerbotten (18 cases per 100 000 inhabitants). All cases reported from the southern parts of Sweden 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.

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

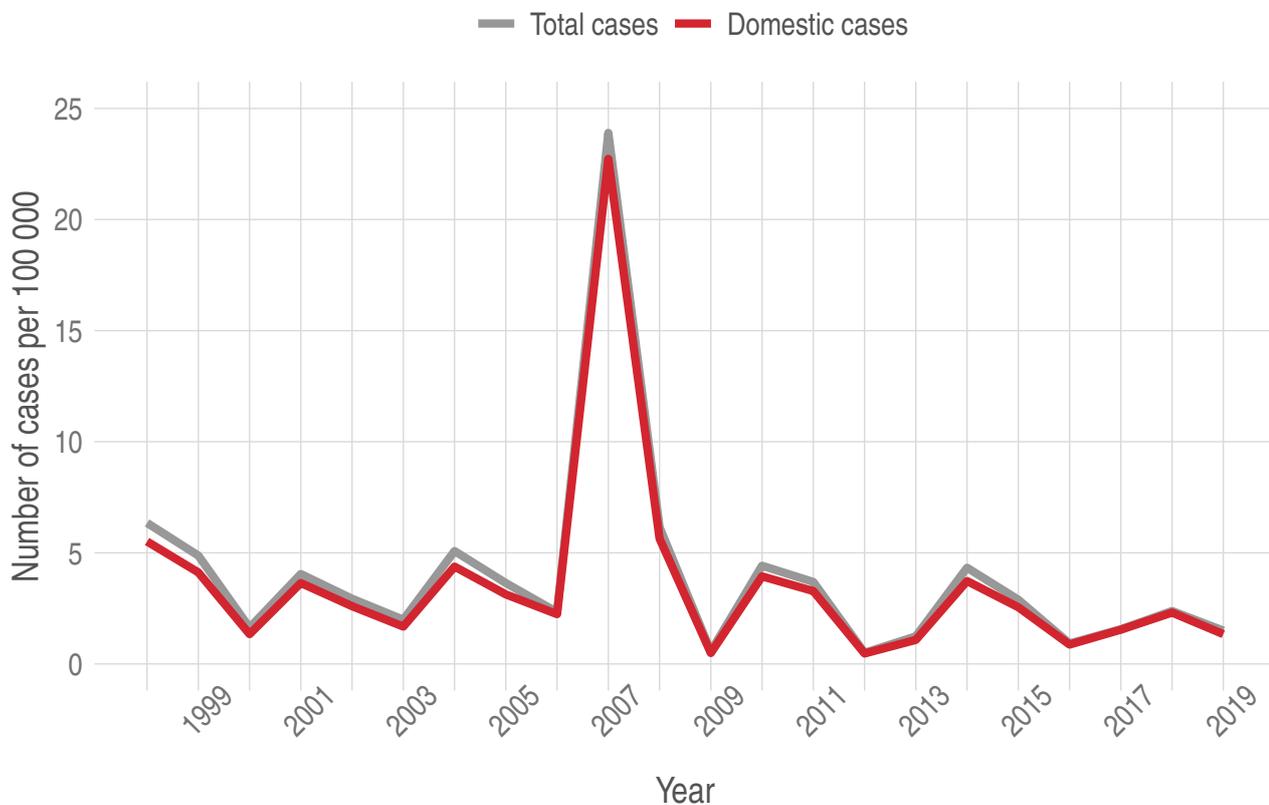


Figure 14: Notified incidence per 100 000 inhabitants of human Nephropathia epidemica in Sweden 1998–2019.

Paratuberculosis

BACKGROUND

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

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

In a study by Frössling and co-workers (2013), the probability of freedom and sensitivity of the surveillance system for MAP was estimated. Results showed that, at the end of 2008, there was a high probability that the Swedish cattle population was free from or had a very low prevalence of MAP.

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.
- Since 2004 all ruminants above one year of age, submitted for postmortem, are sampled and cultured for MAP. Sampled animals also include exotic ruminants like bison and camelids.
- Screening of sheep herds during the years 1993–2011, first with serology, then with faecal culture. The screening of sheep was discontinued in 2012.
- 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, a campaign to raise the awareness of the disease among farmers and veterinarians was initiated to improve the passive surveillance. Bovine practitioners were encouraged to look for and sample cows with low bodyweight, with or without diarrhoea. The 258 samples were analysed by faecal PCR.

DISEASE

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

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

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

LEGISLATION

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

SURVEILLANCE

The overall purpose of the surveillance and the voluntary control programme in beef herds is to document freedom from bovine paratuberculosis and to prevent possible spread by early detection of the infection.

Passive surveillance

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

Post mortem examinations

Sampling is performed on all ruminants above one year of age submitted for post mortem examinations as part of the enhanced passive surveillance for MAP. Samples are taken from the ileal wall, ileal contents and ileocaecal lymph nodes and submitted to the National Veterinary Institute.



Paratuberculosis has never been detected in dairy cattle in Sweden. Photo: Rattthaphong Ekariyasap/Shutterstock.

Active surveillance

Control programme for surveillance in beef cattle

In the voluntary control 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 2019, the voluntary control programme for bovine paratuberculosis encompassed 445 herds, of which 428 are of the highest status. The control programme includes all main beef breeding herds and a smaller number of dairy herds selling calves to beef herds within the programme.

In affiliated herds, individual faecal samples are collected annually for three consecutive years from all cattle over two years of age. Affiliated herds are only allowed to trade with herds of the same status or higher to maintain their level within the programme. After three years of negative test results, the faecal sampling is replaced by postmortem of all deceased or euthanised cattle on the premises where paratuberculosis cannot be excluded as a cause of culling.

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

Cultures are pre-treated with HPC and double incubation. Samples are subsequently cultured on modified Löwenstein-Jensen medium supplemented with mycobactin and on Herrolds Egg Yolk medium for up to 4 months. Faecal samples

from sheep are cultured for up to 6 months on modified L-J with mycobactin. Direct PCR on a new preparation from the stored samples are performed on cultures with mould overgrowth.

Samples collected from clinical suspicions and individual faecal samples from the voluntary beef herd control programme are analysed with direct PCR.

All tests for detection of MAP bacteria are performed at the National Veterinary Institute.

Blood samples are analysed with absorbed ELISA at the Technical University of Denmark.

RESULTS

In 2019, three suspicions of paratuberculosis in cows were raised due to clinical signs of the disease, and one suspicion in an alpaca (*Vicugna pacos*) was raised due to pathological changes detected at post mortem examination. All cases tested negative for MAP with PCR and the suspicions were ruled out.

Moreover, 1235 cattle from 31 herds, 136 sheep from 5 herds, and 6 water buffalo (*Bubalus arnee*) from 1 herd were sampled within the control programme in beef herds. In all, 375 of the cattle samples and 24 of the sheep samples were pooled three and three for analysis at the lab. The remaining samples were analysed individually. For export and health control reasons a total of 192 animals were tested: 186 by serology, all cattle, and 6 by faecal PCR (5 cattle and 1 moose (*Alces alces*)). Two hundred and twenty-eight animals were sampled at post mortem examination; 172 cattle, 50 sheep, 1 goat, 2 bison (*Bison bison*), 1 wisent (*Bison*

bonanus), 1 alpaca and 1 reindeer (*Rangifer tarandus tarandus*). No cases of MAP were detected in the examinations completed in 2019 (Tables 14, 15 and 16).

DISCUSSION

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

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

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

A recent update of the evaluation of the paratuberculosis surveillance programme indicates that the surveillance sensitivity in the last years has decreased. Work is now ongoing to evaluate the possibility of utilising bulk milk samples and slaughterhouse serum samples to increase the surveillance in the dairy cattle population and beef cattle herds not affiliated to the control programme, to improve the surveillance sensitivity.

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 diariernr 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.

Table 14: Cattle sampled in 2019.

Surveillance in cattle	No. of sampled animals	No. of herds
Beef herd surveillance programme ^A	1241	32
Cattle sampled at post mortem examinations	172	154
Cattle sampled for export	191	1

^A Including 6 water buffalo from one herd.

Table 15: Sheep and goats sampled in 2019.

Surveillance in sheep and goats	No. of sampled animals	No. of herds
Sheep sampled in cattle herds within the beef herd surveillance programme	136	5
Sheep sampled at post mortem examinations	50	45
Goats sampled at post mortem examinations	1	1

Table 16: Exotic ruminants sampled in 2019.

Surveillance in exotic ruminants	No. of sampled animals	No. of herds
Exotic and wild kept ruminants sampled at post mortem examination ^A	5	4
Exotic and wild kept ruminants sampled for export ^B	1	1

^A 2 bison, 1 wisent, 1 alpaca, 1 reindeer.

^B 1 moose.

Porcine reproductive and respiratory syndrome

BACKGROUND

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

Sweden has had an active PRRSV surveillance programme since 1998, with Farm & Animal Health collecting samples that are analysed by the National Veterinary Institute. In July 2007, the first case of PRRS in Sweden was detected through this active surveillance programme. Until then, Sweden had been one of only a few countries to declare itself free from PRRSV. At the time of detection, the disease was not widespread so a decision was made to control the outbreak through a modified stamping out procedure. The actions taken to eradicate the disease proved to be effective as, following extensive surveillance during the fall of 2007, Sweden was once again declared free from PRRSV with a high probability by the beginning of 2008. Despite extensive investigation, the source of the outbreak could not be established.

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

DISEASE

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

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

LEGISLATION

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

SURVEILLANCE

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

Passive surveillance

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

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

Active surveillance

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

The revised programme was designed to take into consideration an increased risk of PRRSV introduction and changes in the structure of Swedish pig production, as well as to keep the probability of freedom from PRRS at the same level as it was after demonstration of freedom following the outbreak in 2007. To achieve this, the programme was designed using a between-herd design prevalence of 0.5%,

a within-herd design prevalence of 40% and a risk of introduction of 1 in 5 years. The number of samples needed is calculated yearly taking the outcome of the surveillance in previous years into account. For 2019, the calculated number of samples required was 2400 from the abattoir sampling in addition to the field sampling described above.

RESULTS

Passive surveillance

Ten investigations following clinical suspicions of PRRS were conducted in 2019. In 6 of these herds, reproductive problems such as abortion, stillbirths and weak-born piglets were the primary clinical signs. In 2 herds, respiratory signs and increased mortality in weaned and/or finisher pigs initiated the investigations. In the 2 remaining herds, both reproductive signs in sows and respiratory signs in growing pigs were observed. The number of animals sampled and the methods used during the investigations varied and were dependent on such factors 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.

Also in 2019, one investigation was initiated by gross findings of interstitial pneumonia in two growing pigs during a post mortem examination at SVA. The pigs had been

submitted for examination to investigate the cause of an increase in mortality. PCR analyses of tissues from the dead pigs were negative for PRRS and the herd was subsequently declared PRRS-negative.

Within the programme for enhanced passive surveillance of aborted foetuses, 7 foetuses from 5 herds were examined for the presence of PRRSV genome and all samples were negative.

Active surveillance

In 2019, 647 samples from 42 nucleus herds, multiplying herds and sow pools were analysed. In the abattoir sampling, 2550 samples originating from 506 herds on 851 sampling occasions (some herds were sampled more than once during the year) were analysed. For comparison, the number of samples tested per year since 2010 is given in Table 17.

One field sample from a sow herd was serologically positive by both ELISA and IPMA testing, which prompted an investigation. Additional serum samples were collected from sows in the herd and analysed for the presence of PRRS antibodies. All additional samples were negative and it was concluded that the positive sample was a singleton reactor 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 2019 was >99%.



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: Magnus Aronson.

Table 17: Number of samples and herds tested in the active PRRS surveillance 2009–2019 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

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

^B Some herds were sampled more than once.

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, Nörregård 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

BACKGROUND

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

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

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

DISEASE

Animals

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

Humans

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

LEGISLATION

Animals

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

Humans

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

SURVEILLANCE

Animals

Surveillance in animals is passive. Notification is based on detection of the organism. At SVA detection is performed by PCR targeting the genus of *Chlamydia*. Species identification can be performed by sequencing the PCR fragment.

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 the methods predominantly used.

RESULTS

Animals

In 2019, *C. psittaci* was detected in one of eighteen domestic pet birds tested. In addition, 275 stored samples from wild garden birds sent to SVA for postmortem in 2009–2019, were analysed for *C. psittaci*. In six (2.2%) of the wild birds, *C. psittaci* was detected.

Humans

In 2019, 77 cases of psittacosis were reported, which is more than in any other year during the 2000s (Figure 15). Psittacosis is mainly a domestic infection and only five of the cases were suspected to be infected abroad. Of the cases 54 (70%) were male and 70 (91%) over 50 years old. Contact with birds and bird droppings were considered an important route of transmission. For nearly half (n=36) 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 2019, 56 (73%) of the cases were reported in January–March and December.

DISCUSSION

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

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

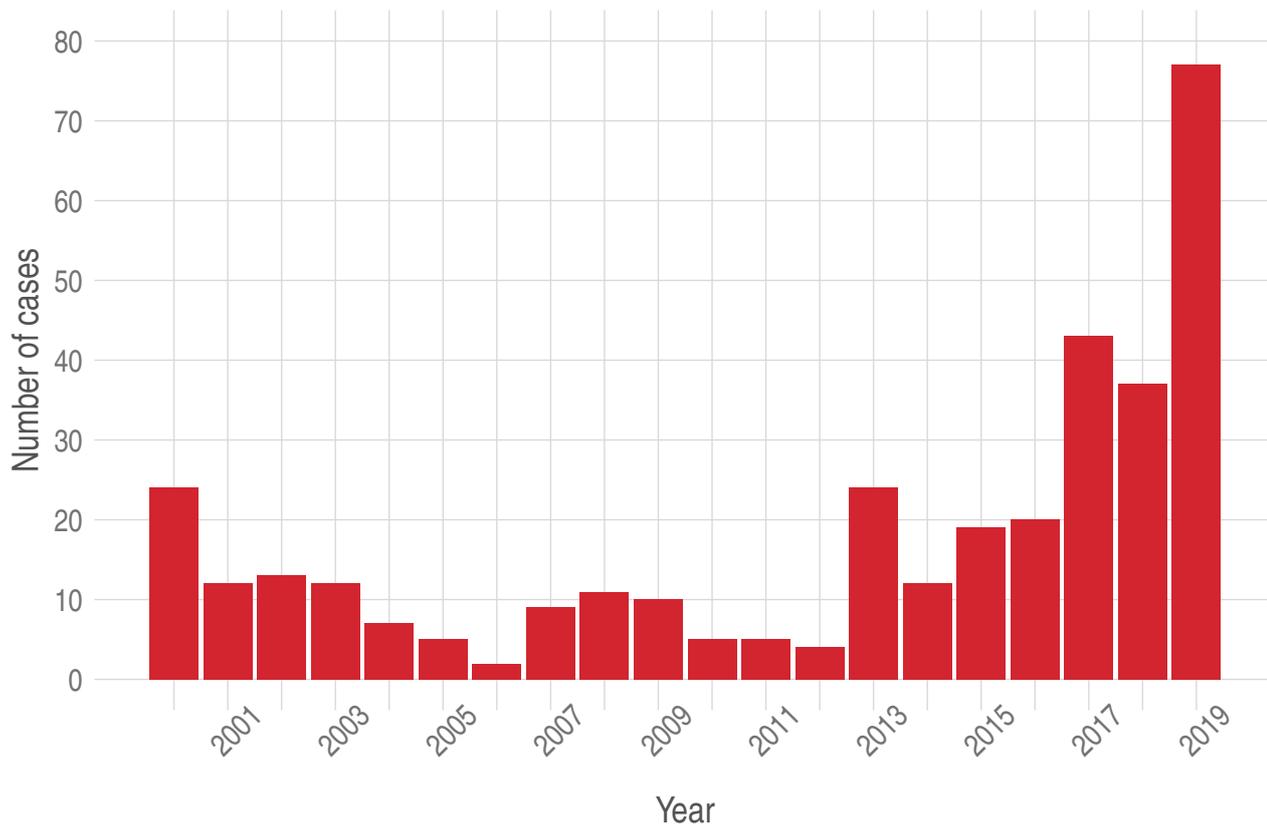


Figure 15: Number of notified human cases of psittacosis in Sweden 2000–2019.

C. psittaci has been detected in a variety of wild bird species, most often in water birds, doves, and pigeons. At present, knowledge on the epidemiology of *C. psittaci* in domestic and wild birds in Sweden is scarce. In a survey performed 2019 of wild garden birds collected during a ten-year period, *C. psittaci* was detected at approximately the same level as in previous Swedish studies of passerines.

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



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.

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. The results support that *C. burnetii* is a rare pathogen in the Swedish sheep and goat populations. In a survey of 99 Swedish moose during 2008–2010 no antibody positive samples were found, indicating that exposure to *C. burnetii* is rare also in this wild species.

In humans, only two domestic cases were reported in the 1980s and 1990s. During the same period, a serological survey in humans identified 28% of sheep farmers and 13% of

veterinarians to be antibody positive, indicating a larger extent of the exposure. However, a prospective study on cases of endocarditis showed that only one of 329 patients had antibodies to *C. burnetii* indicating that chronic Q fever endocarditis is rare. Since Q fever became notifiable in humans in 2004, one to three cases have been reported annually until 2008, when an increase was observed. Only one case was classified as domestic during the period from 2004–2009. In 2010, the situation changed as eight of the totally 11 reported cases claimed to have been infected in Sweden. All these domestic cases were identified as a result of contact tracing when investigating a farm in southern Sweden, which was included in a national survey on dairy herds and where the bulk milk from the cows was shown to be antibody positive for *C. burnetii*.

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.

LEGISLATION

Animals

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

Humans

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

SURVEILLANCE

Animals

Surveillance for Q fever in animals is passive.

Humans

Notification of human cases is mandatory and surveillance is based on identification of the disease by a treating physician or by laboratory diagnosis. Both are obligated to report

identified cases to the regional and national level to enable further analyses and adequate intervention measures. For laboratory verification of the infection, serology and PCR are used.

RESULTS

Animals

Limited testing was done in 2019 on cattle mainly for export reasons. Blood samples from 22 cattle were analysed for the presence of antibodies by complement fixation test or ELISA. Serological tests are no longer performed in Sweden and samples were sent to Denmark for analyses during 2019. Animals from two herds were tested for *C. burnetii* in bulk milk by PCR. In addition, one goat was tested for the agent by PCR in conjunction with the surveillance in aborted foetuses. All samples that were submitted for testing were negative.

Humans

In 2019, eleven cases of Q fever were reported. The cases ranged between 20 and 75 years of age of which seven cases were male. Ten cases were travel-associated where Spain was noted as country of infection for five of them. Six cases were positive for phase II antibodies indicating an acute infection. Phase I antibodies are used to assess chronic Q-fever infections. The antibody test can be negative when the infection is at an early stage. Thereby, PCR should be considered as diagnostic tool when sampling of the patient has been conducted within 14 days of symptom onset.

During the period when Q fever has been a notifiable disease, only about 20% of the reported cases have been women. A similar difference in gender distribution has been described from other countries, but the cause is not clear.

DISCUSSION

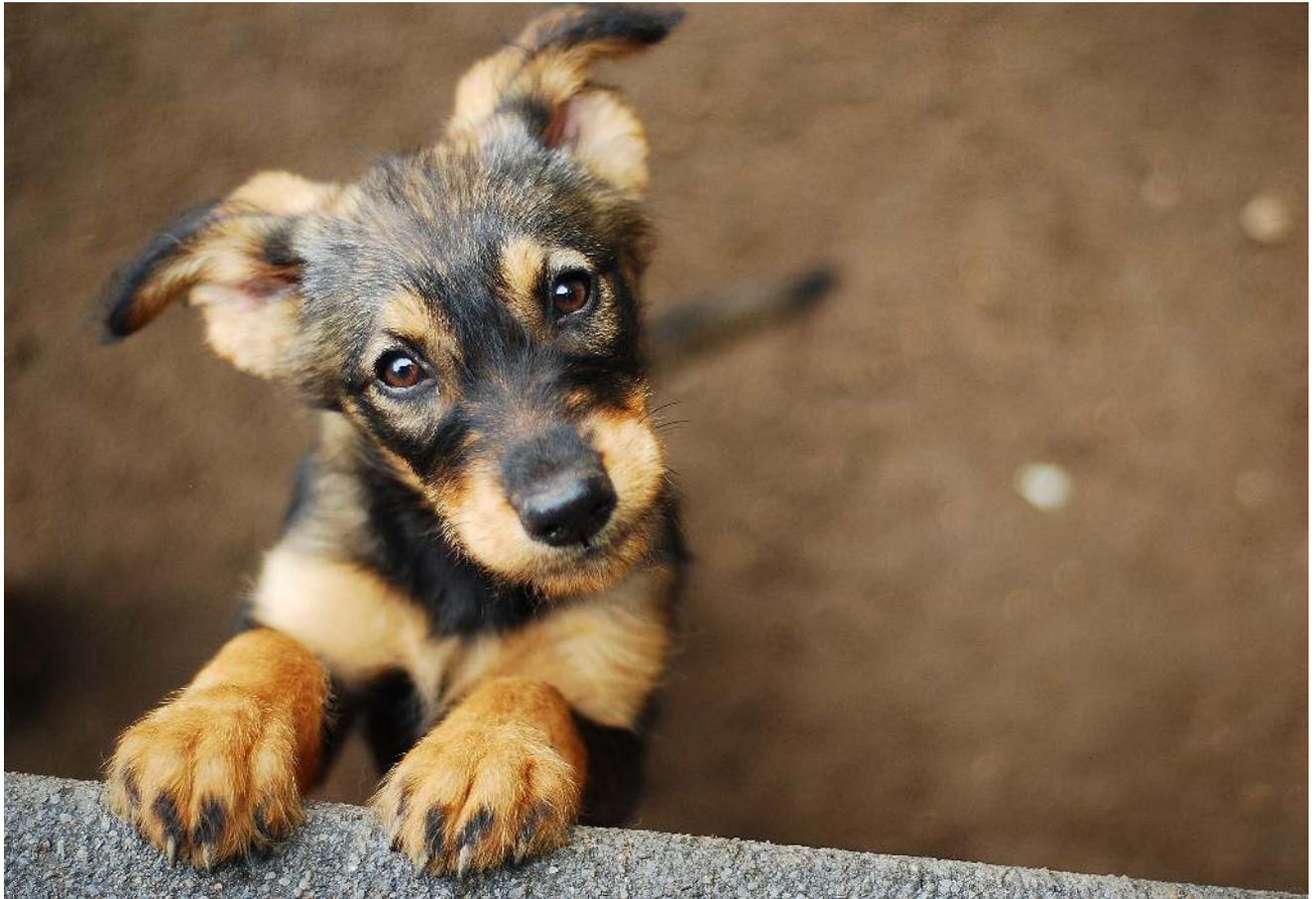
After four years (2008–2011) of active surveillance for Q fever, as well as other related studies, the present surveillance in animals is passive. It is notable that awareness and concern with Q fever as a differential diagnosis for animals has decreased. Due to the nature of the infection, this situation is not likely to change as long as the surveillance remains passive, i.e. dependent on the health or veterinary care seeking behaviour of individuals. Any future prioritisation of Q fever for active surveillance in animals will most likely be influenced by the incidence of human domestic cases, and to some extent also the international situation.

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



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

BACKGROUND

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

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

DISEASE

Humans and animals

Rabies virus infects the central nervous system of humans and mammals. Early symptoms of rabies are non-specific, consisting of fever, headache, and general malaise. As the disease progresses, neurological symptoms appear and may include insomnia, severe anxiety, confusion, slight or partial

paralysis, excitation, hallucinations, agitation, hypersalivation and difficulties in swallowing. The incubation period of rabies is usually 3–6 weeks but may vary from five days to one year.

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

LEGISLATION

Animals

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

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

Humans

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

SURVEILLANCE

Animals

Passive surveillance

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

Active surveillance

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

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 2019, three dogs and two red foxes (*Vulpes Vulpes*) were examined for rabies due to clinical suspicion.

Three dead bats were examined for rabies. In all cases the investigations were requested and paid for by cat-owners whose cats had been exposed to the bats.

In addition, 25 illegally introduced euthanized dogs and seven cats were examined after decision by the Swedish Board of Agriculture. None of the animals had presented clinical signs associated with rabies.

In conclusion, all the above animals that were examined for rabies during 2019 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. 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. However, the greatest risk to people is contact with dogs in countries with endemic dog rabies. In 2019 one woman in Norway died from rabies after having been exposed to a rabid puppy in the Philippines.

The rabies situation in many countries, especially in the EU, is improving due to control and eradication programmes. All countries in the EU are now considered low-risk countries. EU co-finances control, eradication and surveillance programmes in member states as well as in some third countries adjacent to EU.

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 reptiles, all warm-blooded animals, and 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*. Since then, the strategy for control has been to prevent *Salmonella* in all parts of the production chain, from feed to food of animal origin. When Sweden joined the European Union in 1995, the Swedish *Salmonella* control programme was accepted. Sweden obtained additional guarantees for live animals, meat, and egg 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 annually reported 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 constant. 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 animals is low.

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, and cats, whereas infected pigs and poultry are most commonly asymptomatic.

Humans

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

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 feed is also heat-treated. The production of feed is supervised by the Swedish Board of Agriculture which carries out announced and unannounced inspections at feed mills and pet food producers. The control of *Salmonella* in feed is regulated in national legislation (SJVFS 2018:33) as well as in an EU regulation (Commission Regulation (EU) No142/2011).

Animals

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

Food

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

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

Humans

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

MEASURES IN CASE OF FINDINGS OF SALMONELLA Isolates

All suspected isolates of *Salmonella* from non-human sources are sent to the National Veterinary Institute for confirmation, serotyping, resistance testing, and further typing. Index isolates from index cases in animals (first isolate of *Salmonella* in a holding of pig, cattle, goat, sheep, horse or a poultry flock, a companion animal or a wild animal) as

well as other index isolates (other serovars from the holding, findings of *Salmonella* at postmortem or in a lymph node but not confirmed in a holding, *S. diarizonae* serovar 61:(k):1,5(7) in sheep) are resistance tested. From cats and passerine birds, however, a subset of isolates is resistance tested and typed. In addition, one isolate per holding from holdings under restrictions are resistance tested. Isolates of *S. Typhimurium* and *S. Enteritidis* are further typed by MLVA.

All isolates of *Salmonella* from domestic human cases are sent to the Public Health Agency of Sweden for serotyping and further molecular typing. A subset of isolates from travel-associated cases are also typed. In 2013, phage typing of *S. Typhimurium* was replaced by MLVA. During 2016 MLVA was introduced also for *S. Enteritidis*.

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 is 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 feed mill must be thoroughly cleaned and disinfected. Environmental sampling must show negative results before production is resumed.

Animals

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

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 FOCUS: MLVA - a typing technique that will soon be history

Genetic characterisation or 'typing' of bacterial isolates is done to find clusters of potentially related cases of infection, to match isolates from cases to those from suspected sources and to understand the population structure of a pathogen. *Salmonella* Typhimurium and its monophasic variants are together with *Salmonella* Enteritidis the most common causes of human salmonellosis in Sweden, together accounting for over 50% of the cases (data 2019). For these serovars, multi-locus variable number of tandem repeats analysis (MLVA) has been the cross-sectoral typing method of choice during the last decade. In MLVA the number of copies of "tandem repeats" in specific regions of the bacterial genome are determined by PCR and capillary gel electrophoresis. The analysed isolate can be described as a string of copy numbers for each repetitive region or "NA" if the region is missing. A patient isolate of *S. Typhimurium* can for instance be described as 2-13-3-NA-212, and this string can be matched to those of other potentially related isolates or suspected sources. In Sweden, MLVA data has also been used to investigate the spread of specific subtypes with e.g. certain birds, cats and hedgehogs having their own *Salmonella* MLVA variants.

MLVA has been an especially powerful tool for the investigation of international outbreaks and zoonotic transmission as data can easily be exchanged between public health and veterinary laboratories as well as between laboratories in different countries, facilitated by the establishment of shared EU-level protocols. Several foodborne outbreaks due to e.g. contaminated salami, dried herbs and eggs have been solved with the aid of MLVA typing results over the years. In recent years, whole genome sequencing (WGS) has become the gold standard for typing of essentially all bacterial pathogens. WGS is now rapidly replacing all other *Salmonella* typing methods including serotyping, the results of which can be inferred from WGS data. Unfortunately, MLVA profiles cannot currently be reliably extracted from WGS data and comparison with historical data is therefore problematic. In addition, new nomenclature for WGS profiles, clades or strains that would be an equivalent for communication purposes need to be developed.

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 positive horse(s).

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 for preventing recontamination of heat-treated feed. Suspected feed-borne infections are also investigated (see infographic).

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

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

Surveillance of feed mills

The purpose of the surveillance is to ensure the absence of *Salmonella* in the production lines as well as in the feed mill environment. A safety management system is applied in the processing line according to HACCP (Hazard Analysis and Critical Control Points). The management system covers several specific GMP (Good Manufacturing Practices) requirements, according to the Swedish legislation. A minimum of five samples from feed mills that manufacture compound feedstuffs for poultry and a minimum of two samples from those manufacturing compound feedstuffs for other food-producing animals must be collected in the processing line on a weekly basis. These samples are analysed at the National Veterinary Institute (using MSR/V, EN-ISO 6579-1: 2017) 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 (poultry, cattle and pigs and other animals), except for those taken within the control programme at abattoirs, detection of *Salmonella* is performed using the MSR/V (EN-ISO 6579-1: 2017) method or a method validated against it. Measurement of antibodies against *Salmonella* in blood or milk samples of cattle is performed using commercial ELISA tests PrioCHECK[®] *Salmonella* Ab bovine ELISA and PrioCHECK[®] *Salmonella* Ab bovine Dublin.

