

SURVEILLANCE OF INFECTIOUS DISEASES IN ANIMALS AND HUMANS IN SWEDEN 2018



Editor: Ann Lindberg

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

Authors: Anton Andreasson, Charlotte Axén, Mia Brytting, Erika Chenais, Helena Eriksson, Linda Ernholm, Pernille Etterlin, Eva Forsgren, Gittan Gröndahl, Gunilla Hallgren, Anette Hansen, Annelie Hellström, Marika Hjertqvist, Mia Holmberg, Helena Höök, Cecilia Hultén, Cecilia Jernberg, Jerker Jonsson, Pontus Juréen, Ulrika König, Elina Lahti, Ann Lindberg, Mats Lindblad, Anna Lundén, Marie Jansson Mörk, Oskar Nilsson, Maria Nöremark, Anna Ohlson, Faruk Otman, Ylva Persson, Karin Persson-Waller, Thomas Rosendal, Robert Söderlund, Kaisa Sörén, Karl Ståhl, Lena Sundqvist, Magnus Thelander, Karin Troell, Henrik Uhlhorn, Anders Wallensten, Per Wallgren, Stefan Widgren, Ulrika Windahl, Elsie Ydring, Beth Young, Nabil Yousef, Siamak Zohari, Erik Ågren

Cover Photo: Alex Andrews

Copyright of map data: ©EuroGeographics for the administrative boundaries

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. All figures and maps are produced using R software for statistical computing. Development for 2018 has focused on improving the of the importing of content from Word to LaTeX. The method can now import both text and tables from Word, which improves the direct link between author contribution and the final typeset report by allowing authors to design the table layout and content in Word. The tool is available as an R-package available on GitHub (<https://github.com/SVA-SE/mill/>). The report generation R-package and process was designed and written by Thomas Rosendal and Stefan Widgren.

Print: TMG Tabergs AB.

Text, tables, figures and maps may be cited and reprinted only with reference to this report.

Suggestion citation: Surveillance of infectious diseases in animals and humans in Sweden 2018, National Veterinary Institute (SVA), Uppsala, Sweden. SVA:s rapportserie 56 ISSN 1654-7098.

This report may be subject to updates and corrections. The latest version is always available for download at www.sva.se.

Contents

Introduction	3	Listeriosis	55
Overview of active surveillance 2009-2018	4	Nephropathia epidemica	58
Livestock populations and trade in live animals	5	Paratuberculosis	60
Animal registers and data sources used in surveillance	8	Porcine reproductive and respiratory syndrome	63
Institutions, organisations and laboratories involved in surveillance	10	Psittacosis	65
		Q fever	66
Disease Surveillance 2018	13	Rabies	68
Atrophic rhinitis	14	Salmonellosis	70
Aujeszky's disease	15	Scrapie	81
Bluetongue	17	Small Ruminant Lentiviruses	84
Bovine spongiform encephalopathy	19	Strangles	86
Bovine viral diarrhoea	21	Tick borne encephalitis	87
Brucellosis	23	Trichinellosis	89
Campylobacteriosis	25	Tuberculosis	91
Chronic wasting disease	29	Tularaemia	94
Classical swine fever	32	Verotoxinogenic/shiga-toxin producing <i>Escherichia coli</i>	96
Coccidiosis and clostridiosis	34	Yersiniosis	101
Cryptosporidiosis	35	Additional Surveillance 2018	103
Echinococcosis	38	Clinical surveillance	104
Alveolar echinococcosis	38	Poultry health control programme	107
Cystic echinococcosis	40	Infectious diseases in wild boars	109
Enzootic bovine leucosis	41	Infectious diseases and parasites in honeybees	110
Footrot	42	Infectious diseases in fish, crustaceans and molluscs	113
Infectious bovine rhinotracheitis	44	Examination of abortions in food producing animals	117
Influenza	45	Post-mortem examinations in food producing animals	118
Avian Influenza	45	Post mortem examinations in wildlife	120
Swine influenza	49	Antimicrobial resistance in bacteria from animals and food	122
Leptospirosis	52		



Photo by: Hans Braxmeier

Introduction

Surveillance of infectious diseases in animals and humans 2018 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. In fact, this year we celebrate 10 years of integrated reporting of the disease situation with regards to zoonotic infections in Sweden!

A particular focus for this year has been on improving the animal-public health cross-domain analysis, with particular attention to three chapters on zoonoses of high importance; *Campylobacter*, verotoxinogenic *E. coli* and *Salmonella*. The ambition has been to provide a more integrated description of how the surveillance activities in the difference sectors serve to inform one another - all in a true One Health spirit. Specific events have been put “In focus” and the structure of the chapters has been changed to put emphasis on the surveillance activities and what they have achieved. This initiative has been supported by the One Health European Joint Programme (onehealth.eu) as a pilot 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 National Food Agency and the Public Health Agency of Sweden, and this particular initiative is also supported by the Swedish Civil Contingencies Agency.

Over the past few years, *Campylobacter* has received more attention due to several larger outbreaks in humans. In 2018, the annual prevalence of *Campylobacter* positive broiler chicken batches was back to low levels, but nevertheless the integrated cross-sectorial surveillance was triggered in the autumn to reveal an outbreak where the most plausible source was shown to be a hatchery, which has not previously been reported as a possible route of introduction of *Campylobacter* in chicken production. This is just one example of how the combination of integrated surveillance and whole genome sequencing (WGS) will continue to provide new understanding and make it necessary for us to reassess old truths.

2018 was the first year of the EU regulated surveillance programme for Chronic Wasting Disease (CWD), with the first two cases being detected in early 2019. The implementation of the programme is complex. It involves several different species and categories of animals, and requires engagement of voluntary forces as well as agencies that are not commonly involved in animal health surveillance. The importance of having functioning processes for wildlife surveillance can also be exemplified by African Swine Fever (ASF) which has continued to spread in Europe during 2018. In order to strengthen the capacity for early detection much



effort has been put into raising awareness among the public and to engage the hunting community. Still, considering the troublesome situation in south-east Asia, it is clear that ASF-infected meat is only a flight away. Therefore, collaboration with the Swedish customs has been initiated to strengthen awareness also at the border.

This report is subject to constant improvement and development, some more obvious than others. This year we have introduced reporting guidelines for those chapters related to purely animal pathogens. The aim of the guidelines is to facilitate consistent reporting; to ensure all relevant information is included and using harmonised terminology. The reporting guidelines build on experiences from several EU projects, and has 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 are therefore being made available in the form of a wiki on the collaborative platform GitHub (<https://github.com/SVA-SE/AHSURED/wiki>). Feel free to contribute!

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 2018 is provided in this report.

Overview of active surveillance 2009-2018

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 2009–2018 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 from 2009–2018. Filled circles (●) indicate that active surveillance was carried out.

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

Livestock populations and trade in live animals

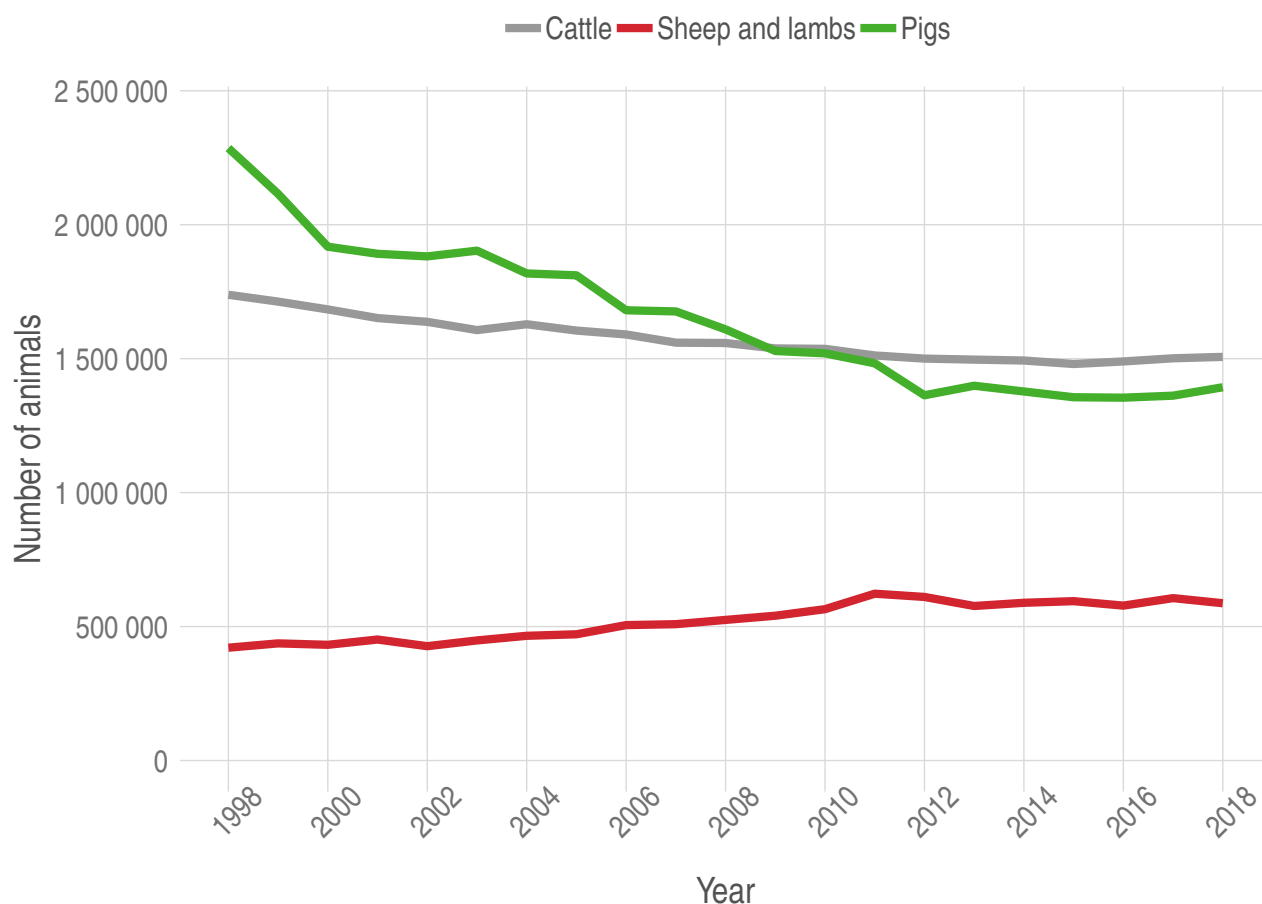


Figure 1: Number of Swedish livestock 1998–2018.

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 in 2018. The statistics for aquaculture reflect 2017.

CATTLE

There are approximately 16 300 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. In 2018, there were approximately 319 000 dairy cows in 3500 holdings, with an average of 92 cows per herd. Nine percent of holdings have 200 or more dairy cows. The number of beef cows has been increasing and, in 2018, this

number was 214 257, with an average herd size of 21 cows.

In total, approximately 410 000 adult cattle and 15 500 calves were slaughtered during 2018. The total milk delivered in 2018 was 2760 million kg. This represents a 2% decrease compared to 2017 and is the lowest production since 1995.

PIGS

The total number of pigs was 1 393 000 (Figure 3) in 2018. For many years this number had been decreasing but, more recently, this trend has been reversed and the population is now increasing. The number of holdings with pigs was 1346, of which 1057 held fattening pigs and 830 held breeding pigs. About 2 646 000 pigs were slaughtered during 2018, as compared to 2 576 000 in 2017.

SHEEP

In 2018, there were 9144 sheep holdings with a total of 295 912 ewes and rams (Figure 4). Sheep holdings in Sweden are usually small-scale enterprises with an average herd size of 32 adult sheep. During 2018, approximately 280 200 sheep were slaughtered, of which 237 000 were lambs. The total slaughter weight was the highest yet recorded.

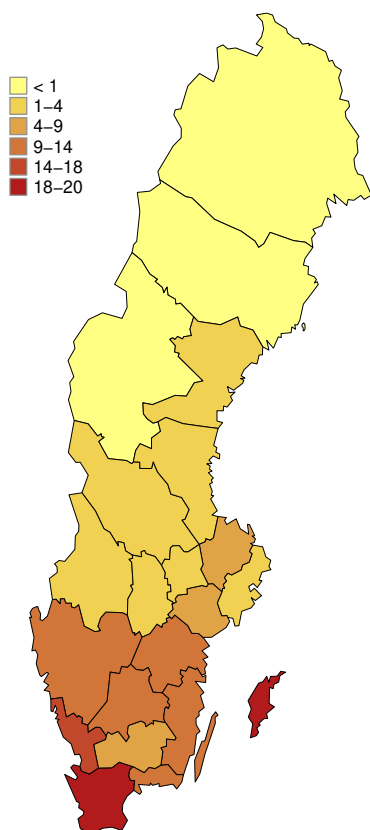


Figure 2: Number of cattle per km² in 21 Swedish counties as of June 2018.

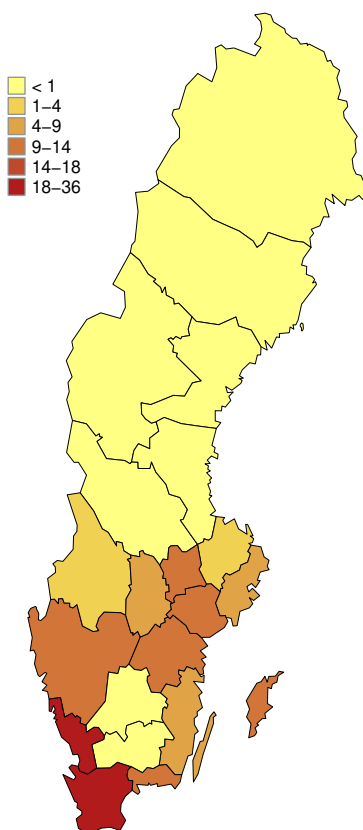


Figure 3: Number of pigs per km² in 21 Swedish counties as of June 2018.

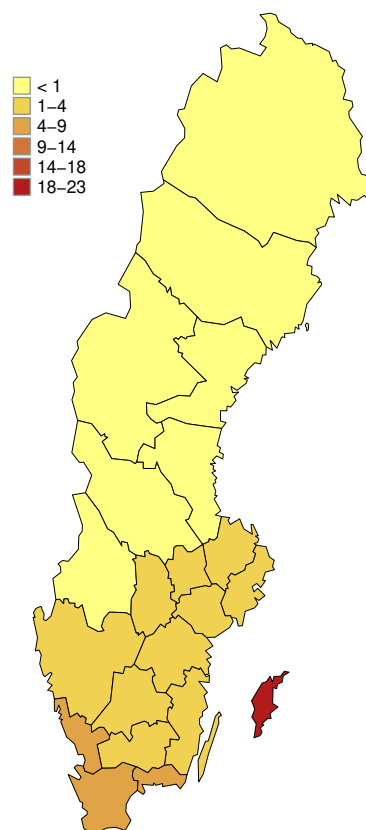


Figure 4: Number of sheep per km² in 21 Swedish counties as of June 2018.

GOATS

In the Central Register of Holdings there are 5059 holdings with goats. Preliminary results (April 2019) from an annual questionnaire show that the number of goats in December 2018 was approximately 15 500. These were kept on a little over 2200 different holdings.

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 2018, there were 7.7 million hens over 20 weeks of age in 3200 commercial holdings, which represents an increase in both population and number of holdings compared to the previous year.

Eggs delivered to wholesalers amounted to 122.8 million kg during 2018.

The number of holdings with broiler production in June 2018 was 213 and approximately 101 million chickens were sent for slaughter during the year. During 2018, 526 000 turkeys were slaughtered.

The production of geese and ducks is very small. In 2018, 15 472 geese, 9150 ducks and no guinea fowl were slaughtered.

FISH AND SHELLFISH

Rainbow trout are the most common farmed fish in Sweden, followed by arctic char, brown trout, eel and salmon, where salmon and sea trout are mainly for restocking of wild populations. Swedish shellfish production is dominated by cultivated blue mussels, of which 2014 tonnes were produced in 2017. All mussel production and 25% of the production of rainbow trout is situated in the coastal district (marine culture), on the west and south/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 2017, there were 49 holdings producing food fish, 56 holdings with fish for restocking, 8 with crayfish for consumption and three with crayfish for restocking. There were six holdings with production of blue mussels and three with oyster production.

The production was 10 881 tonnes of food fish which, when converted to round fresh weight, is the equivalent of 12 834 tonnes. Production has decreased since last year due to the closing of small holdings. Rainbow trout represented the largest production, with 88% of the total production of fish for consumption.

The total production of fish for restocking was estimated to be 924 tonnes. The most common species produced for restocking was also rainbow trout.

To compensate for a decrease in natural reproduction caused by the establishment of hydroelectric power plants, 2.1 million salmon fry and 794 000 sea trout fry were released, mainly in rivers running into the Baltic sea.

REINDEER

In 2018, there were 258 142 reindeer in Sweden, including 57 402 calves, with an average of 54 reindeer per owner. During the 2017/2018 season, 53 150 reindeer were slaughtered. 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 investigation 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 on June 2, 2016 was 77 800. Approximately 2000 horses were slaughtered in Sweden in 2018.

BEEES

In 2018, the number of apiaries in Sweden was 16 477 and the number of colonies was 86 077. These figures, which are approximated by bee inspectors, have decreased in comparison to last year. However, over the last 10 years, these numbers have increased by 44 and 32 percent respectively.

TRADE IN LIVE ANIMALS (LIVESTOCK)

The trade of livestock into and out of Sweden is limited. In 2018, 117 pigs from Norway, two mini pigs from Denmark, 41 cattle from Denmark and one from Finland, two yaks from Germany and seven sheep (all ARR/ARR genotype) from the Netherlands were brought into Sweden. Additionally, 1653 reindeer were brought from Finland for slaughter, and eight alpacas from England and seven llamas from Germany entered Sweden.

Grandparent and parent animals as well as laying stocks entered Sweden as day-old chicks (*Gallus domesticus*) from Germany, Spain and the Netherlands (breeders only). In addition, parent turkeys (*Meleagris gallopavo*) from Great Britain and 13 589 ducks from Denmark and the Netherlands, were brought into the country. Four hundred and twenty hatching eggs (*Gallus gallus*) were brought to Sweden from Germany. Data on the number of imported animals is not available for all poultry.

In total, 48 consignments of honeybees were brought to Sweden for breeding purposes from Denmark, Croatia, Italy,

Malta, Austria, Poland, Slovenia and Germany and Spain.

The number of animals that left Sweden for intra-Union trade during 2018 were: 240 cattle, 2655 pigs (including one mini pig), 93 sheep and three alpacas. In addition, 1665 reindeer left for slaughter in Finland.

Day-old chicks (*Gallus gallus*) and live poultry (*Gallus domesticus*) also left Sweden for intra-union trade in 2018. However, there is no data available on numbers of animals and their destinations.

In total, 1.7 million hatching eggs (*Gallus gallus*) were sent to Poland, Finland, Spain, Hungary, Norway and Russia from Sweden.

A total of 27 consignments of honey bees (*Apis mellifera*) left Sweden for intra-union trade to destinations in Great Britain, Spain, Belgium, the Czech Republic, Germany, Italy, the Netherlands, Poland, Lithuania and Finland.

REFERENCES

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

Personal communication (goats) Magnus Kindström, Djurregisterenheten, Swedish board of Agriculture, April 2018

Swedish Board of Agriculture (2019). "Lantbruksdjur efter län/riket och djurslag. År 1981–2018." [Data accessed 2019-03-13 using pxweb R package 0.9.1], <http://statistik.sjv.se/PXWeb>

Aquaculture in Sweden in 2016, JO 60 SM 1801, SBA (available 2019-04-04 at: <https://www.scb.se>)

Livsmedelsverket (statistics on poultry slaughter)

Sametinget (available 2019-03-28 at: https://www.sametinget.se/statistik_rennaring)

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 reporting to 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 ICARs 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, including approximately 70% 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 farm's water supply and discharge as well as data 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 (i.e. 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 e.g. about animal owners, animals, samples, test results and geolocation. Samples analysed include samples from veterinary practices, different surveillance programs and others. Data exists for 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 with national coverage.

Institutions, organisations and laboratories involved in surveillance

SWEDISH BOARD OF AGRICULTURE

The Swedish Board of Agriculture (SBA) is an expert authority under the Ministry of Innovation and Enterprise, covering the field of agricultural and food policy, 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 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 covers active surveillance, is decided by SBA based on a proposal from the expert authority in the field, the National Veterinary Institute. SBA can also decide on surveillance beyond the 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 lies under 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 epizootic disease preparedness, has National Laboratory functions for several zoonotic and epizootic pathogens, and is also the EU reference laboratory (EURL) for *Campylobacter*.

Several control and monitoring programmes are implemented by SVA in cooperation with stakeholder organisations and relevant authorities. SVA prepares the national surveillance plan that is confirmed and enacted 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 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.

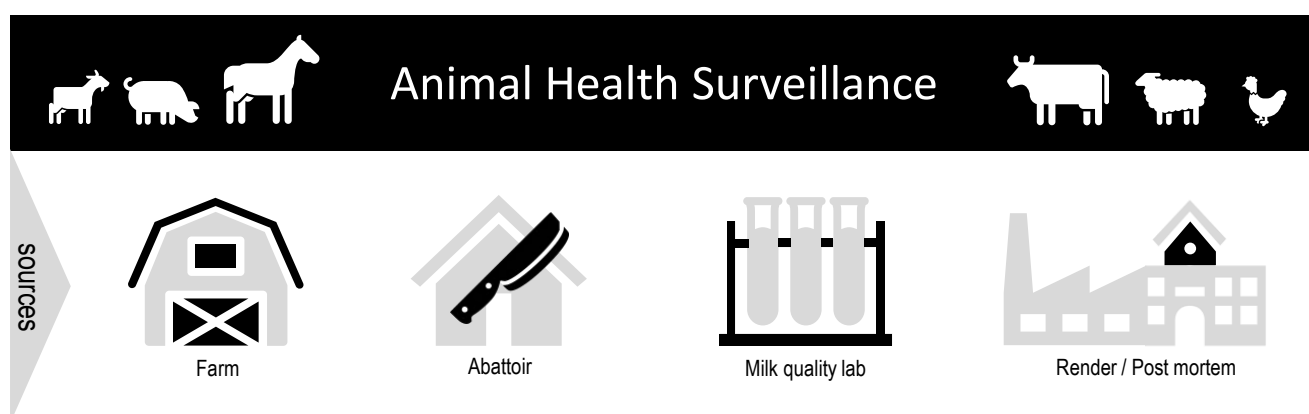
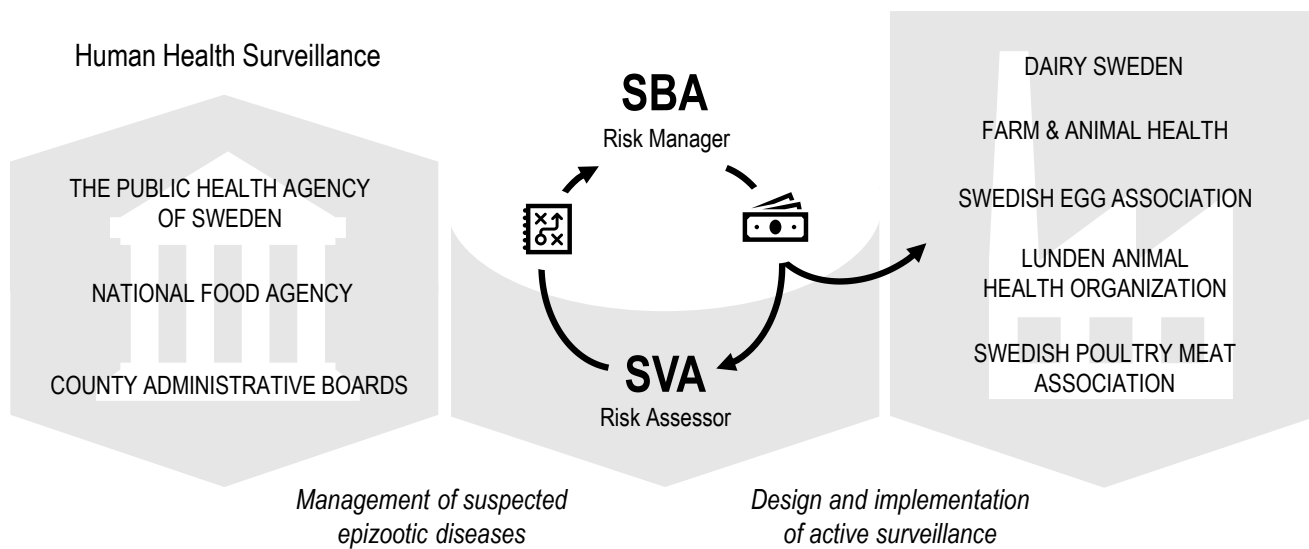
The agency also performs microbiological laboratory analyses, including diagnostics, and supports quality and method development at laboratories engaged in diagnostics of communicable disease pathogens. High containment laboratories have round-the-clock preparedness every day of the year to conduct microbiological 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.

NATIONAL FOOD AGENCY

The National Food Agency (NFA) is a national agency under the Ministry for Enterprise and Innovation. The NFA 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 NFA 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 one hand and the 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 in questions regarding 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



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: Arianna Comin.

County Medical Officers and veterinarians in clinical practice in issues related to zoonoses and “One Health”, and they also carry out regional supervision of animal health and welfare.

VÄXA SVERIGE

Växa Sverige is the largest livestock organisation in Sweden. Växa Sverige is owned by, and works for, its approximate 6000 farmer members. Växa Sverige is an advisor and service provider to dairy and beef farmers, covering most of the geographic area of Sweden.

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 and the voluntary control programme for salmonellosis in cattle. Starting in the autumn of 2015, the salmonella control programme has gradually been replaced with a more general biosecurity programme for cattle (Smittsäkrad besättning). This programme is approved by the SBA and follows the plans and guidelines outlined in SJVFS 2015:17.

FARM & ANIMAL HEALTH

Farm & Animal Health is an advisory company owned by the main meat producing companies and the farmer organisations for pigs, beef and sheep in Sweden. Its aim is to

maintain a high level of health within efficient and profitable pig, beef 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 authorised 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.

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 98% 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 and 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.

Activities also include developing the topic of bee health and how it is affected by pathogens, environmental factors,

pesticides and beekeeping methods. Also included is the National Reference Laboratory for bee health whose activities are carried out in close cooperation with relevant authorities and beekeepers.

BEE INSPECTORS

At the local level, bee inspectors (bitillsynsmän) are experienced beekeepers that are specially trained to examine bee colonies for disease. The main duties of bee inspectors are to examine bee colonies to detect diseases in case of disease suspicion or in connection with requests to move bee colonies from areas classified as protection or surveillance zones. Bee inspectors also issue move-permits and carry out or impose control measures for specific diseases and inform beekeepers about *Varroa* mite treatment. 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. Sweden is divided into just under 500 bee districts and the bee inspectors are responsible for the practical control in each of these. The bee inspector system aims at combating American foulbrood, tracheal mites and varroa mites.

REFERENCES

- Anton Andreasson, National Food Agency (www.slv.se)
- Pernilla Stridh, County Administration Östergötland (www.lansstyrelsen.se) (County Administrative Boards)
- Lena Hult, Swedish Board of Agriculture
- Ann Nyman, Växa Sverige (www.vxa.se)
- Ebba Schwan, Farm & Animal Health (www.gardochdjurhalsan.se)
- Anders Wallensten, Folkhälsomyndigheten (www.folkhal-somyndigheten.se)
- Pia Gustafsson, Swedish Poultry Meat Association (www.svenskfagel.se)
- Magnus Jeremiasson, The Swedish Egg Association (www.svenskaagg.se)
- Erik Lindahl, Lunden animal health organisation (www.lunden.com)
- Ingrid Karlsson, Swedish Board of Agriculture (bee inspectors)
- Eva Forsgren, Swedish University of Agricultural Sciences

Disease Surveillance 2018

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. Atrophic rhinitis was a common disease in pig production but improvements in rearing and disease prevention have caused the disease to gradually fade away. 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 controlled for the presence of toxigenic *P. multocida* at least once a year and every time there is clinical suspicion of AR. Eradication of *P. multocida* is not realistic since it is a ubiquitous bacterium that can affect all mammals. However, anytime AR is suspected in a herd, tests should be performed for the presence of toxigenic *P. multocida*. If toxigenic *P. multocida* is detected, 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* 2005–2018. The samples have been collected in all nucleus and multiplying herds, as well as in production herds suspected for 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

RESULTS AND DISCUSSION

Atrophic rhinitis used to be a common disease, but the disease is now very rare due to efforts made in the early 1990s and the control programme that was initiated in 1995. The latest Swedish herd was diagnosed with AR 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.

Aujeszky's disease

BACKGROUND

Aujeszky's disease (AD) is caused by a herpes virus with the capacity to infect many species, but pigs are the natural hosts. The disease is of importance for pig production worldwide, although in many countries it is controlled in the domestic pig population. AD is widespread in European wild boar populations which may act as reservoirs, but their role in transmitting the disease is not well known. Other species, including cattle, sheep, goats, dogs and cats, develop clinical signs but are not of importance for transmission of the disease as they are considered 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 (current 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 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. 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

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

Active surveillance

In 2018, all samples collected in the abattoir sampling component of the surveillance for porcine respiratory and reproductive syndrome virus (PRRSv), 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 2018, the number of samples required for the abattoir component of the PRRS surveillance programme was calculated to be 2400.

From 2000–2017 there was also active surveillance of AD in wild boar (see chapter on *Infectious diseases in wild boars*). Due to a redistribution of funding, active surveillance for AD in wild boar was not undertaken in 2018 but will be resumed in 2019.

RESULTS

Passive surveillance

In 2018, one clinical suspicion of AD was investigated. In this herd, late-term abortion was the main clinical manifestation. During the investigation, blood samples from sows were analysed for the presence of antibodies to AD. All samples were negative, and the herd was 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 from 2009–2018.

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

Active surveillance

In 2018, 2706 samples from pigs from 514 herds taken on 903 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 detection of 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. The effects of these changes in programme design on the probability of freedom from AD has not previously been evaluated but, because the risk of introduction of AD is considered lower than that for PRRSV, the probability of freedom from AD was assumed to be high. This year, based on the surveillance undertaken in 2018, 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 M-P (2015) A picture of trends in Aujeszky's disease virus exposure in wild boar in the Swiss and European contexts. *BMC Vet Res* 11:277

Bluetongue

BACKGROUND

Bluetongue is a vector borne disease of ruminants and camelids caused by any of 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 also 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) and serum samples were



The bluetongue virus (BTV) is transmitted by haematophagous midges (*Culicoides* spp). Surveillance during 2018 confirms the continued freedom from BTV in Sweden. Photo: Anders Lindström

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

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

Active surveillance

Vectors

Animals

In the 2018 bluetongue surveillance 190 dairy holdings from a risk-based sampling area, comprising the nine most southern 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 2018 until January 2019. Samples were analysed with the milk ELISA routinely used.

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

RESULTS

Bulk milk samples from 189 holdings were tested in the field surveillance. Two clinically suspect cases were investigated and tested during 2018 and found negative. In total 52 serological samples tested for bluetongue 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 2018, 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 thousands of 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, Germany and Switzerland each reported some cases of BTV-8 (using the same definition) found during routine surveillance. The United Kingdom reported a single case of BTV-8 in cattle imported from France.