Poultry

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

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.

Table 18: Sampling scheme of poultry.

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 sock samples	14 d before slaughter	Once a year
Breeders in production	every 2nd week	5 pairs sock samples	14 d before slaughter	3 times under production
Layers in rearing	2 weeks prior to moving	2 pairs sock samples or 2 faecal samples of 75 g	14 d before slaughter	Once a year
Layers in production	every 15th week (start at 22–26 weeks)	2 pairs sock samples or 2 faecal samples of 75 g	14 d before slaughter	Once a year
Poultry for meat production (all species)		2 pairs sock samples or 2 faecal samples of 75 g	14 d before slaughter	Once a year

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 1–2 weeks prior to slaughter. In practice, all poultry flocks are tested prior to slaughter and the results must be available before slaughter.

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

Voluntary programme

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

All broiler and turkey producers belonging to the Swedish Poultry Meat Association are affiliated to the voluntary programme which represents approximately 99% of the slaughtered broilers and 91% of turkeys. This voluntary preventive programme includes the use of all-in all-out production, hygiene measures and a high standard for poultry house construction, such as hygiene 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 an official veterinarian inspects the holding at least once a year.

The organisation Swedish Eggs 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 Infographic).

Compulsory programme

The aim of the programme is to ensure a low prevalence of *Salmonella* in cattle and pig herds. The compulsory part consists of annual faecal sampling from breeding pig herds and gilt-producing herds and biannual sampling from sow pools. In cattle, *Salmonella* testing is performed in all calves <12 months of age that are submitted for postmortem. *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 hygienic programme aiming at decreasing the risk of introduction of *Salmonella* and other infections. Holdings affiliated to the programme receive higher compensation in case of positive findings. In addition, affiliated holdings are entitled to apply for a commercial *Salmonella* insurance. Most breeding herds and many of the large dairy herds are affiliated to this programme.

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

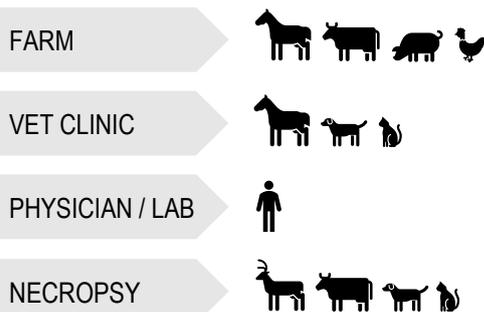
Salmonella screening in dairy herds

In October 2019, a national bulk milk screening was performed including all Swedish dairy herds. A total of 3282 samples were analysed with PrioCHECK® *Salmonella* Ab bovine ELISA (O antigens 1, 4, 5, 12 and 1, 9, 12). All samples with a PP-value higher than twenty (PP>20) in this first test were also analysed with PrioCHECK® *Salmonella* Ab bovine Dublin ELISA (JV dnr 6.2.18-14271/2018).

Scheduled sampling



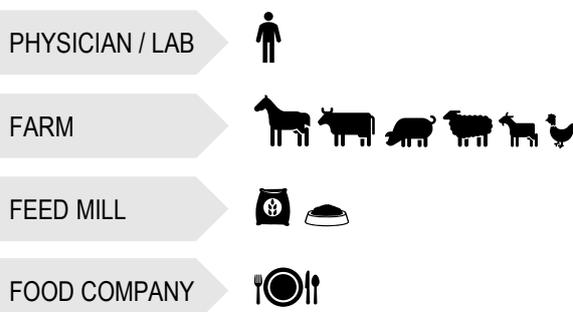
Sampling upon disease suspicion



Voluntary sampling



Sampling following a confirmed case



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

Other animals

Animals are tested for *Salmonella* on clinical suspicion or as part of trace-back investigations (Figure Infographic). Wild animals necropsied at the National Veterinary Institute are also tested for *Salmonella* on suspicion (see chapter on surveillance of wild animals).

Food

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

Approximately 1000 samples per year are tested as part of official sampling by local authorities at food enterprises, other than abattoirs and cutting plants. These samples are analysed mainly using NMKL (nr 71:1999) or a method validated against the standard 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 of these isolates is funded by the Swedish Board of Agriculture, provided that the food business operator agrees that the results are made available to the national authorities. Data from 2007 and onwards are stored in a database at the National Veterinary Institute.

Surveillance at slaughterhouses and cutting plants

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

At red meat cutting plants, approximately 5000 samples are taken annually from meat residues and 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.

Food business operators are obliged to take swab samples from carcasses of sheep, goats, and horses at slaughterhouses for analyses of *Salmonella*, according to the regulation (EG) 2073/2005 on microbiological criteria for foodstuffs. The results of these analyses are not 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 Infographic). 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. All isolates belonging to the serovars *S. Enteritidis*, *S. Typhimurium* and the monophasic variants of *S. Typhimurium* were subtyped using MLVA (multi-locus variable number tandem repeat analysis). 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, 7394 samples were analysed for *Salmonella*; 33 of these samples (0.4%) were positive. Nine serovars were detected; *S. Typhimurium* was the most common (n=19) (Table 19).

In addition, *Salmonella* was detected in 16 out of 1654 analysed batches from feed materials of vegetable origin. The most common serovar was *S. Mbandaka* (n=4). *Salmonella* was detected in 4 out of 1417 batches from feed materials of animal origin and from pet food.

Sweden notified ten findings of *Salmonella* in feed materials and pet food during 2019. All of these concerned intra-community traded or imported feed materials. Seven of them had vegetable origin and the other three were of animal origin.

Animals

Poultry

Salmonella was detected in 2 (0.04%) of 4502 broiler flocks tested in routine sampling before slaughter (Table 20 and Figure 16). *Salmonella* was also detected in 4 of the 692 flocks of layers tested. *Salmonella* was not detected in any breeding flocks, neither in any samples of commercially raised turkeys, geese, ducks, quails, or ostriches. As the poultry registries maintained by the Swedish Board of Agriculture are not sufficiently updated, 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.

Table 19: Serovars of *Salmonella* isolated within feed control in 2019.

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
<i>S. Derby</i>	-	1	-	-	-	-	-
<i>S. Dublin</i>	-	1	-	-	-	-	-
<i>S. Düsseldorf</i>	-	-	-	-	-	1	-
<i>S. Lexington</i>	-	-	-	-	-	1	-
<i>S. Mbandaka</i>	-	-	4	-	-	2	-
<i>S. Muenster</i>	-	-	1	-	-	-	-
<i>S. Saintpaul</i>	-	-	-	-	-	1	-
<i>S. Senftenberg</i>	1	-	2	-	-	1	-
<i>S. Tennessee</i>	-	-	3	-	-	1	-
<i>S. Typhimurium</i>	-	1	3	-	-	19	-
<i>S. Vejle</i>	-	-	-	-	-	1	-
<i>S. enterica</i> sp. <i>diarizonae</i> (IIIb)	-	-	-	-	-	3	-
<i>S. enterica</i> sp. <i>enterica</i>	-	-	2	-	-	3	-
Not typed	-	-	1	-	-	-	-
Total	1	3	16	0	0	33	0
Number of samples	1222	195	1037	576	41	7394	822

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

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

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

Table 20: Results from the *Salmonella* control programme in poultry flocks in 2019.

Animal species	Production type	Production stage	No. flocks tested	No. positives	Percentage	Serovar
<i>Gallus gallus</i>	Meat production	Adult Grand Parent	22	0	0.00%	-
<i>Gallus gallus</i>	Meat production	Adult Parent	148	0	0.00%	-
<i>Gallus gallus</i>	Meat production	Production	4502	2	0.04%	<i>S. Bukavu</i> , <i>S. Reading</i>
Turkeys	Meat production	Adult Parent	4	0	0.00%	-
Turkeys	Meat production	Production	151	0	0.00%	-
<i>Gallus gallus</i>	Egg production	Adult Parent	20	0	0.00%	-
<i>Gallus gallus</i>	Egg production	Production	692	4	0.58%	<i>S. Düsselldorf</i> , <i>S. Kisii</i> , <i>S. Typhimurium</i> (n=2)
Geese	Meat production	Production	5	0	0.00%	-
Ducks	Meat production	Production	10	0	0.00%	-

Cattle

In total, *Salmonella* was detected in 11 new herds in 2019 (Figure 17). *Salmonella* was isolated from six (0.18%) of 3308 mesenteric lymph nodes from cattle at slaughter (Table 21 and Figure 18).

In the bulk milk screening, 4.3% (n=140) of the samples were test-positive in the first ELISA. Of these 140 samples, 40 were also test-positive in the second test, primarily detecting antibodies against *S. Dublin*. There were regional variations in the prevalence of dairy herds with test-positive bulk milk samples ranging from 0% to 24%. The two regions with highest prevalence were Öland and Gotland. In Öland, 24% (33/136) of the herds were test-positive and 31 of these herds were also positive in the second test, indicating present or previous infection with *S. Dublin*, which is

known from previous bulk milk screenings to be at this level in the region. In Gotland 22% (30/139) of the herds were test-positive in the first test, and only one of these were positive in the second test. This can be compared with results from the last bulk milk screening, performed in 2013 when 5% (12/218) of the herds in Gotland were test-positive. As a follow-up, a regional bulk milk screening is planned for spring 2020.

Pigs

Salmonella was detected in three pig herds (Figure 19) and from seven (0.24%) of 2922 lymph node samples taken from adult pigs and from five (0.16%) of 3091 lymph node samples from fattening pigs (Table 21, Figure 18).

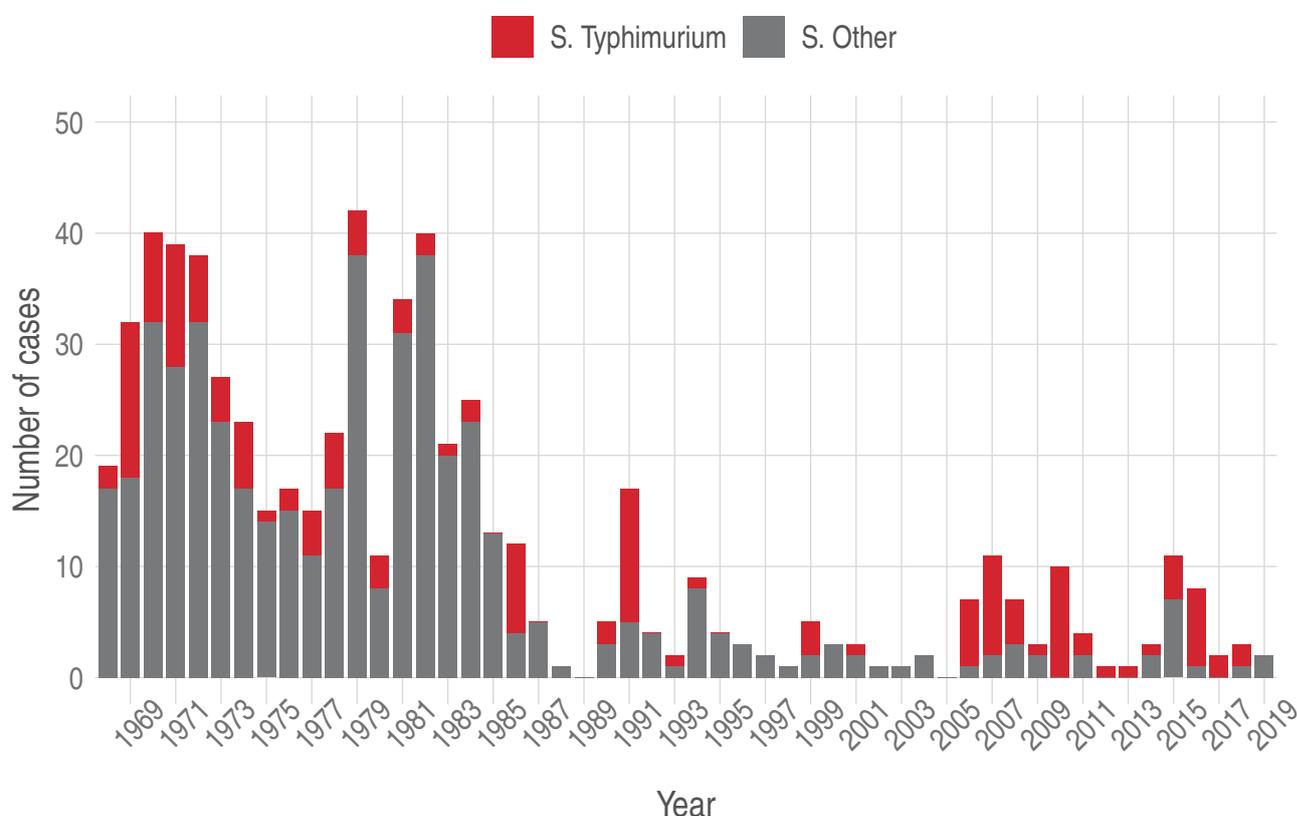


Figure 16: Annual notifications of *Salmonella* in broiler holdings during 1968–2019, breeding flocks included.

Other animals

Salmonella was detected in three stables with horses, in 1179 cats, in 9 dogs, in 21 wild birds (mainly passerine) and in one hedgehog (Table 22).

Food

Within the Swedish *Salmonella* control programme, swab samples were taken from 5935 pig carcasses and 3264 cattle carcasses. Neck skin samples were taken from 2904 poultry carcasses. *Salmonella* was detected in swab samples from one pig and one cattle carcass (Table 21). At cutting plants, *Salmonella* was not detected in any of the 5390 red meat or

the 1244 poultry meat samples taken. (Table 21 and Figure 18).

In addition to the sampling performed within the control programme, 968 samples were taken by national and local authorities. *Salmonella* was detected in three samples. Two samples were taken from vegetables in an investigation of suspected food-borne outbreak, and one sample from pre-cooked crayfish taken in border control (Table 23).

Sweden notified seven findings of *Salmonella* in food during 2019. All these concerned intra-community traded or imported food batches within the food categories meat, crustaceans, and vegetables.

Table 21: Results from the *Salmonella* control programme at abattoirs and cutting plants in 2019.

Animal species	Sample type	No. samples	No. positive	Percentage	Serovar
Cattle	Lymph node	3308	6	0.18%	S. D�usseldorf (n=2), S. Typhimurium (n=4) S. Dublin
	Carcass swab	3264	1	0.03%	
Breeding swine	Lymph node	2922	7	0.24%	S. Agona (n=1), S. London (n=2), Typhimurium (n=4) -
	Carcass swab	2878	0	0.00%	
Slaughter swine	Lymph node	3091	5	0.16%	S. Typhimurium S. Typhimurium
	Carcass swab	3057	1	0.03%	
Cattle and swine	Meat trimmings	5390	0	0.00%	-
Poultry	Neck skin	2904	0	0.00%	-
	Meat trimmings	1244	0	0.00%	-

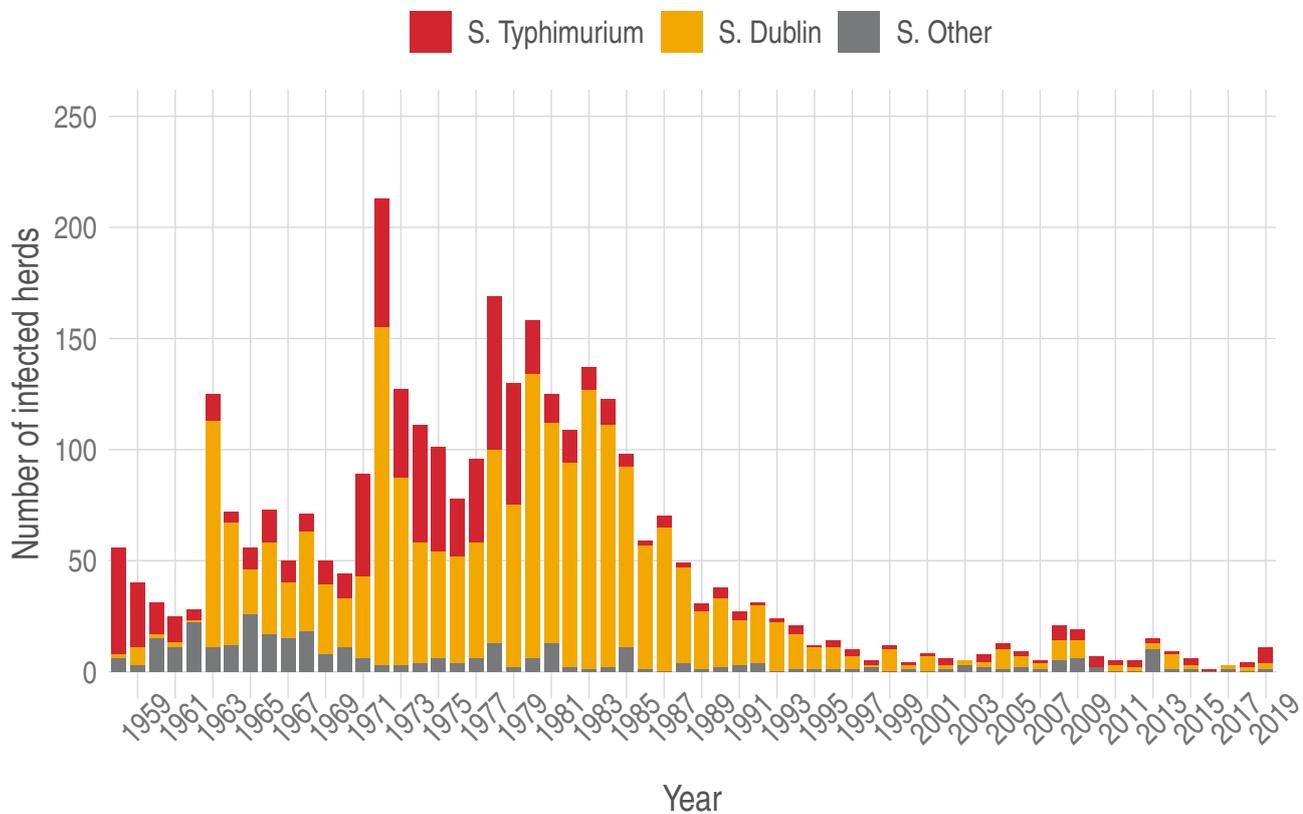


Figure 17: Annual notifications of *Salmonella* in Swedish cattle herds during 1957–2019. Data from 1957 through 1967 is extracted from a graph presented by J.Å. Robertsson (1985).

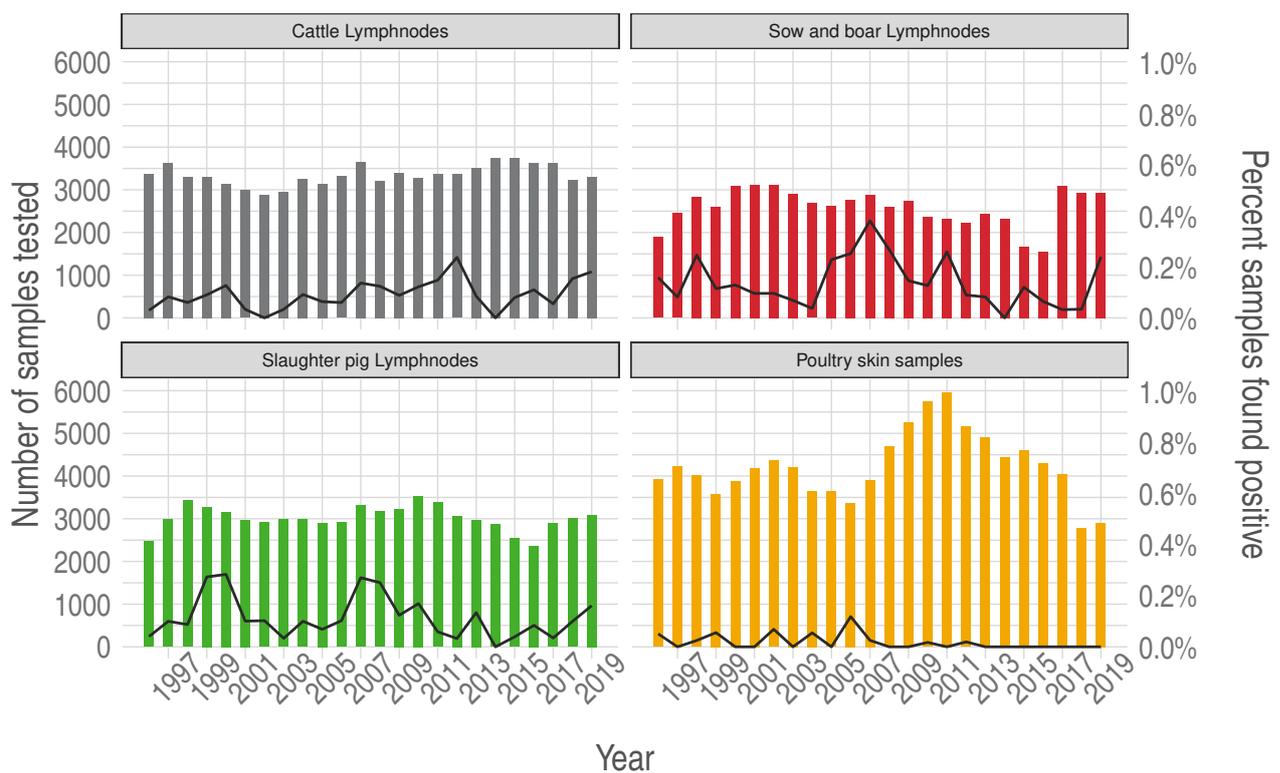


Figure 18: Samples tested (bars - left axis) and percentage of *Salmonella* found (line - right axis) in lymph node samples from cattle, sows and boars and fattening pigs sampled at major abattoirs as well as neck skin samples from poultry at all abattoirs. In 2014, a new laboratory was procured to perform *Salmonella* analyses of samples from abattoirs and cutting plants. The National Reference Laboratory for *Salmonella* and the National Food Agency of Sweden inspected the laboratory and found that the analytical methods and laboratory routines needed improvement. The laboratory results from 2014 and 2015 are therefore considered to be unreliable. Since 2016, another laboratory performs these analyses.

In total, data from serotyped isolates from 479 batches of food or carcasses sampled at retail, slaughterhouses, or other food enterprises between 2010 and 2019 is available. Of these, 283 were from imported food batches, 131 of domestic origin (24 food batches and 107 carcasses) and 65 from food batches of mixed or unknown origin. The distribution of serovars differ between the major food categories (Figure 20). *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*, *S. Infantis* and *S. Enteritidis* were most common. Isolates from lamb meat (mainly originating from swab samples of carcasses) were almost exclusively *S. diarizonae* serovar 61:(k):1,5(7), whereas the composition of isolates from vegetables varied a lot.

Humans

In 2019, a total of 1993 cases of salmonellosis were reported, compared to 2040 cases in 2018 (Figure 23). Domestic cases increased by 13% from 677 cases in 2018 to 763 cases in 2019, resulting in an incidence of 7.4 cases per 100 000 inhabitants. The domestic incidence varies from year to year but has been largely stable over a long period.

A total of 61% of the cases (n=1215) were considered to have been infected abroad. Since 2008, a steep decrease

in the number of travel-associated cases has been noted, despite an increase in international travel.

Among the domestic cases, the median age was 45 years (0–94 years) and the incidence was highest for children younger than 5 years of age with 13.8 cases per 100 000 inhabitants followed by persons over 80 years of age with an incidence of 12.7 per 100 000 inhabitants.

Of the isolates from domestic cases, 90% were serotyped. The most common serovars from domestic cases were monophasic *S. Typhimurium* (24%), *S. Enteritidis* (18%) and *S. Typhimurium* (10%). Of the domestic isolates of monophasic *S. Typhimurium*, MLVA profile 3-14-8-NA-211 (17 cases) was the most common followed by 3-14-11-NA-211 (15 cases) and 3-12-10-NA-211 (14 cases). For *S. Enteritidis*, 3-9-5-4-1 (54 cases) was the most common MLVA profile followed by 3-10-5-4-1 (14 cases). None of the MLVA profiles of *S. Typhimurium* had over ten isolates. Around 70 additional serovars were identified in domestic cases during 2019. Of the cases infected in other countries, 14% were serotyped and *S. Enteritidis* was the most common serovar (46% of the isolates that were typed).

A clear seasonal variation of domestic salmonellosis is usually observed, with most cases occurring during the summer months. During 2019, most domestic cases were reported in early autumn due to several major outbreaks (Figure 22).

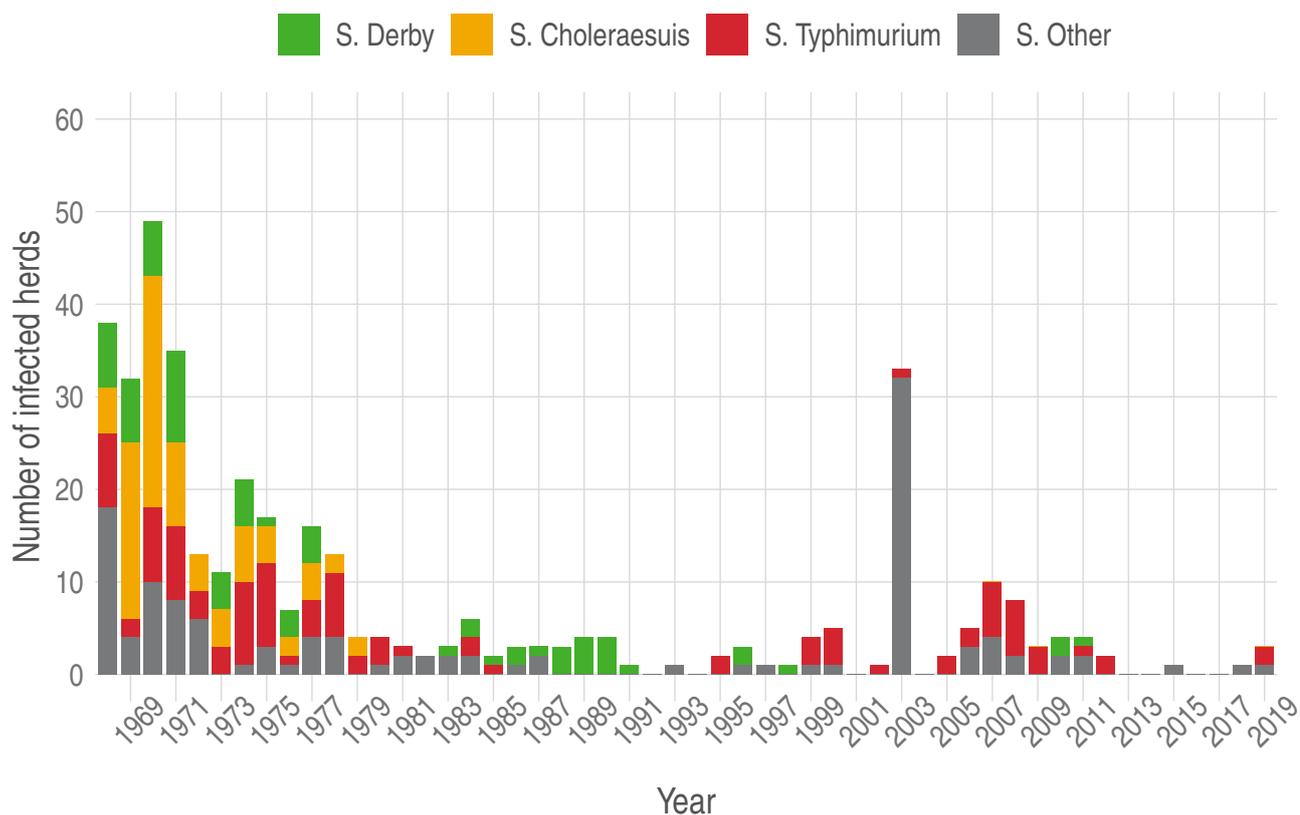


Figure 19: Annual notifications of *Salmonella* in swine herds during 1968–2019. In 2003, a feed borne outbreak of *S. Cubana* occurred in Sweden. In 2016 and 2017, *Salmonella* was not detected in any herd.

Table 22: Reported index cases of *Salmonella* in cats, dogs, horses, wild birds and wild mammals in 2019.

Serovar	Cats	Dogs	Horses	Wild birds	Other wild animals
<i>S. Agona</i>	0	1	0	0	0
<i>S. Derby</i>	0	1	0	0	0
<i>S. Enteritidis</i>	0	0	1	0	1 ^A
<i>S. Hessarek</i>	1	0	0	1	0
<i>S. Newport</i>	1	0	0	0	0
<i>S. Typhimurium</i>	165	10	2	7	0
<i>Salmonella enterica</i> sp. <i>diarizonae</i>	1	1	0	0	0
<i>Salmonella</i> , O:4	1012	1	0	13	0
Total	1179	17	1	21	1
Number of samples	1836	152	57	44	24

^AA hedgehog.

Table 23: Results of *Salmonella* analyses of food samples taken by the authorities in 2019.

Reason for sampling	Total no. of samples	No. of positive samples
Survey	178	0
Routine control	52	0
Suspected food poisoning or complaint	313	2 ^A
Border control	228	1 ^B
Unknown	197	0

^A*S. Enteritidis*, vegetables contaminated at a restaurant.