During 2017, BTV-4 was detected in France, involving several outbreaks on the island of Corsica and subsequent spread to mainland France via movement of live animals. During 2018, one case of BTV-3 was detected on the island of Sardinia, Italy. This serotype is new to Italy but circulating in Tunisia.

During 2012, BTV-14 was detected in cattle in Estonia, Latvia, Lithuania, Poland and Russia. Sequencing was performed and indicated that the positive cases were derived from a common source and suggested significant spread of the virus in the field. The strain was identified as a BTV-14 reference or vaccine strain, possibly indicating the use of a live BTV-14 vaccine.

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 and Switzerland during 2018, again demonstrates that BTV 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, Mieziowska 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 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 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 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), and later by the OIE Scientific Commission and expressed in terms of the Geographical BSE Risk (GBR). 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 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 during 2018 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 necropsy.

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

RESULTS

Feed

In 2018, 35 feed samples were taken at feed mills and one from retail; 32 of these were from feed (21 were cattle feed) and 3 from raw materials for feed production. All of these samples were negative.

Animals

Passive surveillance

In 2018, 42 bovines were examined due to clinical suspicion, all with negative results.

Active surveillance

In 2018, 7456 samples were examined for BSE. All samples were negative. Of these samples 7273 were from fallen stock, 32 samples were from animals with remarks at antemortem inspection before slaughter and 151 samples were from emergency slaughtered animals.

DISCUSSION

No positive BSE cases were detected in Sweden in 2018. 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 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. 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.

At 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



A voluntary control programme with the objective to eradicate BVD from Sweden, without vaccination, was launched in 1993. The programme was made compulsory in 2001. Since 2011, there have been no newly infected herds and the last virus positive animal was born in an infected dairy herd in 2012. Since 2014, Sweden is considered free from BVD. Photo by: Gunilla Hallgren.

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 1993:42 and the compulsory control in SJVFS 2002:31.

SURVEILLANCE

Herds are individually risk categorized based on the number of herds they have purchased from and sold to during the preceding 12-month period.

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

Table 4: Total numbers of samples with different contents of BVDV antibodies tested in 2018.

Sample type	Class/Finding	Herds	Animals
Bulk milk	0–1 ^A	2291	-
Bulk milk	2–3 ^A	0	-
Blood sample at slaughter	Negative	-	8161
Blood sample at slaughter	Positive	-	6
Field sample	Negative	-	27
Field sample	Positive	-	0

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

Table 5: Dairy and beef herd results from testing of BVDV antibodies in bulk milk or blood samples in 2018 divided by herd level risk.

Herd level risk ^A	Herd numbers (N)	Production type	
		Dairy	Beef
<i>Low risk</i>	N of herds	2471	7827
	N of herds tested	897	2114
	N positive	0	5
<i>Medium risk</i>	N of herds	1216	1780
	N of herds tested	853	851
	N positive	0	0
<i>High risk</i>	N of herds	241	405
	N of herds tested	200	232
	N positive	0	1

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

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 2018 are given in Tables 4 and 5.

Diagnostic testing is performed at the National Veterinary Institute. For screening, an indirect antibody ELISA (Svanovir® BVDV-Ab ELISA) 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 2018 is given in Table 4. As shown in Table 4, six samples (all from beef-cattle herds) were antibody positive during the year. Their herds of origin were investigated and considered to be non-infected. In 2018, 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 2018. 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 2018.

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

Brucellosis

BACKGROUND

Brucellosis is caused by 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, however, 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. Brucellosis in humans has been a notifiable disease in Sweden since 2004. Between 4 and 19 human cases have been reported annually. Most of these patients have acquired the infection outside Sweden or via consumption of products from countries where brucellosis is endemic.

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. For rare species, CFT is most commonly used and 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 (Page 117).

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

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.

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 not performed in 2018. From 1997 and onwards, approximately 3000 samples (bulk milk and/or serum samples) have been tested each year for antibodies against *B. abortus*. Samples are selected by systematic random sampling every 6th serum and every 8th milk sample evenly distributed throughout the sampling period from samples collected in the surveillance programmes for bovine viral diarrhoea and enzootic bovine leucosis.

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 surveillance of 2018 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 (5 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 have been tested for antibodies against *B. suis* each year. Beginning in 2009, serum samples are tested every second year, and accordingly, this sampling was not performed in 2018.

RESULTS

Passive surveillance

Animals

During 2018, one clinical suspicion was reported in a bovine dairy herd. The suspicion was ruled out after investigation in the herd and blood samples from five affected testing negative for the presence of antibodies using CFT. No clinical suspicions of brucellosis were seen in any other food-producing animal species.

Within the surveillance of aborted fetuses, 34 bovine, 23 ovine, five caprine, and sixteen pig fetuses were examined for *Brucella* spp. All samples were negative.

Humans

For many years, no domestic cases were reported, and Sweden is therefore considered free from brucellosis. However, since 2010 there has been approximately one domestic case reported annually. Predominantly these cases have, or were suspected to have, consumed unpasteurized milk products from endemic countries. During the time period, one congenital and one laboratory acquired *Brucella* infection were also reported.

In 2018, 11 cases were reported. All but once case reported recent travel history to endemic countries. The most common country of infection was Iraq, which represented more than half of the cases.

Active surveillance

Animals

During 2018, 1935 ovine and caprine serum samples from 397 individual holdings were analysed for *B. melitensis*. All these samples were negative.

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 2018. The long standing and extensive serological screenings performed without finding any infection and the very low number of human cases, only occasionally domestically acquired, confirms that *Brucella* is not present in Swedish food-producing animals. The enhanced passive surveillance in aborted fetuses from food-producing animals is an important part of the surveillance system.

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 seven 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

BACKGROUND

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

Birds are considered the principal reservoir although *Campylobacter* can colonise the intestinal tract of many other animal species. The bacteria are excreted in faeces. *Campylobacter* spp. are fragile organisms but can survive in water for longer periods. The infectious dose for humans is low. A seasonal peak in the summer months is observed in most European countries both in humans and in chickens. 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 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 6). Of these, approximately 20–60% have been reported as domestic. In recent years, due to outbreaks, the majority of cases have been domestic.

SURVEILLANCE

Animals

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

The programme covers 99% of the broilers slaughtered in Sweden. Since 2006, sampling is performed by collecting intact caeca from 10 birds from each slaughter batch at the major abattoirs. When thinning is applied and the time interval between the slaughter batches is longer than four days, samples are taken from both batches. The caeca are pooled into one composite sample per batch. Samples are analysed according to ISO 10272 part 1.

Since 2017, all *Campylobacter* isolates collected in the monitoring programme during two periods of 2.5 weeks, starting week-8 and week-31, have been subjected to whole genome sequencing. The time frames were selected to precede the collection of human domestic isolates.

Food

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



An unusual *Campylobacter* colony on campylobacter mCCDA agar. The incidence in domestic cases decreased by 40% during 2018 from the year before bringing the domestic incidence back to the level prior to 2015. Photo: Frida Wennerholm.

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 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.

National outbreaks are jointly investigated by several authorities, which authorities involved depends on the nature of the outbreak. In 2018 one national outbreak was investigated, see "In Focus".

RESULTS

Animals

In 2018, thermophilic *Campylobacter* spp. were detected in 377 (8.7%) of the 4331 conventionally produced broiler chicken batches tested at slaughter (Figure 5), which is less

IN FOCUS - An outbreak of *Campylobacter jejuni* with an unusual source

In the fall of 2018, an outbreak of *Campylobacter jejuni* with an unusual source within the chicken production was investigated. The outbreak started in the middle of November when the incidence in humans is usually low. Cases could be seen in the whole country. The increase in human cases coincided with an increase in the prevalence of *Campylobacter* in slaughter batches of chicken identified within the *Campylobacter* surveillance programme at SVA. In addition, several employees working at abattoirs were reported with campylobacteriosis in October and November. Isolates from employees and from caecal samples of chicken from three different poultry abattoirs were analysed by whole genome sequencing (WGS). Same sequence types (ST-9198 and ST-148) were identified from human cases and chicken samples. The trace-back investigation showed that farms delivering chicken to these three abattoirs received day-old chicks from the same hatchery. *Campylobacter jejuni* ST-148 was detected from parent flocks delivering eggs to the hatchery. Thus, an unusual pathway of *Campylobacter* introduction was identified as the plausible source of the outbreak. This pathway has previously not been reported as a possible introduction of *Campylobacter* in the chicken production.

than the previous years. Adding up testing of slaughter batches of ecological and free-range production results in a *Campylobacter* prevalence of 9.1%, (401/4394 slaughter batches). However, the monthly prevalence of *Campylobacter* in chicken slaughter batches varied between 0.8% and 16.9% with the highest prevalence in August. The prevalence of *Campylobacter* in incoming batches of poultry also varied between abattoirs.

Food

In August 2018, a survey was performed by the National 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 61% of the 100 samples. *Campylobacter* levels exceeded 10 cfu/g in 25% of the samples.

In addition, 35 samples were taken by national and local authorities from different types of food. Most of these were taken to investigate a complaint or a suspected food poisoning. Neither of them yielded *Campylobacter*.

Humans

A total of 8132 cases of campylobacteriosis were reported in 2018. Of the reported cases, 45% (3645 cases) were domestic. The incidence in domestic cases decreased by 40% from the year before to 35.6 per 100 000 inhabitants. Hence, the domestic incidence is back at the same level as before the years 2015–2017, during which large outbreaks related to chicken consumption affected the incidence. Seen over a longer period however there is an increasing trend in the domestic incidence (Figure 6).

Among the domestic cases in 2018, the median age was 47 years with a spread from 0 to 95 years. Like previous years, the domestic incidence was highest in adults and more men (56%) than women were reported with campylobacteriosis.

In the microbial surveillance programme at the Public Health Agency of Sweden, isolates from cases were collected in March (week 11) and in August (week 34). Of the 119 isolates, all but one was *C. jejuni*. Ten clusters were identified, including 31% of the isolates. In August, isolates from the microbial surveillance programme and isolates from the survey performed by the National Food Agency were analysed by WGS. About 30% of the human isolates clustered with isolates from fresh chicken meat.

DISCUSSION

The domestic incidence of campylobacteriosis was lower in 2018 than in the previous years. The trend over a longer time period is, however, increasing. Most campylobacteriosis cases are considered sporadic but in recent years, several large outbreaks linked to domestically produced chicken have occurred. These outbreaks show the importance of effective control and preventive measures in the poultry production.

In 2018, the annual prevalence of *Campylobacter* in broiler chicken batches was lower than in the previous years (Figure 5). However, an outbreak in late autumn associated with domestic chicken meat and the high detection rate of *Campylobacter* in the survey on retail meat warrant stringent preventive measures. *Campylobacter* prevalence varies considerably between abattoirs, with only a few findings at some abattoirs and higher prevalences 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 leading to a higher amount of potentially contaminated chicken meat at the market.

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. However, there has been a marked change in the

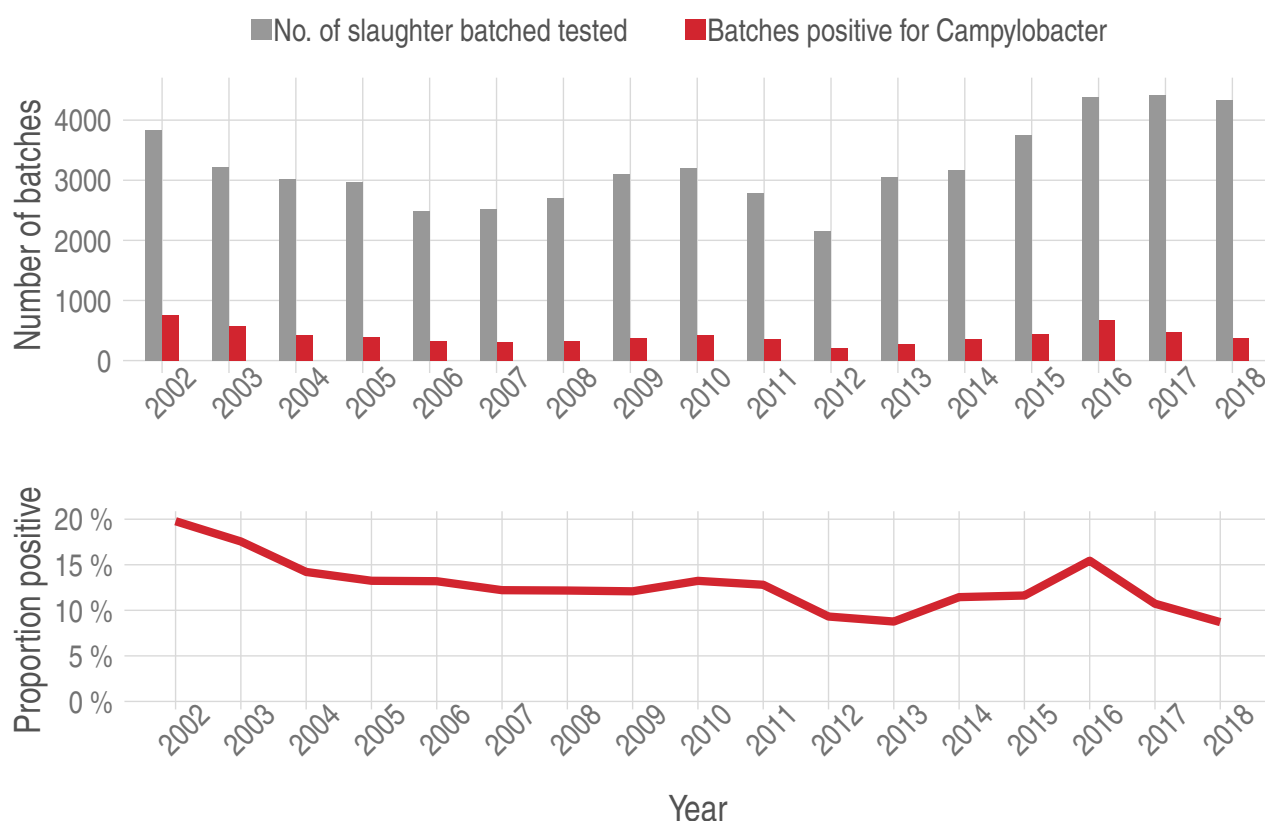


Figure 5: Prevalence of *Campylobacter* in broiler flocks in 2002–2018.

production system and more effort is needed to decrease the number of infected broiler flocks. Also, the outbreak at the end of 2018 was linked to a hatchery and the outbreak 2016/2017 was caused by problems at a slaughterhouse. This shows the importance of biosecurity measures not only at farm level but in the whole production chain.

Broiler carcasses are easily contaminated at slaughter which necessitates that consumers apply good hygiene practices. Strict hygiene in the kitchen is essential to avoid cross-contamination between contaminated raw meat and food that will not be heated such as raw vegetables.

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, 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 National Food Agency requires that weekly samples are taken from June through September. The results from the analyses 2018 were not collected by the competent authority, but they will be from 2019 onwards.

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.

REFERENCES

Folkhälsomyndigheten. Mikrobiologisk övervakning av campylobacter. 2018, <https://www.folkhalsomyndigheten.se/mikrobiologi-laboratorieanalyser/mikrobiella-och-immunologiska-overvakningsprogram/overvakning-av-campylobacter/>.

Hansson I, Nyman A, Lahti E, Gustafsson P, Olsson Engvall E (2015) Associations between Campylobacter levels on chicken skin, underlying muscle, caecum and packaged fillets. Food Microbiol 48:178–181

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

Harvala H, Rosendal T, Lahti E, Olsson Engvall E, Brytting M, Wallensten A, Lindberg A (2016) Epidemiology of Campylobacter jejuni infections in Sweden, November 2011–October 2012: is the severity of infection associated

with C. jejuni sequence type? Infect. Ecol. Epidemiol 6:31079

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: Campylobakter 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

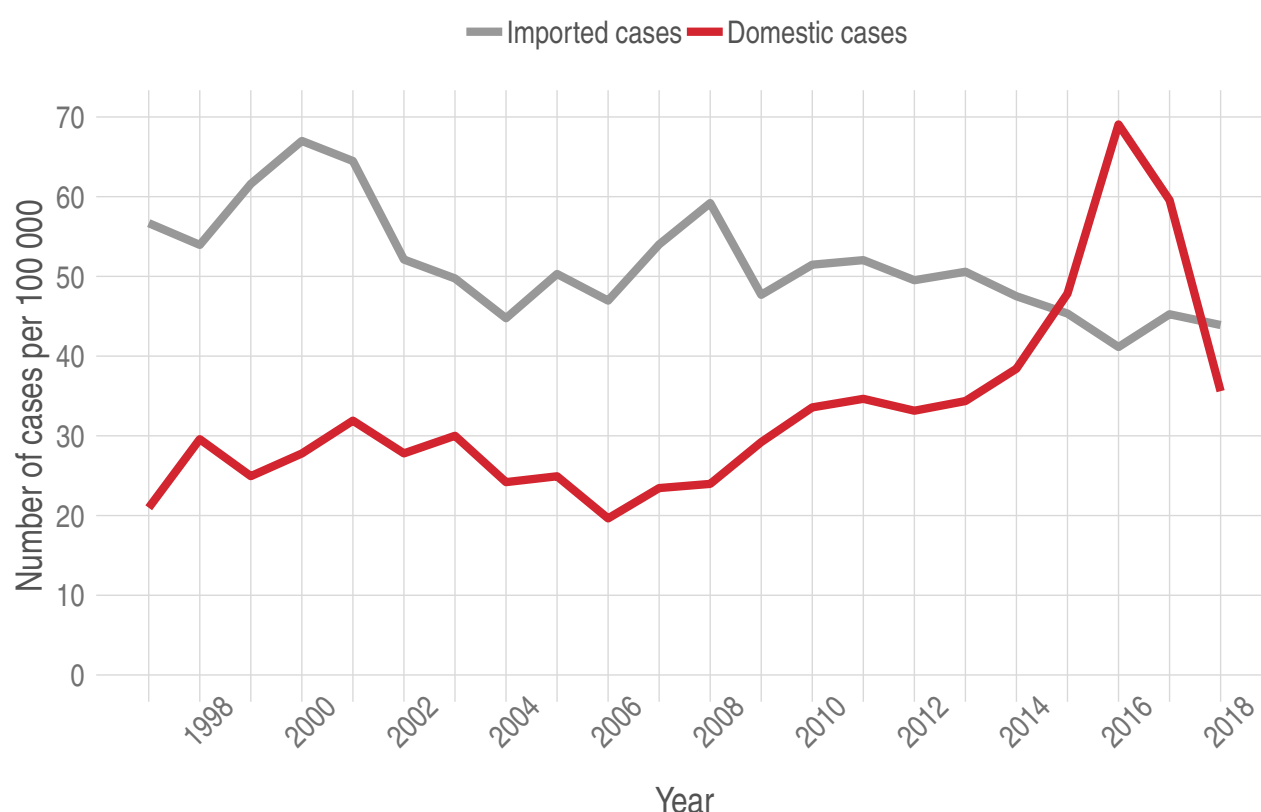


Figure 6: Notified incidence (per 100 000 inhabitants) of human cases of campylobacteriosis in Sweden, 1997–2018. Imported cases are those where the patient has reported travel to another country during the incubation period prior to clinical presentation. Domestic cases are patients that have not recently travelled outside Sweden.

Chronic wasting disease



In response to the detection of Chronic wasting disease in Norway, sampling of adult cervids sent for necropsy to the National Veterinary Institute started during summer 2016. During 2018, an active surveillance of wild, farmed and semidomesticated cervids included a total of 200 cervids tested for CWD in Sweden. Photo: Anders Lindström

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, 2019). Through export of live cervids, CWD has also spread to South Korea.

Until 2016, CWD had not been reported in Europe. In spring of 2016, the first case in Europe was detected in wild reindeer 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 2019) resulted in the detection of the disease in three moose close to the Swedish border (in Selbu and Lierne), one moose in Flesberg near Oslo, one red deer (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. What this means in terms of differences in e.g.

the disease transmission pattern is still unknown, but it has been hypothesised that these “atypical” cases may be spontaneously occurring in older animals (Prisinu et al., 2018).

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.

Although this report concerns surveillance in 2018, it must be mentioned that in March 2019 CWD was reported in Sweden for the first time. The disease was detected in a sixteen-year-old female moose (*Alces alces*) 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 Prisinu et al 2018, such as that it was an older moose and only brainstem was positive. In accordance with EU legislation, intensified sampling will be carried out in the area. The intensified sampling will contribute with epidemiological data indicating if the cases in older moose are contagious or not.

Wild cervid animals cross the border between Sweden and Norway. Some semidomesticated reindeer also cross the border between the countries. In Sweden, reindeer herding is an essential part of the Sami culture; there are no wild reindeer and only Sami people have the rights of reindeer husbandry. Moose and roe deer live in the wild (with few exceptions) and many people are involved in hunting of these species. The farmed cervid species in Sweden are mainly fallow deer and red deer, as well as a low number of moose.

Due to similarities with BSE, which is linked to variant Creutzfeldt Jacobs 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, Wadell 2017). 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 necropsy between 2008 to 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 the disease in the field has been low and as a consequence very few animals have been examined.

DISEASE

From what is known about the type of CWD present in North America, “classical” CWD, the incubation period is long, over a 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 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.

The cases in moose in Norway, Finland and Sweden differ from classical CWD cases as they have all been in old animals and prions have only been detected in the brain and not in lymph nodes. So far, results of increased surveillance do not indicate that these cases are contagious.

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 necropsy to the National Veterinary Institute started during summer 2016. In response to 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 during the moose hunting period.

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 (*Alces alces*), red deer (*Cervus elaphus*), roe deer (*Capreolus capreolus*) and reindeer (*Rangifer tarandus tarandus*) 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 Sami villages (n=51). All animals sampled must be over twelve months of age.

The CWD surveillance programme is implemented 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 on a weekly basis.

Brainstem and lymph node samples are screened with Bio-Rad TeSeE short assay protocol (SAP), using the CWD addendum, at the National Veterinary Institute, Uppsala. The laboratory is the National Reference Laboratory (Regulation (EC) 999/2001) for TSEs. 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 2018, samples were primarily taken from cervids found dead or diseased and road/train killed cervids (assumed to have higher probability of infection), but in a

few cases also from apparently healthy slaughtered/hunted cervids. The samples were collected and sent to the National Veterinary Institute mainly by hunters and animal owners.

RESULTS

The number of samples tested from 2016 to 2018 is detailed in Table 6.

Seventeen investigations following clinical suspicions of CWD were carried out in 2018, all with negative results. In total, 157 moose, 13 red deer, 15 roe deer and 15 reindeer were examined for CWD at the National Veterinary Institute during 2018, all with negative results.

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 during 2018, the first year of the surveillance programme, was much below one third of the 6000 samples to be analysed during the three-year programme. There are several reasons for this. The implementation of the programme is 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 on the other hand quite high, and future efforts will be put into receiving more samples from this group of cervids.

The experience from North America is that classical CWD is very difficult to eradicate or control, and to have a chance, early detection is needed while the prevalence is still low. If this form of the disease, seen also in the wild reindeer in Norway, is present or introduced into Sweden,

it could have large negative consequences for reindeer, wild cervid populations and farmed cervids. Consequently, the disease could also have large consequences for people involved in activities related to, or making their living from, these species. However, if the atypical cases found in Norway, Finland and Sweden can be shown to be spontaneous, the disease could be expected to occur sporadically in all deer populations, without leading to the same severe consequences as classical CWD.

REFERENCES

- Centers for Disease Control and Prevention, <https://www.cdc.gov/prions/cwd/occurrence.html> (accessed 2019-04-01)
- 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
- Prisinu 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
- 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

Table 6: The number of animals tested for CWD per year in Sweden 2016–2018.

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

Classical swine fever



The surveillance for classical swine fever in Sweden was passive under 2018. In previous years, blood samples collected at abattoirs have been used for active surveillance of CSF in domestic pigs. This active surveillance will be reinstated during 2019. Photo: Bengt Ekberg

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 considered one of the most important diseases affecting pig production globally. The disease is considered endemic in much of Asia and South and Central America while the CSF status in Africa and the Middle East is largely unknown. 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 1997–98. These outbreaks led to the implementation of highly effective control and eradication strategies and now large parts of the EU are recognized as being CSF-free. However, over the last 10 years there have been sporadic outbreaks of CSF in both domestic pigs and wild boar in several Eastern European countries including Lithuania (2009, 2011), Latvia (2012–2015) and Ukraine (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. Feeding pigs swill contaminated with CSFV is considered

the main route of spreading the disease to new areas. Because of this, swill feeding of pigs is prohibited in the European Union. Wild boar can also 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.

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, fetal 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 includes sampling of sick or dead animals, examination of the herd for presence of clinical signs and analyses of production results. Due to the similarity in clinical signs, samples are analysed for both CSF and ASF. This strategy is strongly recommended by the EU. During the investigation, the farm is placed under restrictions.

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

Active surveillance

In previous years, blood samples collected in the abattoir sampling component of the surveillance for porcine reproductive and respiratory syndrome (PRRS), carried out by Farm and Animal Health, have also been used for the active surveillance of CSF in domestic pigs. Active surveillance of CSF in hunted Swedish wild boar has also been done yearly from 2000–2017 (see chapter *Infectious diseases in wild boars*). In 2018 however, due to a redistribution of

funding, active surveillance for CSF in domestic pigs and wild boar was not undertaken but will resume in 2019.

RESULTS

Passive surveillance

Four investigations following clinical suspicions of CSF were carried out during 2018, three in domestic pigs and one in captive wild boar. In two of the domestic pig herds the main clinical manifestation was reproductive failure, including abortion and weak-born piglets, while in the third herd, increased mortality with multiple organ hemorrhages in growing pigs were reported. The primary clinical sign in the captive wild boars was sudden, unexplained death. Following the investigations, which included sampling and analysis for CSF, all the herds were declared negative for CSF (the investigations also included testing for African swine fever).

Within the surveillance of aborted fetuses, 14 fetuses from 8 herds were examined for the CSF viral genome and all samples were negative.

Active surveillance

No active surveillance for CSF was undertaken in 2018.

DISCUSSION

The results from the passive surveillance for CSF in Sweden during 2018 add to the documentation of freedom from this infection in the Swedish commercial pig population. During 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 situation regarding CSF in the EU has successively improved in recent years, 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, emphasizes 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 program 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. Clostridiosis 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) 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 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 analysis of the feed for the concentration of anticoccidials is performed and an on-farm investigation of management and general health status is supposed to be carried out.

Condemnation due to liver lesions

The occurrence of hepatic lesions is registered at the abattoir, and if more than 2% of the birds in a flock are affected, samples are sent for histological examination to the National Veterinary Institute. Data on the level of condemnations due to liver lesions are compiled on a quarterly basis, from all abattoirs.

RESULTS AND DISCUSSION

In 2018, 22 broiler flocks were investigated for lesion scoring, and a mean total lesion score (MTLS) above 2.5 was exceeded in 5 flocks. Beginning in 2018 a follow up investigation was supposed to have been performed in flocks exceeding this mean score, but these reports were delayed and could hence not, as required, be compiled in this years SVA report.

98.5 million broilers were slaughtered in Sweden in 2018. Samples for histological examination of the liver were submitted from abattoirs originating from 11 broiler flocks with more than 2% condemnation due to liver lesions. Lesions indicating clostridiosis (i.e. cholangiohepatitis) were observed in 9 flocks. In 2 other flocks, the submitting samples were from flocks with less than 2% condemnation due to liver lesions, therefore a histological examination was not performed.

It was concluded that there is currently no indication of reduced efficacy of anticoccidials in Sweden, despite the increasing occurrence of hepatic lesions at the abattoirs. No longterm trends towards reduced anticoccidial efficacy or increased prevalence of coccidiosis were observed.

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 *C. parvum*, while the zoonotic potential is lower in other species.

The infective life stage, the oocysts, are transmitted between hosts via a 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. However, 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 diarrhea in infants and toddlers, only behind rotavirus. Also, *Cryptosporidium* spp. has been ranked as the sixth most important food-borne 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 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.

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, includes moderate to severe watery diarrhea, low-grade fever, cramping abdominal pain, nausea and vomiting.

LEGISLATION

Animals

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

Humans

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

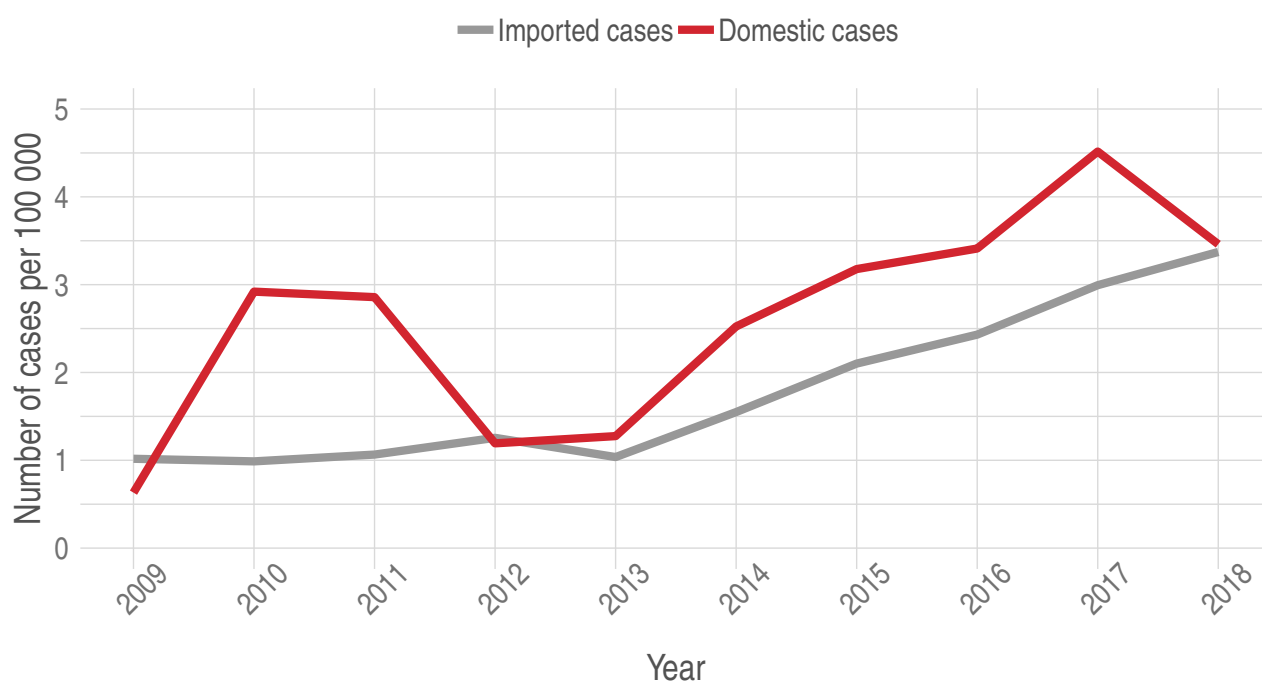


Figure 7: Number of notified human cases per 100 000 inhabitants from 2009 to 2018.