^B*S. Newport*, pre-cooked frozen crayfish

Outbreaks

The number of domestic infections in humans with *Salmonella* was comparatively low during the first half of 2019. However, from July onwards several major outbreaks occurred, which increased the number of cases for the whole year (Figure 22).

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

In the early months of 2019, a large outbreak of *Salmonella* Typhimurium (MLVA profiles 2-[11-15]-[3-4]-NA-212) occurred among cats in Sweden. In total, *Salmonella* was detected in 1179 (64.2%) cats of 1836 tested which was at the same level as in 2018 but more than previously observed. Of the 167 fully serotyped cat isolates, 165 belonged to the serovar Typhimurium. Infected cats were reported predominantly from the regions of Stockholm, Uppsala and Södermanland (65.7% of the cases). Simultaneously, *S. Typhimurium* with the same specific MLVA profiles were detected from 21 passerine birds, 10 dogs, 2 stables with horses as well as in 13 humans.

Outbreak of *S. Enteritidis*

In July 2019, the County of Dalarna informed the Public Health Agency of Sweden about fifteen people with salmonellosis all with an epidemiological link to a local pizzeria/kebab restaurant. All the dishes consumed by the cases contained vegetables, many of them both cucumber

and tomato. Food analyses identified *Salmonella* in sliced cucumber and sliced tomatoes but not in other types of food tested or in whole vegetables. In addition, *Salmonella* was found on a worktop where food was prepared while the restaurant staff sampled were negative. Sequencing of the isolates from the samples of the worktop, sliced vegetables as well as in samples from a total of 50 people who had eaten at or picked up food from the restaurant in July 4–17 revealed an identical type of *Salmonella* Enteritidis ST11. Identical strains were also identified in nine Norwegian patients who had been in Sweden during this time, but it could not be confirmed if they had visited the specific restaurant. Continued source tracing could not reveal the origin of the bacterium.

Outbreak of *S. Newport*

During July through November, 33 persons from 12 counties were notified with *S. Newport*. A case-case study performed by the Public Health Agency of Sweden showed a strong association between being sick with the outbreak strain and eating crayfish. Most of the outbreak cases had eaten a certain brand of frozen pre-cooked Chinese crayfish, which was recalled by the retail company. Following the recall, *S. Newport* was detected in samples of crayfish taken by the retail company and in border control. Whole-genome sequencing showed that the isolates from food clustered with the isolates from the human cases, and the source of infection could thus be confirmed.

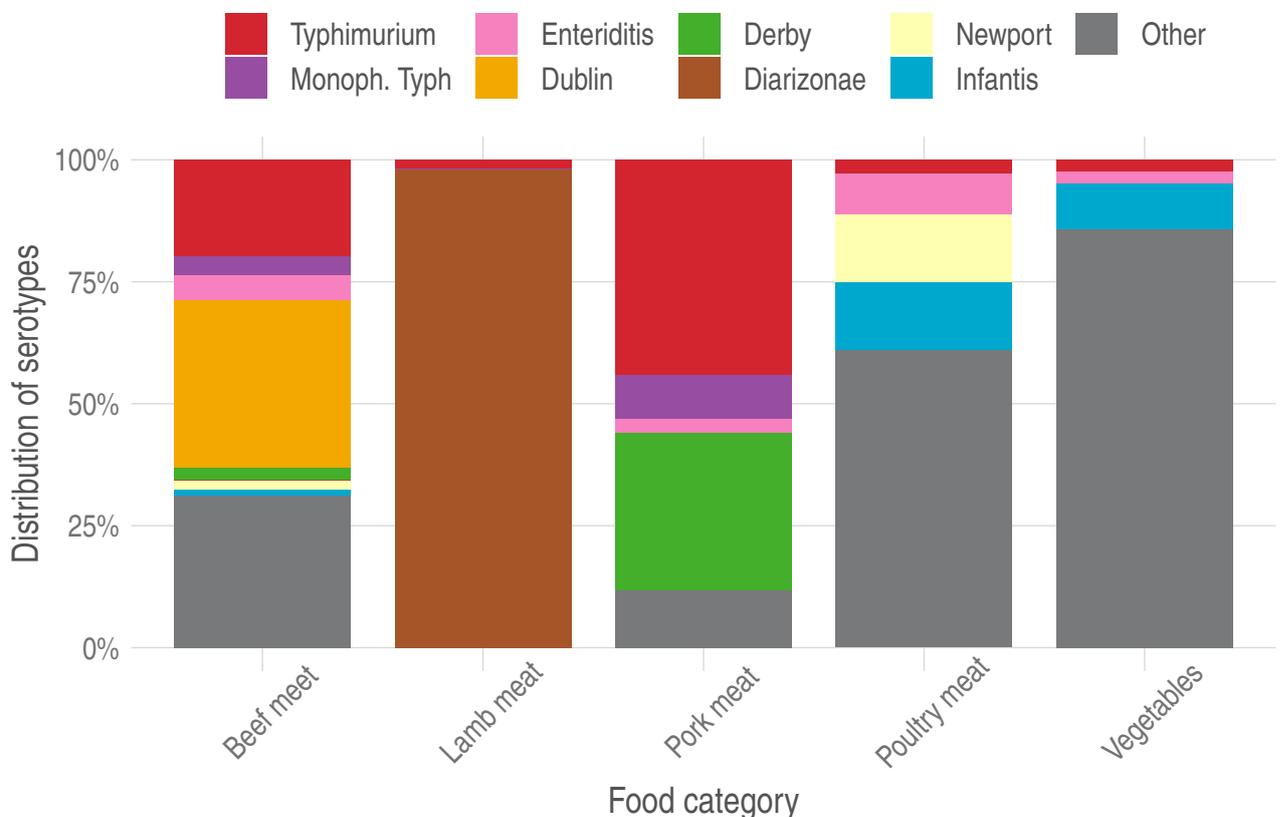


Figure 20: Distribution of *Salmonella* serovars in different food categories. Results of serotyping of isolates from samples taken at retail, slaughterhouses or other food enterprises by authorities or food business operators 2010 – 2019. In total, samples are from 379 batches of food or carcasses (beef meat 157, pork meat 34, poultry meat 36, lamb meat 110, vegetables 42). Food categories with isolates from samples of less than 20 batches of food are not included.

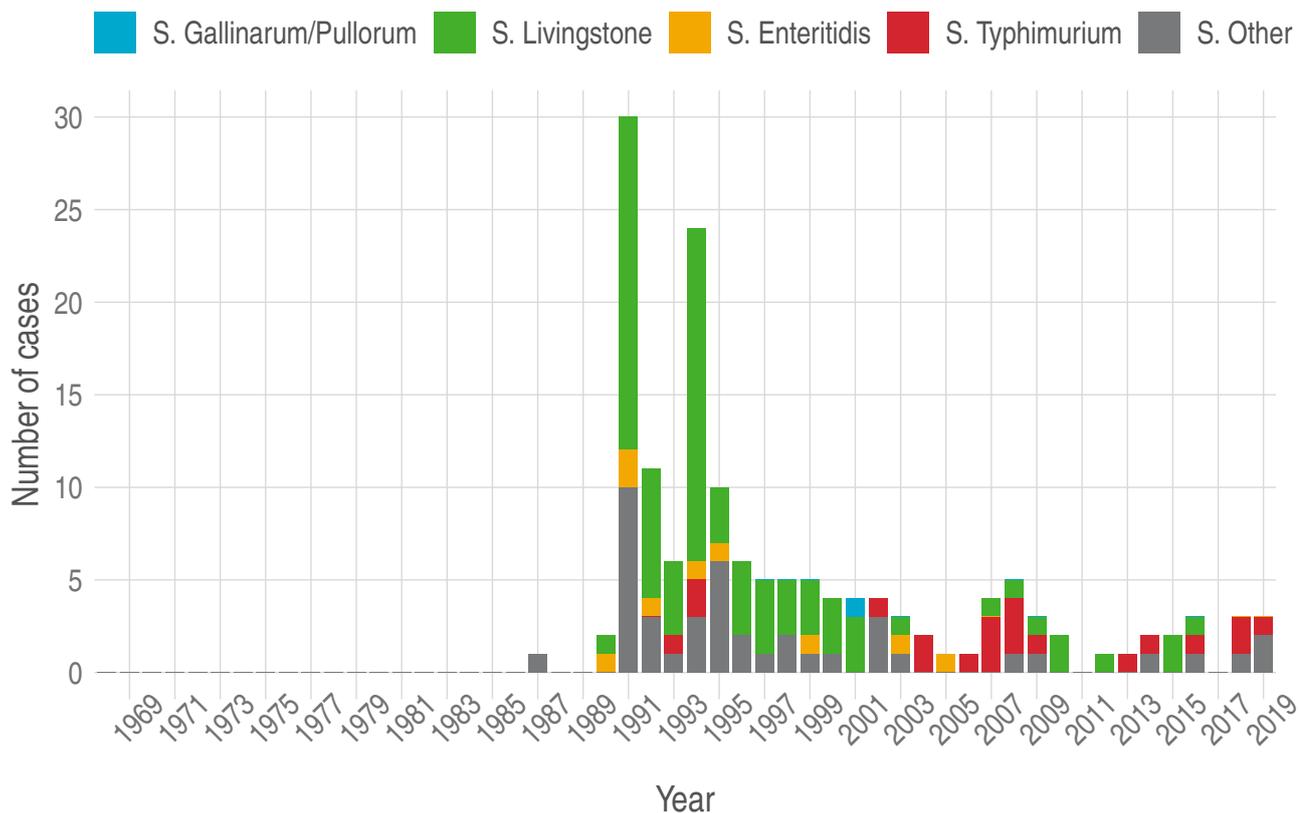


Figure 21: Annual notifications of *Salmonella* in layer holdings during 1987–2019.

Outbreak of monophasic *S. Typhimurium*

In the early autumn 2019, the county of Jönköping reported of an increase in salmonellosis cases to the Public Health Agency of Sweden. The regional clinical laboratory in the county informed that the *Salmonella* isolates all showed unusual phenotypic characteristics on XLD agar plates. They were lacking the traditional black pigmentation of colonies, i.e. they were dihydrogen sulphide negative. The outbreak spread nationally, and a case-control study was conducted. The analysis pointed towards small tomatoes being the likely source. The epidemiological typing also showed that the outbreak strain, a monophasic *S. Typhimurium*, belonged to an unusual sequence type (ST3478), closely related to the more common ST34. In total, 82 cases were identified, and this outbreak highlighted the importance of considering vegetables as a possible vector for transmission.

Outbreak of *S. Mikawasima*

In October 2019, the microbial surveillance programme at the Public Health Agency of Sweden identified a WGS cluster of *S. Mikawasima*. Simultaneously, an Urgent Inquiry was launched in EPIS (ECDC) by Public Health England (PHE) regarding a *S. Mikawasima* outbreak. PHE shared the outbreak sequence, and comparison showed that there was a match with the Swedish outbreak strain. In Sweden, a case-case study was conducted where the control group consisted of salmonellosis cases with differing serovars. In addition, the application SALUT (*Snabb Utredning av Livsmedelsburna Utbrott*) was used as a tool. This application has a database on food habits for the Swedish population that can

be used as a reference for inquiries about food items consumed in the case group. The epidemiological studies did not identify any suspected food item. In total, 36 cases were identified in 12 counties. Internationally, almost 200 cases were reported. No suspected food item was identified as source. However, the spatial and temporal distribution of cases indicated a food source with a short expiry date that had been widely distributed in Europe. *S. Mikawasima* outbreaks have been repeatedly identified in the past in several European countries. This is the third European investigation where Sweden has had cases. None of the previous investigations have pinpointed a food source.

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. The reported travel related incidence in 2019, 11.8 cases per 100 000 inhabitants, is considerably higher than the domestic incidence of 7.4 cases per 100 000 inhabitants.

In the feed sector, in 2019 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=19). All findings were in the feed material intake area, in several different feed mills. This illustrates the importance of handling feed materials in a proper way even if the feed materials have been negatively tested for *Salmonella*.

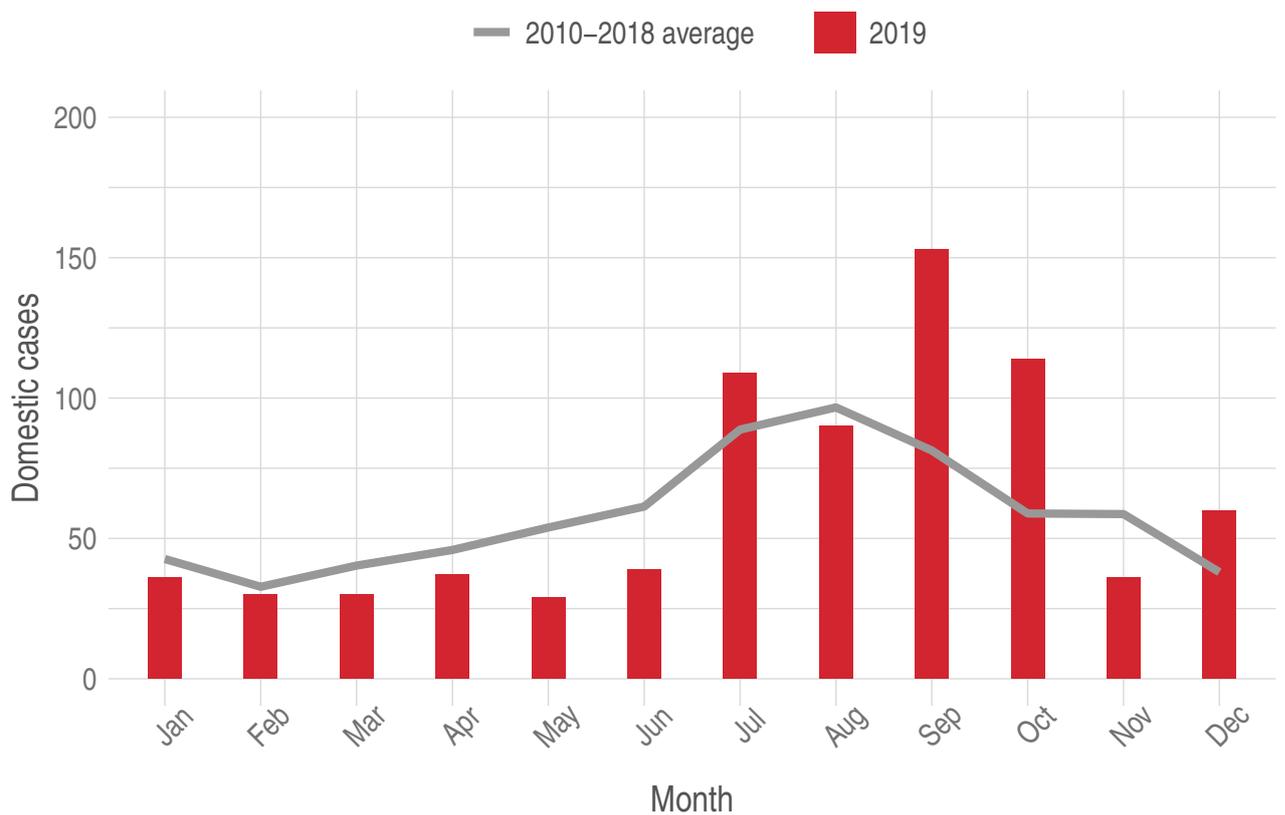


Figure 22: Monthly notifications of domestic human cases of salmonellosis in 2019 and a monthly average for notifications in 2010–2018.



Figure 23: Incidence (per 100 000) of notified human cases of salmonellosis in Sweden, 1997–2019. 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.

In 2019, *Salmonella* was detected in a few flocks of broilers, laying hens and pig herds. As poultry and pig are important sources of salmonellosis in humans a continuous need for strict biosecurity routines are needed in poultry and pig holdings. In 2019, *Salmonella* was detected in 11 cattle herds, which was more than in the previous five years.

The Swedish *Salmonella* control programme has been in place for decades and resulted in a very low *Salmonella* burden in domestic animals (Figures 17, 19 and 21). However, the programme is costly and could be modernised.

Reported domestic human cases of salmonellosis vary from year to year depending on the number of outbreaks. The largest decrease over the past ten years was seen for the travel-associated cases, especially from European countries. This decrease in salmonellosis seems to be the result of the successful implementation of harmonised *Salmonella* control programmes in poultry across the union.

Thailand is the most common country for travel-associated salmonellosis, although the number of cases has decreased in the past years. It is still necessary to inform travellers about the risks of contracting *Salmonella* and other infectious diseases to further decrease the incidence. Also, information about how to prevent secondary transmission to other persons, to the environment and to animals when returning to Sweden is crucial.

Good co-operation 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

Colombe S, Jernberg C, Löf E, Angervall AL, Mellström-Dahlgren H, Dotevall L, Bengnér M, Hall I, Sundqvist L, Kühlmann-Berenzon S, Galanis I, Lindblad M, Hansen A, Rehn M (2019) Outbreak of unusual H(2)S-negative monophasic *Salmonella* Typhimurium strain likely associated with small tomatoes, Sweden, August to October 2019. *Euro Surveill.* Nov;24(47):1900643. doi: 10.2807/1560-7917.ES.2019.24.47.1900643.

EFSA and ECDC (European Food Safety Authority and European Centre for Disease Prevention and Control), 2018. The European Union summary report on trends and sources of zoonoses, zoonotic agents and food-borne outbreaks in 2017. *EFSA Journal* 2018;16(12):5500, 262 pp. <https://doi.org/10.2903/j.efsa.2018.5500>

Robertsson JÅ, *Salmonella* infections in cattle – Cellular and humoral immune reactivity against O-antigens and porins after infection and vaccination with killed and live vaccines. (Page 8, Figure 3). Swedish University of Agricultural Sciences, College of Veterinary Medicine, Department of Veterinary Microbiology, Uppsala, Sweden 1985.

Sundström K, Wahlström H, Ivarsson S, Sternberg Lewerin S (2014) Economic effects of introducing alternative *Salmonella* control strategies in Sweden. *PLoS One* 9:e96446

Söderlund R, Jernberg C, Trönberg 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

Wahlström H, Andersson Y, Plym-Forshell L, Pires SM (2011) Source attribution of human *Salmonella* cases in Sweden. *Epidemiol Infect* 139:1246–53.

Wahlström H, Sternberg Lewerin S, Sundström K, Ivarsson S (2014) Estimation of the expected change in domestic human *Salmonella* cases in Sweden in 2010, given a hypothetical relaxation of the current *Salmonella* control programme. *PLoS One* 9:e89833

Wierup M, Wahlström H, Lahti E, Eriksson H, Jansson DS, Odelros Å, Ernholm L (2017) Occurrence of *Salmonella* spp.: a comparison between indoor and outdoor housing of broilers and laying hens. *Acta Vet Scand* 59:13

Wierup M, Widell S (2014) Estimation of costs for control of *Salmonella* in high-risk feed materials and compound feed. *Infect Ecol Epidemiol* 4:10.3402/iee.v4.23496

Ågren EC, Johansson J, Frössling J, Wahlström H, Emanuelson U, Sternberg-Lewerin S (2015) Factors affecting costs for on-farm control of *Salmonella* in Swedish dairy herds. *Acta Vet Scand* 57:28

Scrapie



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: Whiptop/Shutterstock.

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 misfolded prions (small proteins) induce the same misfolded 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. 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, epidemiological studies on the European level indicate that atypical scrapie

probably is a spontaneously occurring disease which does not seem to spread within or between flocks.

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

DISEASE

The incubation period is long, up to several years. Clinical signs of classical scrapie are related to the neurological system and include altered behaviour and sensation, affected movement and posture, as well as pruritus and skin lesions. The disease is progressive and always fatal. All routes of transmission of classical scrapie have not been established, however, transmission of classical scrapie occurs horizontally within flocks and at lambing, and pastures can be contaminated for long periods of time. Scrapie has, based on epidemiological data, not been considered a zoonotic disease; however, the question is regularly raised.

LEGISLATION

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

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

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

SURVEILLANCE

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

Passive surveillance

All suspicions of scrapie, i.e. sheep or goats showing clinical signs or post mortem findings where scrapie cannot be excluded, must be reported to the authorities. The obligation to report applies to animal owners, veterinarians and everyone else who is responsible for the animals. If the animal is still alive it is examined by a veterinarian who is in close contact with disease experts. If scrapie can still not be excluded the animals is euthanized. Brainstem samples from animals with clinical suspicion of scrapie are examined with Bio-Rad TeSeE short assay protocol (SAP). If inconclusive

or positive the results are confirmed with Bio-Rad TeSeE Western Blot.

Active surveillance

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

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

Except for the northern parts of Sweden, where animal density is low (less than 10% of the sheep population are in this area), it is mandatory to send fallen animals for rendering. In the computerised system for collecting carcasses, roughly every second or every third (adjusted by season) animal is “flagged” for sampling. The carcasses sent for rendering are sampled by employees at the rendering plants. All sheep and goats above 18 months of age sent for post mortem examinations are sampled. This is done by veterinarians or veterinary assistants.

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

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

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

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

RESULTS

Passive surveillance

In 2019, one sheep was examined due to clinical suspicion of scrapie and tested with negative results.

Active surveillance

Sheep

In 2019, the National Veterinary Institute examined 1285 sheep from fallen stock and 32 sheep from flocks under increased surveillance due to Nor98 or under restrictions due to imports, sampled at slaughter. Out of these, all samples were negative for scrapie. The northern part of the country is

under-represented in the sampling and due to problems with rapid decomposition of carcasses during summertime, sampling is not evenly distributed throughout the year. Apart from this, sampling seems fairly representative.

Goats

In 2019, the National Veterinary Institute examined 84 goats from fallen stock for scrapie. All were negative both for classical scrapie and for atypical scrapie.

DISCUSSION

Classical scrapie

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

Regarding the active surveillance, no positive cases have been detected. Continued efforts need to be made to increase samples from the northern parts of the country. From a surveillance point of view, a seasonal variation with less samples during summer is not deemed to have a systematic effect. There was only one reported clinical suspicion of scrapie and efforts are needed to improve passive surveillance.

Atypical scrapie

Since the first case of atypical scrapie was detected 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. Currently, the flocks are put under intensified monitoring in accordance with Regulation (EC) 999/2001. At the European level, two epidemiological studies have concluded that the prevalence is similar in different countries and that the prevalence in positive flocks does not differ from the prevalence in the rest of the sampled population. This pattern differs from the way contagious disease are normally distributed in the population and supports the hypothesis that atypical scrapie is spontaneously 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.

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
- 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 then the genes 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 2019, 112 cases with STEC were reported to develop HUS. When analysing which serotypes and stx profiles that have been associated with HUS during 2005 to 2019 the most prevalent serotype was the domestic serotype O157:H7 clade 8 with 39 (34%) cases, followed by O26 with 15 (13%) cases and O121 with 6 (5%) cases (Table 24). Almost 30 percent of the HUS cases did not have an isolate for typing.

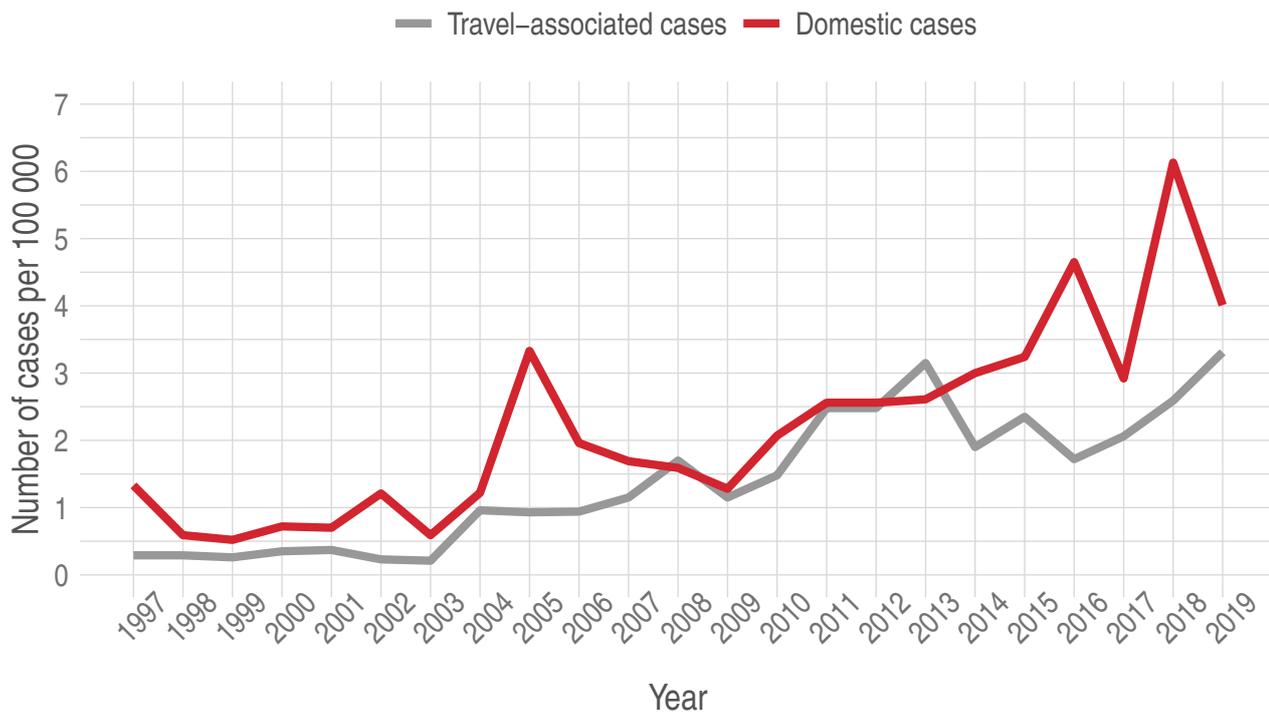


Figure 24: Incidence (per 100 000 inhabitants) of notified human STEC cases in Sweden, 1997–2019. Prior to 2005, only O157 was required to be reported. In 2005, all serogroups of STEC including PCR findings became subject for notification. In 2005, 2016 and 2018, the number of cases increased due to one or more domestic outbreaks.

Table 24: Serotypes and stx-profiles for reported cases with HUS, 2015–2019.

Serotype	stx1	stx1+stx2	stx1a	stx1a+stx2a	stx1c+stx2b	stx2	stx2a	stx2a+stx2c	stx2a+stx2d	stx2b	stx2b+stx2d	stx2c	UNK	Total
Untyped	-	-	-	-	-	1	-	-	-	-	-	-	29	30
ONT:H29	-	-	-	-	-	-	-	-	-	-	1	-	-	1
ONT:H2	-	-	-	-	-	-	1	-	-	-	-	-	-	1
O182:H25	-	-	1	-	-	-	-	-	-	-	-	-	-	1
O175:H21	-	-	-	1	-	-	-	-	-	-	-	-	-	1
O165:H25	-	-	-	-	-	-	-	1	-	-	-	-	-	1
O156	1	-	-	-	-	-	-	-	-	-	-	-	-	1
O153	-	-	-	-	-	1	-	-	-	-	-	-	-	1
O146:H21	-	-	-	-	-	-	-	-	-	1	-	-	-	1
O130:H11	-	-	-	-	-	-	1	-	-	-	-	-	-	1
O117:H7	-	-	1	-	-	-	-	-	-	-	-	-	-	1
O113:H21	-	-	-	-	-	-	-	-	1	-	-	-	-	1
O112ac:H19	-	-	-	-	-	-	-	-	-	-	-	1	-	1
O103	1	-	-	-	-	-	-	-	-	-	-	-	-	1
O77:H41	-	-	-	-	-	-	1	-	-	-	-	-	-	1
O145:H28	-	-	-	-	-	-	2	-	-	-	-	-	-	2
O113:H4	-	-	-	-	3	-	-	-	-	-	-	-	-	3
O157:H7	-	-	-	1	-	-	1	1	-	-	-	-	-	3
O121:H19	-	-	-	-	-	-	6	-	-	-	-	-	-	6
O26	-	1	2	5	-	-	7	-	-	-	-	-	-	15
O157:H7, clade 8	-	-	-	-	-	-	4	35	-	-	-	-	-	39
Total	2	1	4	7	3	2	23	37	1	1	1	1	29	112

LEGISLATION

Animals

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

Food

Detection of STEC in food is not notifiable.

Humans

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

SURVEILLANCE

Animals

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

Passive - Traceback from human cases

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

Active

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

Food

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

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.

Isolates from human cases are sent to the Public Health Agency of Sweden for typing using whole genome sequencing (WGS) to verify molecular serotype, relevant virulence

IN FOCUS: Tracing STEC cases back to farms

When a link between a sporadic human case of STEC and a farm is suspected, a traceback investigation is often performed to find the source of infection. Examples of typical connections leading to a traceback are contact with animals and/or their excrements and consumption of raw milk.

The investigation is initiated by the county medical officer and the county veterinary officer who inform the Swedish Board of Agriculture, and the Board of Agriculture decides whether the farm should be sampled. The farm will not always be sampled, it will depend on the severity and number of cases affected. Any recovered isolates from the farm will be compared to human isolates by whole genome sequencing. If the isolates match, the farm is considered as the likely source of infection.

During 2019, the authorities investigated several minor clusters and sporadic cases of STEC that could be linked to farms and food producing animals. The most commonly found STEC type was O157:H7 clade 8, a domestic subtype known for its potential to cause severe disease. It carries the shigatoxin gene *stx2a*, or more often *stx2a* in combination with *stx2c* and is today the most common subtype to cause domestically acquired HUS. The strain was first established in the 1990s in the county of Halland, situated along the west coast of Sweden and has further spread over the years to the southern parts of the country and to the east coast. In recent years, clade 8 has mainly been found in the regions of Skåne, Blekinge, Småland and on the islands Öland and Gotland (Figure 25). It was not until 2004 that other serotypes of STEC than O157 became mandatory to report, and therefore only O157 was traced to farms before this year.

Tracebacks to farms is a valuable tool for preventing further spread by providing advice to farm owners. They also serve as a basis for monitoring the occurrence and geographical spread of STEC variants capable of causing severe illness in infected humans and serve as an early warning system for introduction of new STEC variants in ruminant populations.

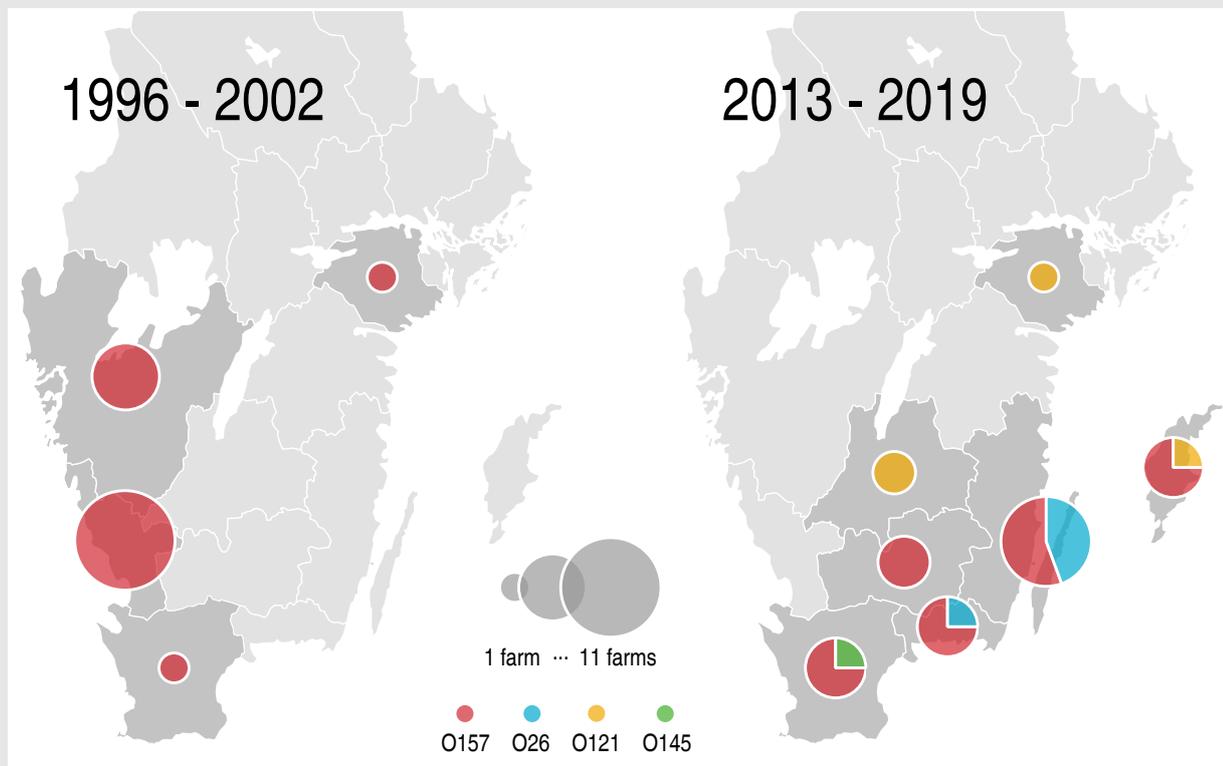


Figure 25: Cattle farms confirmed by genotyping as the source of human infection 1996–2002 (left) and 2013–2019 (right). Serotypes are shown as colors and the size of circles show the number of farms identified during the period, aggregated to county level. Spread of the clade 8 variant of O157 in cattle on the west coast in the late 90's led to a number of farm-associated human cases as well as outbreaks. Since then a notable shift has occurred and clade 8 is now mostly found in the southeastern part of the country. Other serogroups (O26, O121, O145) appear to have become more common as the cause of farm associated human STEC infections over the years. This could reflect improved laboratory capacity and reporting routines for non-O157.

Table 25: Number of reported human cases in comparison to number of cases where an isolate could be retrieved 2019.

Origin of infection	Number of reported cases	Number of isolates typed (%)
Domestic infection	412	237 (58%)
Travel associated infection	331	118 (36%)
Unknown country of infection	13	3 (23%)
Total	756	358 (47%)

genes 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

Passive - Traceback from human cases

During 2019, 12 investigations were performed where cattle or sheep farms were suspected as sources for human infection, see the “in focus” box. An epidemiological association was established on four occasions of STEC O157:H7 stx2a, stx2c (cattle farms), one occasion of O26:H11, stx2a (cattle farm) and one occasion of O121:H19 stx2a (sheep farm). The other farms were either negative or, in two investigations, had non-identical variants.

Active

During 2019 no active surveillance was performed.

Food

In 2019, 75 samples were taken by national and local authorities from different types of food, and analysed for STEC (6 of these only for STEC O157). Most samples (n=60) were taken at border control from bovine meat. STEC was not found in any of these samples. The rest of the samples were mainly taken to investigate complaints or suspected food poisonings and STEC was found in four of these 15 samples. Three of the positive samples (two samples of meat from wild boar and one sample of cevapcici) were collected at the home of a family with two human cases with EHEC infection. The fourth positive sample was a fresh cheese made from unpasteurised milk.

Table 26: Distribution of serotypes and shigatoxin-subtypes in HUS cases in 2019.

Serotype	stx1a+stx2a	stx2a	stx2a+stx2c	stx2b	stx2c	Unknown stx
O157:H7, clade 8	-	2	8	-	-	-
O157:H7	-	-	1	-	-	-
O26	2	2	-	-	-	-
O112ac:H19	-	-	-	-	1	-
O146:H21	-	-	-	1	-	-
O175:H21	1	-	-	-	-	-
Untyped	-	-	-	-	-	4
Total	3	4	9	1	1	4

Humans

In 2019, 756 human cases were reported of which 415 were domestic (55%). The domestic incidence in 2019 was 4 (cases per 100 000 inhabitants), and over a longer period of time an increasing trend is seen (Figure 24). As in previous years, the incidence was highest in children.

STEC-associated HUS was reported in 22 cases of which 18 were domestically acquired infections. Eleven of the HUS cases were children under the age of 10. For 18 of the HUS cases an isolate could be retrieved and thereby serotyped. Ten of the domestic HUS cases belonged to serotype O157:H7, clade 8 (Table 26)

For 58% of the domestic STEC cases, an isolate could be retrieved and thereby serotyped. However, for the travel associated cases only 37% were typed. (Table 25). The reason for the low isolation frequency is not known. It can be influenced by regional analysis algorithms, unusual serotypes that are difficult to isolate or that cases who are infected abroad are seeking care in a later stage of the infection where the concentration of the pathogen is too low for isolation. In total 80 different serotypes were identified. The most common serotypes were O157:H7, O26:H11 and O103:H2. 32 cases were diagnosed with the domestic clade 8 of O157:H7, stx2a and stx2c, 10 (31%) of which developed HUS. The third most common serotype in Sweden, O103:H2, normally carries stx1a and gives milder symptoms. However, during 2019 several cases were infected with the more unusual variant that carried both stx1a and stx2a. This variant was detected for the first time in 2012. The fourth most common serotype 2019 was O91:H14, stx1a, a type associated with mild symptoms. This serotype is another example of STEC serotypes that can carry different variants of *stx* genes. In a retail study 2017–2018 by the Swedish Food Agency, O91:H14 carrying both *stx1a* and *stx2b* was the most common type of STEC isolated from lamb meat. This variant has also been identified in a retail study on Swedish beef meat in 2015. Five cases had co-infections of STEC where two different serotypes were detected.

National outbreak investigations

No national outbreak investigations were performed during 2019.

DISCUSSION

The long-term trend for human cases of STEC infection in Sweden is rising. One known factor contributing to the higher incidence in some regions in Sweden is an increased use in multiplex PCR panels where a higher number of faecal samples are screened for STEC. Thereby, more STEC cases

are identified. The isolation frequency of PCR positive human samples however decreased in 2019, especially for the travel associated cases. Without characterization of isolates, outbreak investigations, identifying highly pathogenic types and comparison with animal, food and environmental isolates is challenging.

In 2019, an unusually high number of farms, 12 in total, were investigated following suspicion of STEC infection spreading e.g. to visitors. All of these farms were located in southern Sweden (see further discussion regarding this type of investigation in the “in focus” box). The repeated occurrence of STEC O26 among farms in recent years is notable, including strains carrying *stx2a* which have historically been rare or absent among Swedish ruminants while being a common cause of severe STEC cases in other countries. This echoes a trend of increasing numbers of human O26 cases in Sweden caused by strains carrying *stx2a*. To further investigate this, a nationwide cattle slaughterhouse prevalence study targeting O26 as well as O157 will be conducted during 2020–2021. The most common cause of HUS cases in Sweden remains the O157:H7 variant known as clade 8, which is endemic in the southeast.

REFERENCES

Frank C, Werber D, Cramer JP, Askar M, Faber M, an der Heiden M, Bernard H, Fruth A, Prager R, Spode A, Wadl M, Zoufaly A, Jordan S, Kemper MJ, Follin P, Muller L, King LA, Rosner B, Buchholz U, Stark K, Krause G, HUS Investigation Team (2011) Epidemic Profile of Shiga-Toxin-Producing *Escherichia coli* O104:H4 Outbreak in Germany. *N Engl J Med* 365:1771–1780

Ivarsson S, Jernberg C, Björkholm B, Hedenström I, Lopez G. Regional Investigation Team, Rapid detection and communication of Swedish cases provided early puzzle pieces in the German STEC O104 outbreak, poster ESCAIDE conference 2011.

Livsmedelsverket. Flink, C. 2019. L 2019 nr 04: Kartläggning av bakterier på lammkött från butik. Livsmedelsverkets rapportserie. Livsmedelsverket, Uppsala.

Sartz L, De Jong B, Hjertqvist M, Plym Forshell L, Alsterlund R, Löfdahl S, Osterman B, Ståhl A, Eriksson E, Hansson H-B, Karpman D (2008) An outbreak of *Escherichia coli* O157:H7 infection in southern Sweden associated with consumption of fermented sausage; aspects of sausage production that increase the risk of contamination. *Epidemiol Infect* 136:370–380

Söderström A, Österberg P, Lindqvist A, Jönsson B, Lindberg A, Blide Ulander S, Welinder-Olsson C, Löfdahl S, Kaijser B, De Jong B, Kühlmann-Berenzon S, Boqvist S, Eriksson E, Szanto E, Andersson S, Allestam G, Hedenström I, Ledet Muller L, Andersson Y (2008) A large *Escherichia coli* O157 outbreak in Sweden associated with locally produced lettuce. *Foodborne Pathog Dis* 5:339–349

National guidelines: Infektion med EHEC/VTEC Ett nationellt strategidokument. Available from: www.folkhalsomyndigheten.se

Small Ruminant Lentiviruses

BACKGROUND

Small ruminant lentiviruses (SRLVs) include caprine arthritis-encephalitis virus (CAEV) and Visna/maedi virus (VMV) in the Retrovirus family. Maedi-visna (MV) is a globally distributed contagious disease in sheep, first described in Iceland in 1939. Caprine arthritis-encephalitis is a common disease in most goat producing countries all over the world. Transmission between animals occurs most commonly via the oral route (mainly via milk and colostrum) but may also occur via inhalation of infected aerosol droplets. The incubation period is long; often 4–5 years. The first case of MV in Swedish sheep was officially reported in 1974. Fifteen years later, the flock-level seroprevalence was 8.2% as demonstrated by sampling of randomly selected sheep at abattoirs. The prevalence of CAE in Sweden is not known, but in a pilot study from 2018, 30% of the herds were seropositive.

Voluntary control programmes for MV and CAE were launched by Farm & Animal Health in 1993 and 1999, respectively, and in 2005 an additional simplified version started, with single sampling of sheep and goats to identify diseased flocks and then in the next step enrol them into the control programme. From 2020, the simplified version is no longer available. The MV and CAE programmes were run in parallel, but from 2020, they are merged into one programme called the MV/CAE programme.

Data from all sampled and controlled flocks have been recorded since 1993.

DISEASE

Only the maedi form of MV is occurring in Swedish sheep flocks; a progressive viral pneumonia. The disease typically remains latent in the flock for several years before appearing with clinical manifestations. In an advanced stage of the disease the typical clinical signs are severe emaciation and respiratory distress in older ewes. After the appearance of clinical signs, the outcome is always fatal within weeks to months. Caprine arthritis-encephalitis occurs in four different forms: arthritis, nervous form, pneumonia and mastitis (hard udder). In Sweden, subclinical disease is probably most common.

LEGISLATION

MV and CAE are notifiable diseases (SJVFS 2013:23). The control programme is regulated through SJVFS 2015:17 (Jordbruksverkets föreskrifter om frivillig organiserad hälsokontroll av husdjur (K 152)).



Caprine arthritis-encephalitis (CAE) is the goat variant of small ruminant lentiviruses. Photo: Bengt Ekberg/SVA.

SURVEILLANCE

The purpose of the control programme is to detect and eradicate MV and CAE from Swedish sheep and goat flocks and to prevent introduction into free flocks. Documentation of the MV/CAE status in the flocks is essential. By identifying infected flocks and taking measures, the spread of MV/CAE stops and eradication is possible. Prevention of introduction of MV/CAE into flocks is crucial.

The programme is based on serological testing of sheep at farm level. A flock-specific MV/CAE status is achieved by repeated blood sampling and testing. Participating farmers sign an agreement that all sheep and goats in the flock are individually identified (according to legislations) and recorded. Purchase of sheep and goats is only allowed from flocks with a similar or higher MV/CAE status.

Three consecutive serological tests are performed on all sheep and goats ≥ 12 months old with an interval of 12–16 months. All samples in each test have to be negative for MV/CAE antibodies. Each test renders an MV-/C-status; M1/C1, M2/C2 and M3/C3. M3/C3-status means that the flock is declared free from MV/CAE. 24–28 months after gaining the M3/C3-status a final test is performed on all sheep/goats ≥ 24 months old and the flock will render an MV/CAE free status. The MV/CAE free status is maintained by an assurance of the animal keeper every second year. An indirect control of the M3/C3/MV/CAE free status holdings is performed by testing of sheep and goats from holdings entering the programme as these new animals are mainly bought from M3/C3/MV/CAE free status flocks. If antibodies are detected in a flock, either the whole herd is culled or other control and eradication measures including selective slaughter is performed, depending on the prevalence of positive sheep and goats within the flock.

The programme is based on serological examination of blood samples for antibodies against MV or CAE virus with an ELISA test (CAEV/MVV Total Ab ELISA IDEXX). Samples with inconclusive or seropositive results are retested using the same ELISA-test and if the results are still seropositive a confirmatory test is performed using AGID (agar gel immunodiffusion) for which the antigen is purchased from the Animal and Plant Health Agency, Weybridge, UK.

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

RESULTS

During 2019, approximately 7539 samples from sheep and goats were analysed in the MV/CAE control programme for antibodies against MV/CAE-virus.

At the end of 2019, 3520 sheep flocks with 128 421 sheep and 306 goat flocks with 2402 goats were enrolled in the programme. This corresponds to about 46% of the

Swedish sheep population, and about 12% of the goat population. 3400 of the flocks were declared free from MV/CAE.

In 2019, 2 sheep flocks and 1 goat flock were considered MV/CAE positive. The rest of the flocks was somewhere in the process from unknown to free, which normally takes 5 years and 4 sampling occasions.

DISCUSSION

It is now more than 25 years since the MV programme was launched. A series of measures have been taken in order to finalise the programme and to reach freedom from disease. A revision of the MV programme was made during 2013 by Farm & Animal Health and the National Veterinary Institute. Since July 2014, the programme has been further refined to improve efficacy and efficiency, e.g. by increasing sampling in risk areas and higher risk flocks and reducing sampling in long-term MV free and well-documented flocks. Currently, the programme is scrutinized again for more cost-effective sampling, diagnostics and control measures. Norway has after a successful programme, declared most herds free from CAE, showing that it is possible to eradicate the disease.

REFERENCES

- Andersson, Ellen, 2019. Böldsjukan och kaprin artrit encefalit hos svenska mjölkproducerande getter: en prevalensstudie och jämförelse av serum och mjölk som provtagningsmaterial. Second cycle, A2E. Uppsala: SLU, Dept. of Clinical Sciences
- Kampen AH, Mork J, Hopp P, Klevar S. The surveillance and control programme for maedi in Norway 2012. Surveillance and control programmes for terrestrial and aquatic animals in Norway. Annual report 2012. Oslo: Norwegian Veterinary Institute 2013
- Lindqvist Å. Kontrollprogram hos maedi-visna hos får. Svensk veterinärtidning 1993, 11, 463–5
- Tine/Helsetjenesten for geit. 2016. Sluttrapport, prosjekt friskere geiter, 2001–2015

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, systematic surveillance by testing is necessary, and it is crucial that the equine industry implements preventive biosecurity strategies for high-risk-situations.

DISEASE

Strangles affects horses, including donkeys and zebras. Common clinical signs include fever, nasal discharge, depression, cough and enlarged submandibular or cervical lymph nodes. Other signs associated with strangles may include: inappetence, dysphagia, painful movements, ruptured abscesses, dyspnoea and swollen limbs; and less commonly: spread of infection to other organs, so called *bastard strangles*. Complications of strangles may be severe and lead to death.

So called *atypical strangles* with mild clinical signs is probably more typical than previously understood, which may lead to large outbreaks due to delayed diagnoses. Also, recent findings indicate that subclinical infections with *S. equi* after an acute outbreak may be far more common than previously understood, and microbiological confirmation of the absence of *S. equi* can be required to rule out the horse being a carrier.

LEGISLATION

Strangles is a notifiable disease in Sweden (SJVFS 2013:23). It is notifiable on clinical suspicion to the County Administrative Board where the horse is residing.

SURVEILLANCE

In Sweden, surveillance for strangles is passive; sampling and diagnostic testing is primarily performed on clinical suspicion. Typically, samples from airways and lymph nodes 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 26 illustrates the number of notified cases per year.

RESULTS

In 2019, there were 48 officially reported index cases of strangles in Sweden, each representing an outbreak in a farm. The trend has been decreasing since 2016, when 115 index cases were reported (Figure 26).

DISCUSSION

The passive surveillance results indicate that strangles is endemic in the Swedish horse population. However, investigations of outbreaks point to a need for screening horses that have recently been moved for, often international, trade purposes, as these horses 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.

REFERENCES

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

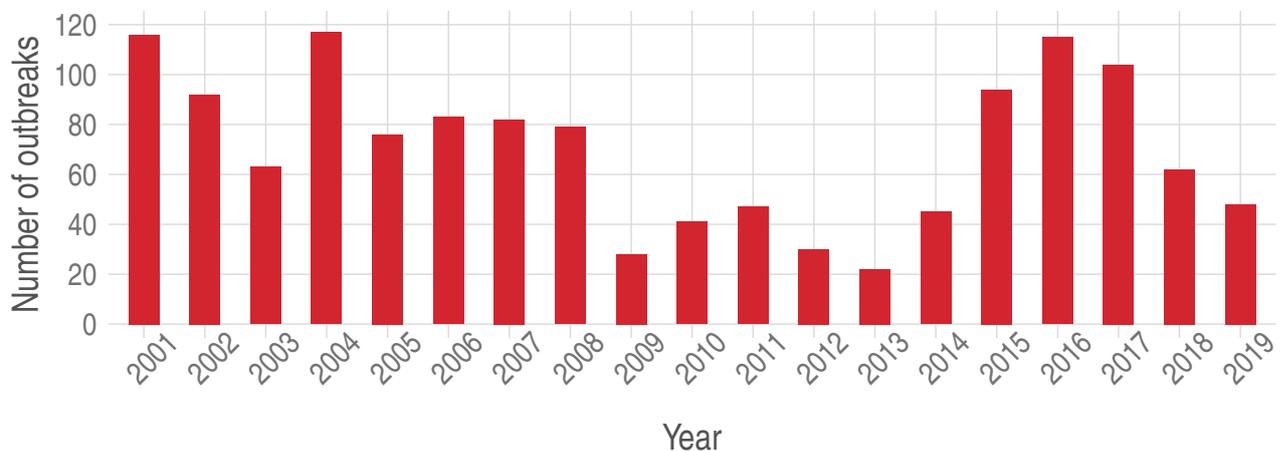


Figure 26: Reported index cases (farm outbreaks) of *Streptococcus equi* infections in horses in Sweden during years 2001–2019. Source: Swedish Board of Agriculture.

Tick-borne encephalitis

BACKGROUND

Tick-borne encephalitis virus (TBEV) belongs to the genus flavivirus in the family *Flaviviridae*. TBEV is endemic in an area ranging from northern China and Japan, through far-eastern Russia to Europe. The virus may cause a neurological infection which may lead to long-term sequelae in the affected patients. The virus is spread by ticks (*Ixodes ricinus* and *I. persulcatus*), which become infected when they suck blood from infected rodents. Wild rodents are the natural reservoir for TBEV. The virus also circulates in the tick population through transovarial transmission without involvement of vertebrate hosts. Large mammals, predominantly ungulates, are important for the maintenance of large tick populations. Humans typically become infected via ticks, although unpasteurised cow, goat and sheep milk and milk products have also been reported as sources. Vaccination of persons living, visiting or working in endemic areas is recommended.

Three sub-types of TBEV are described: the “Western”, “Siberian” and “Far eastern” subtypes. In Sweden, only the “Western” subtype has been identified.

The first case of TBE infection in Sweden was reported in 1954. During the following three decades, 10–40 annual cases were reported. From the mid-1980s a clearly increasing trend has been observed. In recent years about 150–400 cases have been reported annually. A majority of the cases acquire their infections in Sweden. Most have been infected on the east coast of Sweden and in the Stockholm archipelago but in recent decades cases have been observed regularly on the west coast of the country and the infection occurs from the region of Skåne in the south to the regions of Gävleborg and Dalarna in the north. The age distribution

is wide but most of the cases are between 30 and 70 years. There is a slight over-representation of men. A majority of the patients are diagnosed in July to October.

DISEASE

Animals

In general, animals develop a subclinical infection. However, confirmed clinical cases have been reported in dogs and horses. Seroconversion has been demonstrated in grazing domestic animals such as goats, cattle and sheep as well as in wild ungulates. Ruminants may excrete the virus in milk. Wild rodents are considered the natural reservoir for TBEV but are not reported to contract the disease. Serological testing of wild animals, such as moose and deer, has been suggested as an indicator of the circulation of the virus.

Humans

In humans, a biphasic course of the disease is common. The first, viraemic phase lasts for about four days. After an interval of about a week, a meningoencephalitic phase appears in about one third of the patients. The symptoms may include fever, headache, nausea, cognitive dysfunctions or spinal paresis. The mortality is low, about 0.5%. The incubation period of TBE is usually between 7 and 14 days.

LEGISLATION

Animals

TBE is not a notifiable disease in animals in Sweden.

Humans

TBE in humans is notifiable as a viral meningoencephalitis since 2004, according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2013:634).



Figure 27: Incidence (per 100 000 inhabitants) of notified cases of TBE in humans 1988–2019.

SURVEILLANCE

Animals

The surveillance in animals is passive. In 2019, a survey was performed on occurrence of antibodies against TBE virus in bulk milk samples from cattle, goat, and sheep farms in Sweden.

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

In a survey performed in 2019, using an ELISA test, antibodies to TBEV were found in 4 (3.7%) of the 108 tested bulk milk samples.

Humans

In 2019, 359 cases of TBE were reported. This is a small decrease since the year before, but the number of cases nevertheless remained at a relatively high level (Figure 27).

More men (65%) than women were reported with TBE. The incidence was highest among people in the age group 40–79 years, but there were cases reported from 1 to 90 years of age. Normally, there are few young children reported with TBE and this was the case also in 2019 with only two cases among children below the age of 5.

All but six cases had acquired their infections in Sweden. The other countries of infection were Finland, Germany, Lithuania and Norway. The first TBE case became ill as early as in late January and the last in November. The peak occurred in July and August, when most people fell ill. There was a lower incidence during the autumn months of 2019 than during the previous two years with a record number of cases.

As before, the majority of cases were infected in a geographic area that runs like a belt across Sweden, from the regions of Stockholm, Södermanland, Uppsala and Östergötland in the east to Västra Götaland and Värmland in the west (Figure 28). In addition, TBE is widely distributed in several parts of the rest of southern and central Sweden. Cases were reported from the region of Skåne in the south to Gävleborg and Dalarna in the north. TBE is gradually spreading westwards and in 2019 many cases were reported from, for example, the regions of Värmland, Västmanland and Västra Götaland. However, more people than usual were also infected in the regions of Gävleborg and Östergötland.

DISCUSSION

The TBE incidence has shown a significantly rising trend during the last three decades, but similarly to 2017 and 2018 there were still considerably more cases reported in 2019 than expected.

Although most human cases acquire the TBE infection via tick bites the infection can be food-borne. Outbreaks and

Number of cases

- No cases
- 1–3
- 4–7
- 8–14

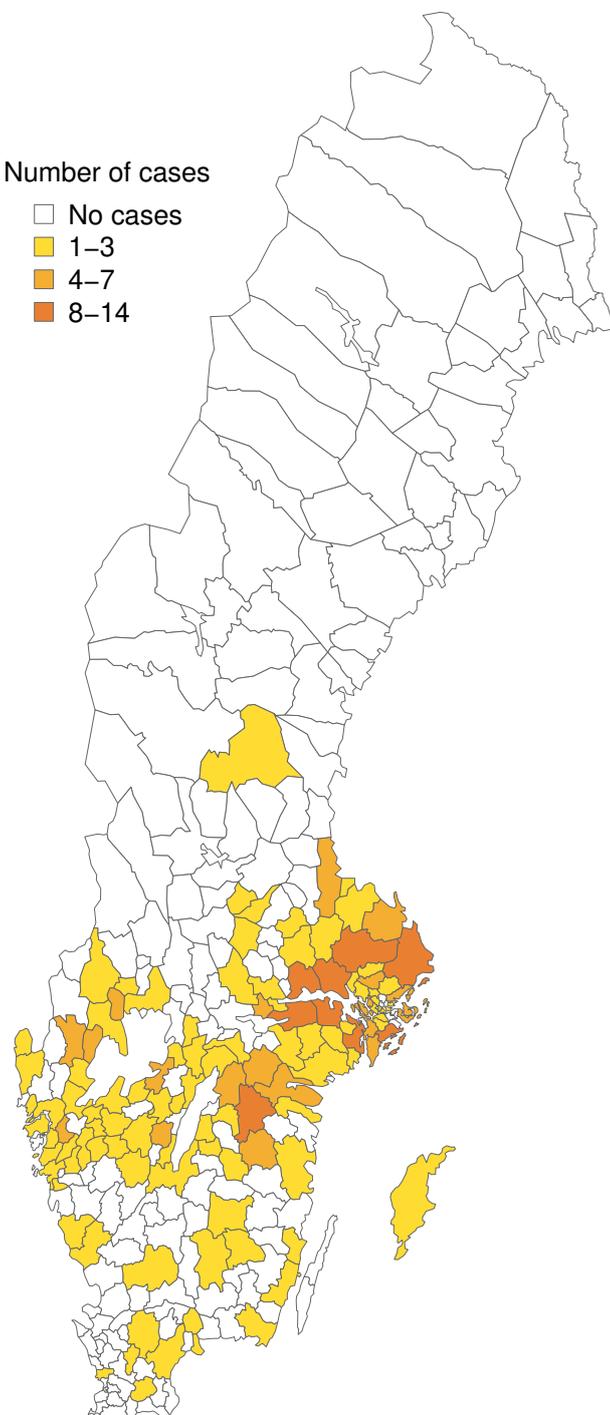


Figure 28: The municipalities of infection of the TBE cases during 2019. ©EuroGeographics for the administrative boundaries.

clusters of cases of TBE caused by consumption of unpasteurised milk or milk products have been described in Baltic, Balkanise and central European countries. The survey performed in Sweden in 2019 showed that the virus circulates in the Swedish population of dairy cattle.

The long-term increase in TBE incidence is probably due to several interacting factors. The most important cause is presumably the very dense population of ticks, a consequence of a large roe deer population from the 1980s up until the recent snowy winters. This situation in combination with a high population of small host animals such as bank voles, and optimal weather for both virus spread and humans spending time outdoors, could explain the large number of cases reported.

Trichinellosis



Trichinella occurs in wild carnivores in Sweden, but the risk of getting infected with the parasite from Swedish food-producing animals is negligible. During 2019, a total of 232 bears were tested for *Trichinella*, all were negative. Photo: Marc Scharping/Shutterstock.

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 and meat products, often cold-smoked, fermented sausages. In Western Europe, the wild boar appears to be the main source of human infection.