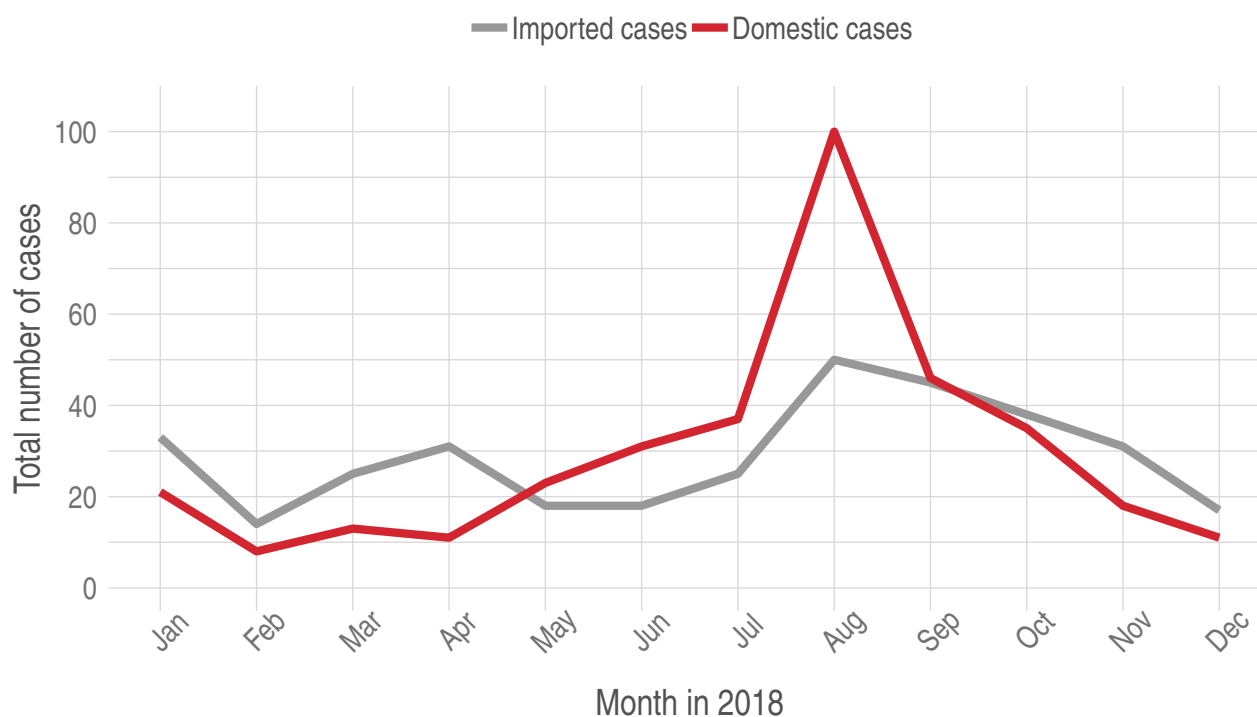


Figure 8: Number of notified human cases of cryptosporidiosis during 2018.

SURVEILLANCE

Animals

The surveillance of *Cryptosporidium* sp. 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

The surveillance in humans is passive. On identification of the disease by the 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.

Also, in 2018, the Public Health Agency of Sweden initiated an enhanced passive surveillance component; a microbiological surveillance program with the aim of determining species and subtypes of all domestic cryptosporidiosis cases in order to better understand the national epidemiology as well as to confirm outbreaks.

RESULTS

Animals

Traceback from the human case of *Cryptosporidium* chipmunk genotype I (mentioned below) resulted in identification of both this species as well as *C. ferret* in the squirrels identified to be the source.

Humans

In 2018, a total of 715 cases of cryptosporidiosis were reported corresponding to an incidence of 7 cases per 100 000 inhabitants. This is comparable to the number of cases reported the year before. (Figure 7). Of all the reported cases the median age was 33 years (0–87 years) and 54 percent

were women (n=384/715). During 2018, 354 cases were reported as domestic, 345 cases as travel-associated and for 16 cases there were no information regarding place of infection. Most of the travel-associated cases were reported from Spain (n=53) followed by Portugal (n=29) and Thailand (n=24). 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.

Usually the majority of cases (both domestic and travel-associated) are reported during the summer months (Figure 8).

In total the laboratory analysed 230 domestic cases in the microbiological surveillance programme. A majority of these, 85 percent (n=196) were *C. parvum* and 9 percent were *C. hominis* (n=20). Other species detected were *Cryptosporidium* chipmunk genotype I (n=8), *C. erinacei* (n=3), *C. meleagridis* (n=2) and *C. ditrichi* (n=1), a relatively new described species.

During 2018 the first transmission of *Cryptosporidium* chipmunk genotype I between a squirrel and human could be confirmed in a joint outbreak investigation between the Public Health Agency of Sweden, the National Veterinary Institute and the local department of communicable disease control. The case was a person working at a small animal rehabilitation centre and in that way came in close contact with squirrels.

DISCUSSION

Even if the total number of reported cases of cryptosporidiosis in humans during 2018 were somewhat lower than 2017 it is still one of the highest numbers reported since the disease became notifiable 2004. The increase of reported cases 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.

In 2018 this increase of cases during the summer months was more significant than previous years (especially during July–September). One possible explanation to this could be the exceptionally warm summer and the increase of exposure in terms of e.g. more frequent bathing, staying and eating outdoors and in that way coming in contact with (farm) animals and their environment.

During 2018, results from the microbiological surveillance program showed that *C. parvum*, was by far the most

common species causing human cryptosporidiosis in Sweden. *C. hominis*, was the second most common species but stood for only a small part of all cases. Another important species identified was *Cryptosporidium* chipmunk genotype I. In 2018 the first case ever in Sweden, and to our knowledge in the world, of zoonotic transmission of *Cryptosporidium* chipmunk genotype I between squirrel and human was confirmed as described above. This species is known to infect humans and is considered an emerging human pathogen in the USA. The prevalence of *Cryptosporidium* chipmunk genotype I among squirrels in Sweden is unknown and needs to be investigated.

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 strictu (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 varies 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 (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 Dalarna County. 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 Södermanland county. 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 Kronoberg county 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.

Within the Emiro research project (finalized in 2016) and the FoMA Zoonosis monitoring programme (<https://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 Södermanlands county in 2013 (Gnesta/Nyköping). One out of 187 *Microtus agrestis* and eight out of 439 *Arvicola amphibius* had metacystode lesions confirmed by PCR and sequencing. Protoscoleces were demonstrated in the *Microtus agrestis* and in three out of eight *Arvicola amphibius*. No lesions were found in *Myodes glareolus* ($n=655$) and *Apodemus* spp. ($n=285$). Within this project, a new infected area was identified in 2014; Väckjö region in Kronoberg county.

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 (<https://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 2018, all free-living wolves submitted to necropsy at the National Veterinary Institute were tested with MC-PCR. In addition, fox scats were collected in an area in Gnesta, Södermanland where the parasite have previously been found in foxes as well as rodents.

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

Animals

During 2018, 31 wolves (*Canis lupus lupus*) and one wolf /domestic dog hybrid, four raccoon dogs (*Nyctereutes procyonoides*) and four dogs were tested with the MC-PCR and all were negative. However, 6 of 13 fox scats collected in Gnesta, Södermanland tested positive.

Humans

In 2018, 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 is considered to be endemic albeit at a very low prevalence 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 that the prevalence of this parasite varies geographically. Regional screenings have previously shown a prevalence of more than 1% in a part of Södermanlands county, 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.

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.

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
- 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

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* 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 (<https://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

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

Animals

E. granulosus was not detected in any animal in 2018.

Humans

In 2018, 25 cases of cystic echinococcosis were reported. Annually around 15–30 cases are reported in Sweden. In 2018, the reported cases ranged in age from 9 to 77 years (median 36 years). Seven cases were women and 18 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 Iraq and Syria with 7 cases each.

DISCUSSION

E. granulosus has not been detected in Sweden in animals since the late 1990s, when it was reported in two reindeer in the northernmost regions of Sweden, bordering Norway and Finland. The parasite is prevalent in several European countries. In Finland it has been detected in wildlife (wolves, moose and reindeer). In other European countries it is 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.

Enzootic bovine leucosis

BACKGROUND

Enzootic bovine leucosis (EBL) is caused by bovine leukaemia virus, 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 characterized 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 2 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 random 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 2018 are given in Table 7.

Diagnostic testing is performed at the National Veterinary Institute. Both milk and sera are analysed using an antibody ELISA (Svanovir® BLV GP-51 ELISA).

RESULTS

No positive samples were found in 2018.

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 2 years of age was positive for EBL. All animals over 6 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 2018.

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

WAHIS Interface. (<http://www.oie.int>). Accessed 2019-05-21.

Table 7: Total numbers of herds and animals tested for EBL antibodies in 2018.

Herd type (sample type)	Herds	Animals
Dairy herds (1 bulk milk sample per herd)	2046	-
Beef herds (blood from 1–3 animals per herd)	2680	7038
Beef herds with at least three animals tested	529	-
Beef herds with two tested animals	1522	-
Beef herds with one tested animal	629	-

Footrot



The Swedish control programme for footrot includes clinical examination and swab samples of the interdigital skin for identification of *Dichelobacter nodosus* and has the goal of eliminating footrot from affected flocks. Photo: Ulrika König

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 within the programme 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.

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 all 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 during August 15 to October 15, when the risk of footrot is highest due to the weather conditions. If no signs of footrot are detected, in all sheep at one occasion, the flock is certified free from footrot (F-status). However, if signs of footrot are documented the following measures are taken: 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.

A total of 369 sheep flocks are affiliated to the control programme.

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.

RESULTS

During 2018, 2 new flocks, within the control programme, were detected with footrot. In 1 of the 2 flocks, virulent strains of *D. nodosus* were detected. In the programme, 369 flocks were certified free from footrot (F-status).

DISCUSSION

The awareness of disease control has been enhanced in the sheep farming community, and their agreement on a trade

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

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

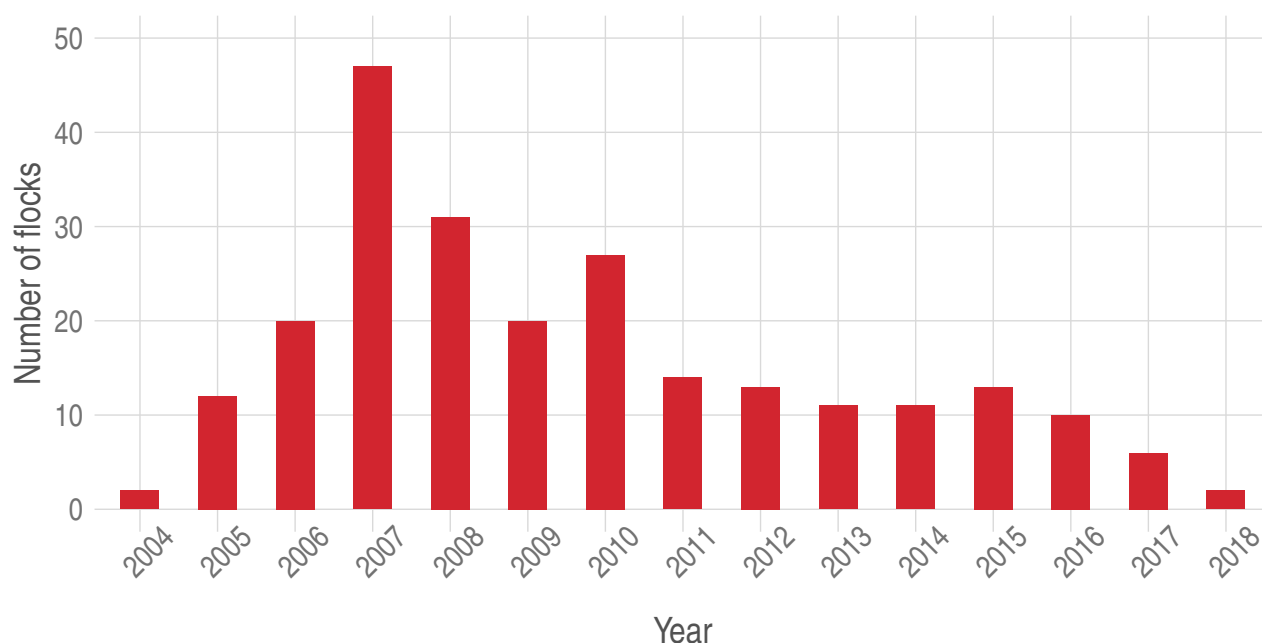


Figure 9: Number of sheep flocks detected with footrot 2004–2018.

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 nineties 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 an indirect ELISA (SVANOVIR™ IBRab, Svanova®). A blocking-ELISA IBR/BHV-1 gB Ab ELISA kit (IDEXX) 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 signs 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/Växa Sverige's 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 centers and all cattle (and other potentially susceptible ruminants) are tested before export and import.

RESULTS

Within the active surveillance, 3368 bulk milk samples and 6929 serum samples from beef cattle were examined. In addition, 215 cattle, 27 alpaca, 2 yak, 1 llama and 1 blesbok were tested as part of health schemes or prior to export. All samples were tested negative.

Two herds were investigated due to clinical suspicions of IBR, with negative results.

DISCUSSION

In summary no herd or individual animal was diagnosed with IBR infection during 2018. 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 member of the Orthomyxoviridae family and divided into four genera, Influenza virus A (IAV), Influenza virus B (IBV), Influenza virus C (ICV) and Influenza virus D (IDV). Influenza A, B, C and D viruses 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 of IAV.

There is only 1 serotype for influenza B viruses (IBV) with two evolutionary lineages, the B/Victoria/2/87-like and B/Yamagata/16/88-like lineages. The single serotype of influenza C viruses (ICV) 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 ICV but soon has been recognized as a new genus; Influenza D virus (IDV). Although the virus was identified among pigs with respiratory illness serological evidence indicates presence of IDV in cattle populations around the globe.

Avian Influenza

BACKGROUND

Avian influenza (AI) viruses are divided into different antigenic subtypes based on the combination of two surface glycoprotein (HxNy). Currently, 18 HA and 11 NA variants have been identified. Except for the 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 avian influenza to human and animal health.

In May 2005, an outbreak of H5N1 led to the death of over 6000 migratory waterfowl in Qinghai Lake in western China. This was the first sustained major outbreak with H5N1 viruses within wild bird populations since 1997. Subsequently, H5N1 outbreaks in wild birds or in 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 HPAIV-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, highly pathogenic avian influenza A(H5N8) viruses belonging to clade 2.3.4.4 of the Gs/Gd-like lineage were detected in wild birds and poultry first in the Republic of Korea, China, Japan and Russian Federation. By autumn the same year, the group A (Buan-like) virus of clade 2.3.4.4 was detected in commercial poultry in Canada and later in December, strains of HPAI were 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 A(H5N8) Buan-like 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 H5N8 subtype belonging to clade 2.3.4.4 group B (Gochang-like) viruses were 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 within the Gs/GD/96-lineage 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 virus A(H5N8) was reported from Hungary. On 4 November, Hungary reported the first outbreak of HPAI H5N8 in poultry. The virus spread rapidly across central Europe with multiple notifications in wild birds, poultry and captive birds.

In November 2016, H5N8 virus was detected in a dead common goldeneye (*Bucephala clangula*) in Skåne county in the southern part of Sweden. Shortly after, a high-biosecurity establishment of laying hens also in Skåne became infected, and the 210 000 animals had to be destroyed. Further cases with HPAI viruses were found subsequently during 2017–2018, as described in this chapter.

Disease Animals

Morbidity in birds infected with HPAIV may be as high as 100%, but 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

Since 2003, more than 860 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. According to the WHO, most of the positive cases have been diagnosed in Egypt, Indonesia and Vietnam. A decrease of cases was noted during the last years, and no case was determined during 2018.

More than 1567 laboratory-confirmed cases of human infection with LPAI H7N9 viruses, including 39% deaths, have been reported since 2013. The first wave in spring 2013 (weeks 7–2013 to 40–2013) resulted in 135 cases, the second wave led to 320 cases (week 41–2013 to week 40–2014), the third wave caused 223 cases, the fourth wave caused 120 cases, the fifth wave resulted in 766 cases, and the sixth wave week 41–2017 to week 40–2018 has only resulted in three cases of H7N9. The last case of human H7N9 was determined January 2018. 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. During the fifth wave, 29 human cases with HPAI H7N9 virus were reported in China. The last human case with HPAI H7N9 was October 2017. The large decrease of human cases with H7N9 is due to introduction of control measures as well as mass vaccination programme in poultry in China.

Since 1998, 50 laboratory-confirmed cases of human infection with LPAI H9N2 virus, including one death, have been reported globally. Cases occurred in China (43), Egypt (4) and Bangladesh (3). During 2018 were three cases of H9N2 reported from China.

A total of 24 laboratory-confirmed cases of human infection with HPAI H5N6 virus, including 6 deaths, have been detected in China since 2014. During 2018, four cases of H5N6 were reported from China.

During 2018 was the first human case with H7N4 determined in China.

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

LEGISLATION

Animals

Highly pathogenic avian influenza 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 2017 is based on Council directive 2005/94/EC and Commission decision 2010/367/EU.

Humans

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

SURVEILLANCE

Surveillance programmes have been carried out annually in all EU member states since 2002 to determine the prevalence of avian influenza viruses, in particular the subtypes H5 and H7. The surveillance program in poultry also aimed at early detect of avian influenza virus subtype H5 and H7 in different species of poultry. Surveillance of wild birds contributes to the knowledge of the threats from wildlife to domestic animal health and serves as an early warning system for avian influenza threat to domestic poultry flocks. From 2006–2010 there was active surveillance of 2000–4500 wild birds annually. Since 2011, the surveillance has been conducted on dead birds submitted for necropsy only.

Poultry

In 2018, sampling was performed in 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 above mentioned sample size, all individuals were sampled. In total, 2187 blood samples were taken. Table 8 gives an overview of all poultry flocks sampled in 2009 to 2018. In addition to the surveillance programme, samples were taken on clinical suspicion of avian influenza. On clinical suspicion of AI or Newcastle disease, laboratory analyses for both diseases are generally performed.

The surveillance programme for 2018 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 to the OIE guidelines.

Wild birds

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 avian influenza is shown in Figure 10. Swab samples (both cloacal and tracheal) taken from these birds were analysed for the detection of avian influenza viral 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 during the influenza surveillance season 1500–2000 samples are collected from sentinel patients with influenza-like illness. These samples are analysed for influenza A and B. If influenza A is detected, further subtyping is performed into 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/characterised. The Public Health Agency of Sweden also performs a specific PCR for H5N1, H5N6 and H7N9 if requested.

RESULTS

Poultry

In 2018, antibodies against influenza virus subtype H5 or H7 was found in three flocks of breeding game birds kept for restocking game. Two of the flocks were mallards which were found negative when subsequently tested by PCR. One flock of pheasants were found to be PCR positive for LPAI of the H5 subtype at follow up. All flocks were sampled within the active surveillance programme (Table 8).

Avian Influenza was investigated following 9 clinical suspicions in poultry or captive birds. Clinical signs as suspicion arose included; increased mortality, production losses and/or eggshell abnormalities. Eight of the suspicions were in commercial flocks (pullets (1), layers (7)) and one in a mixed species hobby flock. All suspicions were investigated by PCR on swab and/or organ samples. The hobby flock was confirmed infected with HPAI H5N6; the other 8 sampled suspicions were PCR-negative for influenza. In the AI positive flock, the symptoms raising the suspicions were increased mortality. One of the layer farms, investigated due to reduced production, was confirmed to have Newcastle disease.

Wild birds

Autumn migrations of wild birds have been implicated in the incursion of HPAIV into Europe in 2005, 2014 and 2016. 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.

In 2018, the HPAI diagnosed was of subtype H5N6 of the European strain, closely related to the H5N8 from

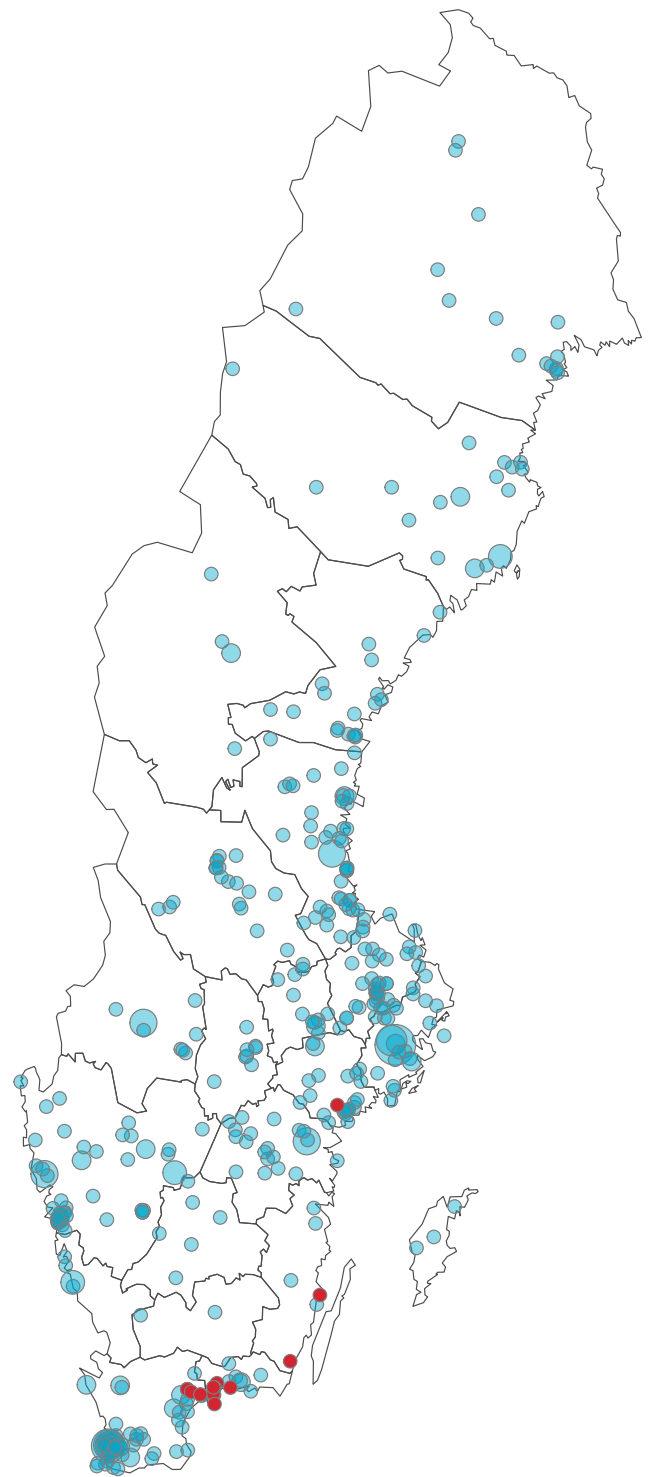


Figure 10: Geographical location of the wild birds analysed for avian influenza in 2018. Point sizes are scaled by the number of birds sampled at a given location. A total of 15 birds were identified positive for influenza H5N6 in 2018.
©EuroGeographics for the administrative boundaries

Table 8: Number of flocks of different poultry categories sampled in 2009–2018.

	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018
Laying hens ^A	61	62	61	52	44	58	68	62	68	65
Free range laying hens ^A	-	-	30	27	16	23	23	30	43	49
Turkeys	17	21	22	19	26	16	18	18	16	16
Ducks	3	4	6	3	1	3	3	4	1	2
Geese	13	11	20	20	13	9	9	7	5	6
Broilers ^B	27	24	39	34	26	12	22	33	23	33
Ratites	6	4	5	3	2	3	3	3	2	2
Breeding hens (parents)	33	34	36	36	36	32	31	34	35	30
Breeding turkeys (parents)	4	3	3	3	3	2	3	3	3	3
Game birds (mallards)	6	7	9	7	7	5	6	7	2	5
Game birds (pheasants)	20	17	15	16	16	12	13	9	13	12
Backyard flocks (geese, ducks)	6	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.

2016/17. The positive findings in wild birds submitted for post-mortem examination were detected from February to June, with most cases in April. Cases were found in wild birds along the eastern and south-eastern coast of Sweden. Although fewer than previous year, positive cases were detected over a longer period and later in the spring.

Within the passive surveillance programme, 455 wild birds of 64 different species were sampled of which 280 bird of prey, 76 water or shore birds and 14 corvids. Fifteen wild birds were PCR-positive for HPAI H5N6, all bird of prey (white tailed eagle (13), common buzzard (2) and northern goshawk (1).), all during the period February to June with the most cases detected in April. All other birds were negative for Influenza A virus.

Humans

No cases of zoonotic influenza were identified among the samples characterised during 2018 in Sweden.

DISCUSSION

The first large outbreak of HPAI in wild birds was reported from China in May 2005. Thereafter wild birds infected with HPAI have been detected in Europe. HPAI may cause disease and death in wild birds, although there seem to be a host-species dependent susceptibility. Wild birds, especially waterfowl, may be infected with LPAI without the presence of clinical symptoms. Considering the capacity of the virus to mutate and become highly pathogenic (HPAI), wild birds may pose a potential risk to poultry since they may host and introduce LPAI into poultry flocks, where the virus may circulate, mutate and become HPAI.

A recent development in the evolution of HPAI H5N1 virus is the emergence of HPAI H5N8 virus. A HPAI H5N8 virus with genes from viruses of the influenza A(H5N1) A/Goose/Guangdong/1/1996 lineage was first detected in birds on live bird markets in China in 2010. This HPAI H5N8 virus is a reassortant virus with the HA gene segment of HPAI H5N1 virus and other gene segments of multiple other AI viruses circulating in eastern China, and is categorized in the new HPAI H5 virus clade 2.3.4.4 (WHO 2015).

This virus caused a large AI outbreak in poultry in South Korea in the winter of 2013/2014, and subsequently spread to Japan, North America, and Europe, causing AI outbreaks there between autumn 2014 and spring 2015. The H5N8 viruses involved in the 2014/2015 outbreaks in Europe and North America belonged to group A(Buan-like) viruses of clade 2.3.4.4, while the 2016/2017 outbreaks in Europe belongs to group B(Gochang-Like) in clade 2.3.4.4. Since the first detection of H5N8 clade 2.3.4.4 group B-Gochang-like viruses at the Ubsu-Nur Lake in May 2016, closely related viruses continued to spread throughout the autumn, winter and spring of 2016–2017, eventually affecting more than 50 countries in Asia, the Middle East, Western, Eastern and Southern Africa and Europe. Countries in the European Union reported outbreaks of HPAI in poultry or captive birds in 24 countries and 19 countries reported outbreaks in wild birds.

In December 2017 the Netherlands reported detection of a novel clade 2.3.4.4 group HP H5N6 subtype virus in wild birds and poultry. Sweden reported its first case of HP H5N6 in February 2018. HPAI was detected 16 times in Sweden for the seasons 2018 0101–20 181 231. All detections were of the A(H5N6) virus subtype, 15 in wild birds and 1 in a flock of captive birds. In addition, one LPAI H5 outbreak in farmed game birds was detected through the routine avian influenza surveillance.

Since June 2018, the virus has not been detected in wild birds or poultry in Sweden. The virus was absent in Europe for several months. However, in August 2018 two dead wild birds infected with H5N6 virus were found in the Netherlands. Later in December one HP H5N6 outbreak in wild birds was notified by Denmark.

Wild birds have played an important role in the arrival and subsequent spread of the H5N8 and H5N6 since the beginning of the epidemics in 2016. All the cases in domestic birds reported in Sweden occurred in areas near wetlands and had a wild birds outbreak reported in close proximity to affected farm.

The ongoing event 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

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

human to pig transmission was the most likely route of infection in the pigs. The isolate expressed a human pandemic H1N1-pdm09 like HA and a H3N2 SIV-like NA that was closely related to Avian-like H1N2 SIV NA from isolates collected in Sweden since 2009. The internal genes were entirely of pandemic H1N1-pdm09 origin which is well adopted to humans. Although the pH1N2 subtype influenza A virus was exclusively prevalent in the Swedish pig population in 2014, the clinical signs of the disease were minor, as later also seen in other countries.

There has not been a regular monitoring of influenza in pigs in Sweden, but serological screenings were performed in 1999, 2002, 2006 and 2010. On each occasion, 1000 porcine sera were analysed for H1N1, H3N2 and H1N2. The screening in 2006 also included analyses for antibodies to H5 and H7. During the past five years, 10–15 herds have been sampled annually with special focus on influenza; in these herds influenza virus has been demonstrated in 3–5 herds per year (Table 9).

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, 5–10 human cases of influenza virus infections with influenza from pigs are reported yearly. Since 2005, 435 humans have become infected with A(H3N2)v in USA and Canada. In 2018, one case of human infection with A(H3N2)v virus were detected in USA. Since 2005, 25 humans have become infected with A(H1N2)v in USA. During 2018, there were twelve cases of A(H1N2)v diagnosed in USA. No human case of A(H1N1)v was determined during 2018. Human infection with swine influenza has been associated with agricultural fairs where people are in close contact with potentially infected pig populations.

LEGISLATION

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

SURVEILLANCE

Animals

Enhanced passive surveillance

During the period from 2009 to 2018, 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 10).

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 initiated 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 2018.

Humans

In Sweden, 1500–2000 samples are collected annually from patients with influenza like illness during the influenza season in a sentinel surveillance system for influenza. These samples are analysed at the Public Health Agency of Sweden for influenza A and B. If influenza A is detected, further subtyping is performed into A(H1N1)pdm09 and A(H3N2). If Influenza A positive samples cannot be subtyped, further characterization is performed to rule out zoonotic influenza A. A further 200–300 influenza positive samples from the diagnostic laboratory are subtyped/characterized.

RESULTS

Animals

Passive surveillance

Samples from 9 herds with respiratory signs were analysed for swine influenza virus in 2018 (Jan 1st to Dec 31st, 2018). No influenza virus was detected.

Active surveillance

No active surveillance was performed in 2018.

Humans

No cases of zoonotic influenza were identified among the characterised samples during 2018 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 9). 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, veterinaries 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 medical 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

- 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.

Table 9: 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 10: Passive and active surveillance for swine influenza in Swedish pig herds from 2014 to 2018.

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	-	-	-	-

^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.

Leptospirosis



Leptospira can cause disease in dogs; surveillance for in dogs is passive and under 2018, 13 seropositive laboratory analyses were reported. Photo: Bengt Ekberg.

BACKGROUND

Several species of the spirochetal bacterium *Leptospira* can cause leptospirosis. All mammals, including humans, are susceptible to one or several *Leptospira* serovars. Leptospirosis occurs worldwide but the dominant serovars vary by region. Cattle and pigs are considered to be reservoirs for *L. Hardjo* and *L. Pomona*, respectively. Serovars known to infect and cause clinical disease in dogs include *L. Icterohaemorrhagiae*, *L. Canicola*, *L. Grippotyphosa*, *L. Pomona*, *L. Sejroe* and *L. Australis*. These are all serovars also known to infect and cause disease in humans. Serovars that can cause disease in horses include *L. Icterohaemorrhagiae*, *L. Grippotyphosa*, *L. Pomona* and *L. Bratislava*.