In Europe, *T. spiralis* and *T. britovi* are the dominant causes of human infections. These species are also detected in Sweden as well as *T. nativa* and *T. pseudospiralis*. *T. pseudospiralis* is mainly isolated from wild boars. In the gut, *Trichinella* larvae develop into adult worms and mate. After mating, the female releases larvae which penetrate the intestinal mucosa and travel via the bloodstream to various organs and muscles. In striated muscles the larvae may survive in an encapsulated form for years.

In Sweden, *Trichinella* has been monitored at slaughter in domestic pigs since the 20th century. From 1970–1990 sporadic cases were detected in domestic pigs, but since 1994 there have been no cases. The parasite is endemic, albeit at a low level, in Swedish wildlife.

The disease is extremely rare in Sweden and detected human cases are usually infected abroad. Since 2004 only seven human cases with confirmed infection with *Trichinella* have been reported; all except one (in 2013) were infected abroad.

DISEASE

Animals

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

Humans

In humans, the disease can range from subclinical infection to fatal disease. The incubation period varies from 5–15 days. Symptoms initially involve diarrhoea and abdominal pain and later muscle pain, fever, oedema of the upper eyelids and photosensitivity. Intestinal stages of the disease respond well to treatment. Cardiac and neurological complications may occur 3–6 weeks post infection. *Trichinella* is not transmitted between humans.

LEGISLATION

Animals

Trichinella is notifiable in animals according to SJVFS 2013:23. Official controls for *Trichinella* in meat is regulated by Commission Implementing Regulation EU 2015/1375 of 10 August 2015.

Humans

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

SURVEILLANCE

Animals

Testing for *Trichinella* is part of routine meat inspection for domestic pigs, horses, wild boars and other animal species that can become infected. Since 2014, Sweden applies reduced testing of domestic pigs from holdings officially recognized to apply controlled housing conditions (EU 2015/2013). The risk of *Trichinella* infection in pigs from such production sites is considered as negligible and only certain categories of pigs have to be tested. In Sweden, all carcasses of breeding sows and boars sent for slaughter are examined, while fattening pigs originating from controlled holdings are not obligated to test for *Trichinella*. Pig production sites without controlled housing conditions should test all their slaughtered domestic pigs. The digestion method is the only method applied in testing for *Trichinella*.

All slaughtered horses, and all wild boars and bears delivered to game handling establishments, are tested for *Trichinella*. Also, most hunters test wild boars and bears consumed in private households. In addition, to monitor the occurrence of *Trichinella* in the environment several species of wild animals are tested for *Trichinella*, including foxes, lynxes, wolves, wolverines, badgers and birds of prey. Testing of *Trichinella* in animals was performed by five laboratories during 2019.

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 2019, the number of tested pigs from controlled housing conditions were 22 928 breeding sows, 269 boars and 1 459 867 fattening pigs. In addition, 503 367 slaughtered pigs (all categories) from uncontrolled housing conditions were tested. The number of slaughtered and tested horse was 1749. *Trichinella* was not detected in domestic pigs or horses.

Trichinella spp. was detected in 5 out of a total of 138 374 (0.004%) wild boar samples and also in 6 lynx, and 2 wolves, see Table 27. These figures are based on results from examination of samples from animals submitted to wild game establishments (19 136 wild boars and 153 bears) as well as samples submitted for testing by private hunters. In addition, samples were taken from selected wildlife species (primarily carnivores) sent to the National Veterinary Institute within the general surveillance program for wildlife diseases.

Humans

No human case of trichinellosis was reported in 2019.

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 27: Findings of *Trichinella* in wild animals 2019.

Animal species	No. samples	No. positives	Percentage (%)	<i>T. britovi</i>	<i>T. nativa</i>	<i>T. pseudospiralis</i>	<i>T. spiralis</i>	<i>T. spp.</i>
Badgers	8	0	0.00%	-	-	-	-	-
Bears	232	0	0.00%	-	-	-	-	-
Beavers	33	0	0.00%	-	-	-	-	-
Beech marten	1	0	0.00%	-	-	-	-	-
Lynx	130	6	4.62%	2	3	-	1	-
Raccoon dog	1	0	0.00%	-	-	-	-	-
Red fox	11	0	0.00%	-	-	-	-	-
Seals	11	0	0.00%	-	-	-	-	-
Wild birds	61	0	0.00%	-	-	-	-	-
Wild boars	138 374	5	0.004%	-	-	5	-	-
Wolves	14	2	14.29%	1	-	-	-	1
Wolverine	1	0	0.00%	-	-	-	-	-
Total	-	13	-	3	3	5	1	1

Tuberculosis

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 1940's was above 300 per 100 000 inhabitants. This was followed by a rapid decline, beginning before effective treatment was available in the early 1950's. Currently, the yearly incidence is 4.8 per 100 000 inhabitants, which is among the lowest in the world. Around 90% of the cases are born outside of Sweden and the vast majority of them are immigrants originating from countries that still have a high incidence of TB. The yearly incidence among people born in Sweden is 1 per 100 000 inhabitants. A large majority of the cases detected in humans in Sweden are caused by *M. tuberculosis* and only a few cases per year are caused by *M. bovis*.

DISEASE

The symptoms caused by TB in both humans and animals depend largely on the localisation of the infection. The disease progresses slowly, and clinical signs may take a long time to develop, even in cases with substantial lesions. Weight loss and sometimes coughing (in cases with respiratory tract infection), ascites (due to infection in intestinal lymph nodes or liver) or mastitis (mainly in cattle with udder infection) can be seen. The incubation period varies from weeks to years.

LEGISLATION

Animals

Suspect and confirmed cases of infection with *Mycobacterium bovis* or *M. tuberculosis*, are notifiable in all animal species according to the Swedish Act of Epizootic diseases (SFS 1999:657, with amendments), other mycobacteria in the *M. tuberculosis*-complex are notifiable according to the Swedish act on notifiable animal diseases and pathogens (SJVFS 2012:24).

Humans

Tuberculosis in humans is a notifiable disease according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2013:634). Contact tracing is compulsory, and the treatment is free of charge. Refusing treatment as a patient when being contagious can lead to detention.

SURVEILLANCE

Passive surveillance

Animals

TB is notifiable both on suspicion and confirmed diagnosis and farmers and veterinarians are obliged to report suspicion of TB. Clinical signs in animals or lesions detected at slaughter, surgery or postmortem of an animal prompt investigations, which may include sampling for histopathology, bacteriology, PCR, tuberculin testing of contact animals and epidemiological investigations.

Surveillance for TB is mainly performed by meat inspection at slaughter of food producing animals. Official inspectors from the Swedish Food Agency perform the inspections. Suspect lesions are sent to the National Veterinary Institute for histology and bacteriology, as described above. For tissue from macroscopic lesions indicating TB, histology and direct smears are performed. If TB cannot be ruled out by histology or if direct smears are positive, culture is performed. Cultures are performed on solid media (Löwenstein-Jensen and Stonebrink's) at the National Veterinary Institute and cultured for up to twelve weeks. Suspected colonies are tested with PCR and, if necessary, with sequencing of a specific gene. Isolates suspected to belong to the *M. tuberculosis*-complex or where the *M. tuberculosis*-complex cannot be ruled out are sent for confirmation, e.g. to the Norwegian Veterinary Institute or the Public Health Agency of Sweden. Positive isolates are further subtyped.

Skin fold tuberculin tests are performed according to EC 1226/2002 (amending annex B of EC 64/432) and SJVFS 2003:33, (K62). The comparative intradermal test is used, mostly at the neck site. In case of positive tuberculin test reactors, the animal is culled and samples from organs with macroscopic lesions and lymph nodes from five different areas (retropharyngeal, submandibular, mediastinal, mesenteric and inguinal) are collected and examined as described above.



The tuberculosis control programme in Swedish farmed deer has been successful and is soon to come to an end. Photo: Jan Miko/Shutterstock.

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, until October 2012, based on regular whole-herd tuberculin testing, or whole-herd slaughter and meat inspection. Since October 2012, tuberculin tests are no longer performed in TB-free herds, but inspections at slaughter and postmortem of animals found dead or euthanized are still required.

A voluntary control programme in alpacas was launched

by Farm & Animal Health in 2015. Testing of alpacas for TB is done using a serological test (Enferplex) instead of an intradermal test as the intradermal test has a demonstrated low sensitivity in alpacas. All adult animals in the herd are serologically tested and all animal purchases and contacts with other herds are recorded.

Furthermore, tuberculin tests are performed at artificial insemination centres and prior to export of animals as required according to EU-legislation (Council Directive 64/432/EEC). Positive animals are treated as suspect cases of TB as described above.

RESULTS

Animals

Due to lesions detected at slaughter, 1 cattle, 1 goat, 10 pigs, 1 red deer and 5 fallow deer were investigated by histology and, where relevant, by culture and PCR. From these samples NTM (Non-tuberculous mycobacteria), from the *Mycobacterium avium/intracellulare*-complex were isolated from 1 red deer and 3 fallow deer (all in the same herd). No other slaughterhouse samples yielded any mycobacteria.

Due to clinical suspicions, macroscopic lesions, or findings of acid-fast bacteria, samples from two dogs and three cats were investigated. *Mycobacterium microti* (which belongs to the *M. tuberculosis*-complex) was isolated from a sample from a swollen prescapular lymph node from one of the dogs, a Swedish born hunting dog. The dog was euthanized, but further macroscopic lesions were not found. No other sample yielded any mycobacteria.

Furthermore, epidemiological investigation of an alpaca herd was done as part of contact tracing as the herd had purchased animals from a herd in UK where TB later had been detected. The herd joined the control program and the animals were serologically tested, with negative results

During 2019, 11 alpacas, 1 llama, and 1 camel were tested serologically in relation to export or import. Within the voluntary control program, 292 alpacas and 1 vicuna were tested, all with negative final results.

In 2019, there were approximately 300 holdings with farmed deer that were considered active. All except two had obtained TB free status. The two herds remaining were 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 2019.

Humans

The total number of detected cases of tuberculosis in humans in 2019 was 491, out of these, three cases of *M. bovis* were reported in humans in 2019; all three cases with extrapulmonary TB and all three most probably infected in their respective country of origin; El Salvador, Kuwait and Syria. All three isolates were unique when analysed with whole genome sequencing.

DISCUSSION

In summary, the overall TB situation in animals and humans remains favourable.

The case of *M. microti* in a dog was the first finding of *M. microti* in animals in Sweden since a finding of *M. microti* in a Suricat (exotic to Sweden) in a Zoo in 1991. *M. microti* has been described to occur in wildlife (e.g. voles) in several countries, and a limited number of cases in livestock, pets and humans have also been described. The epidemiological investigation did not identify the source of infection, but it did reveal that the dog had been in close contact with wildlife. The *M. microti*-situation in Swedish wildlife is largely unknown. *M. microti* has not been reported in humans in Sweden for at least ten years, if ever.

No cases of TB were detected in Swedish livestock during 2019. The officially free status for bovine TB in cattle has been maintained during 2019. Although the surveillance is mainly dependent on inspections of slaughtered animals,

this has been considered sufficient. However, the rate of submission of lesions from slaughtered ruminants has decreased over the years and work has been initiated in 2019 to increase submissions. Work is also ongoing to introduce PCR as initial analytic test. Passive surveillance based on clinical suspicions and post mortem findings will always have a low sensitivity as clinical symptoms and massive lesions are mainly seen in late stages of the infection. The eradication efforts in farmed deer have been successful and the probability that Swedish farmed deer are TB free is high. The aim is to eventually declare all deer herds officially free. Livestock imports to Sweden are very limited, and TB is an internationally regulated disease which means that precautionary measures are taken.

The rapid decline of TB in humans in the 1940's coincided with the eradication of TB in cattle and started before the introduction of effective treatment in the 1950's. 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 Rúa-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



In 2019, the incidence of human cases of tularaemia in Sweden was higher than any of the past 50 years. The high incidence was also associated with an increase in the number of reported dead hares. Photo: Jaro Mikus/Shutterstock.

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 species in Sweden and other countries have detected antibodies but no signs of disease.

Humans

Tularaemia can be manifested in different forms depending on the route of transmission and on the virulence of the organism. The ulceroglandular form is the most commonly diagnosed form and is more frequently seen than the typhoidal form. The pneumonic, oculoglandular and oropharyngeal forms are rarely diagnosed. In the ulceroglandular form, a local ulcer usually appears at the site of infection and the adjacent lymph nodes are enlarged. The general symptoms of tularaemia are high fever, headache and nausea.

LEGISLATION

Animals

Tularaemia is notifiable in animals (SJVFS 2013:23).

Humans

Tularaemia has been a notifiable disease since 1970 according to the Communicable Disease Act (SFS 2004:168) with the amendments of SFS 2013:634.

SURVEILLANCE

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.

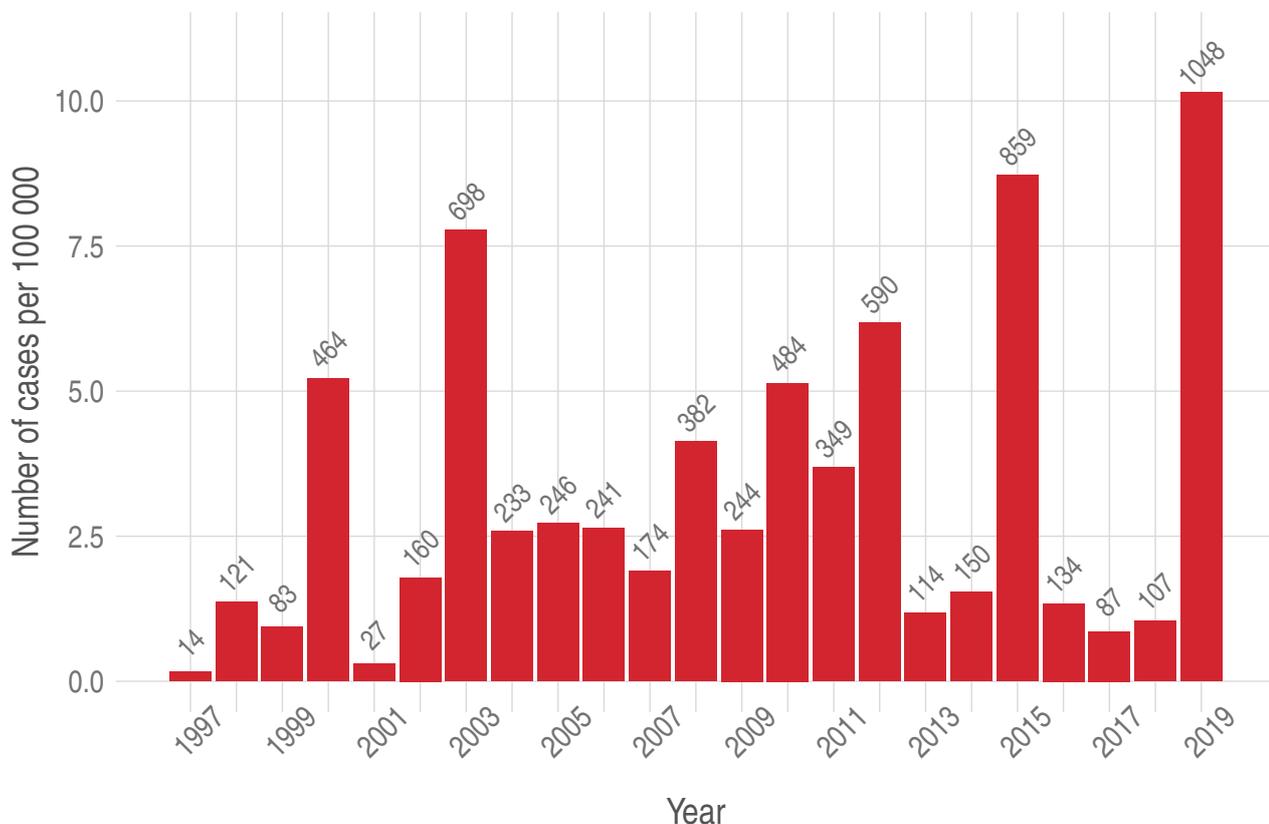


Figure 29: Incidence of notified human cases of tularaemia in Sweden 1997–2019. Bars indicate the incidence per 100 000 inhabitants and adjacent numbers the total number of cases reported.

IN FOCUS: The 2019 tularaemia outbreak

In the summer and autumn of 2019, Sweden experienced its largest outbreak of tularaemia in over 50 years. The beginning of the outbreak was noticed at the end of July in the County of Gävleborg, where residents of or visitors to the town of Ljusdal started to seek health care with fever and swollen lymph nodes. At the beginning of August an increasing number of cases with tularaemia were also registered in the neighboring Counties of Dalarna and Örebro in central Sweden. At the same time, SVA noticed an unusually large number of reports about dead hares from across the country. Tularaemia had been detected in several of the hares.

The following weeks the number of cases increased rapidly, and by the end of the month over 650 people had fallen ill, mainly in the Counties of Dalarna and Gävleborg (Figures 30 and 31). Reports of disease symptoms from these two regions indicated infection through insect bites. Mosquito sampling near a golf course in the aforementioned town of Ljusdal revealed findings of *Francisella tularensis*.

It was not until the last week of September that the disease counts were back to normal for the season. Tularaemia cases in both humans and hares were, in addition to the endemic areas in northern and central parts of Sweden, found far south (Figure 30). The number of examined and diagnosed hares depends on people finding and submitting carcasses for examination. Statistics in humans are more reliable since most affected humans probably will seek health care. It can be assumed that the

geographic distribution of cases and peaks in the number of cases would be roughly similar for hares and humans if all hares were found and examined.

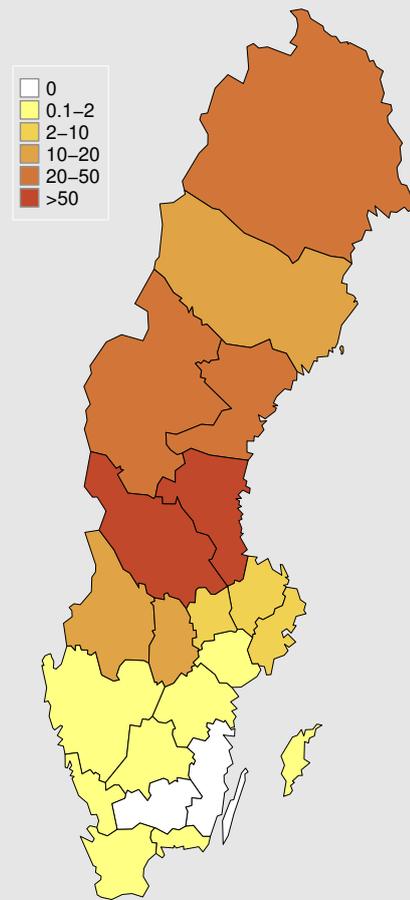


Figure 30: Incidence of reported human tularaemia cases by County in Sweden 2019. The colour scale represents the number of cases per 100 000 inhabitants.

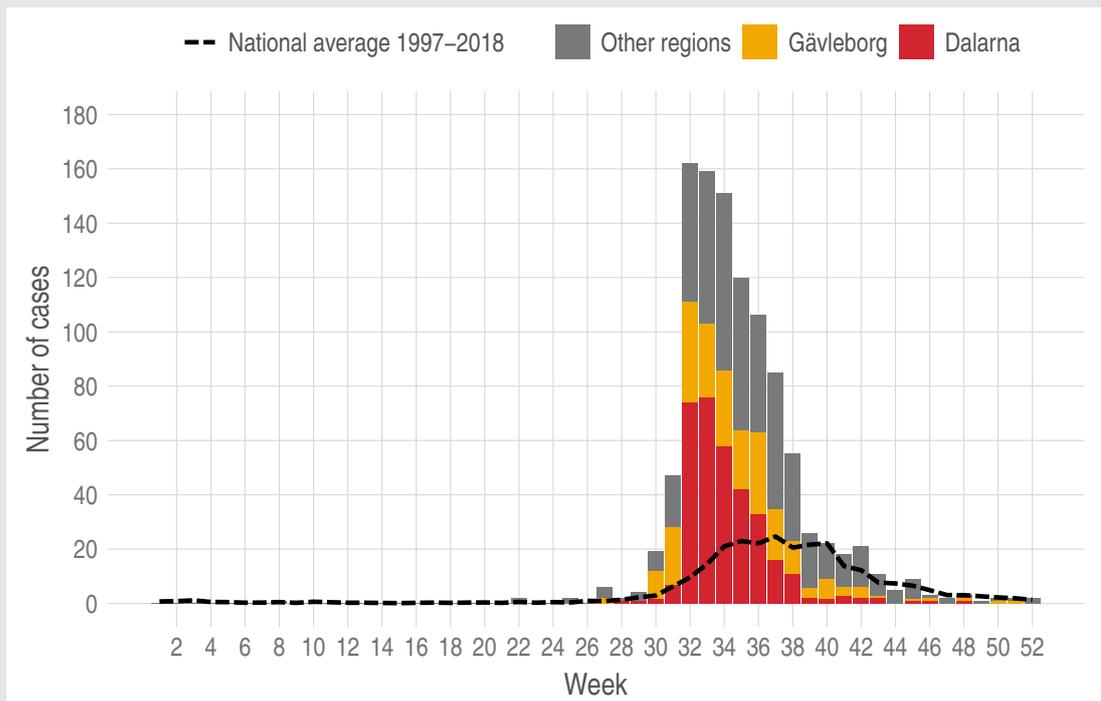


Figure 31: Number of reported human cases per week in 2019 and as an average 1997-2018. For 2019, data for the Counties of Dalarna and Gävleborg are highlighted in red and yellow, respectively.

RESULTS

Animals

In 2019, 128 European brown hares and 48 mountain hares were examined. Due to a tularaemia outbreak during summer and autumn, the number of reports of dead hares and the number submitted for examination were much higher during 2019 compared to years with no outbreaks. *F. tularensis* subsp. *holarctica* was detected in 27 European brown hares and 31 the mountain hares. They all died of an acute disease spread to several organs, quickly leading to death due to septicaemia. The number of tularaemic hares started to slowly increase in July, a peak appeared during August and September followed by a decline in October. The highest number of cases originated from the counties Norrbotten (12 cases), Västerbotten (5 cases), Jämtland (9 cases), Dalarna (6 cases) and Stockholm (5 cases). In the remaining counties where tularaemia was found, the number of cases ranged from one to three. The only counties with no tularaemia diagnosed in hares were Kalmar, Kronoberg, Skåne and Gotland. This could be compared to the outbreak year 2015 when tularaemia was diagnosed in 31 hares, the majority of which originated from an outbreak area in Norrbotten.

Humans

In 2019, 1048 human cases of tularaemia were reported, ten times more than 2018 (n=107) and a higher number than the outbreak year 2015 (n=859) (Figure 29). Of the cases, all but eight were reported as infected in Sweden. For the population as a whole, the incidence was 10.1 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. The reasons behind the annual and regional fluctuations observed are not known.

More men (54%) than women were reported to be infected in 2019, 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.

During 2019, the incidence was highest in the County of Dalarna with 116 cases per 100 000 inhabitants, followed by the County of Gävleborg with 81 cases per 100 000 inhabitants. A number of other Counties also reported many disease cases and an incidence of more than ten cases per 100 000 inhabitants was seen in western Svealand and the whole of Northern Sweden. For all cases except eight, Sweden was designated as country of infection.

During the first half of 2019, only a few cases were reported. The number of cases started to increase in July and peaked in August. A rapid decline was seen in September, which was followed by a more subdued decline during the last months of the year.

DISCUSSION

Tularaemia has been endemic in northern and central Sweden at least since the early 20th century with a marked annual variation. Years with high numbers of cases are often followed by periods when the disease is virtually absent. There is no obvious explanation for these fluctuations. Probably, variations in population sizes of host animals and insect vectors that can transmit infection to humans play a major role which in turn is influenced by factors such as predators, diseases, weather and climate.

During the last two decades, the epidemiology of tularaemia has changed and the number of reported cases in humans and animals, mainly hares, infected south of the previous endemic region is increasing. Since the information on diseased and dead hares is dependent on voluntary reporting and submitting animals for investigation the true numbers are not known. However, the reporting and submissions were remarkably high during 2019 and hares diagnosed with tularaemia were found in most counties, including the south of Sweden. Based on the geographical and temporal distribution of submitted hare cases it can be assumed that the geographic distribution of cases and peaks in number of cases is roughly similar for hares and humans.

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 food-borne 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 killed by heating (pasteurisation and cooking) but can grow at refrigerator temperature and in vacuum and modified atmosphere packaging.

During 2014–2015, a survey of the presence of *Y. enterocolitica* on Swedish finishing pig farms was conducted, involving 105 farms. A herd-level prevalence of 30.5% was found, and the identified bioserotypes were *ail* gene (attachment-invasion locus gene) positive 4/O:3 and 2/O:9, which are considered to be human pathogens. These results indicate that the Swedish domestic pig population has a *Y. enterocolitica* status similar to other pig producing countries in Europe. In 2016, a longitudinal study of 8 previously positive pig herds was conducted. All herds were still positive for *Y. enterocolitica* in at least one of the samples collected, indicating that *Yersinia* is persistent in positive pig production chains.

Human yersiniosis in Sweden is primarily a domestic infection.

DISEASE

Animals

Pigs are asymptomatic intestinal carriers of pathogenic *Y. enterocolitica* and *Y. pseudotuberculosis*. Infection with *Y. pseudotuberculosis* in other animals may vary from asymptomatic to severe mesenteric lymphadenitis and lead to septicæmia and death. *Y. enterocolitica* has occasionally been isolated from cats and dogs with diarrhoea.

Humans

Y. enterocolitica causes gastrointestinal symptoms in humans ranging from mild self-limiting diarrhoea to acute mesenteric lymphadenitis, which might be difficult to differentiate from appendicitis. *Y. pseudotuberculosis* causes

primarily abdominal pain, fever headache and erythema nodosum, a skin reaction. The infection can be complicated by long-term sequelae including reactive arthritis, uveitis and glomerulonephritis (kidney disease).

LEGISLATION

Animals

Y. enterocolitica and *Y. pseudotuberculosis* are not notifiable in animals.

Food

Detection of *Y. enterocolitica* and *Y. pseudotuberculosis* in food is not notifiable.

Humans

Yersiniosis (isolation or identification by PCR of *Y. enterocolitica* (other than biotype 1A) or *Y. pseudotuberculosis* from a clinical sample) is notifiable according to the Communicable Disease Act (SFS 2004:168 with the amendments of SFS 2013:634). Diagnosis of yersiniosis by serology is not notifiable.

In 2012, the case definition for notification of yersiniosis was revised. The previous case definition stated that human pathogenic *Yersinia* was notifiable. In 2013 it was clarified that infection with *Y. enterocolitica* biotype 1A was not notifiable. Notification was also extended to include both culture and PCR identification.

SURVEILLANCE

Animals

Active surveillance for *Yersinia* was not conducted during 2019, but some materials were submitted for routine health examinations or because of clinical disease.

Food

No official control programme exists for *Yersinia spp.* National and local authority may perform sampling as a part of extended official controls or targeted projects. Sampling may be performed by food business operators, but analysis results are not normally reported to the authorities.

Humans

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

RESULTS

Animals

Samples tested for *Yersinia* at SVA during 2019 included 60 samples from mostly zoo and laboratory primates and rodents. *Y. enterocolitica* was isolated from 3 primates,

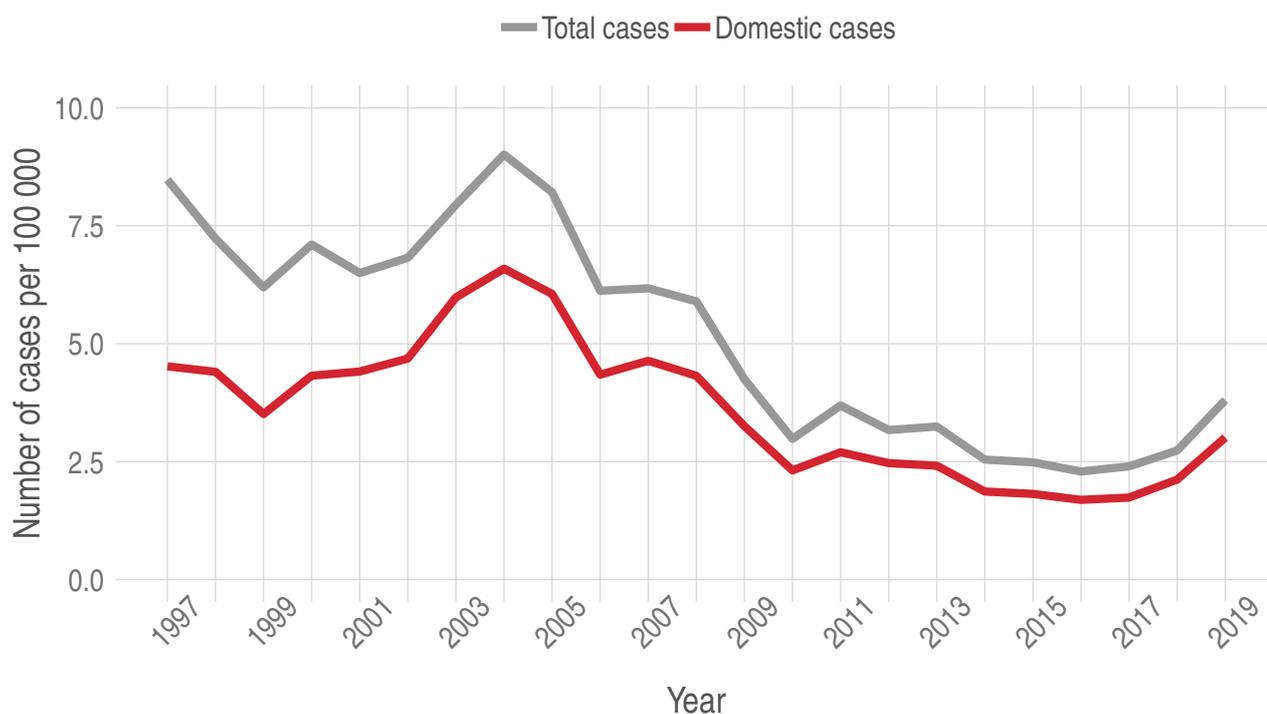


Figure 32: Notified incidence (per 100 000 inhabitants) of human cases of yersiniosis in Sweden, 1997–2019.

Y. pseudotuberculosis from 1 primate, *Yersinia* spp. from 1 rodent and *Y. enterocolitica* in a domestic finishing aged pig as an incidental finding at postmortem.

Food

In 2019, national and local authorities took 14 samples from different types of food. No sample was positive for *Yersinia* spp.

Humans

During 2019, 393 cases were reported (3.8 cases per 100 000 inhabitants). This is the highest incidence in ten years. The proportion reported as infected in Sweden increased from around 75% previous years to near 80% of the cases (Figure 32).

Similar to previous years, the incidence was high among children younger than five years. The incidence was 9.5 (cases per 100 000 inhabitants) for infants and 5.1 for children 1–4 years old, compared to 3.8 for all cases. In 2019, the incidence was also high among persons 15–39 years old (5.5) due to two large outbreaks that particularly affected people of these ages.

Yersiniosis follows a minor seasonal variation with the highest number of cases infected in Sweden during the summer. However, during 2019, the majority of cases were reported during spring with one peak in March and one in May where two larger outbreaks were identified (Figure 33). For the majority of cases species was reported, with 307 being *Y. enterocolitica* and eight *Y. pseudotuberculosis*.

The majority of yersiniosis cases are considered to be 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

Two larger outbreaks were identified in 2019 and both mainly included cases in the age group 15–39. In the first outbreak, an unusual increase of cases of *Y. enterocolitica* and *Y. enterocolitica* O3 biotype 4 was identified. Isolates were sent in to the PHAS for typing using WGS and the majority of isolates formed a tight cluster within sequence type (ST) 18. The outbreak sequence was shared internationally and Denmark reported a match and informed PHAS that they had identified an increase of cases during the same time period. A case-control study was conducted in both countries that indicated an association of cases with the consumption of a fresh vegetable. Specifically, in the Danish case-control study, there was a clear link to fresh spinach from a specific large retail store. A trace-back investigation was conducted and a common producer of fresh spinach was identified supplying both the Danish and Swedish markets via different wholesalers. In total, 57 cases were identified where 37 came from Sweden. The second outbreak was identified immediately after the spinach related outbreak (Figure 33). The majority of cases in this outbreak were reported in May. In total, 30 cases, and all isolates formed a cluster within the same bioserotype of *Y. enterocolitica* as the first outbreak. However, no source could be identified in this second outbreak. Both outbreaks identified a recent challenge with the primary diagnostics of yersiniosis. PCR panels for analysis of bacterial gastroenteritis does not always separate those *Yersinia* that require mandatory notification, *i.e.* those regarded as pathogenic to humans, from the ones that are not notifiable.

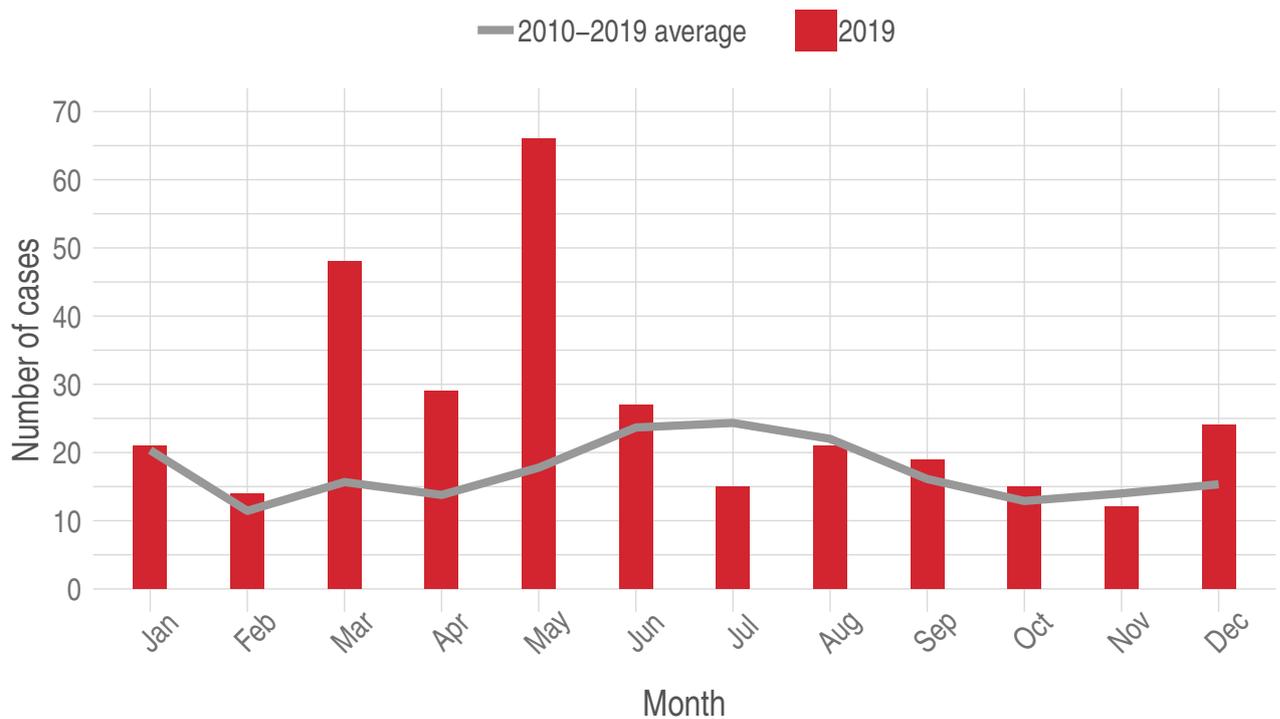


Figure 33: The domestic human case count of yersiniosis by month during 2019 and the mean number of cases per month over the past 10 years illustrates the March and May outbreak peaks during 2019.

DISCUSSION

Since the beginning of the 2000s, the number of reported cases of yersiniosis has decreased not only in Sweden but also in the entire EU. This decrease has occurred without any active interventions in the food chain. The last couple of years, however, the number of cases in Sweden has started to rise again. It remains to be seen if this increase is due to random outbreaks or is the beginning of a new trend with increasing number of cases.

Yersiniosis in humans is considered foodborne and most infected cases are of domestic origin. Outbreaks are rare, and most infections seem to be 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 in the Swedish-Danish outbreak in 2019. Good agricultural practices, as well as, good slaughter hygiene and good manufacturing practices in food processing are essential for control of *Yersinia*.

REFERENCES

Sannö A, Aspán A, Hestvik G, Jacobson M (2014) Presence of *Salmonella* spp., *Yersinia enterocolitica*, *Yersinia pseudotuberculosis* and *Escherichia coli* O157:H7 in wild boars. *Epidemiol Infect* 142:2542–2547

Lindblad M, Lindmark H, Thisted Lambert S, Lindqvist R (2007) Microbiological baseline study of swine carcasses at Swedish slaughterhouses. *J Food Prot* 70:1790–7

Boqvist S, Pettersson H, Svensson A, Andersson Y (2009) Sources of sporadic *Yersinia enterocolitica* infection in children in Sweden, 2004: a case-control study. *Epidemiol Infect* 137:897–905

Swedish Board of Agriculture, National Food Agency, the Public Health Agency of Sweden, the National Board of Health and Welfare and the National Veterinary Institute. *Infektion med Yersinia enterocolitica – ett nationellt strategidokument* ISBN 978-91-7555-116-6 Artikelnr 2013-11-18

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

Additional Surveillance 2019

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 and wild pigs, in its acute form characterised by haemorrhagic fever and high case fatality rates. The disease is endemic in large parts of sub-Saharan Africa and on the Island of Sardinia, Italy, but has expanded its geographical distribution during the last decade. ASF is currently present in large parts of Europe where it continues to spread, in particular among wild boar populations and in spite of the extensive disease control measures implemented. The risk for further spread within EU is considered high. In addition, in August 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 and has since spread to large parts of Asia. With these developments, ASF is currently considered a global threat.

Anthrax

Anthrax is a serious zoonotic disease that may affect most mammals, especially herbivores. It is caused by *Bacillus anthracis*, a spore forming bacterium. The spores are highly resistant and may survive in the soil for decades. The disease was common in Swedish livestock in the beginning of the 20th century, with a significant reduction in frequency of outbreaks during the latter part of the century. During the last decade, however, the disease has re-emerged in the country with reported outbreaks in 2008, 2011, 2013 and 2016. The disease is endemic in most countries of the world.

Foot-and-mouth disease

Foot-and-mouth disease (FMD) is a highly contagious disease of cloven-hoofed animals such as pigs, cattle, sheep and goats. The case fatality rate in FMD is low, but morbidity very high and convalescence is extended, which cause severe production losses. The cost of disease eradication in countries previously free from the disease is extremely high.



Clinical surveillance constitutes a fundamental part of the animal disease surveillance system in Sweden and it depends on the cooperation between many stakeholders in the field (such as animal keepers and veterinarians) and the central veterinary authorities. Photo: Verónica Löfgren.

FMD is endemic in many parts of the world, but since 2011 the disease is absent in Europe. However, the major FMD epidemics that affected several European countries during the last twenty years demonstrated that the continent is continuously at risk for FMD virus introduction, and that early detection is crucial.

Newcastle disease

Newcastle disease (ND) is a highly contagious and often severe disease of domestic poultry and other birds, caused by virulent strains of avian paramyxovirus type 1. Wild birds are important reservoirs of the virus, which is transmitted through direct and indirect contacts between infected and non-infected birds. Since 1995, twenty outbreaks of ND have occurred in Sweden, all of which have been successfully eradicated. Sweden has status of ND free without vaccination (Commission Decision 95/98/EEC).

Table 28: Suspicions of epizootic diseases reported and further investigated between 2014–2019, based on sampling of sick or dead animals.

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

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

^BIncludes wild boar found dead, also described in the specific chapter on infectious diseases in wild boar.

^CIncludes one sheep from the intensified surveillance.

^DDoes not include surveillance of, or cases in, wild birds. One case was negative after autopsy.

^EThe increased number of clinical suspicions in 2018 and 2019 compared to previous years is the result of substantial efforts to detect and notify animals with clinical signs compatible with BSE.

^FDoes not include surveillance of, or cases, in the intensified sampling.

^GOne case was negative after autopsy.

^HReported as cases per herd or owner, surveillance at slaughter included.

LEGISLATION

Clinical suspicions of epizootic diseases, including ASF, anthrax, FMD and ND, must be notified to the Swedish Board of Agriculture in accordance with the Swedish Act of Epizootic diseases (SFS 1999:657 with amendments). This obligation applies to animal keepers, official and private veterinarians, veterinary laboratories, and other relevant stakeholders. Suspicions are investigated after consultation with disease experts at the National Veterinary Institute and following notification to the Swedish Board of Agriculture, and sampling and analysis carried out in accordance with diagnostic manuals of the EC as applicable (ASF 2003/422/EC; FMD 2003/85/EC annex XIII; ND 92/66/EEC annex III). In addition, a number of other infectious diseases are notifiable to the Board of Agriculture and/or the relevant County Administrative Board based on laboratory confirmation or clinical suspicion (SJVFS 2013:23).

SURVEILLANCE

Every year, hundreds of suspicions of serious infectious diseases are reported by field veterinarians, animal owners or private veterinary pathologists to the experts at the National Veterinary Institute. Many of these suspicions can be ruled out already based on anamnesis and initial clinical investigation, whereas others require notification to the Swedish Board of Agriculture and further investigation including sampling of sick or dead animals, with movement restrictions imposed on the farms during the investigation. Also, in cases in which an epizootic disease is not primarily

suspected, but where it cannot be excluded based on clinical investigation, samples can be submitted for laboratory investigation to exclude a diagnosis. This can only be done after discussions with experts at the National Veterinary Institute and in consultation with the Swedish Board of Agriculture. This approach serves to reduce the threshold for submitting samples for analysis of notifiable diseases, and thereby increasing the sensitivity of the system. The Swedish Board of Agriculture covers all costs for veterinary visits, transports, and diagnostic analyses related to the investigation.

African swine fever

Reported cases of increased mortality or serious morbidity, with clinical signs such as haemorrhagic disorders or reproductive failures in pigs are considered suspicions of ASF until ruled out through further clinical investigation. Samples are sent to the National Veterinary Institute for laboratory analyses. Due to clinical similarity, samples from domestic pigs collected for ASF are also analysed for CSF. This strategy is strongly recommended by the EU.

Given the current situation in Europe as regards ASF in wild boar, the surveillance is enhanced, and Swedish public are encouraged to report all findings of dead wild boar. If possible, carcasses or samples are taken in and investigated to rule out ASF as the cause of death (see also specific chapter on infectious diseases in wild boar). Reports of two or more wild boar found dead in the same location, or of wild boar found dead with signs suggesting ASF, are included in the surveillance as clinical suspicions.

Anthrax

Cases with a history of sudden deaths in more than one animal on the premise are considered suspicions of anthrax. Clinical signs such as fever, bloody discharges from the nose, mouth, anus or vagina, uncoagulated blood, subcutaneous oedematous swellings and lack of rigor mortis, as well as recent landscape interventions such as dredging or digging in areas accessible to the animals, strengthens the suspicion. In addition, cases with gross pathological lesions suggestive of anthrax found at postmortem are considered suspicions of anthrax. Samples from suspected cases are sent to the National Veterinary Institute for laboratory analyses.

During 2019, the surveillance in the area affected by anthrax during 2016 was enhanced. All cattle, sheep and wild ruminants found dead in the area, with no obvious cause of death, were investigated 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 National Veterinary Institute for analyses.

Newcastle disease

Reported cases of disease in poultry, or other birds kept in captivity, that present a significant reduction in egg production (egg drop) and deterioration of egg shell quality are considered suspicions of ND, even without more severe clinical signs such as increased mortality, nervous signs and respiratory distress. Samples are sent to the National Veterinary Institute for analyses. Due to clinical similarity, samples from poultry collected for ND are in general also analysed for avian influenza.

In addition, an active ND surveillance component is present within the Poultry Health Control Programme targeting breeding flocks (described in the specific chapter related to this programme).

RESULTS

The suspicions of epizootic diseases that were reported and further investigated based on sampling of sick or dead animals between 2014–2019 are compiled in Table 28.

In 2019, three clinical suspicions of ASF in domestic pigs and two in wild boar were investigated, with negative results. Samples from all suspicions in domestic pigs were also analysed for CSF and PRRS, and one for anthrax, all with negative results. In addition, thirty-three samples from wild boar found dead were analysed for ASF, as part of the enhanced passive surveillance, all with negative results.

Eleven clinical suspicions of anthrax in cattle, two in sheep and one in pig were reported and investigated. In addition, one sheep 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 suspicion of FMD was investigated during 2019.

Ten clinical suspicions of ND were investigated of which one was positive for avian paramyxovirus-1.

Full characterisation including pathogenicity testing in this case was inconclusive and hence why ND was not confirmed. Samples from eight of the suspicions were also analysed for avian influenza with negative result.

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 timelines of detection depends, to a large extent, on the capacity of Swedish hunters to detect, and their willingness to report, findings of dead wild boar. The number of wild boars submitted by the public during 2019 in the enhanced passive surveillance has almost doubled compared to previous years, probably to some extent as a result of increased awareness of ASF among hunters and the general public. However, still less than 40 wild boar found dead were investigated in 2019 as part of the surveillance for ASF. Given the population size of Swedish wild boar (estimated to at least 250 000–300 000) and the expected number of wild boar that would die from other causes than hunting and road kills, and thus constitute the potential sampling frame for the surveillance, this number is 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_get-PDF.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, except for *Mycoplasma synoviae*, are notifiable according to provisions issued by the Swedish Board of Agriculture (SJVFS 2013:23). The diseases included in the programme during 2019 are briefly described below.

Fowl typhoid and pullorum disease

Fowl typhoid and pullorum disease are two poultry diseases caused by *Salmonella enterica* subspecies *enterica* serovar Gallinarum biovar Gallinarum (*Salmonella* Gallinarum, fowl typhoid) and biovar Pullorum (*Salmonella* Pullorum, pullorum disease), respectively. These two biovars of the same serovar are specifically adapted to poultry, and vertical transmission (from the hen to the chicken via the egg) is an important feature, in addition to the common horizontal spread. Pullorum disease mainly affects fetuses and chickens up to 3 weeks of age while *Salmonella* Gallinarum commonly infects and causes disease (diarrhoea, inappetence, production losses and mortality) in older birds. Both biovars are included in the Swedish zoonosis legislation (SJVFS 2004:2) as well as in the European legislation on trade in poultry and hatching eggs (Council Directive 2009/158/EC). The diseases were eradicated from the Swedish commercial poultry population in the beginning of the 1960's. A single case of fowl typhoid (*Salmonella* Gallinarum) was detected in a backyard flock in 1984 but has not been diagnosed since then. *Salmonella* Pullorum is however present in the Swedish backyard poultry population; the last outbreak was diagnosed in 2017.

Mycoplasma gallisepticum, *Mycoplasma synoviae* and *Mycoplasma meleagridis*

Mycoplasma gallisepticum, *M. synoviae* and *M. meleagridis* are important poultry pathogens. However, *M. meleagridis* is only pathogenic for turkeys. These three mycoplasmas can spread both horizontally and vertically. They mainly cause respiratory disease and egg production losses. *Mycoplasma*

gallisepticum and *M. synoviae* may also cause arthritis and are present in the backyard poultry population in Sweden. Testing of breeding flocks for *M. gallisepticum* and *M. meleagridis* (only turkey flocks) is included in the European legislation on trade in poultry and hatching eggs (Council Directive 2009/158/EC). Due to its potential to cause disease and production losses, testing for *M. synoviae* was included in the programme between 1995 and 2010. During a revision of the programme the agent was excluded but is since 1 June 2015 included again. In 2016, testing for *M. synoviae* was further intensified.

Paramyxovirus type 1

Paramyxovirus type 1 may cause outbreaks of Newcastle disease, with egg production losses, increased mortality, nervous signs and respiratory disease; the severity of the disease may vary. The virus is transmitted through direct and indirect contacts with infected birds and for shorter distances also with the wind. Wild birds are an important reservoir. Since 1995, twenty outbreaks of Newcastle disease have occurred in Sweden. The disease is included in the Swedish Act of Epizootic diseases (SFS 1999:657 with amendments). Since all outbreaks have been successfully eradicated, Sweden has a status of Newcastle disease free country without vaccination according to Commission Decision 95/98/EEC.

Egg drop syndrome

Egg drop syndrome virus is a naturally occurring adenovirus in waterfowl (including the wild population) in which it does not cause any clinical disease. In chickens, the clinical signs are only seen during the production period as decreased egg production in an otherwise clinically healthy flock. The virus is able to spread both vertically and horizontally. The Swedish poultry breeding population is free from the disease.

SURVEILLANCE

Serological screening within the programme is administered by the National Veterinary Institute and financed by the Swedish Board of Agriculture and the participating companies. In 2019, eight breeding companies participated in the programme; five broiler-, three laying hen- and one turkey breeding company (one company with both broiler- and laying hen parent flocks). In accordance with the provisions (SJVFS 2010:58), sixty blood samples were taken from the breeding flocks included in the programme, once during the rearing period and several times during the production period. In the majority of the flocks, blood samples are taken by the breeding companies' personnel after delegation from the official veterinarian. In the remaining flocks the official veterinarian takes the samples. The blood samples were sent by mail to the National Veterinary Institute where serological tests were performed. The sampling and testing schemes are presented in tables 29 and 30.

RESULTS

Table 31 gives an overview of all samples taken in breeding flocks of chickens and turkeys, and the laboratory methods used, during 2019. All analysed samples tested negative for paramyxovirus type 1.

Serological reactions to *M. synoviae* were detected in fifteen chicken parent flocks. The majority of these reactions could be linked to a change of method for confirmatory testing used for samples positive in the combined *M. gallisepticum*/*M. synoviae* ELISA. Fourteen flocks were considered free from *M. synoviae* based on clinical status and testing of new samples. However, in one flock new samples obtained two weeks later were also positive for *M. synoviae*.

Three chicken parent flocks were further investigated due to a few positive samples for *M. gallisepticum*. In addition, two chicken parent flocks were investigated due to a few positive samples for *Salmonella* Gallinarum/*Salmonella* Pullorum and Egg Drop Syndrome respectively. 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.

Table 29: Sampling schedule for chicken grandparent and parent flocks. Number of blood samples tested at different weeks of age.

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

Table 30: Sampling schedule for turkey parent flocks. Number of blood samples tested at different weeks of age.

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

DISCUSSION

In conclusion, the results from the serological screening in the Poultry Health Control Programme in 2019 support the status of freedom from several important infectious diseases in the Swedish breeding poultry population. However, the finding of *M. synoviae* antibodies in a chicken breeding flock and possible implications on animal health and production both in the breeding and in offspring flocks need to be further considered. *Mycoplasma synoviae* may spread both horizontally and vertically (from the hen to the chicken via the egg), hence infection in breeders may have consequences for the next generation as well. Infection may result in respiratory signs, articular disease and egg production losses. In addition, eggshell abnormalities associated with infection with *M. synoviae* have been reported. Antibodies to *M. synoviae* were also detected in chicken breeding flocks in 2016 and 2017. As *M. synoviae* is present in e.g. the hobby poultry population it is imperative to keep the breeding flocks under strict biosecurity measures. Wild birds might also play a role in the transmission of *M. synoviae*. Finally, the clinical surveillance of the poultry breeding population is also of utmost importance.

Table 31: Number of sampling occasions for grandparent (GP) and parent (P) flocks of chickens and turkeys and total number of samples tested during 2019.

Agent	No. of sampling occasions			No. of samples			Method
	Chickens		Turkeys	Chickens		Turkeys	
	GP	P	P	GP	P	P	
<i>S. Pullorum</i> / <i>S. Gallinarum</i>	14	99	4	840	5940	240	Serum plate agglutination test, antigen, Ceva Biovac
<i>Mycoplasma gallisepticum</i> / <i>Mycoplasma synoviae</i>	67	446	16	4020	26 760	960	<i>Mycoplasma gallisepticum/synoviae</i> Antibody Test Kit, ID. vet
<i>Mycoplasma meleagridis</i>	0	0	16	0	0	960	Serum plate agglutination test, antigen, Ceva Biovac
Paramyxovirus type 1	14	91	4	840	5460	240	NDV screen competition ELISA, ID.Vet
Egg drop Syndrome-virus	14	99	0	420	2970	0	Antibody haemagglutination inhibition test, antigen, GD Animal Health)

Infectious diseases in wild boar



Surveillance of infectious diseases in wild boar, which has been ongoing since 2000, provides evidence that the Swedish wild boar population remains free from several important diseases, including African swine fever, Classical swine fever and Aujeszky's Disease. Photo: Martin Mecnarowski/Shutterstock.

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 the disease is now found in the wild boar population of nine EU countries.

The Swedish wild boar population is increasing rapidly and is now estimated to be 250 000–300 000 animals. Established wild boar populations are found primarily in the southern parts of the country, but the northern border of the wild boar's range in Sweden is extending and it has, at present, passed the level of the river Dalälven. Surveillance of infectious diseases in Swedish wild boar has been ongoing since 2000. The purposes of this monitoring are to provide

evidence that Sweden is free from several important infectious pig diseases and to enable early detection of new introductions of these diseases into the country.

LEGISLATION

Several diseases capable of infecting wild boar, including ASF, CSF, AD, brucellosis and Porcine reproductive and respiratory syndrome (PRRS), are included in the Swedish Act of Epizootic Diseases (SFS 1999:657 with amendments) and are therefore notifiable upon clinical suspicion. If any of these diseases are suspected or confirmed, measures will be taken to control the disease and to prevent further spread.

SURVEILLANCE

Passive surveillance

An enhanced passive surveillance programme for ASF in wild boars has been in place since 2013. Anyone who finds a dead wild boar can voluntarily submit the whole carcass or samples from it to the National Veterinary Institute for post mortem examination. All submitted samples are analysed for the presence of ASF virus genome with PCR, whether lesions suggestive of the disease are present or not.

Additionally, 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.

Active surveillance

Since 2000, hunted wild boars throughout Sweden have been sampled yearly for surveillance purposes. Hunters voluntarily collect blood samples when free-living wild boars are harvested. The samples are sent to the National Veterinary Institute for analysis for the presence of antibodies to infectious agents that are of importance to domestic pig production. In 2019, the samples were used for the active surveillance of AD and CSF. The samples were tested for antibodies against AD and CSF using ELISA kits (SVANOVIR® PRV-gB-Ab ELISA, Svanova and IDEXX™ HerdChek CSFV Ab Test Kit, respectively). The surveillance was designed to detect these diseases at a 1% prevalence with a 99% confidence level. To reach this level of confidence, it was calculated that 500 samples would need to be submitted for analysis.

RESULTS

Passive surveillance

Two clinical suspicions of CSF or ASF in free-living wild boar were investigated in 2019. In one case, a group of three dead wild boars that showed no obvious cause of death was found by a hunter. All three animals were sampled and tested for CSF and ASF. In the other case, three individual wild boars were found dead without any outward signs of injury or illness in the same area within a short period of time. One of the animals was sampled (the other two carcasses could not be re-located) and tested for ASF. All samples collected during the two investigations were negative.

Thirty-four wild boar that were found dead were submitted by members of the public for examination for the presence of ASF virus genome in 2019. This 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 geographic distribution of the sampled dead wild boars is shown in Figure 34. 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” in this report.

Active surveillance

In 2019, 104 blood samples were collected from hunted wild boar and analysed for the presence of antibodies against AD and CSF. All samples were negative. The geographical distribution of sampled wild boar was roughly correlated to the distribution and density of the Swedish wild boar population (Figure 34) (location information was not available for 13 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 2019 is sufficient to indicate that the prevalence of AD and CSF in the Swedish wild boar population is <3% with a certainty of 95%.

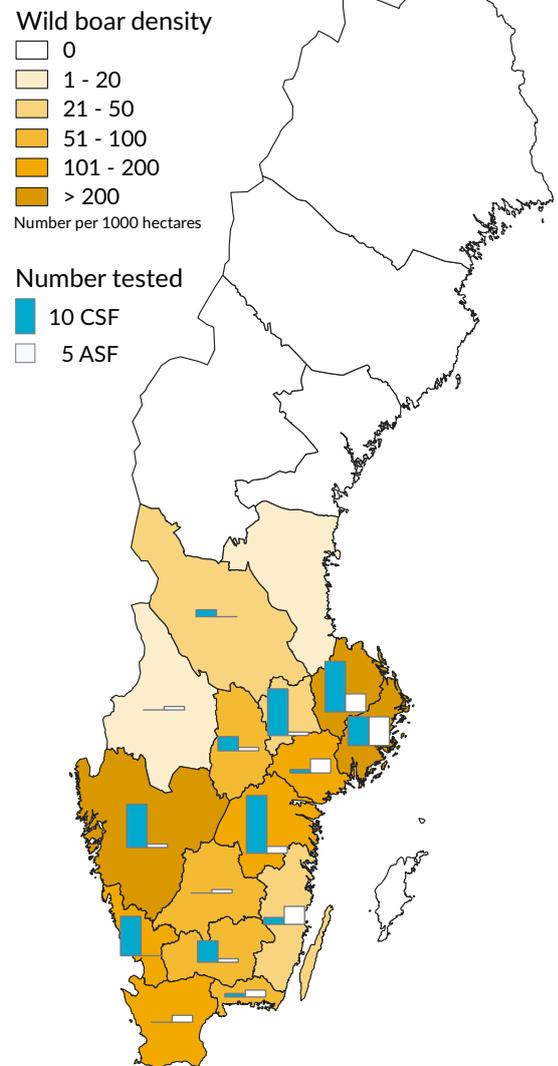


Figure 34: Geographical distribution by county of origin of wild boar samples included in the surveillance. The blue bars indicate the number of hunted wild boar sampled and tested for antibodies against Aujeszky's Disease (AD) and Classical Swine Fever (CSF) in 2019 (total 91). The white bars indicate the number of wild boar found dead and tested for ASF (total 34). The background colours indicate wild boar density based on hunting statistics from 2018 (www.vilt-data.se).

DISCUSSION

The Swedish wild boar population is growing, and the boundary of the population is moving north. In areas where wild boars are already present, the population is also becoming more dense, which increases the risk of direct and indirect contact between wild boars and domestic pigs. The area in Sweden inhabited by wild boars is surrounded by the sea so there is no risk of wild boars migrating into Sweden. Instead, the role of the wild boar in disease spread might be to pick up infectious agents introduced into Sweden by other routes. For example, wild boars could gain access to infected meat or other animal products in garbage or following indirect spread by other means from people, vehicles or equipment. The unfavourable development of the global ASF situation is of special concern and calls for efficient approaches to early detection of disease in the wild boar population. As such, methods to further increase the number of wild boars found dead that are voluntarily submitted by the public for postmortem and ASF testing are currently being investigated.