Seropositivity to *Leptospira* spp other than *L. Pomona* are occasionally confirmed in Swedish pigs, mostly to an indigenous serovar of *L. Sejroe*, *L. Bratislava* and *L. Icterohaemorrhagiae*. An even lower prevalence to the indigenous strain of *L. Sejroe* in cattle has been recorded.

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

Surveillance in other animal species including dogs and

horses is passive only.

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

DISEASE

Animals

L. Hardjo is one of several pathogenic serovars and is associated with disease in cattle, sheep, goats and horses. 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. Sheep and cattle can act as reservoir hosts because the disease may be asymptomatic. *Leptospira* infections in pigs may also be asymptomatic or may give rise to reproductive failure. In piglets, fever, gastrointestinal disorders and jaundice may be present.

The clinical presentations in dogs infected with *Leptospira* range from subclinical to severe clinical illness and

death; liver and/or kidney affection as well as varying degrees of vasculitis is typical. A peracute pulmonary form with high mortality rate is not uncommon.

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

Humans

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

LEGISLATION

Animals

Since 2004, leptospirosis is a notifiable disease on laboratory confirmation in Sweden (SJVFS 2013:23), in all animal species concerned. Single serologically positive samples are reported. 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

Passive surveillance in animals involves mandatory case reporting of laboratory confirmed cases.

The aim of the active surveillance in cattle and pigs is to demonstrate freedom of disease for *L. Hardjo* in cattle and *L. Pomona* in pigs. 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% 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.

Active surveillance in cattle and pigs is at present performed every third year. Animals sampled for export and in breeding centres adds to the active surveillance.

The serological analyses are performed at the National Veterinary Institute. The diagnostic test used for *L. Hardjo* is an indirect ELISA (Prio-CHECK *L. Hardjo*, Antibody detection ELISA, Lelystad, Holland) for both blood and bulk milk samples. Positive blood 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.

Surveillance in dogs and horses is passive. All positive serological titers from 1:100 and above are reported. PCR is available but only recommended as a combination test with a paired blood sample using MAT-analysis, as PCR most often yield negative results and does not identify individual serovars. Blood samples submitted to the National Veterinary Institute are currently tested with MAT for *L. Icterohaemorrhagiae*, *L. Canicola*, *L. Grippotyphosa*, *L. Bratislava*, *L. Saxkoebing*, *L. Sejroe*, *L. Autumnalis* and sometimes *L. Australis*. Some of these serovars have been added in routine diagnostics for dogs in the last two years (2017–2018). The reasons for samples being submitted include suspicion of clinical disease as well as sampling of clinically healthy dogs and horses due to export requirements or suspected leptospirosis in other animals in the household.

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

Animals

No active surveillance was performed in cattle and pigs during 2018. See previous reports for surveillance results from 2016 and earlier. No positive samples were reported in horses. In dogs, thirteen seropositive laboratory analyses were reported. Eleven of these were reported from the National Veterinary Institute.

Furthermore, a serologically positive sample was reported from one wolf and one mouse respectively.

Humans

In 2018, three cases of leptospirosis were reported. Two of the cases had acquired their infections in Asia and one in South America. Cases are commonly infected outside Sweden during leisure activities in contact with water.

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. Ichterohaemorrhagiae*. 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 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 whether positive results are being reported or not by the referring veterinarians is currently unknown. In 2018, the number of samples sent to SVA for PCR analyses instead of MAT analyses increased. 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 in-house ELISA test not distinguishing between different serovars is now available and in use in several animal hospitals and clinics, a

practice which might also lower the number of serological samples sent to the National Veterinary Institute and thereby possibly also the number of positive samples being reported.

In short, leptospirosis in Swedish dogs is currently underreported, and the data; the number of reported positive serovars in 2018 cannot be compared to previous years, neither should data be compared uncritically between previous years. A pilot project investigating background data from animal hospitals including samples analysed at other laboratories is underway, with the aim of optimising a future research project and recommendations regarding seroprevalence, diagnostics and surveillance of zoonotic leptospiral serovars in dogs.

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

Human infections are mainly travel-associated.

REFERENCES

- Lindahl E, Boqvist S, Artursson K, Magnusson U (2011) A field-study on *Leptospira* seroprevalence in dairy cows in four geographical areas in Sweden. *Acta Vet Scand* 53:53
- Boqvist S, Eliasson-Selling L, Bergström K, Magnusson U (2012) The association between rainfall and seropositivity to *Leptospira* in outdoor reared pigs. *The Veterinary Journal* 193:135–9
- 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 refrigeration temperatures, in vacuum packed food and in modified atmospheres. *L. monocytogenes* is often found as an environmental contaminant in food premises. These properties make elimination of *L. monocytogenes* difficult. The main sources of human listeriosis are contaminated food products, such as 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 environment and animals serve as important reservoirs of the pathogen. 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 goat's milk, cold cuts, frozen corn and with ready-to-eat foods. During 2018 the incidence of listeriosis slightly increased compared to the year before and the overall picture is an increasing trend of cases of listeriosis in Sweden (Figure 11).

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 neurological symptoms, 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 mainly 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 mortality rate is high (20–40%). The infection can lead to miscarriage, premature delivery or neonatal death. The incubation period of listeriosis varies from 3–70 days, with an average incubation of 21 days.



Smoked or gravad vacuum-packages fish products are one of the main sources of human listeriosis. Photo: Miia Ranta - CC BY-SA 2.0.

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. Notifications are based on clinical cases and laboratory analyses. The diagnosis can be based on histological findings at necropsy or by detection of the organism by cultivation methods using enrichment in selective broth followed by culture on selective and non-selective agar. Identification is made by biochemical methods. 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.

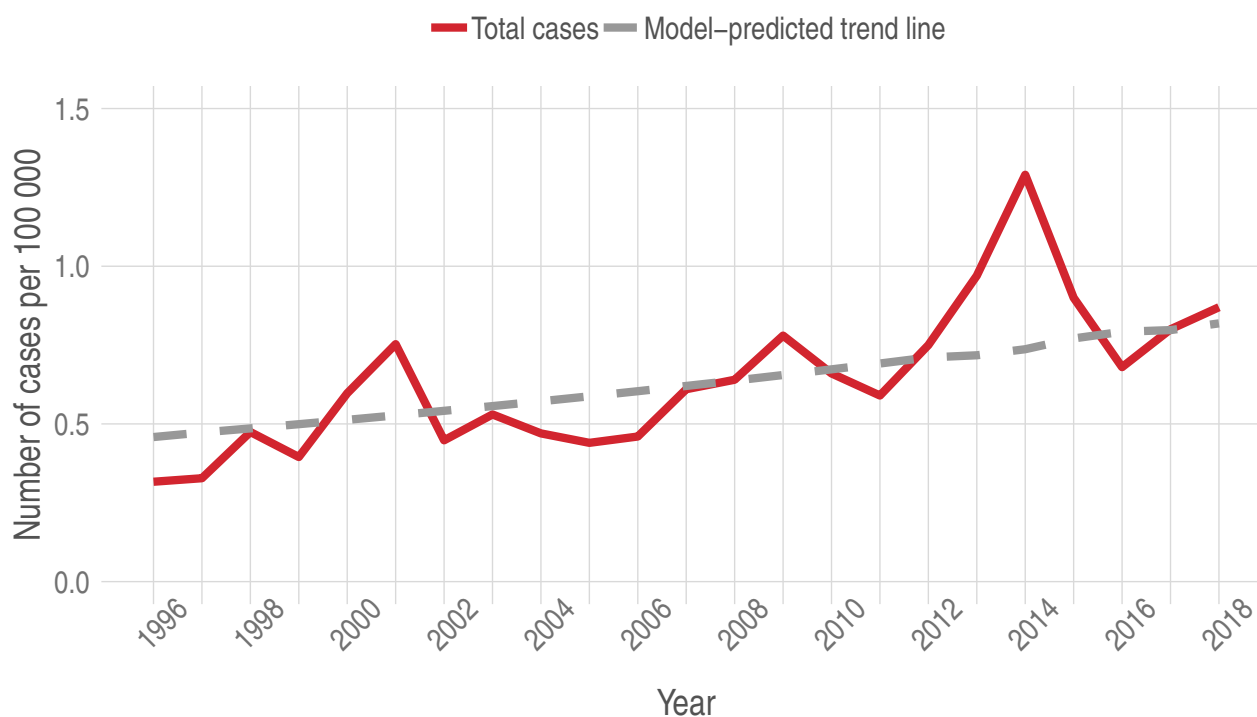


Figure 11: Notified incidence (per 100 000 inhabitants) of human cases of listeriosis in Sweden 1996–2018 and a model-predicted trend.

Humans

The surveillance in humans is mandatory and 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, ie. ST-type, is defined by WGS.

RESULTS

Animals

In 2018, listeriosis was reported in 16 sheep, five cattle, two goats, two dogs, two horses, one hedgehog and in one monkey.

Food

In 2018, 410 samples from different types of food were sampled by national and local authorities and analysed for presence of *L. monocytogenes* in qualitative analysis (Table 11). *L. monocytogenes* was detected in nine samples. Levels were quantified in seven of these and ranged from < 10 cfu/g to 50 cfu/g.

Humans

In 2018, 89 cases of listeriosis were reported (incidence 0.9 cases per 100 000 inhabitants). (Figure 11). This was a minor increase in number of cases compared to the year before when 81 cases were notified. The majority of the cases reported with listeriosis belong to the older age groups. In 2018, the median age was 71 years and 57% were people

over 70 years. As previous years, the highest incidence was found in the age group over 80 years (6.1 cases per 100 000 inhabitants). Of the reported cases, 52% were women. In total 29% of the reported cases died within one month from diagnosis.

Listeriosis is most often a domestic infection. During 2018, 86 of the reported cases (97%) noted Sweden as country of infection.

In 2018 all but five (94%) of the human isolates were sent in to the Public Health Agency of Sweden for typing. The most common molecular serotypes were IIa (68%), IVb (24%), IIb (7%) and IIc (1%). In addition to serotypes, sequence types (ST) are also identified through WGS. Different STs can belong to the same serotype and during 2018 the most common STs were ST-8 belonging to serotype IIa and ST-1 belonging to serotype IVb. Identical isolates within the same ST have been identified during several years. This might indicate that some of these strains have been established in production facilities and occasionally contaminate food products causing illness in patients. During 2018 a total of 13 cases had identical isolates belonging to three different ST-clusters identified since 2015 (8 cases within IIa-ST155, 3 cases within IIa-ST37, 2 cases within IIa-ST14).

During 2018, an outbreak of listeriosis was identified in the county of Västra Götaland. A total of seven cases with onset of disease between February and May had an identical serotype IVb ST-1 strain. The outbreak strain could be detected in ready-to-eat food from a local food producer and the products were recalled.

In addition to the outbreak, one case had an identical strain of serotype IVb ST-6 causing the European outbreak linked to frozen corn in 2015–2018.

Table 11: Food samples analysed for *L. monocytogenes* in 2018.

Reason for sampling	No. of samples	No. of positive samples	Food in which <i>Listeria</i> was detected
Survey	52	0	-
A routine control or verification sample	45	0	-
Investigation of a complaint or a suspected food poisoning	50	6	5 Prepared dishes, 1 vegetable
Unknown	263	3	2 Fish (raw), 1 Prepared dish
Total	410	9	

DISCUSSION

During 2018 the incidence of listeriosis slightly increased compared to the year before and the overall picture is an increasing trend of listeriosis since 1983. (Figure 11). The same trend has been observed in other European countries. The reasons for the increase remain unclear but are most likely related to a combination of factors such as an ageing population, a widespread use of immunosuppression medications and consumer preference changes to more ready-to-eat foods. The European Centre for Disease Prevention and Control (ECDC) collaborate with the member states to strengthen the molecular surveillance to be able to detect cross-border clusters and outbreaks of *L. monocytogenes*. This collaboration, including also the European Food Safety Authority (EFSA), is essential in the investigation of food-borne outbreaks in Europe.

The case fatality rate of listeriosis is high. Approximately one third of the patients die within three months. Since most of the patients suffer from severe underlying diseases the impact of listeriosis is difficult to estimate. The microbiological criteria for *L. monocytogenes*, set in 2005, determine the standard the industry has to achieve for their products to be considered safe for consumers.

Continued surveillance of *L. monocytogenes* in humans and in food and food processing environments will be essential for understanding the sources for human infection and providing tools to prevent infections. 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

European Centre for Disease Prevention and Control/European Food Safety Authority. Multi-country outbreak of *Listeria monocytogenes* serogroup IVb, multi-locus sequence type 6, infections probably linked to frozen corn – 22 March 2018. Stockholm: ECDC/Parma: EFSA; 2018.

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

Parihar VS, Lopez-Valladares G, Danielsson-Tham ML, Peiris I, Helmersson S, Unemo M, Andersson B, Arneborn M, Bannerman E, Barbuddhe S, Bille J, Hajdu L, Jacquet C, Johansson C, Löfdahl M, Möllerberg G, Ringberg H, Røcourt J, Tjernberg I, Ursing J, Henriques-Normark B, Tham W (2008) Characterization of human invasive isolates of *Listeria monocytogenes* in Sweden 1986–2007. *Foodborne Pathogens and Dis* 5:6

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

Nephropathia epidemica



Humans may be exposed to aerosols containing 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: pen_ash (<https://pixabay.com>).

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 12). 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 2018, 243 cases of NE were reported, which was an increase in comparison to the previous year (Figure 12). The median age among all cases were 54 and most reported cases were males in the age category 30 and older. Consistent with previous years, more cases were reported in men (58%) 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 have acquired their infections in Sweden. In 2018, there was only seven 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 Västerbotten (29 cases per 100 000 inhabitants) followed by the County of Norrbotten with (24 cases per 100 000 inhabitants). This regional pattern is consistent with previous years. One case in the County of Skåne had no travel history to endemic areas during the incubation time and thus are suspected to have contracted the disease within the county. This is the first time a case has been reported to contract NE in the far south of Sweden.

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

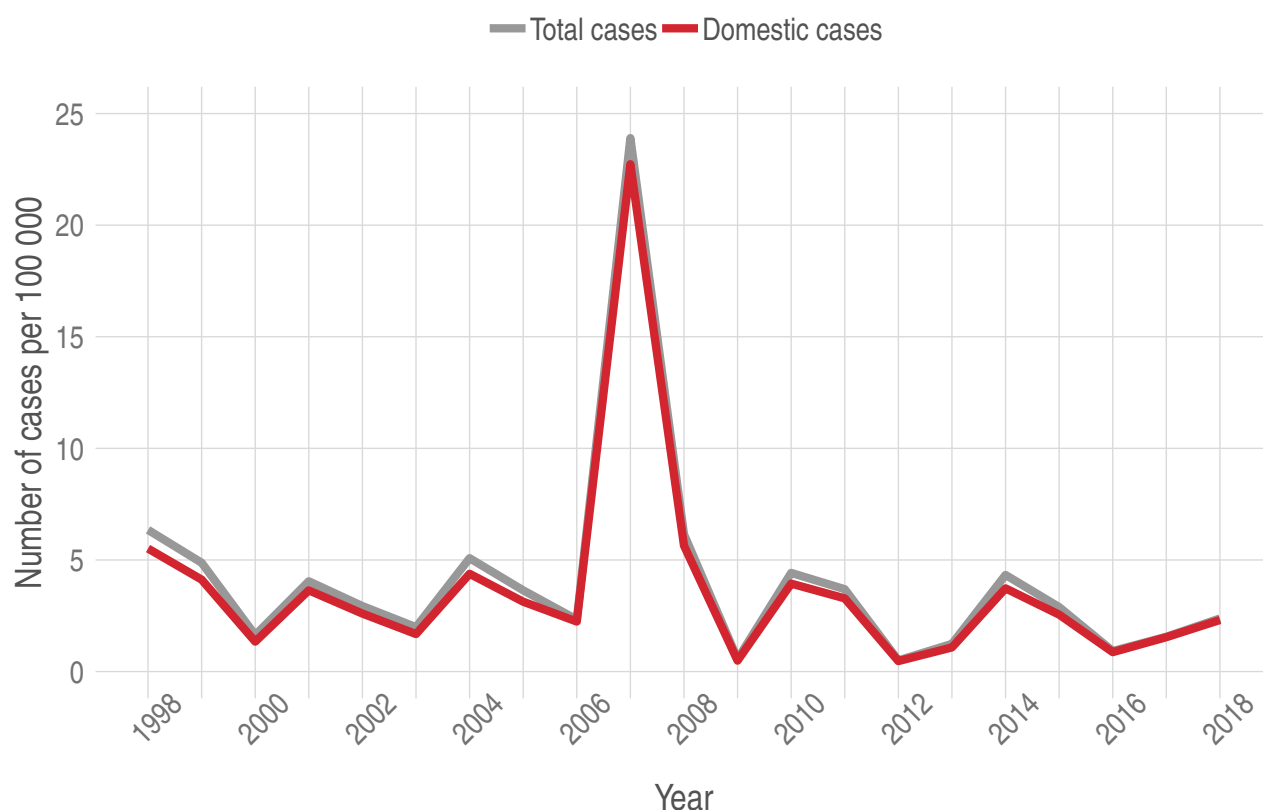


Figure 12: Notified incidence (per 100 000 inhabitants) of human Nephropathia epidemica in Sweden 1998–2018.

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 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 necropsy, are sampled and cultured for MAP. Sampled animals also include exotic ruminants like buffalo 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 is 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. Whole-herd slaughter with subsequent sanitation and tracing of animal movements is performed if MAP is detected in a herd.

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 necropsy.

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.

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 2018, the voluntary control programme for bovine paratuberculosis encompassed 454 herds, of which 425 are of the highest

Table 12: Cattle sampled in 2018.

Surveillance in cattle	No. of sampled animals	No. of herds
Beef herd surveillance programme ^A	1481	29
Cattle sampled at post mortem examinations	153	135
Cattle sampled for export	9	1

^A Including 4 water buffalo from one herd.

Table 13: Sheep and goats sampled in 2018.

Surveillance in sheep and goats	No. of sampled animals	No. of herds
Sheep sampled in cattle herds within the beef herd surveillance programme	13	3
Sheep sampled at post mortem examinations	105	86
Goats sampled at post mortem examinations	7	7

Table 14: Exotic ruminants sampled in 2018.

Surveillance in exotic ruminants	No. of sampled animals	No. of herds
Exotic and wild kept ruminants sampled at post mortem examination	7	6
Exotic and wild kept ruminants sampled for export ^A	3	2

^A 2 forest reindeer 1 blesbok.

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 and all purchased animals from one year 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 necropsy of all euthanised or deceased cattle on the premises where paratuberculosis cannot be excluded as a cause of culling.

Health controls for export reasons

Nine cattle were tested by serology for export reasons. Ten sheep, two forest reindeer (*Rangifer tarandus fennicus*) and one blesbok (*Damaliscus pygargus*) were tested by faecal PCR. 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.

RESULTS

In 2018, one suspicion of paratuberculosis in a cow was raised due to pathological changes detected at post mortem examination. The cow tested negative for MAP with PCR and the suspicion was ruled out. Moreover, 1477 cattle from 28 herds, 13 sheep from 3 herds, and 4 water buffalo from 1 herd were sampled within the control programme in beef herds. In all, 579 of the cattle samples were pooled three and three and 135 as pools of five for analysis at the lab. The remaining samples were analyzed individually. For export reasons a total of 22 animals were tested: 9 by serology, all cattle, and 13 by faecal PCR (10 sheep, 2 forest reindeer (*Rangifer tarandus fennicus*) and 1 blesbok (*Damaliscus pygargus*)).

Two hundred and seventy-two animals were sampled at post-mortem examination; 153 cattle, 105 sheep, 7 goats, 1 alpaca, 1 camel, 2 kept deer, 1 bison, 1 yak and 1 water buffalo. No cases of MAP were detected in the examinations completed in 2018 (Tables 12, 13 and 14).

DISCUSSION

If present at all, the prevalence of MAP in Swedish ruminants remains at a very low level.

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 been detected in no 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. Initiated last year, work is now ongoing to evaluate the possibility of utilising bulk milk samples to increase the surveillance in the dairy cattle population 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.

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.

In 1998, an active PRRSV surveillance programme was launched in Sweden, 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 and inappetence for a few days. 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. In fattening pigs, the infection mainly causes respiratory signs.

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

Because PRRS is notifiable on clinical suspicion by both veterinarians and farmers, 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 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

In the current active surveillance programme, which has been in effect 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 on 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 2018, the calculated number of samples required was 2400 from the abattoir sampling in addition to the field sampling described above.

RESULTS

Passive surveillance

Two investigations following clinical suspicions of PRRS were conducted in 2018. Reproductive problems were the primary clinical signs in both cases, with one herd reporting

late-term abortions and the other reporting abortions, high piglet mortality and non-pregnant sows. The number of animals sampled and the methods used during the two 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. Following sampling and testing, both herds were declared negative for PRRSV.

Within the programme for enhanced passive surveillance of aborted foetuses, 14 foetuses from 8 herds were examined for the presence of PRRSV genome and all samples were negative.

Active surveillance

In 2018, 784 samples from 54 nucleus herds, multiplying herds and sow pools were analysed. In the abattoir sampling, 2707 samples originating from 514 herds on 903 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 15.

One abattoir sample was serologically positive by both ELISA and IPMA testing which prompted an investigation. In addition to further serological testing in the herd, the investigation included an examination of the herd for clinical signs of PRRS and an assessment of production data. No signs of PRRS were noted in either the herd examination or the production assessment and all additional samples were negative for PRRSV antibodies. The investigation therefore concluded 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 2018 was >99%.

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, Agren EC, Eliasson-Selling L, Sternberg-Lewerin S (2009) Probability of freedom from disease after the first detection and eradication of PRRS in Sweden: Scenario-tree modeling 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)
- Lindberg A, 2008. PRRS-översyn av övervakningsprogrammet. SVA D-nr 2008/429 (In Swedish)

Table 15: Number of samples and herds tested in the active PRRS surveillance 2009–2018 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

^A Jordbruksverket statistikdatabas ().

^B Some herds were sampled more than once.

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

C. psittaci 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

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. For laboratory verification of the infection, serology and PCR are the methods predominantly used.

RESULTS

Animals

In 2018, *C. psittaci* was detected in one of thirteen domestic pet birds tested.

Humans

Psittacosis is mainly a domestic infection. Of the 37 cases reported during 2018 only 2 were suspected to be infected abroad, 25 (68%) of the cases were male and 28 (76%) of the cases were 50 years or older. Most cases reported that they had been in contact with birds or bird droppings. For the remaining cases there were no obvious routes of transmission. All cases were reported from the south of Sweden.

DISCUSSION

At present, knowledge on the epidemiology of *C. psittaci* in domestic and wild birds in Sweden is scarce. The organism is occasionally notified in pet birds.

REFERENCES

- Rehn M, Ringberg H, Runehagen A, Herrmann B, Olsen B, Petersson AC, Hjertqvist M, Kühlmann-Berenzon S, Walsten 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

Q fever



Surveillance for Q fever in animals is passive. Limited testing was done in 2018 on cattle and sheep mainly for export reasons. National surveys of Swedish sheep herds indicate that *Coxiella burnetii* is a rare pathogen in this population. Photos by: Maya Hoffman

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*.

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. Limited testing was done in 2018 on cattle and sheep mainly for export reasons. Blood samples from 9 cattle and 18 sheep were analysed for the presence of antibodies by complement fixation test or ELISA. Animals from five herds were tested for *C. burnetii* in bulk milk by PCR.

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. For laboratory verification of the infection, serology and PCR are used.

RESULTS

Animals

Bulk milk from one cattle herd tested positive for Q fever with PCR. All other samples that were submitted for testing were negative.

Humans

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. In 2018, seven cases of Q fever were reported with a median age of 60; five of the cases were male and two females. All cases were reported to be infected abroad and predominantly in Spain.

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 will most likely remain a function of 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



European bats may carry European Bat Lyssavirus (EBLV), but not classical rabies. Six dead bats were examined for rabies during 2018. In three cases, humans had been exposed to them in a way that could pose a risk of rabies exposure. All bats tested negative for rabies. Photo: Anders Lindström

BACKGROUND

Rabies is caused by a lyssavirus in the family *Rhabdoviridae*, and can infect all warm-blooded animals. 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), but not classical rabies. 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 passive. 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 2018, five dogs and four cats were examined for rabies due to clinical suspicion. Furthermore, five racoon dogs were examined for rabies as part of the raccoon dog project (<https://jagareforbundet.se/vilt/invasiva-frammande-arter/Mardhundsprojektet/forvaltning/>).

Six dead bats were examined for rabies. In three cases humans had been exposed to them in a way that could pose a risk of rabies exposure.

In addition, 35 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 2018 tested negative.

Humans

No human cases were reported during the year.

DISCUSSION

During the recent decades, 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.

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 has been implemented almost every year. The next surveillance will probably be conducted during 2020. 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 as well as 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.

A total of 2000–3000 human cases of salmonellosis have been annually reported to the Public Health Agency of Sweden. A majority (70–80%) of these cases were infected abroad. During the last decade, the total incidence has decreased. This is due to a decrease in cases infected abroad, whereas the domestic incidence remains constant. The low proportion of domestic infections is unique to Sweden compared to many other countries. The source of the investigated outbreaks is often imported food. The contribution to the human disease burden from domestic animals is low.

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.

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

Feed raw 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 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 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

IN FOCUS - Outbreaks of *Salmonella* Typhimurium in passerine birds, cats, dogs and humans

Serovars of *Salmonella* occur in a wide spectrum of hosts ranging from host generalists to host specialists where the latter preferentially only infect a single species. A specific type of *Salmonella* Typhimurium (MLVA profiles 2-[11-15]-[3-4]-NA-212) is a host specialist that has caused outbreaks of septicaemia and mortality in wild birds reported in Sweden, Norway, the United Kingdom and Switzerland. These outbreaks tend to occur in the late winter or early spring, and most commonly among certain species passerine birds. The infected birds are an easier prey for cats which in turn become infected. Cats and birds can then transfer the infection to humans. In the early months of 2018, a large outbreak of *Salmonella* Typhimurium occurred among cats in Sweden. In total, *Salmonella* was detected in 1185 of 1760 samples from cats which was the highest number ever recorded. Infected cats were reported in all regions in Sweden. Simultaneously, *S. Typhimurium* with the specific MLVA profiles were detected from 26 passerine birds, 10 dogs as well as in 16 humans. To protect public health, communication efforts to raise awareness and recommendations for good hand hygiene when maintaining bird feeders and handling infected cats and were put in place. The number of cases of this type of *S. Typhimurium* vary between years but the reasons for these variations are not fully understood. However, the differences appear to be related to variations in the population sizes and migrations of passerine birds.

Table 16: 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

on a weekly basis. These samples are analysed at the National Veterinary Institute (using MSRV, 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 MSRV (EN-ISO 6579-1: 2017) method or a method validated against it.

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.

Compulsory programme

All breeding flocks with more than 250 birds are tested (Table 16). 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 or faecal samples taken from all parts of the building or the department where the bird flock is kept. From rearing flocks, two pairs of sock samples are taken and pooled into one whereas five pairs pooled into two are taken from the breeding flocks in production.

All holdings that sell eggs for consumption are sampled (Table 16). 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 programme are to prevent introduction of *Salmonella* into the poultry holding, minimise the risk of the spread of the infection to animals and humans. A voluntary programme has been in place for more than 40 years. Producers affiliated to the voluntary programme receive higher financial compensation in case of a finding of *Salmonella*. All broiler and turkey producers belonging to the Swedish Poultry Association are affiliated to the voluntary programme which represents approximately 99% of the slaughtered broilers. 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.

Cattle and pig herds

This programme includes a compulsory and a voluntary component.

Compulsory programme

The aim of the programme is to ensure a low prevalence of *Salmonella* in cattle and pig. compulsory part consists of annual faecal sampling from breeding pig herds and gilt-producing herds and biannual sampling from sow pools. In

Table 17: Serovars of *Salmonella* isolated within feed control in 2018.

Serotype	Feed material of animal origin ^A	Pet food	Feed material of oil seed origin ^B	Feed material of cereal grain origin	Other plants ^C	Process control feed mills	Process control rapeseed crushing plant
S. Agona	-	-	1	-	-	1	-
S. Bere	-	-	1	-	-	-	-
S. Bispebjerg	-	-	-	-	-	1	-
S. Emek	-	-	1	-	-	-	-
S. Fresno	-	-	1	-	-	-	-
S. Kedougou	-	-	1	-	-	-	-
S. Kottbus	-	-	-	-	-	1	-
S. Mbandaka	-	-	4	-	-	1	-
S. Newport	-	-	-	1	-	-	-
S. Poano	-	-	1	-	-	-	-
S. Senftenberg	-	-	2	-	-	-	-
S. Typhimurium	-	-	-	-	-	10	-
S. Vejle	-	-	-	-	-	1	-
<i>S. enterica</i> sp. <i>diarizonae</i> (IIIb)	-	-	-	-	-	1	-
<i>S. enterica</i> sp. <i>enterica</i>	-	-	4	-	-	-	-
Total	0	0	13^D	1	0	16	0
Number of samples	1261	199	1280	637	50	7840	824

^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, peanut and sunflower seed.

^CPeas, algae, beans, guar meal, herbs (dried), berries and hemp.

^DIn one of the unit positive for *Salmonella* four different serotypes were found.

cattle, *Salmonella* testing is performed in all calves <12 months of age that are submitted for necropsy. *Salmonella* testing is also performed in conjunction with necropsies if an infection is suspected based on macroscopic findings. All imported animals are also tested and on clinical suspicion, any herd or single animal should be tested for *Salmonella*.

Voluntary programme

The voluntary programme is a preventive hygienic programme aiming at decreasing the risk of introduction of *Salmonella*. 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.

Other animals

Animals are tested for *Salmonella* on clinical suspicion or as part of trace-back investigations. Wild animals necropsied at the National Veterinary Institute are also tested for *Salmonella* on suspicion.

Food

Control of *Salmonella* is an important part of in-house quality control programmes in most food enterprises in Sweden. 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.

Surveillance at abattoirs 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 is proportional to slaughtering capacity. The number of samples taken is calculated to detect a prevalence of 0.1% (CI 95%) in cattle, pig and poultry carcasses at a national level. Altogether, approximately 20 000 samples from cattle, adult pigs, fattening pigs and poultry are collected at abattoirs annually.

Abattoirs sample sheep carcasses for analyses for *Salmonella* according to regulation (EG) 2073/2005 on microbiological criteria for foodstuffs. The results from the analyses are not collected by the competent authority.

At red meat cutting plants, approximately 5000 samples are taken annually from crushed meat and meat scrapings and approximately 900 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.