Infectious diseases and parasites in honeybees

BACKGROUND

Every beekeeper in Sweden has the responsibility to prevent the spread of bee diseases and is obligated to register the location of their apiaries to the responsible County Administrative Boards (CABs). There is no national bee register, but the number of apiaries and colonies are estimated by the local bee inspectors and reported to the respective CABs. The health of honeybees is controlled by local bee inspectors, appointed and given the responsibility over local inspection districts by seven of the CABs. Sweden is divided into around 400 bee districts and in each of these the local bee inspectors are responsible for the practical control of the apiaries located in the 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, including American foulbrood and *Varroa* and tracheal mite infestations. There are regulations for the import and export 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 must be made to the SBA at each point of entry. The conditions for import are the same in all EU Member States. If bees are introduced without permission, it is considered a violation of the law on smuggling goods.

DISEASES AND LEGISLATION

All veterinarians, as well as laboratories analysing samples from honeybee colonies, are obligated to notify the SBA if American or European foulbrood (AFB and EFB, respectively), tracheal mite infestation/acariosis (*Acarapis woodi*), *Varroa mite* infestation/varroosis (*Varroa destructor*), *Tropilaelaps* mite infestation (*Tropilaelaps* spp) or the small hive beetle (*Aethina tumida*) are found. This is regulated in the bee diseases act (1974:211), the ordinance of bee diseases (1974:212) and the SBA's regulation (SJVFS 1992:38) on the control of American foulbrood, *Varroa* and tracheal mites in honeybees, as well as the SBA's regulation on notification of animal diseases and infectious agents (SJVFS 2012:24). A beekeeper needs a permit issued by a bee inspector to move the bees out of an area which has been declared infected with AFB by the SBA. Visual inspection of clinical symptoms 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 present earlier, the bee inspector notifies the CAB, which in turn notifies the SBA. The SBA then declares the area in which the apiary is situated infected/infested. Bee inspectors can send samples of diseased brood, larvae, pupae or adult bees to the National Reference Laboratory for Bee

Health (NRL) at the Swedish University of Agricultural Sciences (SLU), where the diagnosis of honeybee diseases included in the legislation is performed on behalf of the SBA. This is a yearly, laboratory-based, passive surveillance of honeybee diseases.

American foulbrood

American foulbrood (AFB) of honeybees is a contagious bacterial disease caused by the spore-forming bacterium, *Paenibacillus larvae*. The disease is widely distributed across the world causing great economic losses in apiculture and is notifiable in most countries. As the name indicates, the disease only affects the larval stages of honeybees. AFB is highly infectious, lethal to the individual honeybee larva and potentially lethal to infected colonies. AFB is a statutory notifiable disease in the European Union in the framework of trade and export requirements (Directive 92/65/EEC). In many European countries, Sweden included, the disease is controlled through burning of symptomatic colonies 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 tylosine). 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 symptomatic honeybee colonies within a 3 km radius from the infected apiary. Also, apiaries outside the 3 km radius that have in any way been in contact with infected colonies through beekeeping management are inspected and sampled.

European foulbrood

European foulbrood (EFB), is a serious disease of honeybees caused by the bacterium *Melissococcus plutonius*. EFB affects mainly young honeybee larvae usually between 4 and 5 days old. A massive loss of brood resulting from severe infection weakens the colony and can lead to its collapse. Regional variations in disease burden have been reported and recent decades have seen dramatic increases in the incidence of EFB in parts of Europe. Large disease outbreaks have been identified in areas previously thought to be disease free, such as Norway.

Tracheal mite infestation (acariosis)

The honeybee tracheal mite *Acarapis woodi* is an internal parasite of the respiratory system of adult honeybees.



Honeybees guarding the nest entrance. Photo: Apinordica AB.

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 1989 and in the county of Skåne in 1991. The regulations from the SBA has 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 Västerbotten, Jämtland, Väster-norrland and Norrbotten).

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 are visually inspected for the occurrence of *Tropilaelaps* mites. The mite has not been reported as being present in Europe.

The small hive beetle

The small hive beetle (*Aethina tumida*) is endemic to sub-Saharan Africa, but has spread to many other locations, including North America, Australia and the Philippines, and was introduced into Europe in 2014, when it was detected in Calabria and Sicily. The Commission has defined protective measures to prevent the spread of the beetle and the incidence is still limited to these areas in southern Italy.

The small hive beetle can be a destructive pest of honeybee colonies, causing damage to comb, stored honey and pollen. The primary damage to colonies and stored honey is caused through the activity of the larvae tunnelling through honeycombs, feeding and defecating, causing discolouration and fermentation of the honey. If a beetle infestation is sufficiently heavy, they may cause bees to abandon their hive.

SURVEILLANCE

Passive surveillance

Passive disease surveillance of honeybee diseases and parasites is done through diagnostics related to disease outbreaks, and results are reported by the NRL to the SBA yearly.

Enhanced passive surveillance by visual inspection of clinical symptoms 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 where diseases are detected are reported by

the bee inspectors to the CABs. For results over time, see Figure 35.

RESULTS

Samples from a total of 2071 bee hives in 315 beekeeping operations were analysed by the NRL for bee health in 2019. The results are shown in Table 32.

The national bee inspectors performed visual inspection of disease symptoms in 8944 colonies in 1966 apiaries and reported symptoms of AFB in 147 bee hives in 88 apiaries. See Figure 35.

No active surveillance was conducted during 2019.

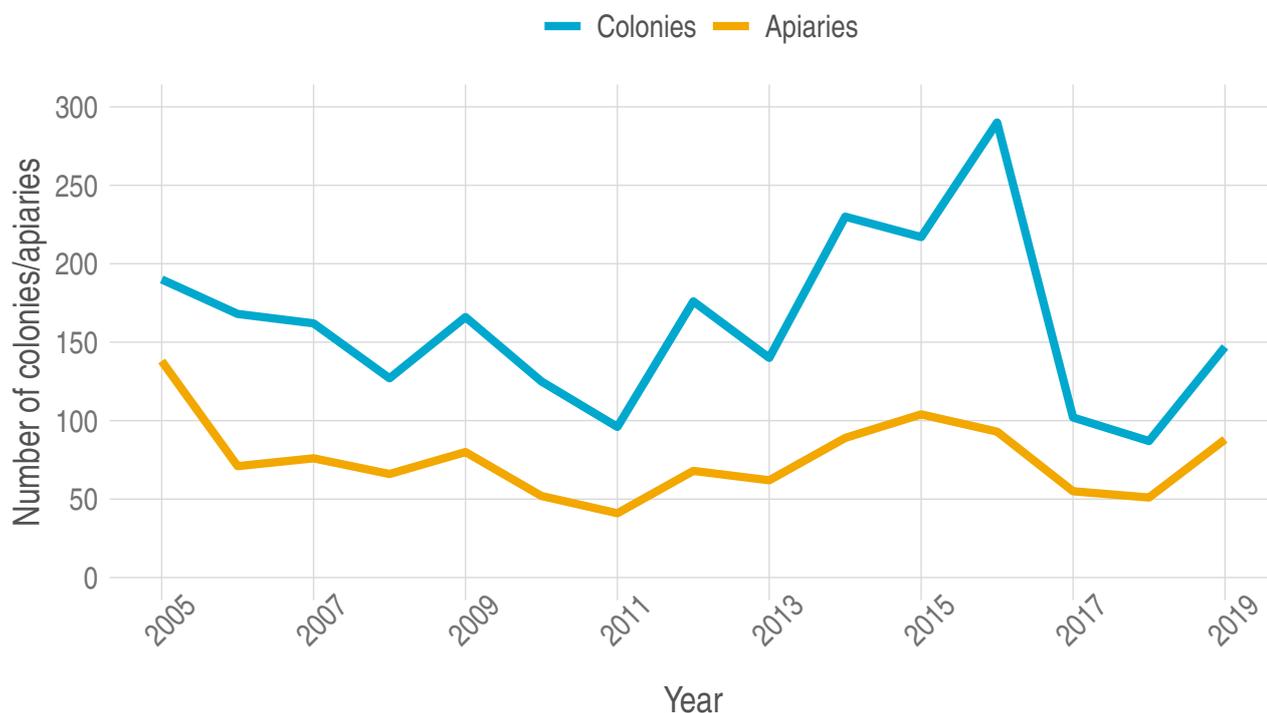


Figure 35: Number of new cases of American foulbrood in 2005–2019 in bee colonies and apiaries, based on reports from bee inspectors to the County Administrative Boards. A total of 8944 colonies in 1966 apiaries were inspected in 2019.

Table 32: Number of samples from the Swedish honeybee population analysed at the NRL for bee health during 2019. 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 beehives	No. of infected/infested beehives	No. of beehives with symptomatic brood
AFB	194	58	33	1813	374	82
EFB	1	0	-	1	0	0
<i>A. woodi</i>	7	0	-	19	0	0
<i>Varroa mites</i>	107	22	3	232	40	4
<i>Tropilaelaps</i>	0	0	-	0	0	0
<i>A. tumida</i>	6	0	-	6	0	0

DISCUSSION

The reporting of AFB incidence has, thus far, been based on the information that the bee inspectors report to the CABs based on visual observation of clinical signs (Figure 35). In a 2016 baseline study of honeybee diseases (presented in “Surveillance of infectious diseases in animals and humans in Sweden 2017”), microbiological cultivation of *P. larvae* from samples of adult bees was used. This method was previously shown to be well correlated with clinical signs of disease (Nordström et al., 2002; Locke et al., 2019). Only young larvae develop clinical signs, but adult bees are carriers of the bacterium. In the 2016 baseline study, the subclinical presence of the bacterium in a selection of the country’s apiaries was investigated. The bacteria could not be detected in most of the examined apiaries (94%), which is an important argument for simplifying the regulations on the management and movement of bee colonies in the country. It is important to highlight that there are many apiaries in areas free from this pathogen and that this status is worth preserving.

Starting January 2019, the bee inspectors have the option to send samples of adult bees to the NRL for the detection of *P. larvae*, which has led to a more than 10-fold increase in the number of hives analysed for the presence of *P. larvae* (Table 32). This is a complement to visual inspection of honeybee colonies in connection to outbreaks of AFB and is a useful tool for the bee inspectors to track symptomatic colonies.

The bacterium *Melissococcus plutonius*, which causes EFB, was detected in only two apiaries in Östergötland in the 2016 baseline study, and only one additional confirmed case has been reported since then. Historically, EFB has been considered to be less serious than AFB but reports of more aggressive forms of the bacterium and more serious disease outbreaks have become increasingly common in recent years. A few years ago, Norway had an outbreak of EFB that led to extensive investigations and sanitation, which highlights the value in continued monitoring for this disease to prevent outbreaks in Sweden.

After the introduction of the *Varroa* mite in Sweden, the SBA introduced regulations to prevent or at least slow down the spread of the mite in the country. This has not completely prevented the spread but has led to the fact that we still have apiaries in the northern parts of the country that are apparently free from *Varroa* mites. This can be further confirmed by the results of the 2016 baseline survey which reinforces earlier observations and reports from bee inspectors. In the county of Norrbotten, however, there have been findings of *Varroa* mites in Haparanda, Övertorneå, Kalix and Luleå, which may be a result of introduction of the disease from northern Finland where the mite is present. *Varroa* mites has also been detected in parts of Västerbotten, Västernorrland and Jämtland, but they seem to be limited outbreaks.

In the 2016 baseline survey, DWV was detected in all counties except Västerbotten, Jämtland, Norrbotten and Västernorrland. The spread of DWV coincides with the presence of *Varroa* and follows the spread of the mite. In Västernorrland, the mite has recently been introduced and the virus infection has not yet spread. Another virus associated with *Varroa* is ABPV, which was detected only in a single apiary on Gotland and one in Skåne. It is possible that the virus is so virulent that it kills its host faster than it can effectively spread. This could explain why the less virulent virus DWV has such a high incidence while ABPV is rare. It is also worth noting that the counties where ABPV is detected, Gotland and Skåne, are the counties where *Varroa* was first introduced into the country. At that time (late 80s, early 90s), ABPV was the most dominant *Varroa*-associated virus in Europe before being surpassed by DWV. Perhaps it is that ABPV was established in parts of the honeybee population in these counties before DWV became more widely spread.

The lack of a national bee register makes it difficult to organise and collect samples of bees. As a result of the new EU legislation on animal health, *Regulation (EU) 2016/429 of the European Parliament and of the Council on transmissible animal diseases and amending and repealing certain acts in the area of animal health (“Animal Health Law”)*, registers of all animals kept in husbandry for food production will be mandatory. The legislation is however so far not in place but will hopefully be so when the new animal health regulation will be applicable in April 2021. This would 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 as a basis for legislation and prevention measures regarding honeybee health.

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. (<https://www.sva.se>)
- 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

Infectious diseases in fish, crustaceans and molluscs



Juvenile rainbow trout with suspicion of flavobacteriosis. Photo: SVA.

BACKGROUND

All registered aquaculture farming sites are obligated to participate in the Official Health Control Programme, regulated in accordance with SJVFS 2014:4 and by Council Directive 2006/88/EG. Sweden has a very good health status in aquaculture as well as in wild populations of fish and shellfish. None of the serious diseases that occur throughout Europe 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 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 compensate for the lack of natural migration.

LEGISLATION AND DISEASES

All Swedish fish farms have participated in surveillance for the diseases mentioned below since the late 1980s in accordance with Commission Decision 2001/183/EC (now replaced by Commission Implementing Decision (EU) 2015/1554) and Council Directive 2006/88/EC. Sweden has an approved disease-free zone status (2002/308/EC) for Viral haemorrhagic septicaemia (VHS) and Infectious haematopoietic necrosis (IHN) (2008/427/EC). Additional

guarantees are in place for the whole country for Spring Viraemia of Carp (SVC), and for the inland zone for Infectious Pancreatic Necrosis (IPN) (2010/221/EU). The inland zone has an eradication programme for Renibacteriosis/bacterial kidney disease (BKD) and the coastal zone for IPN (2010/221/EU). These diseases are included in the Swedish legislation on notifiable diseases (SJVFS 2013:23). Further, IHN, VHS, IPN (other than 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, and for Crayfish plague in crayfish. These diseases are also regulated by the Swedish legislation on notifiable diseases (SJVFS 2013:23). Other notifiable diseases such as furunculosis (*Aeromonas salmonicida salmonicida*/ASS), yersiniosis/Enteric redmouth disease (ERM), Marteiosis and Bonamiosis (shellfish) and Whitespot disease (crayfish) are not actively tested for within surveillance programmes.

Infectious haematopoietic necrosis (IHN) and viral haemorrhagic septicaemia (VHS)

Both diseases are caused by rhabdoviruses and occur frequently in Europe. They are transferred horizontally, but vertical transmission cannot be completely ruled out for IHN. Both diseases have greatest impact in freshwater rainbow trout (*Oncorhynchus mykiss*) aquaculture but have also been detected in several other species. Infected fish exhibit behavioural changes, lethargy and abnormal swimming

(whirling). The fish are anaemic with varying degrees of haemorrhage in multiple organs. VHS also exists in a marine form, and a low prevalence in wild populations of sensitive species cannot be excluded in the Swedish coastal zone since the virus has been identified in wild fish from Skagerrak and the Bornholm basin. IHN was found in two Bothnian bay farms in Finland in 2017, but the virus has not yet been identified in Sweden.

Infectious pancreatic necrosis (IPN)

IPN is caused by a birnavirus 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 findings. IPN appears sporadically in Swedish east coast farms.

Renibacteriosis (BKD)

BKD is caused by a gram-positive bacterium, *Renibacterium salmoninarum*. The infection can be transmitted both horizontally and vertically. The disease favours low water temperatures, and outbreaks mainly occur at temperatures between 7 and 15°C.

Salmon and arctic char are most susceptible to BKD and mortality can reach 80%. In rainbow trout, the disease is chronic with a continuous low mortality of about 5–10%, however outbreaks of up to 40% mortality can occur. Infected fish may have reduced growth and disease can result in a deterioration of the meat quality. BKD is present in a few farms in the Swedish inland zone.

Spring viraemia of carp (SVC)

SVC is caused by a rhabdovirus. The disease occurs in Asia and several European countries. SVC is not present in Sweden. The virus has been detected in several fish species in the cyprinid family and is transmitted horizontally. Clinical signs are usually general, such as darkening, exophthalmia and a slow breathing. The fish swim lazily with sporadic periods of hyperactivity. Other common findings are pale gills, ascites and haemorrhages in the skin and gills. Internally, haemorrhage is found in various organs including muscle, swim bladder and the brain.

Koi herpes virus (KHV) infection

KHV is a herpesvirus and affects common carp (*Cyprinus carpio*) and variants thereof, including koi. The virus was first detected in 1998 and has since then been reported from all continents except Australia. The virus is transmitted horizontally. KHV can cause severe problems and is associated with high mortality. Infected fish usually swim at the surface and have an increased breathing frequency. Symptoms 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. There were two Swedish outbreaks with 90–100% mortality in 2018.

Crayfish plague

Crayfish plague is caused by an aquatic fungus (*Aphanomyces astaci*) that spread from the United States to Europe in the late 1800s with live crayfish. 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, reduced coordination and balance difficulties.

Crayfish plague is spread in the southern parts of Sweden.

White spot disease (WSD)

WSD is caused by a *Whispovirus* (WSSv) that can infect a wide range of aquatic crustaceans, including marine, brackish and freshwater prawns, crabs, crayfish and lobsters. Outbreaks occur at water temperatures of 18–30°C. The most common clinical sign is white spots in the exoskeleton, but 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. The virus can be present in imported frozen raw giant shrimps. There is a non-negligible risk that the virus will be introduced to the aquatic environment by anglers using these shrimps for bait. The consequences are difficult to predict but the virus may have a negative impact on Swedish crustacean populations. WSSv has never been detected in Sweden.

Marteiliosis

Marteiliosis, a disease in oysters and blue mussels, is caused by a unicellular parasite (*Marteilia refringens* in oysters and *M. pararefringens* in blue mussels). The parasite needs a crustacean (*Paracartia grani*) as an intermediate host. The disease causes reduced fitness, impaired growth and resorption of the gonads and hence reduced reproductive capacity. *M. pararefringens* is present on the Swedish west coast.

Bonamiosis

Bonamiosis is a disease in oysters caused by the protistan parasite *Bonamia ostreae*. The parasite invades and destroys the haemocytes. Usually, the only sign of disease is increased mortality in the infected oyster population. *B. ostreae* is found along the European Atlantic coast as far up as Denmark, where it has now been found in Limfjorden.

SURVEILLANCE

Within the Official Health Control Programme, there is active surveillance for the viruses causing 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 category I and II are tested every year and every second year, respectively, but farms within risk category III are only tested upon suspicion of disease. The aim of the Official Health Control Programme is to document freedom from disease and to contribute to the maintenance of this status.

There is also active surveillance in imported quarantined fish (eel - IPN and koi/carp - KHV). Active surveillance is also done when potential invasive alien species - like the marble crayfish - are discovered.

Passive disease surveillance has been done through diagnostics related to disease outbreaks in farms and wild fish.

Crayfish plague is monitored by passive surveillance and testing is done based on suspicion of disease outbreaks.

DIAGNOSTIC PROCEDURES

All diagnostic virus analyses are performed according to recommendations by the EU (EU 2015/1554) or the OIE aquatic manual at the Swedish reference laboratory for fish diseases at the National Veterinary Institute. Pooled organ material (for VHS, IHN and IPN spleen, kidney, heart/brain are tested, for SVC spleen, kidney, brain and gill are tested) by a cell culturing method. 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 (rt-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 co-habituated rainbow trout are sampled for detection of virus. In the case of carp/koi, only a few fish may be sampled. KHV is tested on individual fish (pooled gill and kidney) by PCR.

BKD is tested on kidney tissue from individual fish and demonstrated by an ELISA method. Verification is done by rt-PCR. Thirty fish are sampled in regular farms, and in restocking farms up to 120 fish (all females) are sampled after stripping of roe.

A. astaci is demonstrated by light microscopy and cultivation and verified by rt-PCR, and WSSv is detected by rt-PCR. The number of sampled animals varies from case to case.

RESULTS

Official health control programme for fish farms and crustacean surveillance

The number of samples analysed and results are shown in Table 33. In summary, the active surveillance detected six cases of BKD and one case of IPN (one case=one outbreak). Four of six BKD cases were reinfections of recently sanitised farms.

Voluntary health control programme for fish farms

There were five recorded outbreaks of “other” notifiable diseases in fish during 2019. Furunculosis (ASS) was detected in four farms. One farm had recurrent disease and concurrent BKD infection, and another farm within the same company also got infected. The other two farms were unrelated cases. Yersiniosis was detected in one sea based farm.

Few cases (n=6) of flavobacteriosis due to *Flavobacterium psychrophilum*, usually the predominant production disease, were detected compared to previous years (15–30 cases in the last 10 years). Instead, *Aeromonas* bacteria other than *A. salmonicida salmonicida* or *A. salmonicida* atypically dominated with 16 cases. The cause for this shift is unknown. *Flavobacterium columnare* was detected in five disease cases during the summer.

Voluntary health control in wild fish

Due to the detection of IPN genogroup 6 in broodstock trout from Lake Vänern in December 2016, the County Boards of Värmland and Västra Götaland took an initiative to sample 500 wild trout and salmon from the lake in 2017. During 2017–2018, a total of 609 fish caught in the lake or broodstock that returned from the lake to the river and five organ pools with unknown number of fish (n=1–10) were investigated by virus cell culture. No virus was detected. Since only 279 of the 609 fish were caught in the lake, one more sampling was performed in 2019. A total of 41 fish were investigated for presence of virus in 2019. No virus was detected.

Outbreaks in wild fish, crustaceans and molluscs

One arctic char that had been caught in lake Vättern 2018 (frozen after catch) and had multiple small skin wounds was suspected to have spawning rash, a specific form of BKD, was confirmed to be infected.

Suspicion of crayfish plague was investigated in five outbreaks of mortality in noble crayfish and three cases with signal crayfish. Crayfish plague was not detected in any of the noble crayfish cases. Crayfish plague was detected in two of the signal crayfish cases. One case concerned collapse of a signal crayfish population and it cannot be excluded that the plague was involved, although signal crayfish are generally resistant to clinical infection. One case was a follow up from a water system where the plague had previously been identified. In the third case, neither crayfish plague nor any other pathogen was detected. The crayfish was sent in because the meat had turned black at boiling.

One case of mortality in Norwegian lobsters was also handled. A few different bacteria were identified, and investigation of fixed shell with underlying tissue identified severe thinning of the cuticula and widespread muscular necrosis. No certain diagnosis could be made, but idiopathic muscle necrosis with secondary bacterial infection was suspected.

DISCUSSION

The number of farms that were sampled are listed in Table 33. Swedish aquaculture has a good health status, where all severe diseases of EU/OIE importance are absent.

The most problematic disease to control is renibacteriosis/BKD, due to its vertical transmission and variable clinical presentation. 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 four years, ASS has been causing problems in one BKD infected farm and mortalities continued despite antibiotic treatment. The reason is probably the underlying BKD infection, facilitating the ASS infection and itself being accelerated by the concurrent ASS infection. Control of BKD is expected to be improved by modified sampling and improved methodology, from today's post mortem sampling to an *in vivo* method. Additional resources must be invested in risk-based analysis of individual aquaculture farms to get a more reliable assessment for health surveillance.

Table 33: Samples taken in the Swedish surveillance programmes for notifiable diseases in fish, crustaceans and molluscs. One case=one outbreak.

Disease	No. of sampled production sites	No. of infected production sites	No. of tested individuals	No. of tested pools	No. of infected individuals/pools
Fish					
VHS	64	0	-	431	-/0
IHN	64	0	-	431	-/0
IPN	64	1	-	431	-/1
SVC	2 ^A	0	7 ^A	6	0/0
KHV	2 ^A	0	7	5 ^B	0/0
BKD	73 ^C	7 ^C	3363	-	32/-
Crustaceans					
<i>Aphanomyces astaci</i>	15 ^D	4 ^D	30	-	10/-
WSSv	0	-	-	-	-/-
Molluscs					
<i>Bonamia ostreae</i> ^E	4	0	150	0	0/-
<i>Marteilia refringens</i> ^E	4	0	150	0	0/-

^A One import company. No aquaculture farms were tested.

^B Pools of 2 individuals.

^C one production site represents a wild arctic char.

^D A total of 15 locations were sampled, representing 10 separate waterways with wild crayfish and one laboratory with crayfish. Four waterways were positive.

^E This sampling was performed as part of a project within the European Sea and Fisheries Fund.

Abbreviations:

VHS	Viral haemorrhagic septicemia
IHN	Infectious Haematopoietic Necrosis
IPN	Infectious pancreatic necrosis
SVC	Spring viraemia of carp
KHV	Koi herpesvirus
BKD	Bacterial Kidney Disease

Examination of abortions in food producing animals

BACKGROUND

Post mortem examinations are considered important for early detection and national surveillance for infectious and emerging diseases. As mentioned in the chapter “Post mortem examinations in food producing animals”, the Swedish Board of Agriculture has financed a programme to encourage such examinations for the past 20 years. However, some infections do not produce lesions that can be detected at postmortem or cause only non-specific macroscopic changes. Brucellosis, porcine reproductive and respiratory syndrome (PRRS) and classical swine fever (CSF) are examples of infections that may be present without specific macroscopic findings at postmortem. Moreover, the clinical picture in herds affected by these diseases can be non-specific, which may cause a delay before the suspicion of these infections occurs in clinical surveillance.

SURVEILLANCE

This surveillance component was introduced in 2008. It includes examinations for brucellosis in all ruminant foetuses and for brucellosis, PRRS and CSF in all pig foetuses submitted for postmortem through the post mortem examination programme. These infections often cause abortion, so by sampling aborted foetuses the sampling occurs within a risk group. This increases the chance of detecting the infectious agents, if present. The Swedish Board of Agriculture finances the sampling and testing of foetuses for *Brucella*, PRRS and CSF. The National Veterinary Institute (SVA) is responsible for the organisation of the aborted foetus examination programme. Samples from aborted foetuses are either submitted to SVA by veterinarians performing post-mortem at regional laboratories or are taken from foetuses submitted directly to SVA for post mortem examination. All

diagnostic testing is performed at SVA. Testing for the presence of CSF virus and PRRS genome is done by PCR, and for *Brucella* by bacterial culture.

RESULTS

In 2019, a total of 67 foetuses from 44 herds were examined (Table 34). This represents an increase from 2017, when the lowest number of foetuses was submitted for postmortem since the surveillance programme started in 2008. However, this number remains below the 140 foetuses that were expected to be examined during the year. All analysed samples were negative for *Brucella*, PRRS and CSF.

DISCUSSION

The post mortem examination and sampling of aborted foetuses is an important part of the national surveillance for infectious and emerging diseases. This was demonstrated in 2012–2013, when the then newly-identified Schmallenberg virus (SBV) was detected in Sweden through the surveillance of aborted foetuses. At that time, in addition to testing for *Brucella*, ruminant foetuses were also examined for the presence of SBV. Testing for SBV did not continue beyond 2013, because the disease became established in Sweden and elsewhere in the EU with limited economic impact and was therefore delisted at EU level.

Since 2008, the number of foetuses of different species submitted for examination has varied from year to year. In 2013, the number of ruminant foetuses submitted was extraordinarily high, most likely because of concerns about SBV. For the last six years, the number of submissions has been less than anticipated across all species (Table 34). Activities to increase awareness about the opportunity to submit aborted foetuses among veterinarians and animal producers will be undertaken in 2020.

Table 34: Number of foetuses (herds^A) investigated by species from 2010–2019 through the aborted foetus examination programme.

Species	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019
Cattle	62	21	63	114	32 (27)	29 (23)	34 (23)	20 (18)	34 (28)	21 (20)
Goat	9	3	5	4	2 (2)	0	2 (2)	2 (1)	5 (3)	3 (2)
Sheep	70	45	79	89	28 (14)	31 (21)	16 (13)	22 (15)	23 (16)	12 (8)
Alpaca	5	0	0	0	0	2 (1)	1 (1)	0	0	0
Bison	0	0	1	0	0	0	1 (1)	0	0	0
Wisent	0	2	1	0	0	0	0	0	0	0
Gnu	0	0	0	1	0	0	0	0	0	0
Pig	61	51	54	46	31 (12)	17 (10)	43 (22)	6 (4)	16 (9)	31 (14)
Water buffalo	0	0	0	0	0	0	0	1 (1)	0	0
Total	207	122	203	259	93 (55)	79 (55)	97 (62)	51 (39)	78 (56)	67 (44)

^ANumber of herds not available prior to 2014

Post mortem examinations in food producing animals

BACKGROUND

Early detection of infectious diseases is of utmost importance to prevent negative consequences. For diseases with severe clinical signs, the first line of defence is the detection of disease by animal owners, field veterinarians and pathologists. International and national experiences show that post mortem examinations remain a vital part in disease control and detection of emerging diseases.

As post mortem examinations are considered an important part of early detection and national disease surveillance, a specific programme for such examinations started in the early 1990s. The Swedish Board of Agriculture finances the programme, complemented by fees from animal owners. Farm & Animal Health is responsible for the organisation of the post mortem examination programme.

SURVEILLANCE

The programme subsidises post mortem examinations in all food producing animals, poultry and exotic ungulates. Poultry were included in the programme in 2007 and domesticated exotic ungulates in 2008. Since 1999, approximately 3000 animals have been examined yearly within the programme. In conjunction with post mortem examinations, samples are collected from defined categories of animals for surveillance of antimicrobial resistance, salmonellosis, transmissible spongiform encephalopathies (TSE) and paratuberculosis. Aborted ruminant and pig fetuses submitted for post mortem examination are sampled for brucellosis, porcine reproductive and respiratory syndrome (PRRS) and classical swine fever (CSF) (see chapter “Examination of abortions in food-producing animals”).

The programme also includes training for large animal practitioners and veterinary employees of the post mortem examination facilities. To facilitate skill development, yearly courses are offered and quarterly newsletters are produced.

Transportation of the carcasses to the laboratories is arranged and financed by the animal owner. This can be a problem for large animals, particularly when the distance between the farm and post mortem examination facility is large.

RESULTS

In 2019, post mortem examinations were performed at six different laboratories, all located in the southern half of Sweden: Skara (Farm & Animal Health), Kävlinge (Farm & Animal Health), Uppsala (the National Veterinary Institute (SVA) and the Swedish University of Agricultural Sciences (SLU)), Visby (Farm & Animal Health) and Karlskoga (Farm & Animal Health). Large animals, such as adult cattle, were examined at all laboratories except Skara, which does not have the facilities to handle large animals. To facilitate post mortem examination of large animals in

the area around Skara, a programme was started in 2019 to have necropsies of all animals weighing more than 10kg performed by an experienced ambulatory veterinarian on the farm, instead of transporting carcasses long distances to other laboratories.

A total of 2214 post mortem examinations were performed within the programme during 2019. The distribution of species examined over the last 15 years is shown in Table 35. The total number of examinations in 2019 was lower than in recent years and was caused primarily by a drop in the number of sheep and farmed deer carcasses submitted for postmortem. This decrease can be partially explained by decreases in animal numbers and financial hardship caused by the drought in Sweden in 2018. In 2019, 94 cases were diagnosed with a notifiable disease at post mortem examination (Table 36).

Since 2017, a Remote Digital Autopsy (RDA) method has been used to facilitate timely post mortems of large animals in remote areas of Sweden. This method utilizes a process where a simplified gross post mortem examination is done at the farm. Digital photographs of key organs are taken and, together with available anamnestic information, sent to a pathologist for a presumptive diagnosis. 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. In 2019, RDA was used for the first time for post mortem examinations of reindeer.

DISCUSSION

Post mortem examinations are a vital part of the national surveillance for infectious and emerging diseases, as illustrated by the detection of 94 index cases of notifiable disease in 2019. Post mortem examination is also an important tool that helps veterinarians solve animal health problems at the individual farm. The number of post mortem examinations performed each year varies but has remained at approximately 3000 per year over the last decade. Pig submissions were on a steady decline but seem to have settled at around 500 animals per year. The number of cattle and sheep examined has been stable at around 800 and 500 animals, respectively, but for the last three years, the number of sheep undergoing post mortem examination has declined. Poultry submissions show the most variation from year to year. 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.

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. Unfortunately, the relatively new RDA method has yet to increase the number of large animal post mortem examinations performed. It is hoped that the new on-farm post mortem examination programme started in 2019 in the area around Skara, a region with high animal density but without a large animal post mortem examination facility, will increase the number of post mortem examinations performed in the region. Performing post mortem examinations on-farm has allowed for fresher material to be examined and collected for further diagnostics, which improves the chances of reaching

a diagnosis. The programme has been appreciated by both producers and veterinarians and will therefore continue in 2020.

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 35: Number of food producing species submitted for post mortem examination, 2005–2019.

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

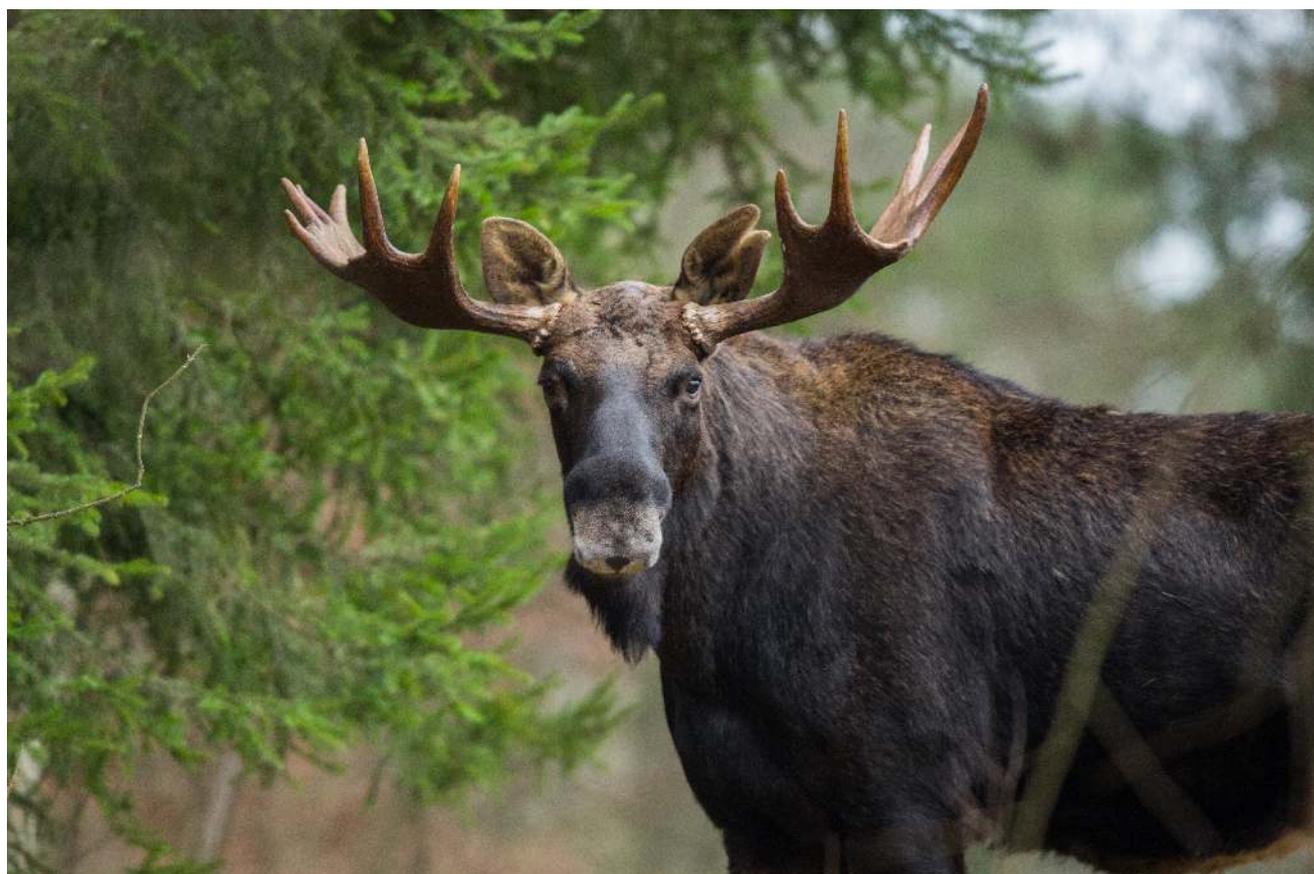
Table 36: Number of index cases of a notifiable disease diagnosed from samples taken at post mortem examination, 2003–2019.

Disease	2013	2014	2015	2016	2017	2018	2019
Anthrax	0	0	0	1	0	0	0
Avian rhinotracheitis	1	0	0	0	0	0	0
Blackleg	7	4	19	26	25	24	25
Bovine Malignant Catarrhal fever	3	1	1	6	6	2	2
Chorioptes (sheep/goat)	-	-	-	-	1	0	0
Duck Viral Enteritis ^A	-	1	0	0	0	0	0
Fowl Cholera (pasteurellosis)	0	0	0	3	4	2	0
Fowl typhoid (<i>S. Gallinarum</i>)	0	0	0	0	3	0	0
Gumboro (Very virulent IBDV)	-	-	-	-	5	4	0
Infectious Bronchitis	0	0	0	0	0	0	0
Infectious laryngotracheitis	36	35	26	26	17	20	21
Influenza, pigs	1	1	0	0	1	0	0
Influenza A typ (H1N1) 2009	3	0	0	0	1	0	0
Listeriosis	49	31	22	20	22	22	9
Lymphoma (not EBL)	0	0	0	2	0	0	0
<i>Mycoplasma gallisepticum</i>	0	4	4	0	1	7	32
<i>Mycoplasma</i> , poultry (not <i>gallisepticum</i>)	0	0	0	2	0	0	0
Necrotic haemorrhagic enteritis (<i>Clostridium perfringens</i> type C)	0	0	0	0	0	0	0
Salmonellosis	2	3	3	1	2	2	5
Total	102	80	75	87	88	83	94

Statistics from Farm & Animal Health.

^AThis disease was not diagnosed in Sweden prior to 2014.

Post mortem examinations in wildlife



A male moose (*Alces alces*), one of the most important game species in Sweden. The finding of chronic wasting disease (CWD) in Swedish moose in 2019 is a concern for game management, hunters and wildlife disease researchers. Continued surveillance of CWD in cervids is important to improve the knowledge of this new disease in Sweden. Photo: Szczepan Klejbuk/Shutterstock.

BACKGROUND

A general surveillance programme for diseases of wildlife based on pathology and ancillary testing was established in Sweden in the late 1940s. The surveillance programme is financed partly by annual state hunting permit fees, and partly by governmental funding. The aim of the general and targeted wildlife disease surveillance programmes is to monitor the health status of wildlife 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 and can serve as an indicator of environmental and ecosystem health. The National Veterinary Institute (SVA) is the only laboratory in Sweden where post mortem examination of fallen wildlife is performed. The OIE national focal point for wildlife is located at SVA and submits reports of OIE listed diseases in wildlife, as well as OIE specified non-listed wildlife diseases.

SURVEILLANCE

The general public, local authorities, and especially hunters submit wildlife that is found dead, or found sick and then

ethanised, to the National Veterinary Institute 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 are tested at various commercial labs or SVA before consumption. All large carnivores (brown bear, lynx (*Lynx lynx*), wolf (*Canis lupus*) and wolverine (*Gulo gulo*)) found dead, euthanised or shot in licensed hunting are submitted to SVA for postmortem as skinned carcasses or tissue samples. Whenever possible, disease causing agents are identified and cause of death established.

RESULTS

In 2019, whole carcasses or parts of 2452 free-ranging wild animals were submitted to the Department of Pathology and Wildlife Diseases, not including examined farmed or captive wildlife species.

The most important wildlife disease event in 2019 was the discovery of three cases of chronic wasting disease (CWD, a prion disease of cervids), in three older female moose in the county of Norrbotten. Two cases were detected in the ongoing national monitoring of CWD and the third case was found in the follow-up targeted surveillance during

the 2019 moose hunt in that area. For more details, see the CWD chapter.

The first case of usutu virus in Sweden was found in 2019, in a blackbird from the island of Öland. Surveillance of usutu virus and West Nile fever virus was carried out during the year in a citizen science project, with a good response of reporting and submitting dead passerine birds.

A major outbreak of the bacterial disease tularaemia, caused by the bacterium *Francisella tularensis*, was noted during the summer and autumn, with numerous reports of dead hares and multiple confirmed positive cases in hares submitted to SVA. Many human cases of tularaemia were also diagnosed in this time period (see also specific chapter on tularaemia). The last time there was a major outbreak of similar magnitude of tularaemia in both hares and humans, was in 2015. A study of culled muskrats (*Ondatra zibethicus*), an invasive alien species, showed antibodies against *F. tularensis* in 14% of examined carcasses. This finding gives support to the hypothesis that tularaemia may have been involved in the crash of the Swedish muskrat population the past decades.

Information efforts to increase awareness among the public, and especially hunters, to report dead wild boar for

screening of African swine fever (ASF) has resulted in a slow but continuous increase of tested carcasses (see specific chapter on Infectious diseases in wild boar. Use of the SVA online form (rapporteravilt.sva.se) to report dead wild boar and other fallen wildlife has increased significantly in 2019. No cases of ASF were found in 2019.

DISCUSSION

The general disease surveillance in wildlife is based on citizen science, with the interested public and hunters especially, reporting and submitting samples. A high public interest in wildlife health and conservation continues to make this work possible, together with state financing. Among the healthcare community and relevant authorities, it is well recognised that wildlife disease surveillance is an integral part of the One Health concept. The surveillance results (Table 37) show that Sweden has few serious infectious disease threats in wildlife.

REFERENCES

SVA annual report (årsredovisning) 2019. SVALA-data on wildlife diagnoses 2019. SVA report: Wildlife disease monitoring in Sweden 2019.

Table 37: OIE listed and non-listed wildlife diseases and number of outbreaks/cases 2019.

Disease	Number of cases	Species affected
Avian pox	1	Great tit
Avian tuberculosis	1	Common buzzard
Chronic wasting disease	3	Moose
European brown hare disease	44	European brown hare
Myxomatosis	2	Wild rabbit
Pigeon paramyxovirus	19	Pigeon
Poisoning	22	<i>Lead poisoning</i> : Greylag goose (1), White tailed eagle (19), Golden eagle (1). <i>Yeast dough/ethanol poisoning</i> : Hedgehog (1)
Rabbit Hemorrhagic Disease	4	Wild rabbit
Salmonellosis ^A	35	Bullfinch (10), Common redpoll (10), Jackdaw (14), Greenfinch (1)
Sarcoptic mange	11	Lynx (7), Wolf (2), Red fox (2)
Toxoplasmosis	1	European brown hare
Trichinellosis	19	Lynx (6), Raccoon dog (1), Wild boar (5), Wolf (2)
Tularemia	58	European brown hare (27), Mountain hare (31)
Total	232	

^AThe selection criteria for the number of cases with salmonellosis differ from the definition of index cases. Here, all individuals diagnosed with salmonellosis are listed. Thus, the figures presented in this table include both bacteriologically confirmed and non-confirmed cases and more than one case per geographical location.

Antibiotic resistance in bacteria from animals and food

BACKGROUND

The National Veterinary Institute (SVA) has the mission to monitor and analyse the development of antimicrobial resistance in bacteria from animals and food of animal origin. This also includes implementation of the mandatory harmonised monitoring of antibiotic resistance in bacteria from food-producing animals and food thereof, dictated by EU legislation. The monitoring activities are carried out through the Swedish Veterinary Antibiotic Resistance Monitoring Programme (Svarm), which has been running since 2000.

The objectives of Svarm are to detect changes in trends in resistance and to provide a basis for recommendations on the use of antibiotics in animals. Three types of bacteria are monitored: zoonotic bacteria, specific animal pathogens and indicator bacteria from healthy animals and meat. In addition, both intestinal content from healthy farm animals and fresh meat are screened for *E. coli* producing extended spectrum beta-lactamases (ESBL), AmpC-enzymes and carbapenemases. The rationale for monitoring indicator bacteria, i.e. commensal *Escherichia coli* and *Enterococcus* spp. from the normal intestinal flora of healthy animals, is that resistance among these bacteria reflects the selection pressure caused by the use of antibiotics in an animal population. These commensal bacteria can also be a reservoir of mobile resistance genes that can reach humans through the food chain. Thus, the prevalence of resistance in bacteria that contaminate meat reflects the magnitude of the potential human exposure to such reservoirs in food-producing animals.

The Svarm programme conforms to directive (2003/99/EG) and subsequent decisions (2013/652/EU). According to the directive, resistance in *Salmonella*, *Campylobacter jejuni* and indicator bacteria shall be regularly monitored in broilers, turkeys, pigs and cattle using harmonised methodologies. Briefly, for Sweden, this implies that each year, isolates of *Salmonella* from all notified outbreaks in food-producing animals, as well as 170 isolates of *Campylobacter* from either broilers or pigs, are tested for antibiotic susceptibility. Also, 170 isolates of *E. coli* from intestinal content of healthy broilers or pigs are tested each year. In addition, each year 300 samples of intestinal content and 300 samples of fresh retail meat from either broilers or from pigs and cattle are screened for ESBL/AmpC- and carbapenemase producing *E. coli*. Due to small production volumes, it is not mandatory for Sweden to investigate *Campylobacter* or indicator bacteria from healthy turkeys or cattle. It is not mandatory to screen for ESBL/AmpC- or carbapenemase producing *E. coli* in these animal categories either. However, sometimes such investigations are still performed, on a voluntary basis.

In addition to the mandatory monitoring described above, Svarm is complemented with data on resistance in clinical isolates of bacteria from the routine testing of clinical submissions at SVA. Svarm is also complemented with data from research projects and specifically from the Svarm-Pat project focusing on resistance in animal pathogens from farm animals. SvarmPat is run in cooperation with Farm & Animal Health and is financed by the Swedish Board of Agriculture.

Results of Svarm, i.e. data on antimicrobial resistance in bacteria from animals and food, are presented in a yearly report together with data on sales of antimicrobials for use in animals. These results are published together with corresponding data for human medicine from the Swedres programme at the Public Health Agency of Sweden in an integrated report - Swedres-Svarm - available at www.folkhalsomyndigheten.se or at www.sva.se/swedres-svarm. The different data sources compiled in this report are illustrated schematically in Figure 36.

LEGISLATION

As mentioned above, parts of the antibiotic resistance monitoring performed in Sweden are regulated by EU legislations (2003/99/EG and 2013/652/EU). The latter of these is currently under revision and some changes to the monitoring within EU can be expected from 2021. Furthermore, there is also national legislation indirectly affecting the antibiotic resistance monitoring. More precisely, findings of carbapenemase producing Enterobacteriaceae (ESBL_{CARBA}) and methicillin-resistant coagulase-positive staphylococci (e.g. MRSA and MRSP) in animals are notifiable in Sweden (SJVFS 2012:24 with amendments).

SUMMARY OF RESULTS

From an international perspective, Sweden still has a favourable situation regarding antibiotic resistance in bacteria in humans and animals. This confirms that our strategies to promote the rational use of antibiotics and to limit the spread of antibiotic resistance are effective. Over the last decades, the sales of antibiotics in Sweden have decreased for both humans and animals. In addition, the sales of broad-spectrum antibiotics have decreased while the use of narrow-spectrum antibiotics has increased. Despite this, many of the monitored types of antibiotic resistance have continued to increase over the years, even if exceptions to these negative trends occur.

Antibiotic sales for veterinary use

In 2019, reported sales of antibiotics for animals were 9601 kg, of which 58% were narrow-spectrum penicillins. The corresponding figures for 2010 were 14 117 kg and 53%, respectively.

Since the withdrawal of growth-promoting antibiotics from the market in 1986, the total sales of antibiotics have decreased by around two thirds when corrected for population sizes over time. During the 1990s, sales of veterinary products for medication of groups of animals decreased, and in the past decade there has also been a decrease in sales of products for use in individual animals (Figure 37).

Extended spectrum beta-lactamase (ESBL) producing Enterobacteriaceae

ESBL-producing Enterobacteriaceae are rare among animals in Sweden. Previously, the occurrence in intestinal samples from broilers was high, but it has decreased in recent years. In 2019, the occurrence of ESBL-producing *E. coli* in intestinal samples from pigs and broilers as well as samples of pork and beef were investigated with screening

methods. Such bacteria were isolated from 3% of the intestinal samples from pigs and broilers respectively, and <1% and 0% of the pork and beef samples of Swedish origin. Bacteria that form ESBL_{CARBA} have not been detected in animals in Sweden.

Methicillin resistant *Staphylococcus aureus* (MRSA)

The occurrence of methicillin-resistant *Staphylococcus aureus* (MRSA) in animals in Sweden is still low, which limits the spread from animals to humans. MRSA was found sporadically in dog, cat, horse, rabbit and goat in 2019, and MRSA with *mecC* was detected in samples from hedgehogs in a research project. In companion animals, the same types of MRSA as in humans dominate, indicating a human source of MRSA in these animals. In horses, livestock-associated MRSA clonal complex 398 is the most common.

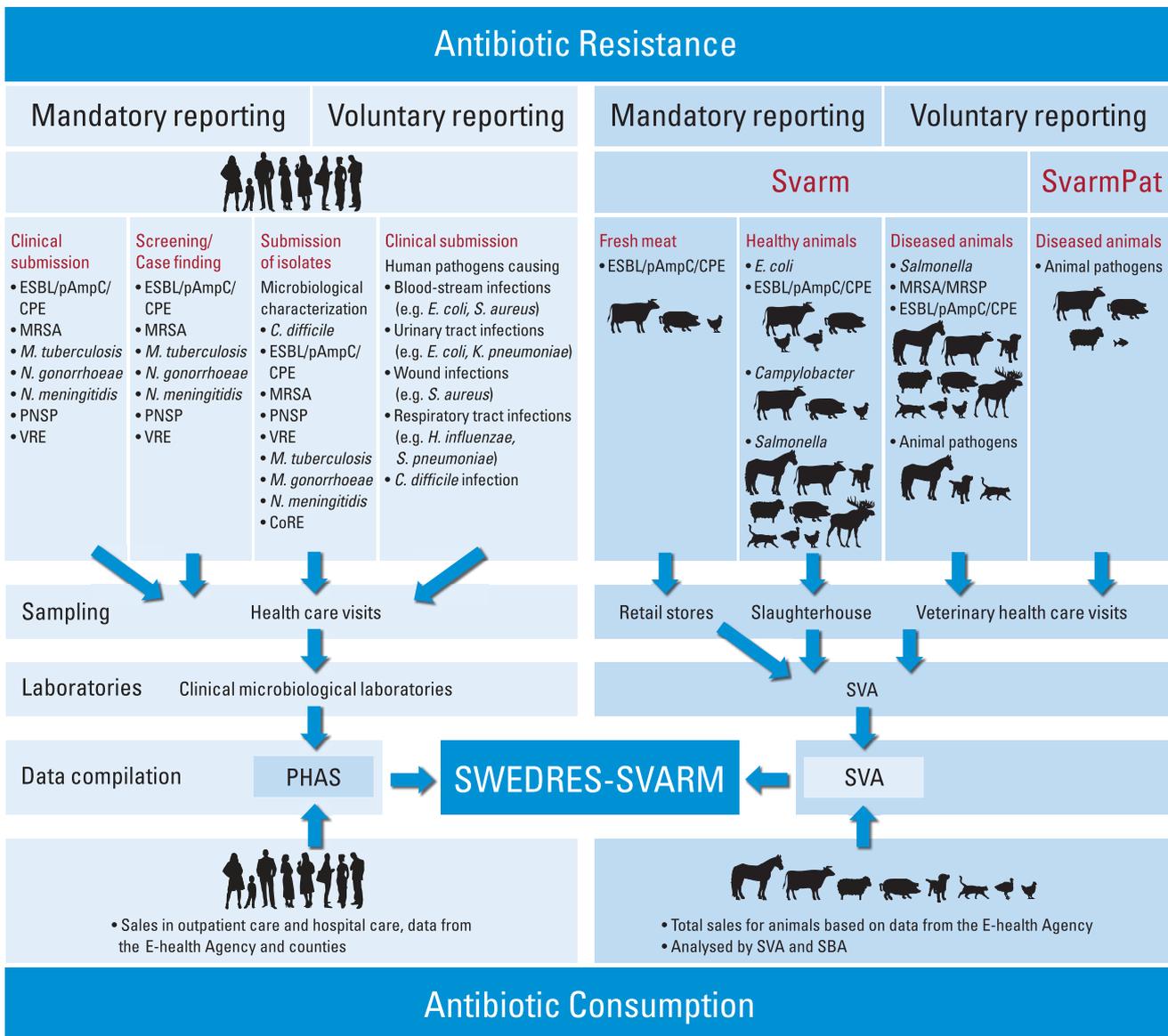


Figure 36: A schematic illustration of data included in the Swedres-Svarm report.

Methicillin resistant *Staphylococcus pseudintermedius* (MRSP)

In 2019, the number of reported cases of methicillin-resistant *Staphylococcus pseudintermedius* (MRSP) in animals was at the same level as in previous years. In total 48 cases of MRSP were notified to the Swedish Board of Agriculture, and isolates from 42 cases (38 dogs, 3 cats and 1 horse) were available for further investigations. All isolates were resistant to three or more substances, i.e. multi-resistant. The epidemiology of MRSP is becoming more diverse compared to earlier years with several sequence types occurring. MRSP in humans is not notifiable.

Resistance in zoonotic pathogens

Salmonella is rare in animals in Sweden, and few incidents involve antibiotic-resistant strains. Resistance to fluoroquinolones is rare and in 2019 a strain with ESBL resistance was for the first time detected, in an environmental sample from a farm. Isolates from human invasive infections with *Salmonella* are markedly more resistant, which makes animals in Sweden an unlikely source for these infections.

Campylobacter from animals in Sweden are generally susceptible to relevant antibiotics, and resistance to erythromycin, for example, is most uncommon.

Infections, either in humans or in animals, caused by

Salmonella and *Campylobacter* are usually not treated with antibiotics.

Resistance in animal clinical isolates

Bacteria causing clinical disease in animals are mostly susceptible to antibiotics relevant for treatment. Respiratory pathogens from farm animals and horses are generally susceptible to benzylpenicillin, but penicillin resistance is common in *Staphylococcus pseudintermedius* from dogs and occurs in *S. aureus* from horses and *S. felis* from cats. Resistance in *E. coli* occurs in all animals but is most prominent in enteric isolates from young calves and pigs. Susceptibility testing for guidance in antibiotic therapy is warranted, especially for staphylococci, *E. coli* and, *Brachyspira* spp.

Resistance in indicator bacteria from healthy animals

Antibiotic resistance in *E. coli* from the intestinal flora of healthy animals serves as an indicator for the presence of resistance in an animal population. The prevalence of acquired resistance in such commensal bacteria also indirectly reflects 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 generally low, and the situation is favourable in an international perspective.

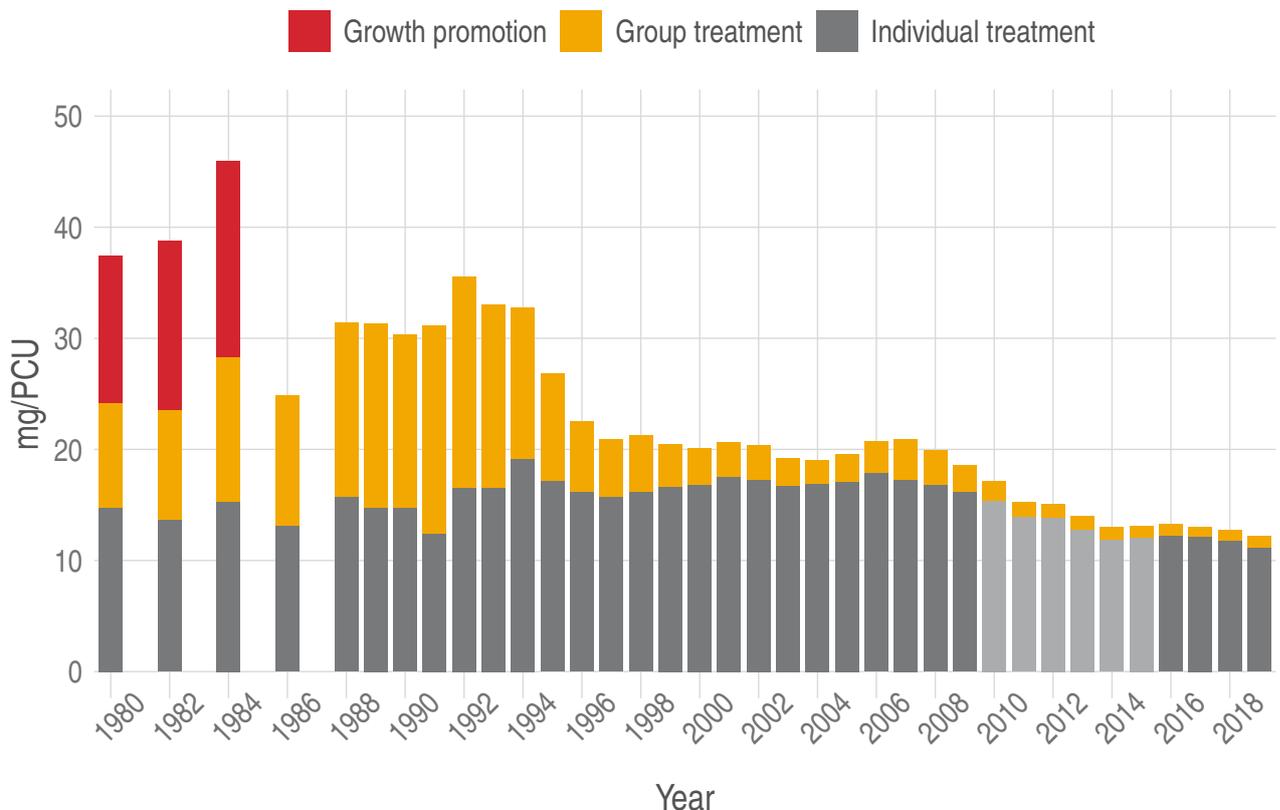


Figure 37: Sales of antibiotics for animals expressed as mg per population correction unit (PCU). Data from 2010–2015 are uncertain because of a lack of completeness mainly affecting injectable products (indicated in a lighter grey). In the present figure, all products (including tablets) are included while in data presented in the European surveillance of veterinary antimicrobial consumption tablets are excluded when calculating mg/PCU.