Humans

Surveillance in humans is based on identification of the disease by a 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

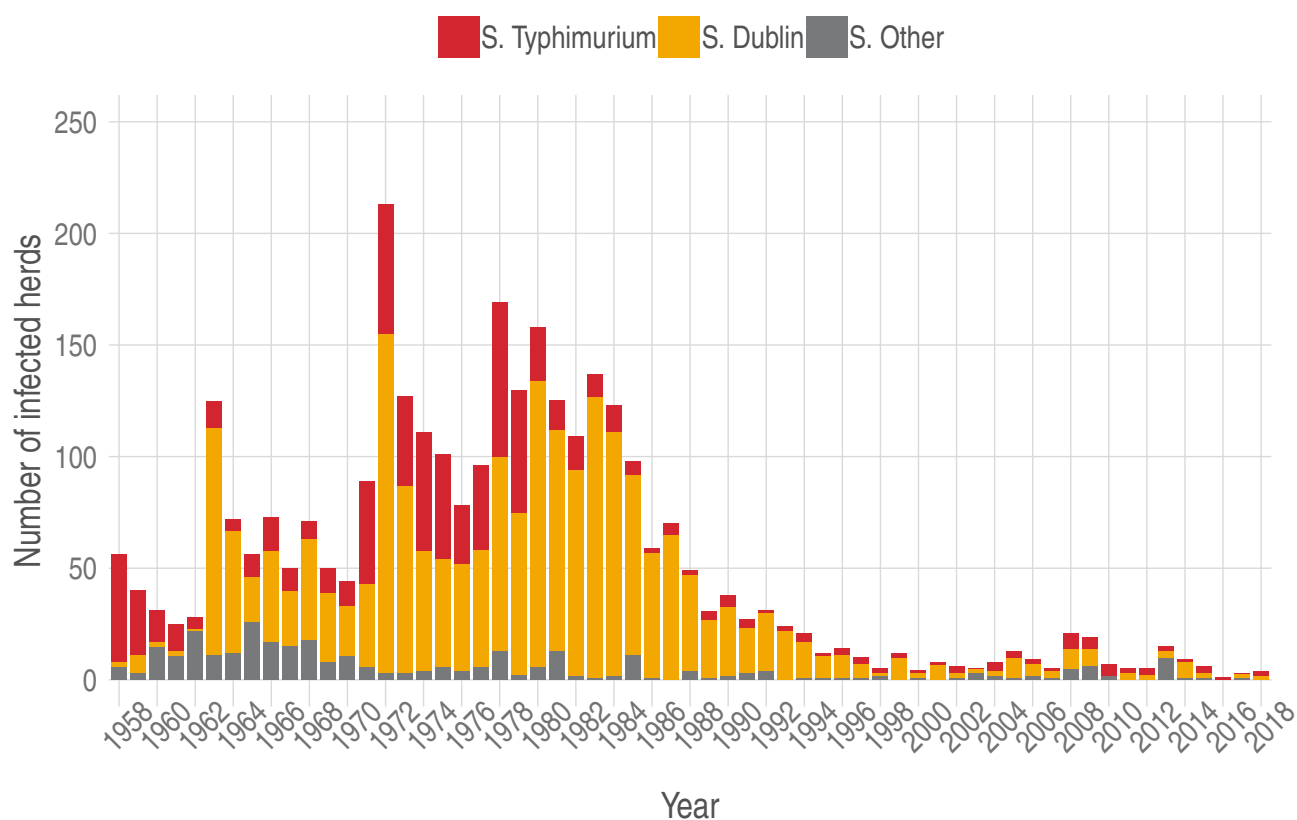


Figure 13: Frequency of notifications of *Salmonella* in Swedish cattle herds during 1957–2018. Data from 1957 through 1967 is extracted from a graph presented by J.Å. Robertsson (1985).

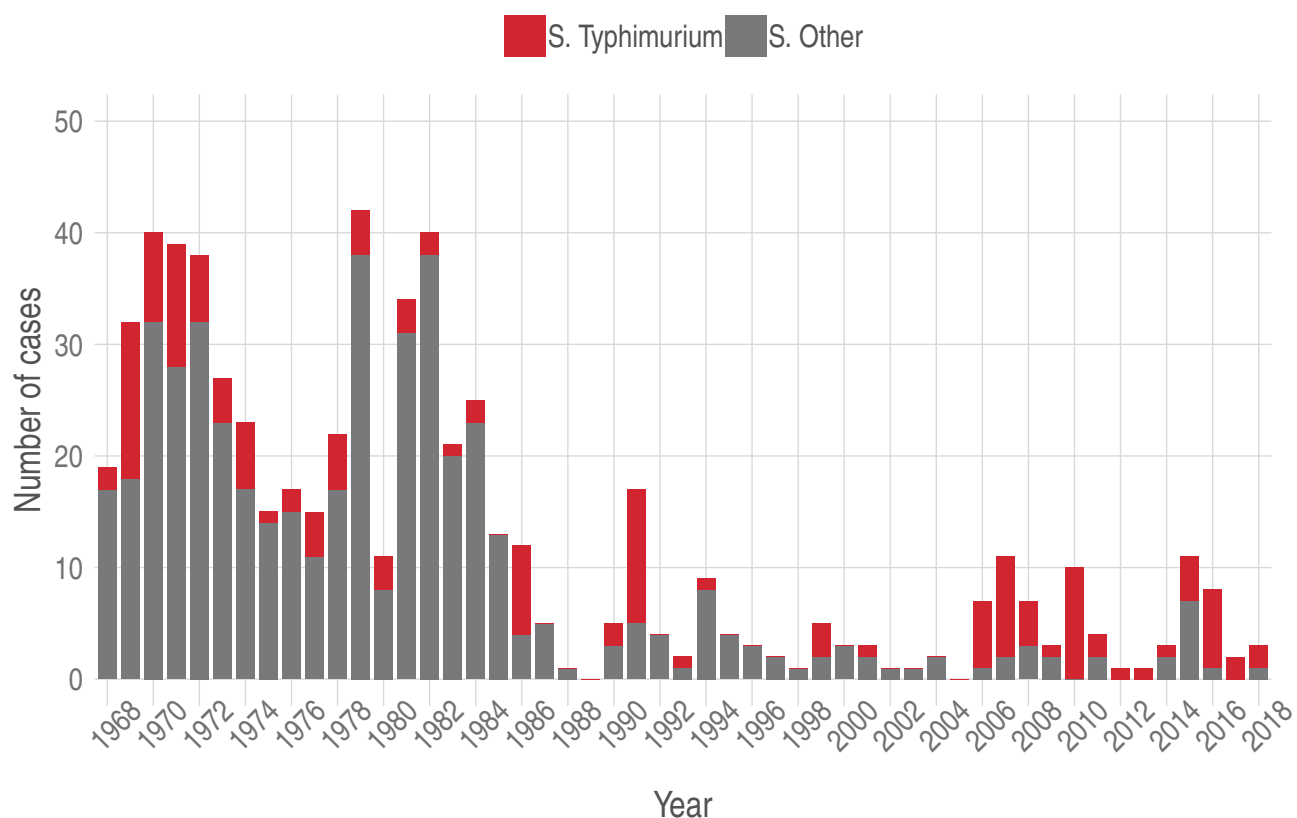


Figure 14: Frequency of notifications of *Salmonella* in broiler holdings during 1968–2018, breeding flocks included.

Table 18: Results from the *Salmonella* control programme in poultry flocks.

Animal species	Production type	Production stage	No. flocks tested	No. positives	Percentage	Serovar
<i>Gallus gallus</i>	Meat production	Adult Grand Parent	26	0	0.00%	<i>S. Mbandaka</i> , <i>S. Typhimurium</i> (n=2)
<i>Gallus gallus</i>	Meat production	Adult Parent	137	0	0.00%	
<i>Gallus gallus</i>	Meat production	Production	4955	3	0.06%	
Turkeys	Meat production	Adult Parent	4	0	0.00%	<i>S. Mbandaka</i> (n=2), <i>S. Typhimurium</i> (n=2)
Turkeys	Meat production	Production	166	0	0.00%	
<i>Gallus gallus</i>	Egg production	Adult Parent	20	0	0.00%	
<i>Gallus gallus</i>	Egg production	Production	678	4	0.59%	<i>S. Mbandaka</i> (n=2), <i>S. Typhimurium</i> (n=2)
Geese	Meat production	Production	15	0	0.00%	
Ducks	Meat production	Production	21	0	0.00%	

measures. *Salmonella* spp. is part of the microbial surveillance programme at the Public Health Agency of Sweden and domestic isolates are sent in for serotype determination and for cluster detection. All isolates belonging to serovars *S. Enteritidis*, *S. Typhimurium* and the monophasic variants of *S. Typhimurium* are subtyped using MLVA (multi-locus variable number tandem repeat analysis). For outbreak investigations, whole genome sequencing is used. 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 *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, 7840 samples were analysed for *Salmonella*; 16 of these samples (0.2%) were positive. Seven serovars were detected; *S. Typhimurium* was the most common (n=10) (Table 17).

In addition, *Salmonella* was detected in 14 out of 1967 analysed batches from feed materials of vegetable origin. The most common serovar was *S. Mbandaka* (n=4). *Salmonella* was not detected in any of the 1460 batches tested from feed materials of animal origin and from pet food.

Animals

Poultry

Salmonella was detected in 3 (0.04%) of 4955 broiler flocks tested in routine sampling before slaughter (Table 18 and Figure 14). *Salmonella* was also detected in 4 of the 678 flocks of layers tested. *Salmonella* was not detected in any breeding flocks, neither in any samples of commercially raised turkeys, geese, ducks, quail or ostriches.

Cattle

In total, *Salmonella* was detected in four new herds in 2018 (Figure 13). *Salmonella* was isolated from five (0.15%) of 3242 mesenteric lymph nodes from cattle at slaughter (Table 19 and Figure 15).

Pigs

Salmonella was detected in one pig herd (Figure 16) and from one (0.03%) of 2930 lymph node samples taken from adult pigs and from three (0.10%) of 3003 lymph node samples from fattening pigs (Table 19, Figure 15).

Other animals

Salmonella was detected in 1185 (67.3%) cats of 1760 tested (Table 20), which was more than previously observed. Of the 308 fully serotyped cat isolates, 305 belonged to the serovar *Typhimurium*.

Salmonella Typhimurium was detected in one horse submitted to an animal hospital.

In addition, *Salmonella* was detected in 17 dogs, 26 wild birds (mainly passerine), one hedgehog and one wild boar (Table 20).

Food

Within the Swedish *Salmonella* control programme, swab samples were taken from 5879 pig carcasses, 3272 cattle carcasses and neck skin samples from 2780 poultry carcasses. *Salmonella* was detected in one pig carcass sample (Table 19). At cutting plants, 5173 samples of red meat and 1118 samples of poultry meat were taken. *Salmonella* was not detected in any of these samples (Table 19 and Figure 15).

In addition to the sampling performed within the control programme, 697 samples were taken by local authorities. *Salmonella Typhimurium* and monophasic *Salmonella* (O:4,5:i:-) were detected in two samples of salami taken in an outbreak investigation (Table 21).

Humans

In 2018, a total of 2040 cases of salmonellosis were reported, compared to 2279 cases in 2017 (Figure 18). Domestic cases decreased by 15% from 798 cases in 2017 to 677 cases in 2018, giving an incidence of 6.6 cases per 100 000 inhabitants. The domestic incidence varies from year to year but has been largely stable over a longer period.

A total of 66% of the cases (n=1355) were determined 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 42 years (0–99 years) and the incidence was highest for persons over

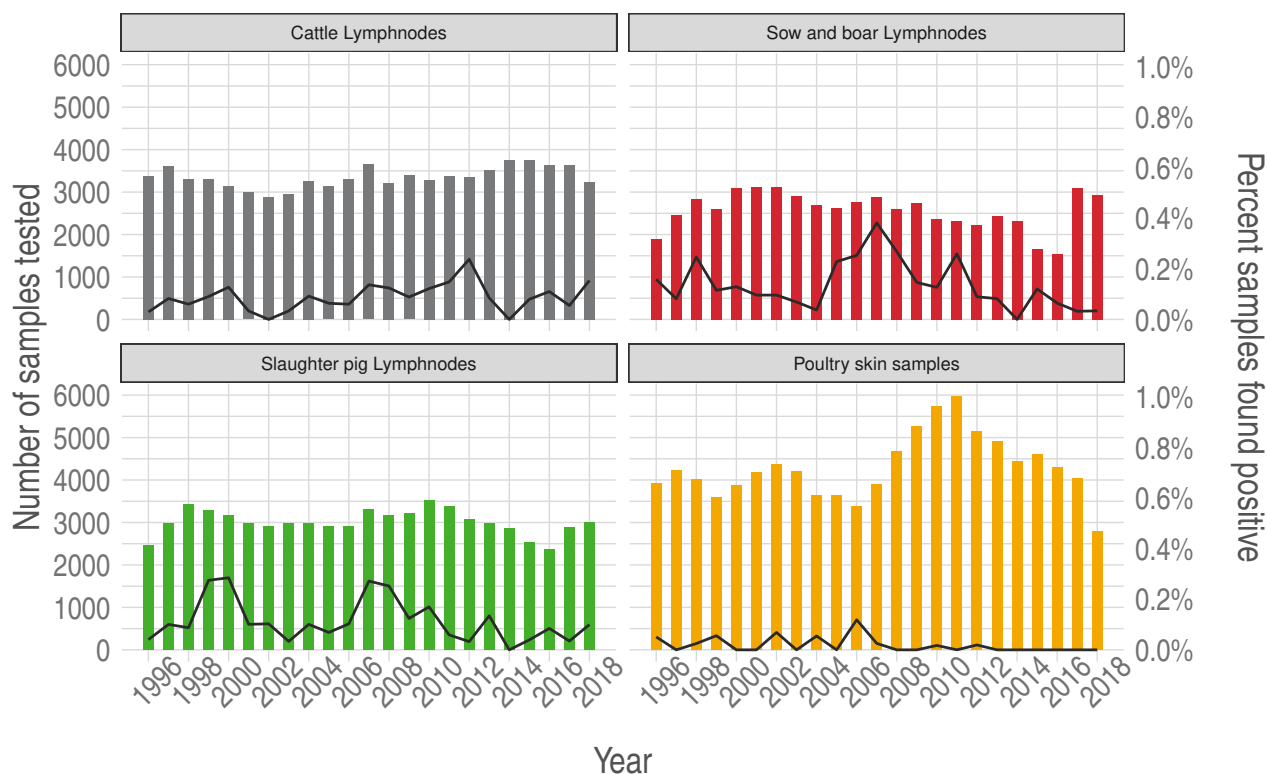


Figure 15: Samples tested (bars - left axis) and percentage of *Salmonella* found (line - right axis) in lymph node samples from cattle, sows and boars and fattening pigs sampled at major abattoirs as well as neck skin samples from poultry at all abattoirs. In 2014, a new laboratory was chosen to perform *Salmonella* analyses of samples from abattoirs and cutting plants. The National Reference Laboratory (NRL) 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.

80 years of age with 11.6 cases per 100 000 inhabitants followed by children 1–4 years of age with an incidence of 10 per 100 000 inhabitants.

Of the isolates from domestic cases, 91% were serotyped. The most common serovars from domestic cases were *S. Enteritidis* (19%), *S. Typhimurium* (17%) followed by monophasic *S. Typhimurium* (12%). Profile 2-10-7-3-2 (41 cases) was the most common MLVA profile of *S. Enteritidis*. Of the domestic isolates of *S. Typhimurium*, MLVA profile 2-17-N-N-211 (19 cases) was the most common followed by 2-14-3-N-212 (13 cases) and of the isolates of monophasic *S. Typhimurium* MLVA profile 3-11-10-N-211 (18 cases) was the most common. Around seventy additional serovars were identified in domestic cases during 2018. Of the cases infected in other countries, 18% were serotyped and *S. Enteritidis* was the most common serovar (42% of the isolates that were typed).

A clear seasonal variation of domestic salmonellosis is usually observed, with most cases occurring during the summer months. This was also apparent during 2018, with a peak in July and August.

DISCUSSION

The low proportion of domestic *Salmonella* infections in humans is unique to Sweden, Norway and Finland when compared to most other European countries. This reflects the low *Salmonella* burden in domestic animals and food. The

total reported incidence in 2018, 20 cases per 100 000 inhabitants, is considerably higher than the domestic incidence of 6.6 cases per 100 000 inhabitants.

In the feed sector, in 2018 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=10). 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*.

In 2018, *Salmonella* was detected in three broiler- and four layer-flocks, which was more than the previous year. This highlights a continuous need for strict biosecurity routines. Unfortunately, the poultry registries maintained by the Swedish Board of Agriculture are not sufficiently updated, which complicates supervision of the control and outbreak investigations and results in uncertain estimates of the poultry population. Therefore, the Swedish figures on the number of flocks within the programme and the number of flocks not sufficiently sampled, can only be considered estimates. To supervise *Salmonella* control in poultry, some County Veterinary Officers have needed to create their own poultry databases. It is estimated that approximately 20% of the poultry flocks lack an annual veterinary inspection.

In 2012, *Salmonella* Dublin was detected for the first time in decades in cattle herds in the southern county of

OUTBREAK INVESTIGATIONS OF HUMAN CASES

Seven domestic outbreaks of *Salmonella* were investigated during 2018 with altogether 152 cases. The largest outbreak of *Salmonella* during 2018 was caused by the serovar *S. Bovismorbificans* with a total 40 cases from 13 counties. No common source was found but beetroot sprouts were suspected as a source. Early in 2018, a cluster of 17 cases with serovar *S. Mikawasima* was identified and the same serovar was also detected in cases from Denmark, Germany and the United Kingdom. An international outbreak investigation was conducted but no source could be identified.

Re-occurring *Salmonella* outbreaks linked to salami

In 2018, *Salmonella* Typhimurium, MLVA profile 3-10-10-NA-211, was implicated in an outbreak with a salami being the confirmed source of infection. In total, 18 cases were laboratory confirmed and the majority reported having eaten a specific type of truffle salami from Italy. The outbreak strain was detected in two opened packages of truffle salami and the finding was reported in RASFF (Rapid Alert System for Food and Feed). During the last three years, salami has been implicated in five national *Salmonella* outbreaks in Sweden with 156 reported cases. In four of the investigations, the outbreak strain could be isolated from suspected salami sausages. In 2017, an outbreak with *S. Typhimurium*, MLVA profile 3-19-11-N-311, with 72 confirmed cases was investigated. A Spanish fuet salami was suspected early and the outbreak strain could be detected from samples from several of these sausages. In 2016, there were three national outbreak investigations concerning salami sausages. Salami sticks with a monophasic *S. Typhimurium*, MLVA-profile 3-12-8-NA-211, caused an outbreak with 42 verified cases. Furthermore, eleven cases of monophasic *S. Typhimurium*, MLVA profile 3-14-9-NA-211, were reported, and the outbreak strain was detected in a sample of a salami cacciatore. Finally, the same serovar but with another MLVA profile 3-13-9-NA-211 caused an outbreak with 13 reported cases. The seven cases answering a questionnaire had eaten salami, however there was no suspected food item to be sampled and analysed.

Skåne. Altogether, 13 infected herds were detected in 2012–2015. All but one of them were located within a radius of 10 km, in a cattle dense area of Skåne. The only infected herd outside this region had purchased cattle from one of these herds. No newly infected herds were detected during 2016 or 2017, and the outbreak declined. However, during 2018, two herds with *S. Dublin* were detected, both of which had been infected with this serovar previously, and two herds with *S. Typhimurium*.

In order to present a context for the history of *S. Dublin* in Swedish cattle herds, data was obtained for the period 1958–1967 (Figure 13). This indicates that *S. Dublin* did not become dominant as a serovar in Swedish cattle herds until 1963, when 102 cattle herds were detected with this serovar that still today is a challenge.

In 2018, *Salmonella* was detected in one pig herd (Figure 16). This is consistent with the low incidence of *Salmonella* in pigs in previous years. However, the decrease in the number of pig herds in Sweden during the last few years may also play a role in the low incidence.

Reported domestic human cases of *Salmonella* 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 *Salmonella* cases 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 in order 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.

Routine MLVA typing and comparison of *S. Typhimurium* and *Enteritidis* isolates from humans, animals, food, feed and the environment has proved to be a useful tool to detect clusters and outbreaks.

The Swedish *Salmonella* control programme has been in place for decades and resulted in a very low *Salmonella* burden in domestic animals (Figures 13, 16 and 17). However, the programme is costly and could be modernised.

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, but 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.

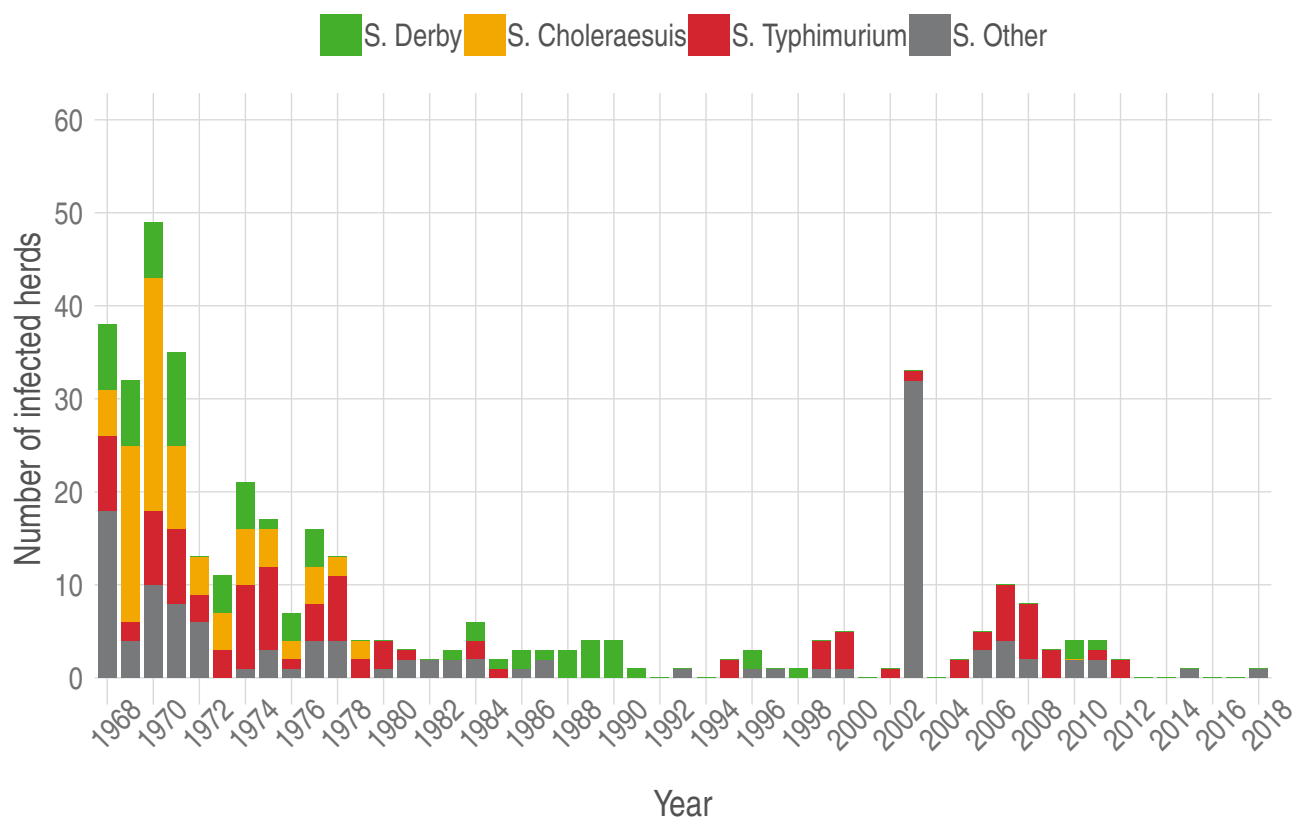


Figure 16: Frequency of notifications of *Salmonella* in swine herds during 1968–2017. In 2016 and 2017, *Salmonella* was not detected in any herd.

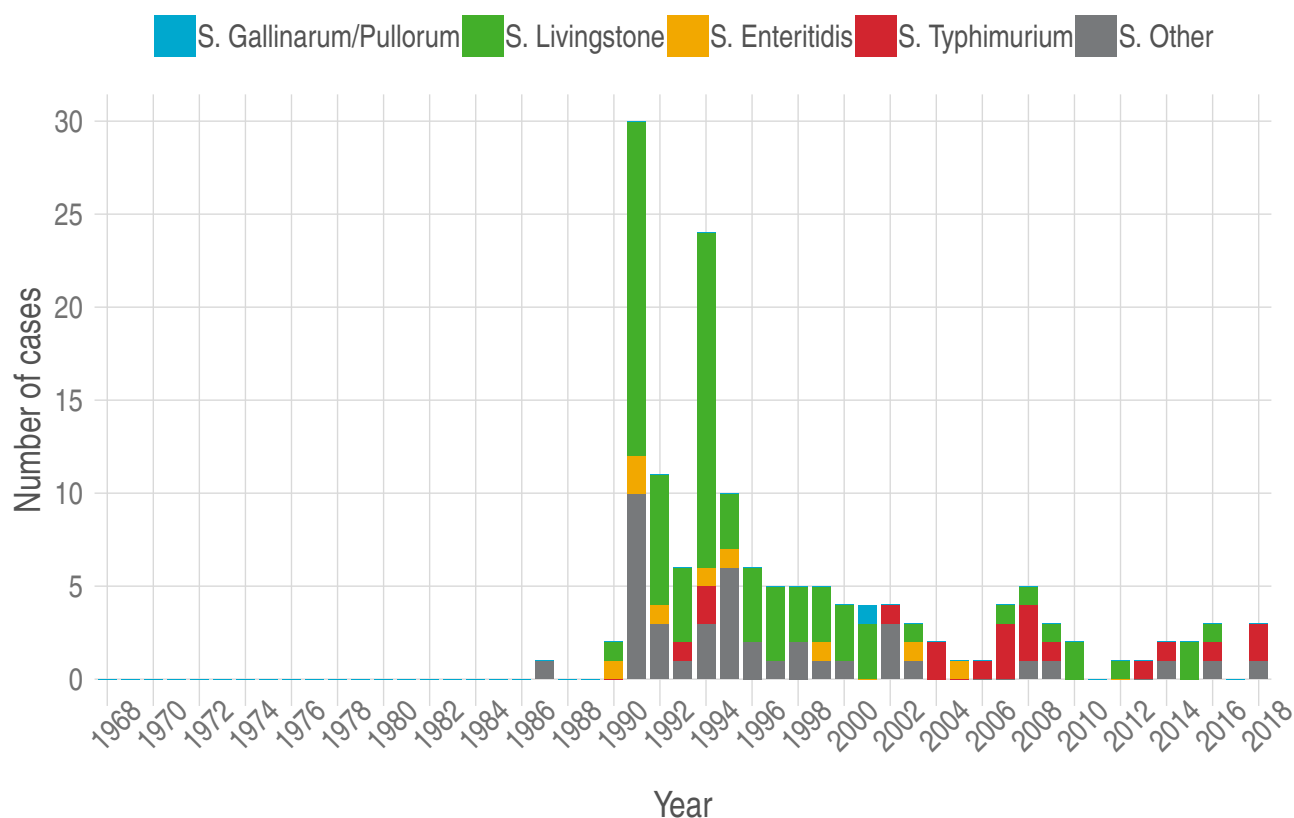


Figure 17: Frequency of notifications of *Salmonella* in layer holdings during 1968–2018.

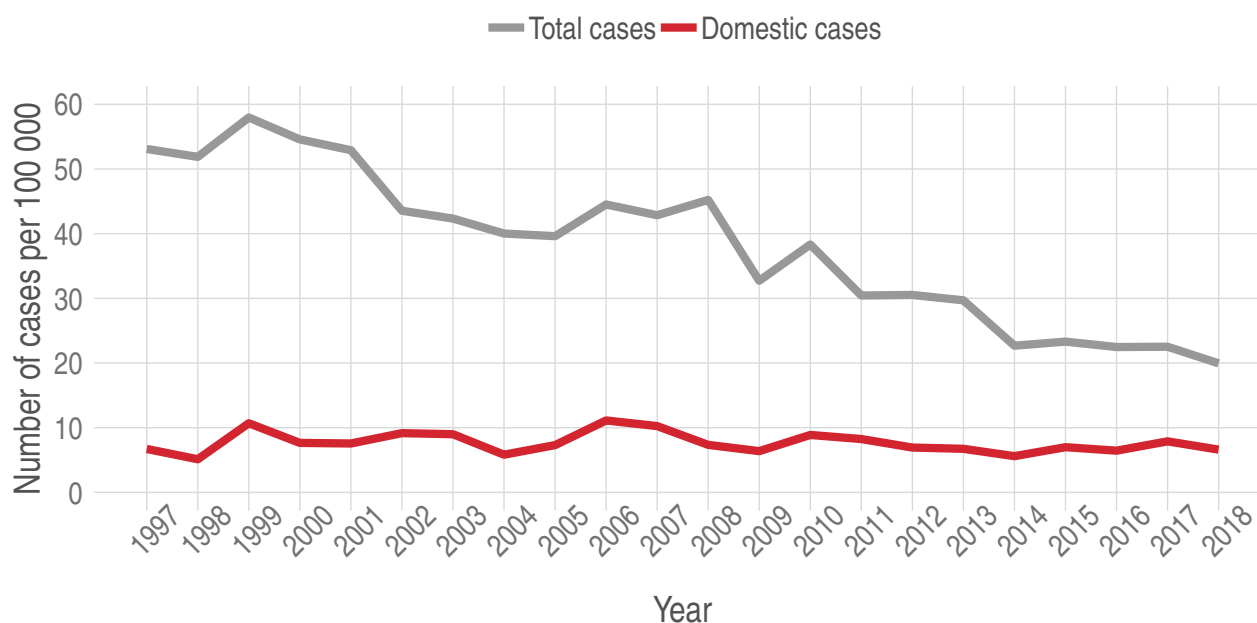


Figure 18: Incidence (per 100 000) of notified cases of human salmonellosis in Sweden, 1998–2018.

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 *Salmonella 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 *Salmonella 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 with amendments).

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 necropsy 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. Already in 2013, phage typing of *S. Typhimurium* was completely 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)

Table 19: Results from the *Salmonella* control programme at abattoirs and cutting plants in 2018.

Animal species	Sample type	No. samples	No. positive	Percentage	Serovar
Cattle	Lymph node	3242	5	0.15%	S. Dublin, S. Duesseldorf ^A , S. Mikawasima ^A , S. Typhimurium, S. enterica sp. enterica O4:b:-
	Carcass swab	3272	0	0.00%	
Breeding swine	Lymph node	2930	1	0.03%	S. Hessarek S. Typhimurium ^A
	Carcass swab	2926	1	0.03%	
Slaughter swine	Lymph node	3003	3	0.10%	S. Typhimurium ^B
	Carcass swab	2953	0	0.00%	
Cattle and swine	Meat scrapings	5173	0	0.00%	
Poultry	Neck skin	2780	0	0.00%	
	Meat scrapings	1118	0	0.00%	

^AIsolation from a pooled sample.

^BOne of these isolated from a pooled sample.

(https://ec.europa.eu/food/safety/rasff_en). Measures are always taken when *Salmonella* is detected in feed samples. *Salmonella* positive feed materials are usually treated with organic acids. After acid treatment the feed material must be re-tested negative before use in feed production. Finished feed containing *Salmonella* must be withdrawn from the market. Extended sampling and cleaning are done in the production line if *Salmonella* is detected in the weekly surveillance. If *Salmonella* is found before heat treatment the contaminated part of the production line is thoroughly cleaned and disinfected, usually by dry cleaning, followed by disinfection. If *Salmonella* is found after heat treatment, the 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 Veterinary Officer. 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 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 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.

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

REFERENCES

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.

Sternberg Lewerin S, Skog L, Frössling J, Wahlström H (2011) Geographical distribution of *Salmonella* infected pig, cattle and sheep herds in Sweden 1993–2010. *Acta Vet Scand* 53:51

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

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-Forsell 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

Table 20: Reported index cases of *Salmonella* in cats, dogs, horses, sheep, wild birds and wild mammals in 2018.

Serovar	Cats	Dogs	Horses	Sheep	Wild birds	Other wild animals
<i>S. Agona</i>	-	1	-	-	-	-
<i>S. Enteritidis</i>	-	-	-	-	-	1 ^A
<i>S. Hessarek</i>	1	-	-	-	-	-
<i>S. Infantis</i>	-	2	-	-	-	-
<i>S. Konstanz</i>	1	-	-	-	-	-
<i>S. London</i>	-	3	-	-	-	-
<i>S. Typhimurium</i>	305	10	-	-	16	-
<i>Salmonella enterica</i> sp. <i>diarizonae</i> =61:-:1,5	-	-	-	15	-	-
<i>Salmonella enterica</i> sp. <i>diarizonae</i>	1	-	-	-	-	-
<i>Salmonella enterica</i> sp. <i>enterica</i> (I) = 6,7:-:1,5	-	-	-	-	-	1 ^B
<i>Salmonella enterica</i> sp. <i>enterica</i> (I) = 4,5:i:-	-	-	1	-	-	-
<i>Salmonella</i> , O:4	877	1	-	-	10	-
Total	1185	17	1	15	26	2
Number of samples	1760	152	57	- ^C	52	33

^AA hedgehog.

^BA wild boar.

^CThe number of tested samples from sheep was not available.

Table 21: Food samples analysed for *Salmonella* in 2018.

Reason for sampling	Total no. of samples	No. of positive samples
Survey	54	0
Routine control	63	0
Suspected food poisoning or complaint	361	2 ^A
Border control	96	0
Unknown	123	0

^A*S. Typhimurium*. *S. enterica* sp. *enterica* O:4,5:i:-.

Scrapie



Sweden has a negligible risk for classical scrapie. As part of the active surveillance for scrapie during 2018, the National Veterinary Institute examined 106 goats from fallen stock for scrapie. All were negative both for classical scrapie and for atypical scrapie. Photo: Ylva Persson

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 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 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 symptoms 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 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 95% level of confidence of detecting classical scrapie if it is present in that population at a prevalence rate 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 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 investigation 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 2018, no sheep or goats were examined due to clinical suspicion of scrapie.

Active surveillance

Sheep

In 2018, the National Veterinary Institute examined 1766 sheep from fallen stock and 87 sheep from flocks under increased surveillance due to Nor98 sampled at slaughter. Out of these, all samples were negative for classical scrapie and three were positive for atypical scrapie Nor98. The northern part of the country is under-represented in the sampling and

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

Goats

In 2018, the National Veterinary Institute examined 106 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 were no reported clinical suspicions 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. For the very first time in 2018, more than one case was found in the same flock, but it was a large flock and the animals were not born in the same herd. 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

Small Ruminant Lentiviruses



During 2018, approximately 9141 samples from sheep flocks were analysed in the Maedi-visna (MV) control programme. Of the 4097 flocks enrolled in the programme, 3753 were declared free from MV. Photo: Ylva Persson

BACKGROUND

Maedi-visna (MV) is a globally distributed contagious disease in sheep, first described in Iceland in 1939. The causative agent is a lentivirus in the Retrovirus family. Transmission between animals occurs most commonly via the oral route (mainly via milk) 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. A voluntary control programme for MV was launched by Farm & Animal Health in 1993, 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. The simplified version is not regulated within the Swedish legislation and does not require the same obligations from the farmers. The control programme and the simplified version of it are running in parallel.

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. In highly infected flocks clinical signs can also appear in younger sheep. After the appearance of clinical signs, the outcome is always fatal within weeks to months.

LEGISLATION

MV is a notifiable disease (SJVFS 2013:23). The control programme is regulated through SJVFS 1993:42 (Jordbruksverkets föreskrifter om organiserad hälsokontroll av husdjur (K 152).

SURVEILLANCE

The purpose of the control programme is to detect and eradicate MV from Swedish sheep flocks. Documentation of the MV status in the flocks is essential. By identifying infected flocks and taking measures, the spread of MV stops

and eradication is possible. Prevention of introduction of MV into flocks is crucial.

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

Serological testing is performed on all sheep older than one year. Negative serology grants the flock an M1-status. A second sampling performed 12–16 months later grants an M2-status if all samples are negative for MV antibodies. This procedure is repeated 12–16 months later and a negative result grants an M3-status, which means that the flock is declared free from MV. The MV free status is maintained by an assurance of the animal keeper. An indirect control of the M3 status holdings is performed by testing of sheep from holdings entering the programme as these new animals are mainly bought from M3 status flocks. If antibodies are detected in a flock, either the whole herd is culled or other eradication measures including selective slaughter is performed, depending on the prevalence of positive sheep within the flock.

Goat herds can also be enrolled in the MV programme.

The programme is based on serological examination of blood samples for antibodies against MV virus with an AGID-test (agar gel immunodiffusion) for which the antigen is purchased from the Animal and Plant Health Agency, Weybridge, UK. Samples with inconclusive or seropositive results are retested with an ELISA (Elitest MVV/ CAEV, Synbiotic), which is also used for flocks under partial eradication and for very small flocks with less than five sheep.

Post mortem examinations and histopathology are still 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 in sheep (eg. Brucellosis, where all samples were negative in 2018).

RESULTS

During 2018, approximately 9141 samples from sheep (and a few goat) flocks were analysed in the MV control programme for antibodies against MV virus.

At the end of 2018, 4097 flocks with 152 627 sheep were enrolled in the programme and 3753 of these flocks were declared free from MV. For goats, 277 flocks with 2286 goats were enrolled in the MV/CAE programme. This corresponds to about 50% of the Swedish sheep population, and about 15% of the goat population.

Within the simplified programme, 1264 samples from 44 flocks were analysed.

In total during 2018, 3 flocks were considered positive of which one was a sheep flock, one was a goat flock and one had both sheep and goats. Two flocks were detected in the simplified programme.

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. A revision of the MV programme was made during 2013 by Farm & Animal Health and the National Veterinary Institute. Since July 2014, the programme was further refined to increase sampling in risk areas and higher risk flocks and reduce sampling in long term MV free and well documented flocks. Studies on the routes of introduction and appearance of MV in sheep flocks are desired to further understand how to conclude the programme, as well as investigations into the advantages and disadvantages of different diagnostic tests.

REFERENCES

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

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. 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 information must be disseminated about the disease and how it can be prevented, detected and stopped. It is equally important to understand and combat the social stigma associated with this disease. During the last decade, an array of new diagnostic tools has become available, to the benefit of surveillance and control.

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 that may appear are: 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 unnecessary 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 to the County Administrative Board where the horse is residing, already on clinical suspicion.

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) to the National Veterinary Institute. Numbers from other veterinary laboratories are not available.

A yearly summary of notified, confirmed cases of strangles per county is produced by the Board of Agriculture and presented below (Figure 19).

Detection of *S. equi* is influenced by 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.

RESULTS

In 2018, there were 62 officially reported index cases of strangles in Sweden, each representing an outbreak in a farm. During the previous 5 years, the average number of officially reported index cases was 75 per year.

DISCUSSION

The passive surveillance results indicate that strangles is endemic in the Swedish horse population.

Investigations of outbreaks point to a need for screening horses that have recently been moved for trade purposes, as these horses appear to be involved in most of the investigated acute outbreaks. It would also be of benefit with a programme for tracking the spread of strangles, by DNA characterisation of different isolates.

REFERENCES

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

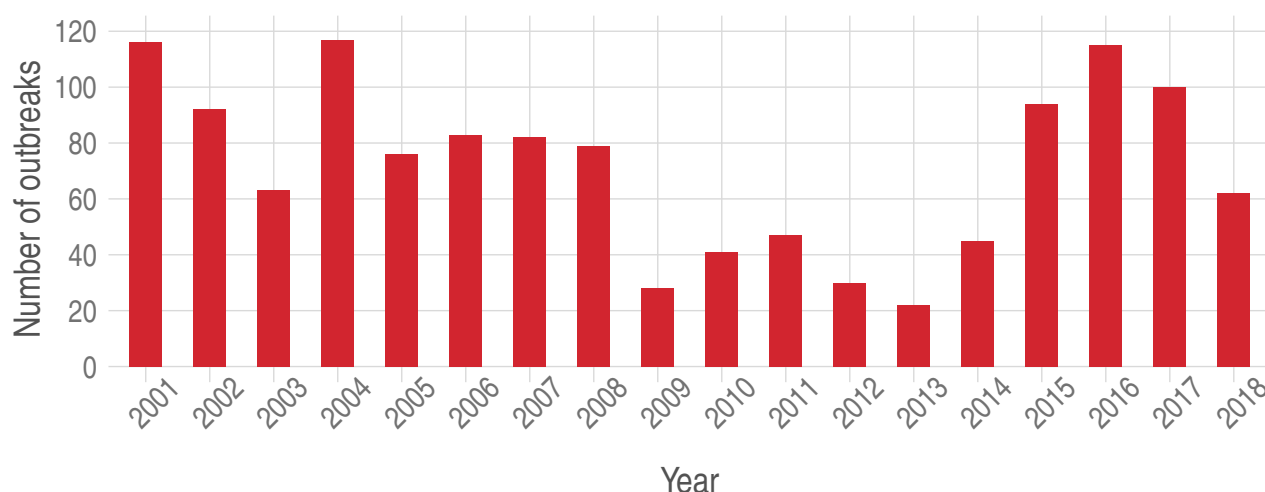


Figure 19: Reported index cases (farm outbreaks) of *Streptococcus equi* infections in horses in Sweden during years 2001–2018. Source: Swedish Board of Agriculture

Tick-borne encephalitis

BACKGROUND

Tick-borne encephalitis virus (TBEV) belongs to the genus flavivirus in the family *Flaviviridae*. TBE virus 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 county of Skåne in the south to Gävleborg in the north. The age distribution is wide but most of the

cases are between 30 and 70 years. There is a slight overrepresentation 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. Wild rodents are considered the natural reservoir for TBEV but are not reported to contract the disease. Roe deer have been suggested as an indicator of the prevalence 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

Demonstration of TBE virus or antibodies in animals is not notifiable.

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 20: Number of notified cases of TBE in humans 1988–2018.

SURVEILLANCE

Animals

The surveillance in animals is passive. During 2017, six dogs were tested for TBE antibodies.

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

Animals

One of the dogs was positive; it is however not known if clinical signs in this dog were caused by TBEV infection.

Humans

In 2018, 385 cases of TBE were reported. This is about the same number as the year before, which was a record year with more reported cases than ever before (Figure 20). On a longer term, since 2005 the TBE incidence has shown a significantly rising trend of 5% each year.

More men (66%) than women were reported with TBE. The incidence was highest among people in the age group 50–69 years, but there were cases reported from 5 to 92 years of age. Normally, there are few young children reported with TBE, but in 2018 there were less than usual as no cases in children below the age of 5 were reported.

All but seven cases had acquired their infections in Sweden. As usual, most of the imported cases had been infected in Finland (three cases in 2018).

The first TBE case became ill in mid-April and the last in mid-December. The peak occurred in September, when more cases were reported to have fallen ill than during any year before. There were also more cases falling ill during the exceptionally warm month of May than it use to be.

The geographic distribution of the disease was mainly, as in previous years, concentrated in the coastal areas of Stockholm, Södermanland and Uppsala counties, both along the lake of Mälaren and the Baltic Sea (Figure 21). The incidence was highest in the counties of Södermanland (17 cases per 100 000 inhabitants) and Uppsala (11 cases per 100 000 inhabitants). However, the infection also occurs in many other parts of the country; from the county of Skåne in the south to Gävleborg in the north. TBE is successively spreading westwards and in 2018 there were unusually many cases infected in for example the counties of Värmland, Västmanland, Västra Götaland and Örebro.

DISCUSSION

The TBE incidence has shown a significantly rising trend during the last three decades, but similarly to 2017 there were still considerably more cases reported in 2018 than expected. The extreme drought during several weeks in the summer does not seem to have had a large effect on the number of cases that might have been expected given that the ticks are very sensitive to dehydration. The heat and sun

Number of cases

- No cases
- 1–3
- 4–7
- 8–13
- 14–17

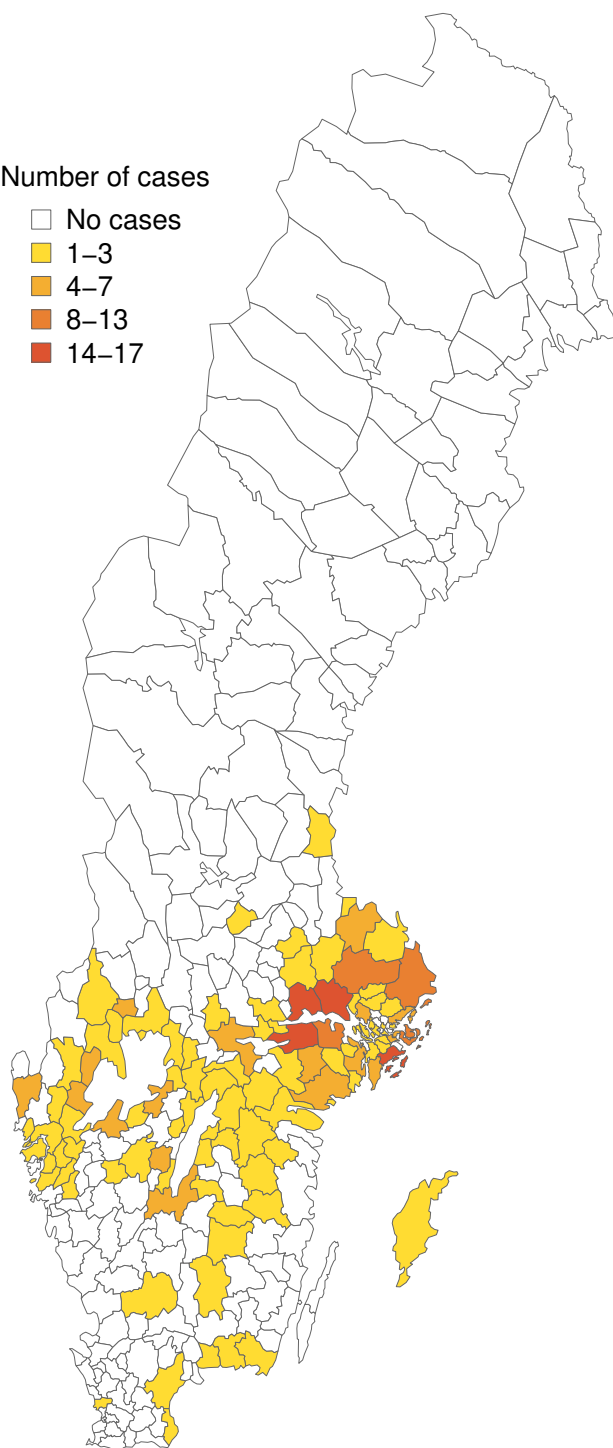


Figure 21: The geographic distribution of the place of infection of cases of TBE during 2018.

©EuroGeographics for the administrative boundaries.

probably had an opposite effect on human behaviour, so that people were exposed to a greater extent than usual.

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 is extremely rare in Swedish food-producing animals and the few human cases detected during the last decades were most often infected abroad. However, the parasite is endemic in wildlife, albeit at a low level. During 2018, a total of 232 lynx were tested for the *Trichinella* of which 6 were positive. Photo: Karin Bernodt.

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 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 2018.

Humans

Surveillance in humans is passive.

RESULTS

Animals

In 2018, the number of tested pigs from controlled housing conditions were 25 981 breeding sows, 392 boars and 1 494 474 fattening pigs. In addition, 580 203 slaughtered pigs (all categories) from uncontrolled housing conditions were tested. The number of slaughtered and tested horse was 1324. *Trichinella* was not detected in domestic pigs or horses.

Trichinella spp. was detected in 9 out of a total of 106 055 (0.008%) wild boar samples and also in 6 lynx, 1 raccoon dog and 3 wolves, see Table 22. These figures are based on results from examination of samples from animals submitted to wild game establishments (14 558 wild boars and 116 bears) as well as samples taken by private hunters.

Humans

No human case of trichinellosis was reported in 2018.

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 22: Findings of *Trichinella* in wild animals 2018.

Animal species	No. samples	No. positives	Percentage (%)	<i>T. britovi</i>	<i>T. nativa</i>	<i>T. pseudospiralis</i>	<i>T. spp.</i>
Badgers	11	0	0.00%				
Bears	232	0	0.00%				
Beaver	4	0	0.00%				
Lynx	53	6	11.32%	1	5		
Lion	1	0	0.00%				
Raccoon dog	23	1	4.35%		1		
Roe deer	1	0	0.00%				
Seal	2	0	0.00%				
Tiger	1	0	0.00%				
Wild boars	106 055	9	0.008%	1		7	1
Wolves	17	3	17.65%	1	2	-	-
Total	-	19	-	3	8	7	1

Tuberculosis



Wild fallow deer in Sweden. A control programme for tuberculosis in farmed deer was introduced in 1994 and the last case was identified in 1997. Today Sweden is free from tuberculosis. Photo: Karin Bernodt.

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 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 5.3 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.

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*, *M. tuberculosis*, or other mycobacteria in the *M. tuberculosis*-complex, are notifiable in all animal species according to the Swedish Act of Epizootic diseases (SFS 1999:657, with amendments).

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

As TB is notifiable on suspicion, clinical signs in animals or lesions detected at slaughter or necropsy of an animal prompt official investigations, including sampling for bacteriology, tuberculin testing of contact animals and epidemiological investigations.

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. Histology and direct smears are performed on all materials. 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 to the Norwegian Veterinary Institute or the Public Health Agency of Sweden. Positive isolates are further subtyped.

A positive finding of *M. bovis* or *M. tuberculosis* in animals would 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.

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

Surveillance for TB is mainly performed by meat inspection at slaughter of food producing animals. Official inspectors from the National Food Agency perform the inspections. Suspect lesions are sent to the National Veterinary Institute for histology and bacteriology, as described above.

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 necropsy 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 suspicions as described above.

RESULTS

Animals

Due to lesions detected at slaughter, four cattle, two sheep and seventeen pigs were investigated by histology and, where relevant, by culture. From these samples NTM (Non-tuberculous mycobacteria), from the *Mycobacterium avium/intracellulare*-complex were isolated in two pigs. No other slaughterhouse samples yielded any mycobacteria. Due to clinical suspicions or lesions found at necropsy, samples from one yak, one camel, one goose, one dog and three cats were investigated. NTM (Non-tuberculous mycobacteria), from the *Mycobacterium avium/intracellulare*-complex was isolated from the goose. No other sample yielded any mycobacteria.

In 2018, there were 302 holdings with farmed deer that were considered active and had obtained TB free status. Seven herds were not considered free. These herds are exempted from regular testing. Instead, to obtain a free status they must slaughter 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 2018.

During 2018, 22 alpacas and 8 llamas were tested serologically before export or import. Within the voluntary control programme, 322 alpacas and 6 camels were tested, all with negative final results.

Humans

Three cases of *M. bovis* were reported in humans in 2018; all three cases with extrapulmonary TB and all three most probably infected in Syria. There were no connections between the cases except for having the same country of origin. All three isolates were unique when analyzed with whole genome sequencing.

DISCUSSION

In summary, the overall TB situation in animals and humans remains favourable.

No cases of TB were detected in Swedish animals during 2018. The officially free status for bovine TB in cattle has been maintained during 2018. Although the surveillance is mainly dependent on inspections of slaughtered animals, this is considered sufficient. However, the rate of submission of lesions from slaughtered ruminants should be improved. Passive surveillance based on clinical suspicions and necropsy 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 the remaining deer herds officially free.

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.

REFERENCES

- Alvarez J, Bezos J, Juan Ld, Vordermeier M, Rodriguez S, Fernandez-de-Mera IG, Mateos A, Domínguez L. Diagnosis of tuberculosis in camelids: old problems, current solutions and future challenges. *Transbound Emerg Dis*. 2012 Feb;59(1):1–10. doi: 10.1111/j.1865-1682.2011.01233.x. Epub 2011 Jun 2
- Rhodes S, Holder T, Clifford D, Dexter I, Brewer J, Smith N, Waring L, Crawshaw T, Gillgan S, Lyashchenko K, Lawrence J, Clarke J, de la Rua-Domenech R, Vordermeier M. Evaluation of gamma interferon and antibody tuberculosis tests in alpacas. *Clin Vaccine Immunol*. 2012 Oct;19(10):1677–83. Epub 2012 Aug 22.
- Wahlström H, Frössling J, Sternberg Lewerin S, Ljung A, Cedersmyg M, Cameron A (2010) Demonstrating freedom from infection with *Mycobacterium bovis* in Swedish farmed deer using non-survey data sources. *Prev Vet Med* 94:108–118

Tularaemia

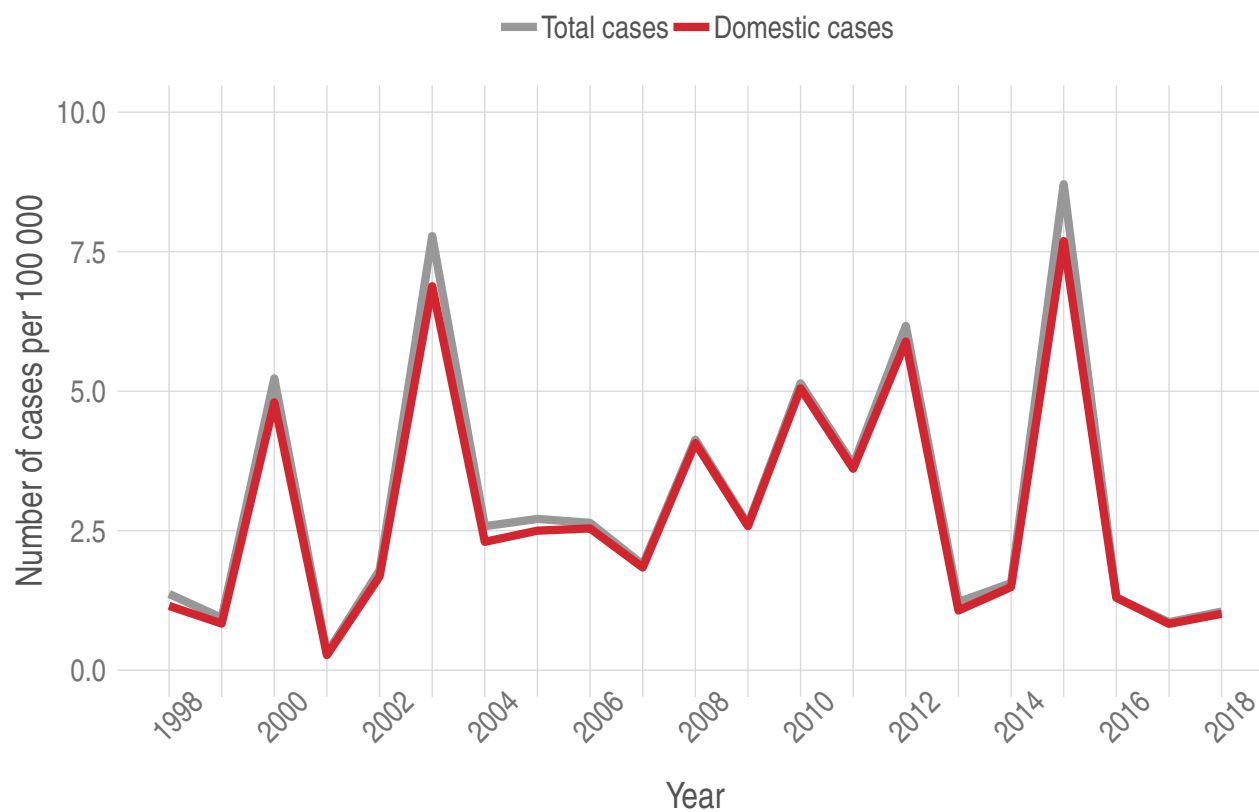


Figure 22: Incidence of notified human cases of tularaemia in Sweden 1998–2018.

BACKGROUND

The bacterium *Francisella tularensis* is the causative agent of tularaemia, a disease affecting many animal species, including humans. 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. Although many different animal species can be infected, tularaemia is typically found in hares and small rodents.

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.

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, the pathological presentation of the disease is a disseminated multi-organ septicaemic form.

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.

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. For laboratory verification of the infection, serology, PCR and isolation of the bacteria are used.

RESULTS

Animals

In 2018, 26 European brown hares and six mountain hares were examined. *F. tularensis* subsp. *holarctica* was detected in five European brown hares and none of the mountain hares. Four of the five hares had died of an acute disease spread to several organs, finally ending with sepsis. One hare had a slightly different presentation with fibrous pneumonia and pleuritis, but *F. tularensis* was only detected in the kidney pelvis and was not associated with the thoracic lesions. The tularaemic hares originated from: Stockholm (one hare), from counties south and southwest of Stockholm, Östergötland (two hares), and Västra Götaland (two hares). The number of cases in 2018 is approximately at the same level as in other years without outbreaks, for example seven cases in 2017, six in 2016 and two in 2014. This could be compared to the outbreak year 2015 when tularaemia was diagnosed in 31 hares, the majority coming from an outbreak area in Norrbotten.

Humans

In 2018, 107 human cases of tularaemia were reported. As a rule, there are large natural fluctuations in the number of tularaemia cases observed between years and in different regions. This is probably due to several factors; among others are the extent of infection in reservoir species and number of mosquitoes, as well as weather conditions. Even though the tularaemia incidence has varied a lot between years, the increasing trend in incidence in the last decades is significantly different in comparison to the same time period before 1992.

More men (61%) than women were reported to be infected in 2018, 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 their somewhat different activities.

As in previous years, except for a few sporadic cases, tularaemia was only reported from the northern, western and central parts of Sweden. During 2018, the incidence was highest in the County of Dalarna with 8.4 cases per 100 000 inhabitants, followed by the County of Örebro with five cases per 100 000 inhabitants. In 2018, four cases were reported with unknown country of infection; the remaining 103 cases were reported to have been infected in Sweden.

During the first half of the year, just a few cases were reported each month. The number of cases started to increase in July and peaked in August. During the last month of the year the number of cases subsided.

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. The reservoir for the bacterium between outbreaks has not been clearly identified. During the last two decades, the epidemiology of tularaemia has changed and the number of reported cases in humans and animals, mainly European brown hares, infected south of the previous endemic region has increased. In animals, outbreaks of tularaemia have in some countries been associated with a rise in rodent and hare populations, but this has not been confirmed in Sweden. It is possible that the European brown hare has become an important carrier of *F. tularensis* in many areas, but its epidemiological role remains unclear.

Verotoxinogenic/shiga-toxin producing *Escherichia coli*

IN FOCUS - O157:H7 CLADE 8 - A VIRULENT STRAIN OF E. COLI THAT IS ENDEMIC IN SWEDEN

In the summer of 2018, Sweden experienced one of the largest outbreaks in the country. The outbreak was serious, especially because of the strain implicated. It was a subtype of O157:H7 called clade 8, known for its potential to cause severe disease such as HUS. It carries the vero/shigatoxin gene *stx2a*, or more often *stx2a* in combination with *stx2c* and is today one of the most common subtypes to cause domestically acquired HUS. The strain was first established in the 1990s in the county of Halland and has further spread over the southern parts of the country. In recent years, clade 8 has mainly been found in Skåne, Blekinge, Småland and on the islands Öland and Gotland. In 2005 it caused, what still holds to be the largest VTEC/STEC outbreak in Sweden with 135 cases. Lettuce that had been irrigated with contaminated water from a stream where grazing cattle in the environment upstream was the probable source. A farm with cattle in the area was found positive for O157:H7. During the outbreak of 2005 and the outbreak in 2018, 8 and 12% of the cases developed HUS, which is significantly higher than as yearly reported (2–4%). In two minor outbreaks in 2002 and 2017 involving this strain, 11 and 38% of the reported cases developed HUS. The pathogenic potential shown by this strain has led to joint efforts by Swedish authorities to map and monitor the occurrence and molecular epidemiology of clade 8 among Swedish animals and humans. Efforts have been made to reduce the risk of infection for example through, advice to animal owners and food producers. At present, there is no effective method for combating VTEC/STEC among animals, but in the long term the hope is that the occurrence can be reduced by e.g. vaccination.

BACKGROUND

Verotoxinogenic *Escherichia coli* (VTEC) or, synonymously, shigatoxin-producing *Escherichia coli* (STEC), 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.

VTEC/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.

SURVEILLANCE

Animals

Surveillance of VTEC/STEC in animals is both enhanced passive and active and consists of traceback investigations from human STEC cases and 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 since 1997 and the results of the studies are summarised in Table 24. In these 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 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 2018, ten cattle or sheep farms were investigated as suspected sources for human infection. An epidemiological association was established in two cases of VTEC/STEC O157:H7 clade 8 (one sheep farm and one farm with both cattle and sheep) and one case of STEC O26:H11 (cattle farm).

Active

During 2017–2018, a national survey was performed by the National Veterinary Institute in which 1164 faecal samples from cattle were collected from abattoirs and analysed for STEC O157 and STEC O121, see Table 24. In the survey, STEC O157 was detected in 46 samples of which 12 samples were clade 8. Additionally, STEC O121 was detected in 3 samples. All cattle with positive samples originated from central and southern Sweden.

Food

From autumn 2017 through spring 2018, a survey was performed by the National Food Agency in which 300 samples of lamb meat were collected at retail and analysed for STEC. In the survey, STEC was detected in 35% of the 300 samples by qualitative analyses. The prevalence of STEC differed depending on country of origin. Among the three major countries of origin, STEC was most common in lamb meat from Ireland (64%), followed by Sweden (43%) and New Zealand (19%). The most common serotype was STEC O91:H14. According to the FAO and WHO's risk classification model, all but three of the 123 STEC isolates belonged to the low-risk classification level associated with milder symptoms such as diarrhoea and stomach cramps in humans.

In addition, 121 samples were taken by national and local authorities from different types of food and analysed for STEC (11 of these only for STEC O157). The majority, 100 samples, were of beef meat and taken in border control. The rest of the samples were mainly of different types of food taken to investigate a complaint or a suspected food poisoning. Neither of the 121 samples was positive for STEC.

Humans

In 2018, 892 human cases were reported of which 627 were domestic (70%). The domestic incidence in 2018 was 6.1 (cases per 100 000 inhabitants), twice as high as the year before, and over a longer period of time an increasing trend

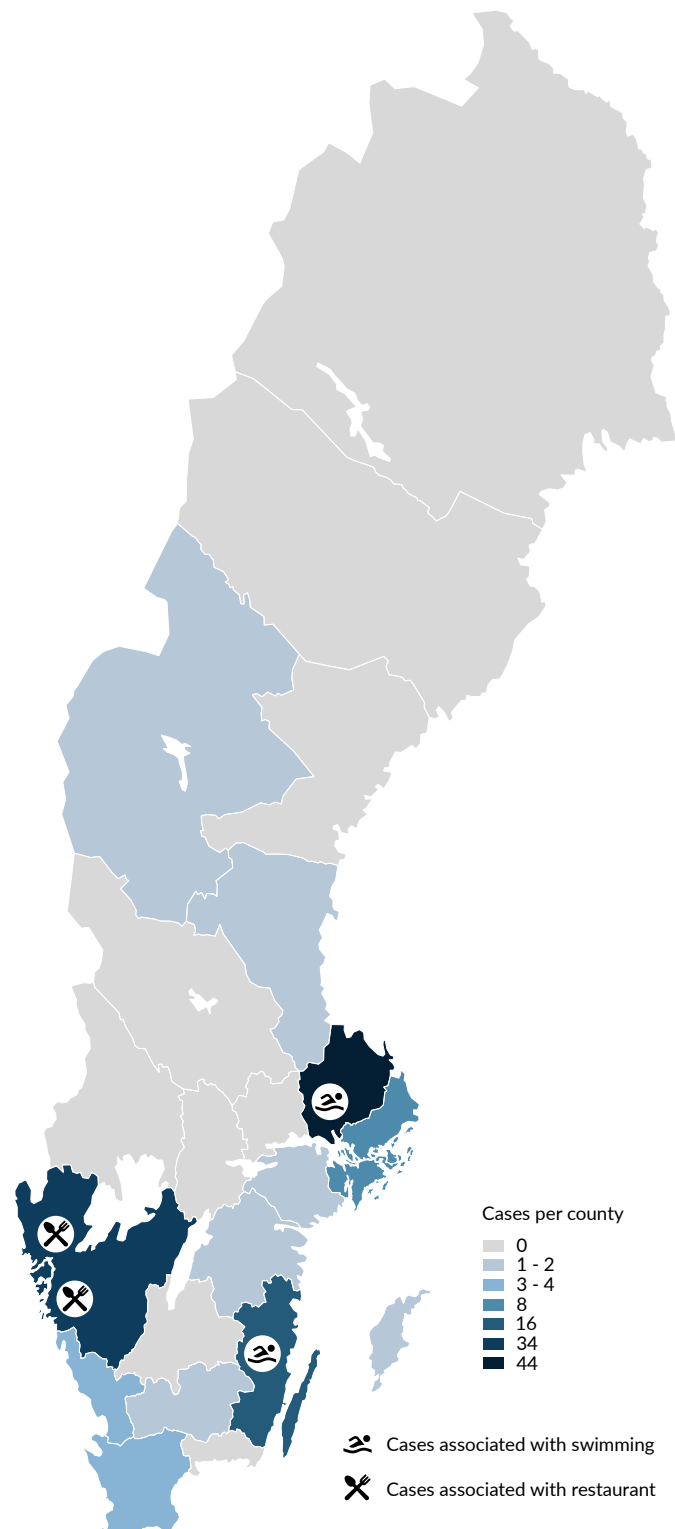


Figure 23: Cases of O157:H7 clade 8 during the 2018 summer outbreak by county of infection, or if unavailable county of residence. Icons indicate clusters of cases linked to two restaurants and two lakes. County map from Statistics Sweden (<https://www.scb.se/>).

is seen (Figure 24). The increase in 2018 was seen throughout the country and especially during summer and early autumn, the period where most cases are usually reported. A large outbreak during the summer contributed to the increase but also without the outbreak, the number of cases was the

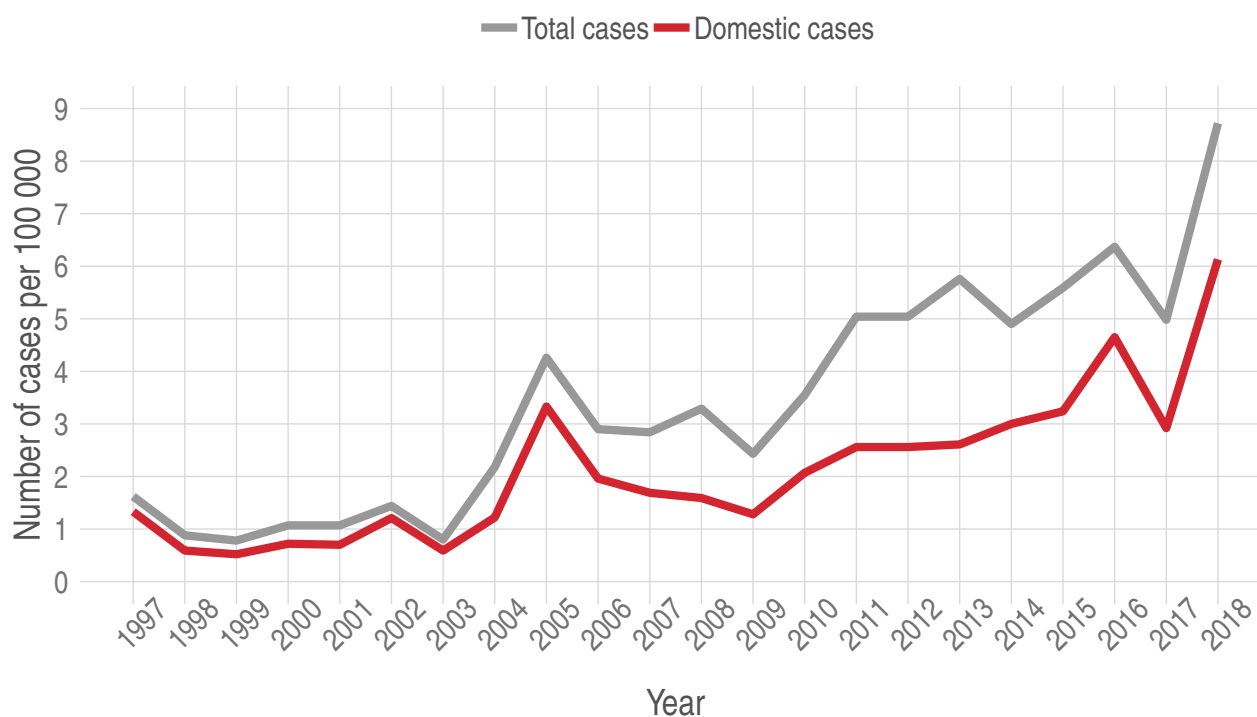


Figure 24: Notified incidence per 100 000 inhabitants of human EHEC cases in Sweden, 1997–2018.

highest ever reported. The effect that the unusual high summer temperatures could have had on the domestic incidence of STEC has not been analysed. As in previous years, the incidence was highest in children.

STEC-associated HUS was reported in 40 cases of which 36 were domestically acquired infections. The majority of HUS cases were children under the age of 10. For 31 of the HUS cases an isolate could be retrieved and thereby serotyped (Table 23). Eighteen of the domestic HUS cases belonged to serotype O157:H7, clade 8, of which 14 belonged to the summer outbreak.

In 67% of the domestic STEC cases, an isolate could be retrieved and thereby serotyped. The most common serotypes were O157:H7, O26:H11, O121:H9 and O103:H2. For O26:H11, more isolates are identified with *stx2a* or *stx1a* in combination with *stx2a*. Previously, this serotype has almost exclusively borne *stx1a* alone, a type that usually cause milder disease than *stx2a*.

NATIONAL OUTBREAK INVESTIGATIONS

National outbreaks are jointly investigated by several authorities; which authorities depends on the nature of the outbreak. During the summer of 2018, one of the largest VTEC/STEC outbreaks ever seen in Sweden occurred. A total of 116 cases was microbiologically or epidemiologically linked to the outbreak, of which 14 developed HUS. Cases were spread across the country but with some accumulation of cases linked to two restaurants and two public outdoor baths, see Figure 23. The source of infection was not identified but is likely to have been food-borne since people fell ill in different parts of the country. Locally, it also seems that the infection was spread from person to person via the outdoor bathing sites. In addition, a national case-control study

was conducted. The study did not identify any specific food items likely to have caused the outbreak but showed, in line with regional investigations, that cases were more exposed to having eaten at restaurants, specifically pizzerias, compared to controls.

Also, an outbreak of STEC O26:H11, *stx1a* occurred in late summer 2018 affecting 13 persons. The source of infection was not identified but the outbreak is likely to have been food-borne, mainly due to the geographical distribution of cases.

DISCUSSION

The trend in domestic incidence continued to increase in 2018, even without including the cases from the summer's large outbreak. The ongoing change toward using multiplexed PCR panels when faecal samples are analysed for gastrointestinal pathogens is likely to increase the number of detected cases but to which extent is not known.

Several investigations were performed based on suspected associations with farms and food items. Most reported cases from humans are in counties with high cattle density, typically in the southern parts of Sweden. Many of these regions are however more densely populated, in addition to historically a higher ratio of faecal samples analysed for STEC. The screening frequency of STEC in faecal samples of children with diarrhoea has, in a previous investigation, been shown to also be the highest in the southern parts. The higher numbers of cases infected abroad, which can also be found in these parts of Sweden, can partly be explained by the differences in screening routines, but the cause has not been fully investigated.

The prevalence among cattle, based on samples taken at slaughter, has since 2005 been in the range of 2.2–3.5%. In

Table 23: Distribution of serotypes and shigatoxin-subtypes in HUS (haemolytic uraemic syndrome) cases in 2018.

Serotype	stx1a+stx2a	stx2a	stx2a+stx2c	stx2a, stx2d	stx2b, stx2d
O157:H7, clade 8	-	-	18	-	-
O26:H11	2	3	-	-	-
O121:H19	-	2	-	-	-
O130:H11	-	1	-	-	-
O113:H21	-	-	-	1	-
O165:H25	-	-	1	-	-
O77:H41	-	1	-	-	-
ONT:H29	-	-	-	-	1
ONT:H2	-	1	-	-	-

these studies, STEC O157:H7 has predominantly been isolated from cattle in southern Sweden and rarely from the northern two thirds of the country. In the latest surveys, positive STEC O157 samples have also been analysed by whole-genome sequencing, e.g. for identifying the subtype clade 8. There is a tendency for geographical clustering of clade 8.

DISEASE

Animals

Animals do not develop clinical disease.

Humans

The clinical picture may vary from asymptomatic infection to non-haemorrhagic or haemorrhagic diarrhoea associated with abdominal cramps. Most patients fully recover. In recent years, approximately 3% of the cases in Sweden have developed HUS, which is characterised by acute renal failure, thrombocytopenia, and microangiopathic haemolytic anaemia; a condition that may lead to death. 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.

LEGISLATION

Animals

Since 1999, VTEC/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 that are pathogenic to humans 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.

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

Table 24: Surveillance of VTEC O157 in faecal and ear samples collected from cattle and sheep at abattoirs in Sweden during 1996–2018. Since 2011, positive faecal samples have been further analysed to identify hypervirulent strains (clade 8).

Year	Species	Faecal samples			Ear samples	
		Total	Positive (%)	Clade 8	Total	Positive (%)
1996–1997	Cattle	3071	37 (1.2)	-	-	-
1997–1998	Cattle	2308	7 (0.3)	-	-	-
1999	Cattle	2057	14 (0.7)	-	-	-
2000	Cattle	2001	34 (1.7)	-	-	-
2001	Cattle	1998	36 (1.3)	-	-	-
2002	Cattle	2032	29 (1.4)	-	-	-
2005–2006	Cattle	1758	60 (3.4)	-	-	-
2007–2008	Sheep	492	9 (1.8)	-	105	2 (1.9)
2008–2009	Cattle	1993	65 (3.3)	-	446	54 (12.1)
2011–2012	Cattle	2376	73 (3.1)	15	500	41 (8.2)
2014–2015	Cattle	1492	33 (2.2)	5	-	-
2017–2018	Cattle	1164	46 (3.5)	12	-	-

Yersiniosis

BACKGROUND

The genus *Yersinia* has been associated with human and animal diseases for centuries; it was identified in the late 19th century and reclassified into its own genus in the mid-20th century. Two enteropathogenic species of the genus are zoonotic: *Yersinia enterocolitica* and *Yersinia pseudotuberculosis*. Pigs are considered the main reservoir of *Y. enterocolitica*. *Yersinia* bacteria are widespread in nature, among which nonpathogenic strains are most frequent. The most common human pathogenic bioserotype is *Y. enterocolitica* 4/O:3.

Wild animals, especially rodents and birds are considered the principal reservoir of *Y. pseudotuberculosis*. Both *Y. enterocolitica* and *Y. pseudotuberculosis* are frequently found in pig tonsils and porcine intestinal contents. Infections caused by *Y. enterocolitica* are thought to be foodborne and pigs are considered the main source of infection. The sources and vehicles of *Y. pseudotuberculosis* infections in humans remain unclear 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); however, they are able to grow at refrigerator temperature and can therefore grow in food that is kept cool. In addition, they can grow in vacuum and modified atmosphere packages.

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.

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. Prolonged carriage has been reported. 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 2018, 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 passive.

RESULTS

Animals

Samples tested for *Yersinia* at SVA during 2018 included 83 samples from mostly zoo and laboratory primates. *Yersinia* was not isolated from any of these samples.

Food

In 2018, two samples were taken by national and local authorities. Both samples were taken from air-dried ham to investigate a complaint or a suspected food poisoning. One sample from the ham was positive for *Yersinia enterocolitica*.

Humans

Yersiniosis is mainly an infection of domestic origin. Of the 280 cases reported in 2018, 77% were infected in Sweden. For the cases infected abroad, Spain, Greece and Cuba are the most frequent travel destinations.

The domestic incidence of yersiniosis was higher in 2018 compared to the previous years but seen over a longer time period there is a statistically significantly decreasing trend in the incidence (Figure 25).

Similar to previous years, the incidence was highest among children younger than five years. The incidence was 4.3 (cases per 100 000 inhabitants) for infants and 8.0 for children 1–4 years old, compared to 2.7 for all cases.

Yersinia has previously had a clear seasonal variation with the highest number of cases infected in Sweden during the summer. However, for the past five-year period, there is no statistically significant difference between the summer months and the rest of the year.

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.

The ham positive for *Yersinia enterocolitica* (mentioned above in Results-Food) was suspected to have caused an outbreak in a restaurant. Six people fell ill but no isolates from the human cases were available and therefore the source of infection could not be confirmed.

DISCUSSION

Since 2004, 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.

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. Thus, 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

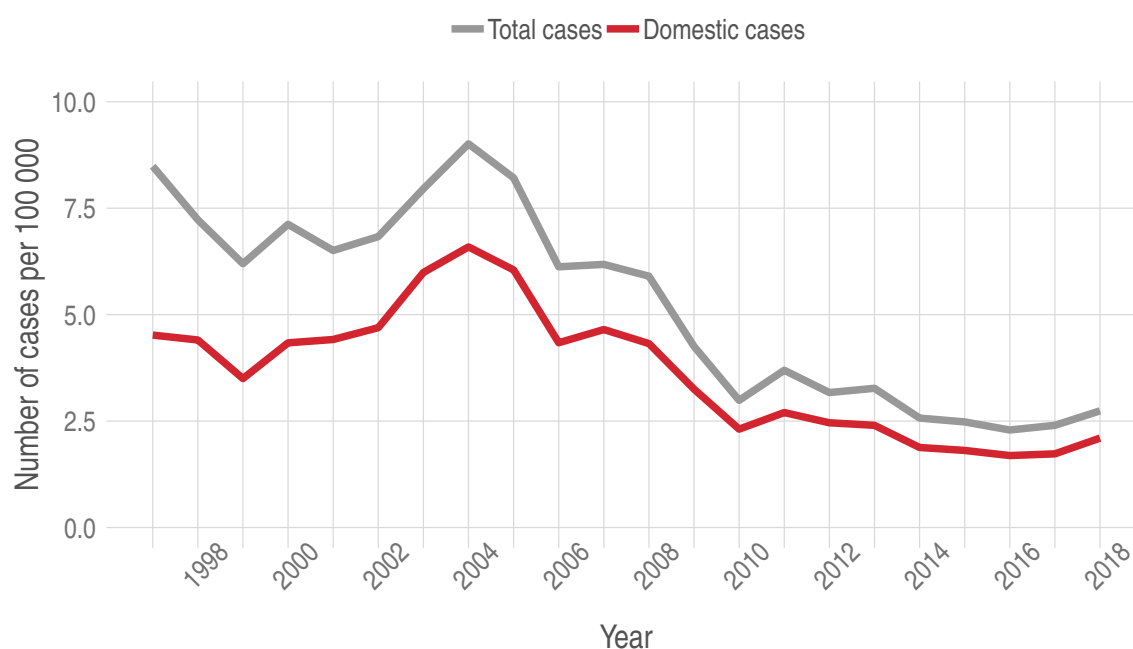


Figure 25: Notified incidence (per 100 000 inhabitants) of human cases of yersiniosis in Sweden, 1997–2018.

Additional Surveillance 2018

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. Outbreaks have since then been reported from large parts of China, as well as from Mongolia, Vietnam, Cambodia, North Korea and Laos. 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 makes this



African swine fever is currently present in large parts of Europe where it continues to spread. The risk for further spread within EU is considered high and Swedish hunters are encouraged to report all findings of dead wild boar. Photo: Marisa04 - Pixabay.

disease especially important in countries previously free from the disease. 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 decade 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 avulavirus 1 (previously called avian paramyxovirus type 1) in the family of paramyxoviruses. Wild birds are important reservoirs of the virus, which is transmitted through direct and indirect contacts between infected and non-infected birds. Since 1995, sixteen outbreaks of ND have occurred in Sweden, all of which have been successfully eradicated. Sweden has status of ND free without vaccination (Commission Decision 95/98/EEC).

LEGISLATION

Clinical suspicions of epizootic diseases, including ASF, anthrax, FMD and ND, must be notified to the Swedish Board of Agriculture in accordance with the Swedish Act of Epizootic diseases (SFS 1999:657 with amendments). This obligation applies to animal keepers, official and private veterinarians, veterinary laboratories, and other relevant stakeholders. Suspicions are investigated after consultation with disease experts at the National Veterinary Institute and following notification to the Swedish Board of Agriculture, and sampling and analysis carried out in accordance with diagnostic manuals of the EC as applicable (ASF 2003/422/EC; FMD 2003/85/EC annex XIII; ND 92/66/EEC annex III).

In addition, a number of other infectious diseases are notifiable to the Board of Agriculture and/or the relevant County Administrative Board based on laboratory confirmation or clinical suspicion (SJVFS 2013:23).

SURVEILLANCE

Every year, hundreds of suspicions of serious infectious diseases are reported by field veterinarians, animal owners or private veterinary pathologists to the experts at the National Veterinary Institute. Many of these suspicions can be ruled out already based on anamnesis and initial clinical investigation, whereas others require notification to the Swedish Board of Agriculture and further investigation including sampling of sick or dead animals, with movement restrictions imposed on the farms during the investigation. Also, in cases in which an epizootic disease is not primarily suspected, but where it cannot be excluded based on clinical investigation, samples can be submitted for laboratory investigation to exclude a diagnosis. This can only be done after discussions with experts at the National Veterinary Institute and in consultation with the Swedish Board of Agriculture. This approach serves to reduce the threshold for submitting samples for analysis of notifiable diseases, and thereby increasing the sensitivity of the system. The Swedish Board of Agriculture covers all costs for veterinary visits, transports, and diagnostic analyses related to the investigation.

African swine fever

Reported cases of increased mortality or serious morbidity, with clinical signs such as haemorrhagic disorders or reproductive failures in pigs are considered suspicions of ASF until ruled out through further clinical investigation. Samples are sent to the National Veterinary Institute for laboratory analyses. Due to clinical similarity, samples from domestic pigs collected for ASF are also analysed for CSF. This strategy is strongly recommended by the EU.

Given the current situation in Europe as regards ASF in wild boar, the clinical surveillance is enhanced, and Swedish hunters are encouraged to report all findings of dead wild boar. If possible, carcasses or samples are taken in and investigated to rule out ASF as the cause of death (see also specific chapter on infectious diseases in wild boars).

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 post-mortem are considered suspicions of anthrax. Samples from suspected cases are sent to the National Veterinary Institute for laboratory analyses.

During 2018, the clinical 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 2014–2018 are compiled in Table 25.

Four clinical suspicions of ASF in domestic pigs and one in wild boar were investigated, with negative results. Samples from all suspicions were also analysed for CSF, two were analysed for PRRS and one for Aujeszky's disease, all with negative results. In addition, thirteen samples from wild boar found dead were analysed for ASF, with negative results.

Eleven clinical suspicions of anthrax in cattle were reported and investigated. In addition, two cattle, one sheep, and two moose found dead were investigated as part of the enhanced clinical 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 2018.

One outbreak of ND in poultry was confirmed in 2018. The suspicion was raised after an acute egg drop of 50% in a layer flock with approximately 5000 birds. In addition, eight other clinical suspicions of ND in poultry were reported and investigated with negative results. Samples from seven of these suspicions were also analysed for avian influenza with negative results.

DISCUSSION

Clinical surveillance constitutes a fundamental part of the animal disease surveillance system and is particularly important as regards early detection of epizootic and/or emerging diseases. This surveillance component depends on the level of cooperation and trust between the relevant stakeholders in the field (including animal keepers and official and private veterinarians, among others) and the central veterinary authorities, but also on the level of knowledge and

awareness among all involved. In Sweden, cooperation between the relevant stakeholders is long-standing at a high level, and the level of knowledge and awareness as regards epizootic diseases as well as the obligation to report suspicions thereof is considered good. Based on this and given the relatively high numbers of suspicions of epizootic diseases investigated each year, the performance of the clinical surveillance is considered adequate. However, a systematic evaluation of this performance has never been carried out. Therefore, to get a better understanding of the coverage and representativeness of the clinical surveillance and thus the performance, and to identify gaps, an evaluation of the clinical surveillance using data from the last ten years is currently underway.

As regards ASF, given the current situation in Europe and globally, the risk for introduction to Swedish wild boar is considered increased. In case of introduction, early detection is crucial in order to prevent a longer-term establishment of the disease. The timeliness 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. Despite information and awareness campaigns carried out

in this regard during the last few years, targeting the hunting community, and in spite of a well-established network of hunters, which is fundamental for the general surveillance for diseases in wildlife (also described in the specific chapter on Post mortem examinations in wildlife), less than 20 wild boar found dead are investigated annually as part of the surveillance for ASF. Given the population size of Swedish wild boar (estimated at 250 000) and the expected number of wild boar that would die from other causes than hunting, 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. http://ec.europa.eu/food/audits-analysis/act_getPDF.cfm?PDF_ID=11146

Table 25: Suspicions of epizootic diseases reported and further investigated between 2014–2018, based on sampling of sick or dead animals.

Disease	Investigated ^A (Confirmed)					
	2013	2014	2015	2016	2017	2018
African swine fever ^B	17 (0)	6 (0)	17 (0)	20 (0)	18 (0)	18 (0)
Anthrax	18 (1)	18 (0)	11 (0)	74 (15)	34 (0)	16 (0)
Aujeszky's disease	2 (0)	2 (0)	1 (0)	2 (0)	0 (0)	1 (0)
Avian influenza ^C	12 (1)	16 (0)	15 (0)	17 (2)	28 (4)	9 (1)
Bluetongue	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)
BSE	4 (0)	3 (0)	1 (0)	2 (0)	2 (0)	0 (0)
CWD	0 (0)	0 (0)	0 (0)	0 (0)	1 (0)	17(0)
Classical swine fever	4 (0)	5 (0)	3 (0)	5 (0)	3 (0)	4 (0)
FMD	2 (0)	1 (0)	1 (0)	1 (0)	0 (0)	0 (0)
IBR	3 (0)	1 (0)	0 (0)	0 (0)	0 (0)	2 (0)
Lumpy skin disease	0 (0)	0 (0)	1 (0)	1 (0)	0 (0)	0 (0)
Newcastle disease	15 (0)	25 (3)	15 (0)	17 (1)	29 (3)	8 (1)
Paratuberculosis	4 (0)	7 (0)	3 (0)	5 (0)	5 (0)	1 (0)
PRRS	9 (0)	4 (0)	5 (0)	5 (0)	2 (0)	2 (0)
Rabies	8 (0)	5 (0)	10 (0)	3 (0)	6 (0)	9 (0)
Tuberculosis	8 (0)	14 (0)	8 (0)	6 (0)	9 (0)	7(0)
West Nile fever	2 (0)	1 (0)	2 (0)	1 (0)	2 (0)	0 (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.

^CDoes not include surveillance of, or cases in, wild birds.

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 2018 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*

M. 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. *M. 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.

Avian avulavirus 1

Avian avulavirus 1 (previously 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, sixteen 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 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 2018, 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 26 and 27.

RESULTS

Table 28 gives an overview of all samples taken in breeding flocks of chickens and turkeys, and the laboratory methods used, during 2018. All analysed samples tested negative for *M. gallisepticum* and avian avulavirus 1.

Serological reactions to *M. synoviae* were detected in sixteen chicken flocks (fourteen parent flocks and two grandparent flocks). This could later be linked to a change of method for confirmatory testing used for samples positive in the combined *M. gallisepticum*/*M. synoviae* ELISA. Two flocks were sampled at 60 weeks of age and no additional samples were available from these flocks. The remaining fourteen flocks were later considered free from *M. synoviae* based on clinical status and testing of new samples.

Nine chicken parent flocks were further investigated due to a few positive samples for egg drop syndrome. In addition, one chicken parent flock and one turkey parent flock were investigated due to a few positive samples for *Salmonella Gallinarum*/*Salmonella Pullorum* and *Mycoplasma meleagridis* 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.

DISCUSSION

In conclusion, the results from the serological screening in the Poultry Health Control Programme in 2018 support the status of freedom from the infections included in the Swedish breeding poultry population. However, clinical surveillance of the poultry breeding population is also of utmost importance.

Table 26: 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	72
<i>S. Pullorum</i> / <i>S. Gallinarum</i>	-	60	-	-	-	-
<i>Mycoplasma gallisepticum</i>	60	60	60	60	60	60
<i>Mycoplasma synoviae</i>	60	60	60	60	60	60
Avian avulavirus 1	-	-	-	60	-	-
Egg drop syndrome-virus	-	30	-	-	-	-

Table 27: 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
Avian avulavirus 1	-	-	-	60

Table 28: Number of sampling occasions for grandparent (GP) and parent (P) flocks of chickens and turkeys and total number of samples tested during 2018.

Agent	No. of sampling occasions			No. of samples			Method
	Chickens		Turkeys	Chickens		Turkeys	
	GP	P		GP	P		
S. Pullorum / S. Gallinarum	16	95	4	960	5700	240	Serum plate agglutination test, antigen, ID.Vet
Mycoplasma gallisepticum / Mycoplasma synoviae	75	439	16	4500	26 340	960	Mycoplasma gallisepticum/synoviae ID screen indirect ELISA, ID. vet
Mycoplasma meleagridis	0	0	16	0	0	960	Serum plate agglutination test, antigen, ID.Vet
Avian avulavirus 1	16	88	4	960	5280	240	NDV screen competition ELISA, ID.Vet
Egg drop Syndrome-virus	16	95	0	480	2850	0	Antibody haemagglutination inhibition test, antigen, in-house (Until May 2017. From May 2017 antigen from GD Animal Health)

Infectious diseases in wild boars

BACKGROUND

Wild boars are susceptible to contagious diseases that affect domestic pigs and they therefore can play a role in spreading disease to and from domestic pigs. This is particularly true for classical swine fever (CSF) which has been transmitted between wild boars and domestic pigs in several European countries. Also, the ongoing spread of African swine fever (ASF) in Eastern Europe and within the EU involves wild boar, and the direct and indirect contacts between domestic pigs and wild boar in these areas hamper the control and management of the disease. The Swedish wild boar population is increasing rapidly and was estimated at 250 000 animals before the reproductive season of 2018. The northern border of the wild boar's range in Sweden is extending and has at present passed the level of the river Dalälven. Since the year 2000, hunted wild boars from throughout the country have been blood sampled yearly for surveillance purposes. These samples are sent to the National Veterinary Institute for analysis for antibodies to infectious agents that are of importance for domestic pig production. Also, due to the worrying ASF situation in Eastern Europe and within the EU, an enhanced passive surveillance programme for ASF in wild boars that are found dead has been in place since 2013.

LEGISLATION

Several diseases capable of infecting wild boar, including ASF, CSF, Aujeszky's disease, brucellosis and 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

Anyone who finds a dead wild boar can voluntarily submit the whole carcass or organ samples from it to the National Veterinary Institute for postmortem examination. All submitted samples are analysed through the wild boar enhanced passive surveillance programme 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

From 2000–2017, blood samples from hunted wild boar, submitted voluntarily by hunters, have been used for the active surveillance of Aujeszky's disease, CSF and *Brucella suis*. In 2018 however, due to a redistribution of funding, no active surveillance of wild boars was undertaken. This activity will be resumed in 2019.

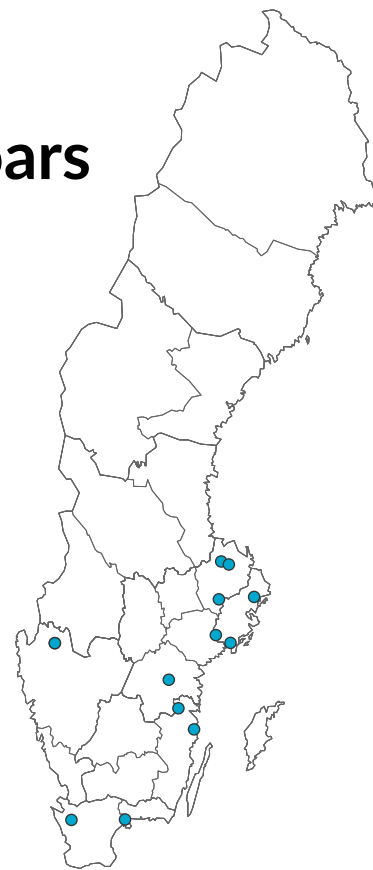


Figure 26: The locations where dead wild boars tested for African Swine Fever (ASF) were found. ©EuroGeographics.

RESULTS

Passive surveillance

No investigations based on clinical suspicion of disease were conducted in free-living wild boar in 2018.

Thirteen wild boar that were found dead were examined for the presence of ASF virus genome and all analyses were negative. The geographic distribution of the sampled dead wild boars is shown in Figure 26. Additional post mortem findings in these wild boars are reported in the chapter “*Post mortem examinations in wildlife*” in this report.

Active surveillance

No active surveillance of wild boars was undertaken in 2018.

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 ASF situation in Russia, Eastern Europe and within the EU is of special concern and calls for efficient approaches to early detection of disease in the wild boar population. As such, methods to increase the number of wild boars found dead that are voluntarily submitted by the public for post-mortem and ASF testing are currently being investigated.

Infectious diseases and parasites in honeybees

BACKGROUND

Every beekeeper in Sweden has the responsibility to prevent the spread of bee diseases and are 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 must be reported by the beekeepers and recorded by 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. The country is divided into approximately 500 bee districts and the bee inspectors are responsible for the actual 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 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, 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 a parish which has been declared infected with AFB by the SBA. Visual inspection of clinical symptoms of AFB and *Varroa* mites are 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 parish in which the apiary is situated infected/infested. Bee inspectors can send samples of diseased brood, larvae or pupae 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 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 all other apiaries within a 3-km radius from the infected apiary.

European foulbrood

European foulbrood (EFB), is a serious disease of honeybees caused by the bacterium *Melissococcus plutonius*. EFB affects mainly young honeybee larvae usually between 4 and 5 days old. A massive loss of brood resulting from severe infection weakens the colony and can lead to its collapse. Regional variations in disease burden have been reported and recent decades have seen dramatic increases in the incidence of EFB in parts of Europe. Large disease outbreaks have been identified in areas previously thought to be disease free, such as Norway.

Tracheal mite infestation (acariosis)

The honeybee tracheal mite *Acarapis woodi* is an internal parasite of the respiratory system of adult honeybees. The tracheal mite has spread through global beekeeping exchanges and has been reported from all European countries except Sweden. It is therefore regulated in Swedish legislation.

Varroa mite infestation (varroosis) and associated virus infections

The honeybee parasitic mite, *Varroa destructor*, was originally confined to the Eastern honeybee, *Apis cerana*, where a stable host-parasite relationship exists due to a long period of coevolution. After a shift in the last century, from the native host to the Western honeybee, *Apis mellifera*, the mite dispersed around the globe and is currently considered the greatest threat to honeybees and apiculture worldwide. The mite was reported in Europe in the late 1970s, 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. *Varroa* mites have so far not been reported from the northern half of Sweden (Västerbotten as well as most of Jämtland, Västernorrland, Norrbotten, Dalarna and Gävleborg) except close to the Finnish border. The rest of the country has a varying level of infestation.

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 *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, the Philippines and was recently reported in 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 honey combs, 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 reported by the NRL to the SBA yearly (Table 29).

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 a parish which is declared infected by the SBA. All inspections are reported by the bee inspectors to the CABs (Figure 27).

Active surveillance

No active surveillance was conducted during 2018

DISCUSSION

The reporting of AFB incidences has, thus far, been based on the information that the bee inspectors report to the CABs based on visual observation of clinical signs (Figure 27). 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. 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 in the ongoing discussion between beekeepers and the regulatory authorities about 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.

The bacteria *Melissococcus plutonius* that 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 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 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. 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 been 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 organize and collect samples of bees. There has been resistance to a central bee register from some beekeepers, but an initiative has now been taken by the CABs and the SBA to establish a register. The legislation is however so far not in place but will hopefully be so when the new animal health

regulation enters into force 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>)

Table 29: Number of samples from the Swedish honeybee population analysed at the NRL for bee health during 2018. Testing conducted based mainly on clinical suspicions.

Disease/parasite	No. of tested beekeeping operations	No. of infected/infested operations	No. of tested bee hives	No. of infected/infested bee hives
AFB	92	42	123	57
EFB	6	0	8	0
<i>A. woodi</i>	2	0	12	0
<i>Varroa</i> mites	18	16	36	27
<i>Tropilaelaps</i>	0	0	0	0
<i>A. tumida</i>	0	0	0	0

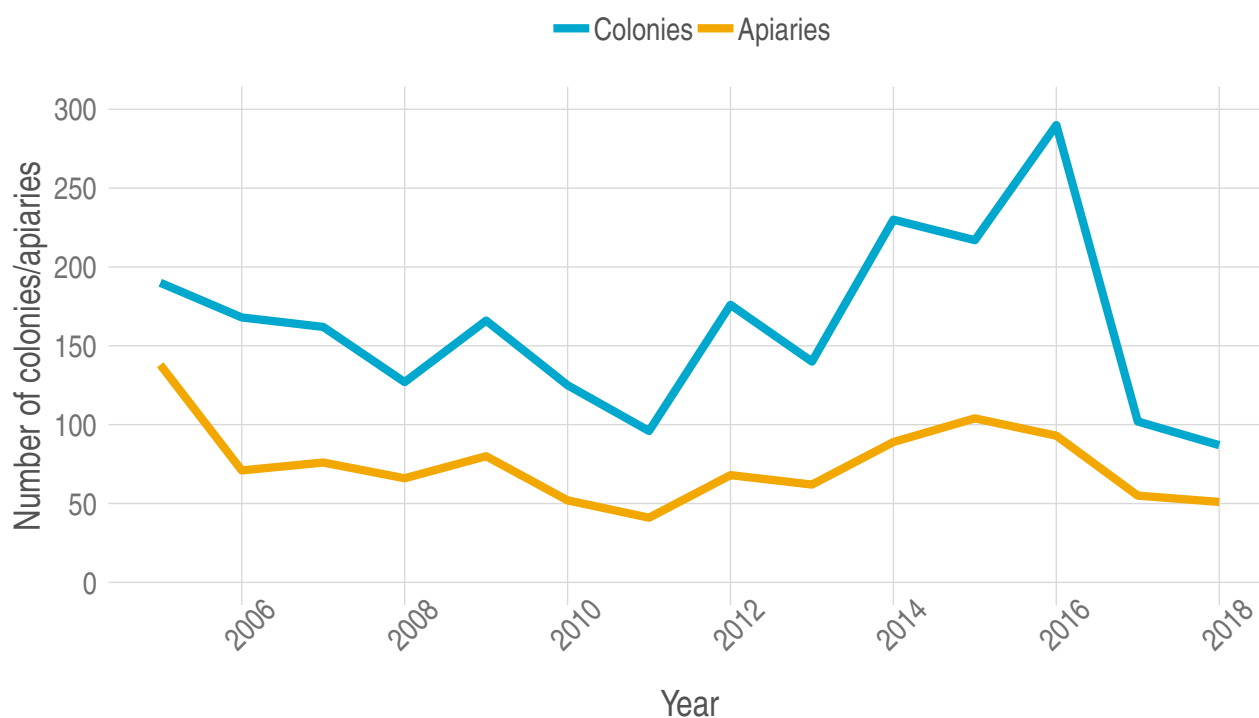


Figure 27: Number of new cases of American foulbrood during 2005–2018 in bee colonies and apiaries based on reports from bee inspectors to the County Administrative Boards

Infectious diseases in fish, crustaceans and molluscs



Pathological findings as a result of Koi herpes virus (KHV) include gill necrosis and secondary bacterial or parasitic infections of the gills and skin. The prevalence of this disease in Sweden is not known but two Swedish outbreaks in 2018 resulted in a mortality of 90–100%. Photo by: Charlotte Axén

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 1980's 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), Marteiliiosis 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 that 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.

IPN has severe consequences, with high mortality in young fish, and is considered as 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. Mortality rates vary and can reach 90%. 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 7–15°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 a number of 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 haemorrhage 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 1800's 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 is infected the first sign is high mortality in affected populations. Disease in the individual is characterised by behavioural changes such as moving 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 also 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 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 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 (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 2 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 30. In summary, the active surveillance did not detect any of the listed diseases in fish, but crayfish plague was detected in five new locations (one case=one outbreak):

Voluntary health control programme for fish farms

There were two recorded outbreaks of “other” notifiable diseases in fish during 2018. Furunculosis (ASS) was again identified in an inland farm with concurrent BKD infection and proliferative kidney disease (PKD) was identified in another inland farm.

Two koi farmers had outbreaks of KHV in August, when water temperatures were extremely high. Another koi farmer suspected presence of CEV (Carp edema virus) in his imported koi, and presence of the virus was confirmed by necropsy and PCR. This was the first time CEV was recorded in Sweden.

Flavobacteriosis due to *Flavobacterium psychrophilum* continues to be the dominant cause of production disease in fry and young fish. Resistance against oxolinic acid and oxytetracycline is becoming more and more common in the bacterium. The cause for this is not known. Usually florfenicol (for which there is yet no resistance) is used for treatment of the bacterium, and the other two antibiotics are rarely used in aquaculture. *Aeromonas salmonicida atypical* (formerly *achromogenes*) and *Flavobacterium columnare* were detected in disease cases during the summer, but the problems due to these bacteria were less severe than expected considering the high water temperatures.

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. In 2018, a total of 115 adult salmon and trout caught in the lake, and 155 broodstock fish from Forshaga avelsstation were investigated by virus cell culture. No virus was detected. Together with 339 fish (broodstock and fish caught in the lake) and five organ pools with unknown number of fish (n=1–10) investigated in 2017, the sum is now up to 609 fish without any new infections detected. Since only 279 of the 609 fish were caught in the lake, one more sampling will be performed in 2019.

Outbreaks in wild fish, crustaceans and molluscs

One outbreak of disease and mortality occurred in signal crayfish during the hot summer. Analyses for crayfish plague and whitespot syndrome were negative. The suspected cause of the problem is oxygen deprivation, since bottom oxygen levels were measured to be extremely low at the location.

DISCUSSION

The number of farms that were sampled are listed in Table 30. Swedish aquaculture has a good health status, where all severe diseases of 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: the last three 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. The number of identified new crayfish plague outbreaks are at the same level as in 2018, but the disease is spreading upstream in already infected water systems. The spread is probably facilitated by human activities.

Table 30: 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	71	0	-	542	-/0
IHN	71	0	-	542	-/0
IPN	71	0	-	542	-/0
SVC	1	0	-	15	-/0
KHV	4 ^A	2 ^B	8	-	4/0
BKD	61	0	3056	-	0/-
Crustaceans					
<i>Aphanomyces astaci</i>	19 ^C	5 ^C	47	-	26/-
WSSv	2 ^D	0	3	7	0/0
Molluscs					
<i>Bonamia ostreae</i> ^E	5	0	150	0	0/-
<i>Marteilia refringens</i> and <i>Marteilia pararefringens</i> ^E	5	0	150	0	0/-

^A 2 import companies, 2 private holdings with ornamental fish. No aquaculture farms were tested.

^B 2 private holdings with ornamental fish.

^C Wild crayfish. A total of 19 locations were sampled, representing 9 separate waterways. 5 waterways were positive.

^D 1 shrimp farm, 1 lake with disease in signal crayfish.

^E This sampling was performed as part of a project within the European Sea and Fisheries Fund.

Abbreviations:

VHS	Viral hemorrhagic 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

Postmortem examinations are considered important for early detection and national surveillance for infectious and emerging disease. As mentioned in the chapter “Postmortem 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 necropsy 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 on post-mortem. 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 necropsy through the postmortem examination programme. These infections often cause abortion so, by sampling aborted foetuses, the sampling occurs within a risk group. This increases the chance of detecting the infectious agents, if present. The Swedish Board of Agriculture finances the sampling and testing of foetuses for *Brucella*, PRRS and CSF. The National Veterinary Institute (SVA) is responsible for the organisation of the aborted foetus examination programme. Samples from aborted foetuses are either submitted to SVA by veterinarians performing postmortems at regional laboratories or are taken from fetuses submitted directly to SVA for postmortem examination. All diagnostic testing is performed at SVA. Testing for

the presence of CSFV and PRRS genome is done by PCR and for *Brucella* by bacterial culture.

RESULTS

In 2018, a total of 78 foetuses from 56 herds were examined (Table 31). This represents an increase from 2017, when the lowest number of foetuses was submitted for necropsy 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 postmortem 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 is now considered endemic.

Since 2008, the number of foetuses of different species submitted for examination has varied from year to year. For example, the numbers of ruminant foetuses submitted in 2013 were extraordinarily high, most likely because of concerns about SBV. For the last five years, the number of submissions has been less than anticipated, with the number of submitted pig foetuses being particularly low (Table 31). Actions have been taken to increase these numbers, such as reminding herd veterinarians about the opportunity to submit aborted foetuses for examination. These actions will continue and will be complemented by awareness-raising activities directed towards farmers.

Table 31: Number of foetuses (herds^A) investigated by species from 2010–2018 through the aborted foetus examination programme.

Species	2010	2011	2012	2013	2014	2015	2016	2017	2018
Cattle	62	21	63	114	32 (27)	29 (23)	34 (23)	20 (18)	34 (28)
Goat	9	3	5	4	2 (2)	0	2 (2)	2 (1)	5 (3)
Sheep	70	45	79	89	28 (14)	31 (21)	16 (13)	22 (15)	23 (16)
Alpaca	5	0	0	0	0	2 (1)	1 (1)	0	0
Bison	0	0	1	0	0	0	1 (1)	0	0
Visent	0	2	1	0	0	0	0	0	0
Gnu	0	0	0	1	0	0	0	0	0
Pig	61	51	54	46	31 (12)	17 (10)	43 (22)	6 (4)	16 (9)
Water buffalo	0	0	0	0	0	0	0	1 (1)	0
Total	207	122	203	259	93 (55)	79 (55)	97 (62)	51 (39)	78 (56)

^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 effects. 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 experience 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 in the early detection and national disease surveillance, a specific programme for such examinations started in the early nineties. The Swedish Board of Agriculture finances the programme, complemented by fees from the 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, around 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 salmonellosis, paratuberculosis, TSE and antimicrobial resistance.

The programme also include training of veterinarians, both large animal practitioners and veterinary employees at the post-mortem 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 owner. This can be a problem for large animals, particularly when the distance between the farm and post-mortem facility is large.

RESULTS

During 2018, post-mortem examinations were performed at five different sites, all located in the southern half of Sweden: Skara (Animalycen AB), Kristianstad (Farm & Animal Health), Uppsala (the National Veterinary Institute 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 four of these sites, Uppsala, Kristianstad, Karlskoga and Visby.

A total of 2360 post-mortem examinations were performed within the programme during 2018, which is less compared to recent years, mainly explained by varying numbers in poultry and declining numbers of examinations in sheep.

The distribution of species examined over the last 10 years are shown in Table 32. The variation in the number of

animals submitted for post-mortem examination within the largest livestock producing sectors (pigs, cattle, sheep and poultry) is illustrated in Figure 32.

In 2018, 83 cases were diagnosed with a notifiable disease at post-mortem examination. Table 33 shows the number of reported index cases of notifiable diseases.

To facilitate timely necropsies of large animals in remote areas of Sweden, a project financed by the Board of Agriculture and carried out by SLU during 2017–2018 trained sixteen Swedish veterinarians in a field necropsy method, developed by the Feedlot Health Management Services in Canada. The method “Remote Digital Autopsy” (RDA) utilises 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.

In 2019 an additional project “post-mortem examinations performed at farms” will be carried out in the area around Skara, where one of the laboratories are located. This project will hopefully increase the number of post-mortems of large cattle in the area, as the actual laboratory cannot handle animals larger than 250 kgs of weight. From 2019, Farm & Animal Health will take over all the activity of the post-mortems in Skara from the company Animalycen which was in charge during 2018.

DISCUSSION

Post-mortem examinations are a vital part of the national surveillance for infectious and emerging diseases, as illustrated by the detection of 83 index cases of notifiable disease in 2018. Post-mortem examination is also an important tool for the veterinarians to solve animal health problems at the individual farm. During the last decade, the number of post-mortem examinations has been around 3000 per year with a shift in species examined. Pigs were on a steady decline but seems to have settled at around 500 animals per year. The number of cattle and sheep examined has been stable around 800 and 500 animals, respectively, but for the last two years the number of sheep undergoing a post-mortem examination has declined. Poultry shows a varied number of post-mortem examinations over the last few years. Partially, this is explained by differences in the occurrence of outbreaks or other animal disease situations leading to periods of increased necropsies.

A regional imbalance can be seen in that more examinations are done in the 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 RDA method has not yet increased the large animal post-mortem examinations. Hopefully the upcoming project on “at-farm post-mortem examinations” in the south west of Sweden will result in more examinations.

This project covers an area with, by Swedish standards, high animal density but without a post-mortem facility for large animals close by.

Distance, and transportation method to facilities where thorough post-mortem examinations can be performed, is important for quality reasons. A long delay before cold storage and examination will result in more cadaverous changes and will influence the quality of the post-mortem examination negatively. A project financed by the Swedish Civil Contingency Agencies on improving transportation and logistics for transportation of dead animals submitted for post-mortem, to improve quality of the examinations, was initiated and carried out in 2014–2015. The project resulted in better logistics and better post-mortem examinations due to less carcasses affected by cadaverous changes. The designated transports have, in part, been funded by an extra fee for

the farmers using the service and by the programme. Even though this was a successful and appreciated service it was partly discontinued during 2018 due to lack of funding, limiting the service to approximately twice a week instead of daily.

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 32: Number of submissions to post-mortem examination of food producing species, 2008–2018.

Year	Pigs	Cattle	Sheep	Goat	Farmed deer	Poultry	Exotic ungulates	Reindeer	Other	Total
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

Table 33: Number of index cases of a notifiable disease 2013–2018, diagnosed from samples taken at post-mortem examination.

Disease	2013	2014	2015	2016	2017	2018
Anthrax	0	0	0	1	0	0
Avian rhinotracheitis	1	0	0	0	0	0
Blackleg	7	4	19	26	25	24
Bovine Malignant Catarrhal fever	3	1	1	6	6	2
Chorioptes (sheep/goat)	-	-	-	-	1	0
Duck Viral Enteritis ^A	-	1	0	0	0	0
Fowl Cholera (pasteurellosis)	0	0	0	3	4	2
Fowl typhoid (<i>S. Gallinarum</i>)	0	0	0	0	3	0
Gumboro (Very virulent IBDV)	-	-	-	-	5	4
Infectious Bronchitis	0	0	0	0	0	0
Infectious laryngotracheitis	36	35	26	26	17	20
Influenza, pigs	1	1	0	0	1	0
Influenza A typ (H1N1) 2009	3	0	0	0	1	0
Listeriosis	49	31	22	20	22	22
Lymphoma (not EBL)	0	0	0	2	0	0
<i>Mycoplasma gallisepticum</i>	0	4	4	0	1	7
<i>Mycoplasma</i> , poultry (not <i>gallisepticum</i>)	0	0	0	2	0	0
Necrotic haemorrhagic enteritis (<i>Clostridium perfringens</i> type C)	0	0	0	0	0	0
Salmonellosis	2	3	3	1	2	2
Total	102	80	75	87	88	83

Statistics from Farm & Animal Health.

^AThis disease was not diagnosed in Sweden prior to 2014.

Post mortem examinations in wildlife



The general disease surveillance in wildlife is based on citizen engagement, with the interested public and hunters, reporting and submitting samples. A high public interest in wildlife health and conservation, together with state financing continues to make this work possible. Photo: Erik Agren

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 euthanised, 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 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 necropsy as skinned carcasses or tissue samples. Whenever possible, disease causing agents are identified and cause of death established.

RESULTS

In 2018, whole carcasses or parts of 1751 free-ranging wild animals were submitted and examined at the Department of Pathology and Wildlife Diseases, not including examined farmed or captive wildlife species.

Some specific studies in wildlife in 2018 involved extensive dermatitis in moose and infectious diseases of muskrat (*Ondatra zibethicus*), an invasive alien species. A doctoral thesis on Lagovirus in rabbits, causing rabbit viral haemorrhagic disease type 2 was finalised in 2018 at SVA, as part of a large European study on this disease. The first finding of this disease in mountain hares (*Lepus timidus*) was part of the dissertation.

Active surveillance of avian influenza identified some cases of highly pathogenic H5N8 in white tailed sea eagles. Outbreaks of pigeon avian virus (previously PMV-1) were also noted in 2018.

Chronic Wasting Disease (CWD) screening of fallen or euthanised sick cervids continued in Sweden as the EU regulated screening running between 2018 and 2020 was initiated. All cases tested in 2018 were negative, but to be noted, the first two CWD positive moose (*Alces alces*) cases were

found in northern Sweden in March and May 2019. For more details, see the CWD chapter.

Screening of fallen wild boar for African swine fever (ASF) increased during 2018 as information efforts have increased awareness among the public, and especially in hunters. No cases of ASF have been found in 2018.

DISCUSSION

The general disease surveillance in wildlife is based on citizen engagement, 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 34) show that Sweden has few serious infectious disease threats in wildlife.

REFERENCES

SVA annual report (årsredovisning) 2018. SVALA-data on wildlife diagnoses 2018. SVA report: Wildlife disease monitoring in Sweden 2018 (to be published during 2019)

Table 34: OIE non-listed wildlife diseases and number of outbreaks/cases reported to the OIE for 2018.

Disease	Number of cases	Species affected
Avian influenza	17	Goshawk (1), White-tailed eagle (14), Buzzard (2)
Avian pox	5	Great tit (1), Jackdaw (1), Magpie (1), Raven (1), Redwing (1)
Echinococcosis	5	Red fox
Myxomatosis	4	Wild rabbit
Rabbit Hemorrhagic Disease (RHD)	15	Wild rabbit
Salmonellosis	20	Bullfinch (7), Common redpoll (7), Siskin (3), House sparrow (1), Greenfinch (1), Hedgehog (1)
Sarcoptic mange	18	Lynx (8), Wolf (5), Red fox (3), Raccoon dog (2)
Trichinellosis	19	Lynx (6), Raccoon dog (1), Wild boar (9), Wolf (3)
Tularemia	3	European brown hare
Total	106	

Antimicrobial 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 from 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, 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 indicates 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 in indicator bacteria shall be regularly monitored in broilers, turkey, pigs and cattle using harmonised methodology. 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, each year 170 isolates of *E. coli* from intestinal content of healthy broilers or pigs are tested. 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 and cattle. It is not mandatory to screen for ESBL/AmpC- and 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 <https://www.folkhalsomyndigheten.se> or at <https://www.sva.se/swedres-svarm/>. The different data sources compiled in this report are illustrated schematically in Figure 28.

LEGISLATION

In Sweden, findings of carbapenemase producing Enterobacteriaceae (ESBL_{CARBA}) and methicillin-resistant coagulase-positive staphylococci in animals are notifiable (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 consumption of antibiotics in Sweden has decreased in both humans and in 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 in veterinary medicine

In 2018, reported sales of antibiotics for animals were 10 042 kg, of which 58% were narrow-spectrum penicillins. The corresponding figures for 2009 were 15 368 kg and 50%, 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 29).

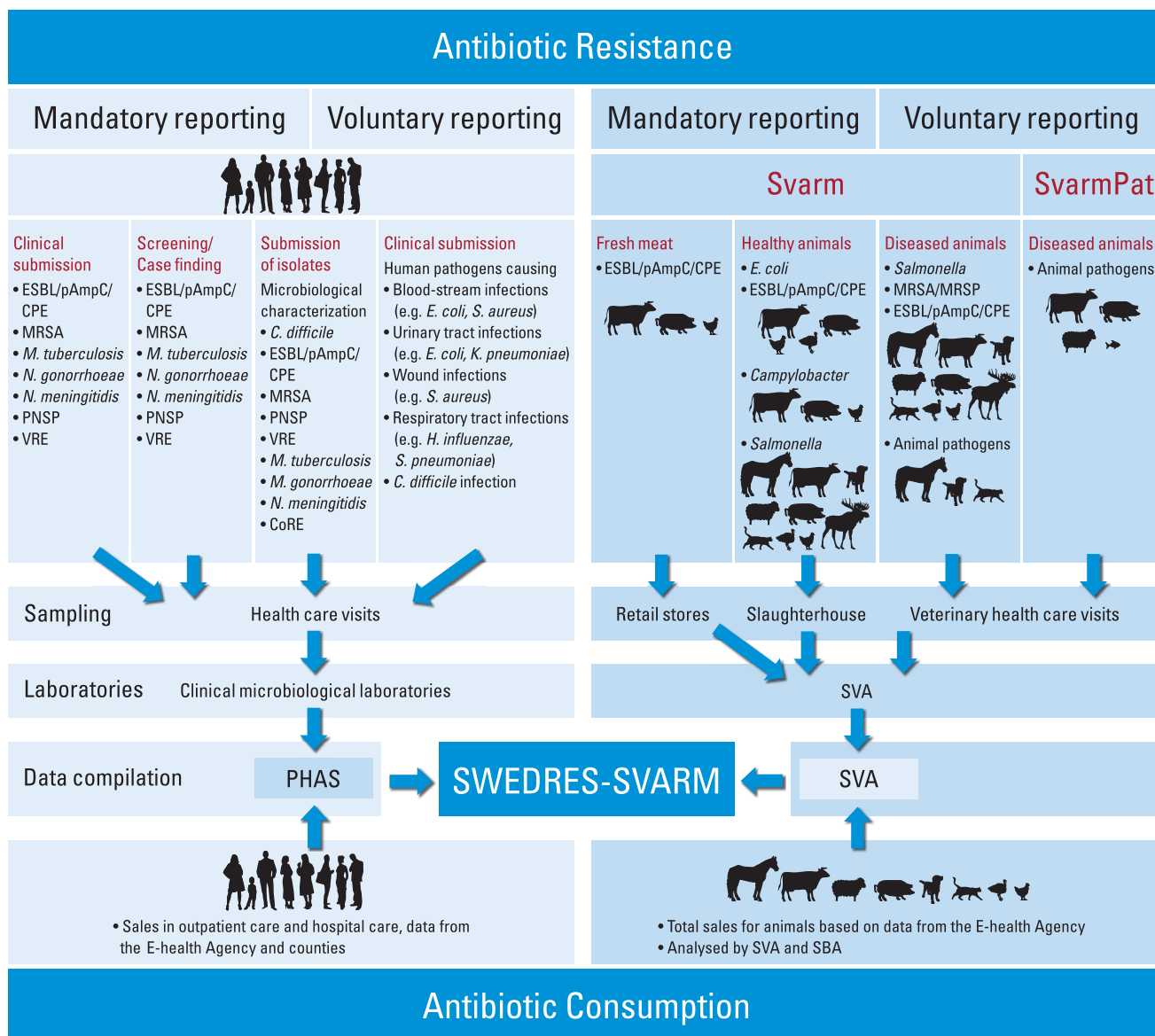


Figure 28: A schematic illustration of data included in the Swedres-Svarm report.

Extended spectrum beta-lactamase (ESBL) producing Enterobacteriaceae

ESBL-producing Enterobacteriaceae are, with the exception of broilers, rare among animals in Sweden. In 2018, the occurrence of ESBL-producing *E. coli* in caecal and meat samples from broilers, caecal samples from turkeys, and intestinal samples from cattle under one year of age were investigated with screening methods. Such bacteria were isolated from 13% of the intestinal samples and 12% of the meat samples from broilers of Swedish origin. This is a significant decrease from previous years and is most likely explained by decreased occurrence of ESBL-producing *E. coli* in the breeding pyramid. ESBL-producing *E. coli* were isolated from 3% of samples from cattle under one year but not from samples from turkey. Bacteria that form ESBL_{CARBA} have not been detected in animals in Sweden.

Methicillin resistant *Staphylococcus aureus* (MRSA)

The occurrence of MRSA in animals in Sweden is still low, which limits the spread from animals to humans. MRSA was found sporadically in cats, dogs and horses in 2018, 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.

Methicillin resistant *Staphylococcus pseudintermedius* (MRSP)

In 2018, there were 57 cases of methicillin-resistant *Staphylococcus pseudintermedius* (MRSP) notified to the Swedish Board of Agriculture. All cases except one were related to dogs. This number is about the same level as in recent years. 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. Strains with ESBL resistance have never been found in isolates from animals in Sweden, and resistance to fluoroquinolones is rare. Isolates

from human invasive infections 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. Susceptibility testing for guidance in antibiotic therapy is warranted, especially for staphylococci, *E. coli* and, *Brachyspira* spp.

Resistance in indicator bacteria from healthy animals

Antibiotic resistance in *E. coli* from the intestinal flora of healthy animals serves as an indicator for the presence of resistance in an animal population. The prevalence of acquired resistance in such commensal bacteria also indirectly indicates the magnitude of the selective pressure from the use of antibiotics in an animal population. The prevalence of resistance in indicator bacteria from animals in Sweden is generally low, and the situation is favourable in an international perspective.

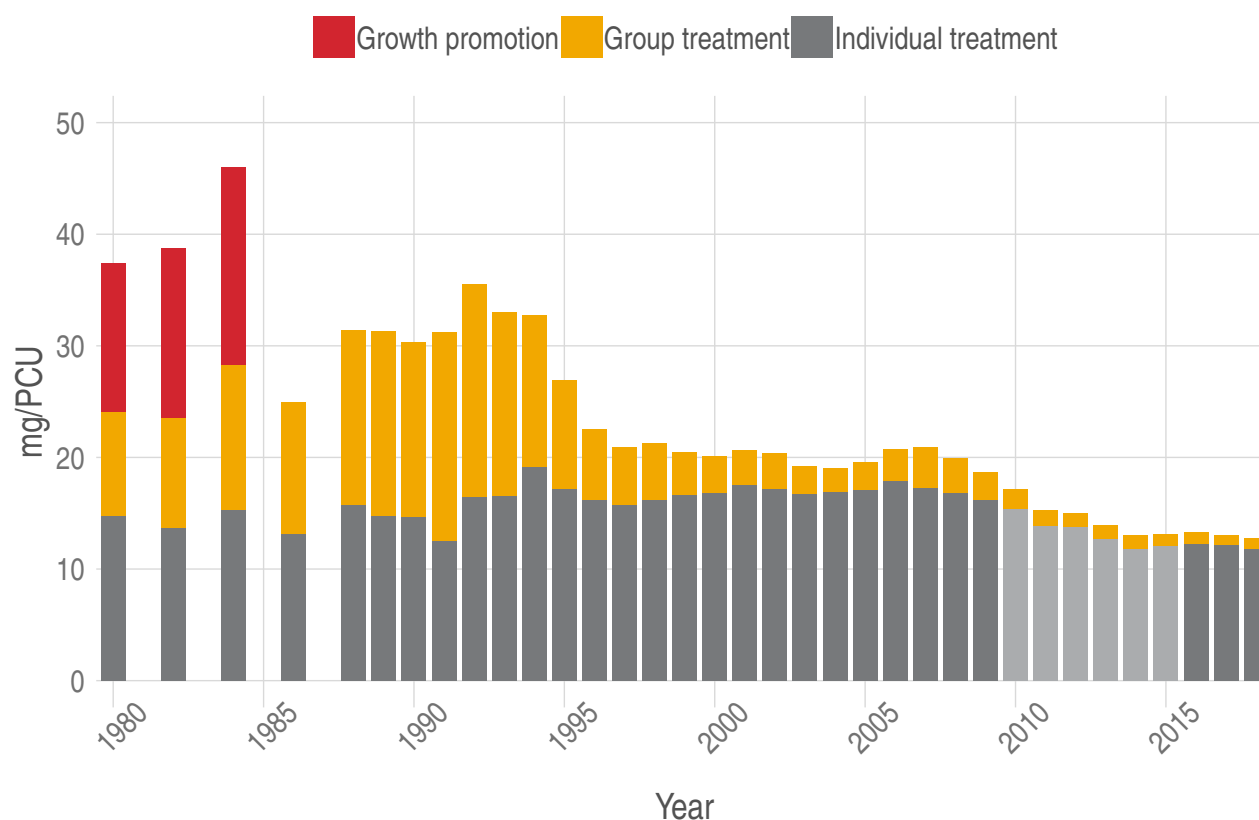


Figure 29: Sales of antibiotics for animals expressed as mg per population correction unit (PCU). Data from 2010–2015 are uncertain because of a lack of completeness mainly affecting injectable products (Indicated in a lighter grey). All products (including tablets) are included, while in the data presented in the European surveillance of veterinary antimicrobial consumption, tablets are excluded when calculating mg/PCU.

