

SURVEILLANCE OF INFECTIOUS DISEASES

IN ANIMALS AND HUMANS IN SWEDEN 2022

*Chapter excerpt:
Cryptosporidiosis*



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

Layout: The production of this report continues to be accomplished using a primarily open-source toolset. The method allows the source text to be edited independently of the template for the layout which can be modified and reused for future reports. Specifically, the chapter texts, tables and captions are authored in Microsoft Word and then converted to the LaTeX typesetting language using a custom package written in the R software for statistical computing. The package uses the pandoc document conversion software with a filter written in the lua language. Most figures and maps are produced using R and the LaTeX library pgfplots. Development for 2022 has focused on generalising the R package to accommodate conversion into formats other than LaTeX and PDF, with a focus on markdown files which can be published as HTML websites using the Quarto publishing system. The report generation R package and process was designed by Thomas Rosendal, Wiktor Gustafsson and Stefan Widgren.

Print: TMG Tabergs AB

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Suggestion citation: Surveillance of infectious diseases in animals and humans in Sweden 2022, National Veterinary Institute (SVA), Uppsala, Sweden. SVA:s rapportserie 89 1654-7098

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Cryptosporidiosis

BACKGROUND

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

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

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

DISEASE

Animals

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

Humans

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

SURVEILLANCE

Animals

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

Humans

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

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

LEGISLATION

Animals

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

Humans

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

RESULTS

Humans

In 2022, a total of 716 cryptosporidiosis cases were reported corresponding to an incidence of 6.8 cases per 100 000 inhabitants (Figure 17). Among reported cases, the median age was 38 years (0–90 years) and 55 percent were women (n=392/716). In 2022, the majority of reported cases were infected in Sweden (n=550), 146 cases were infected abroad and for 20 cases information was missing.

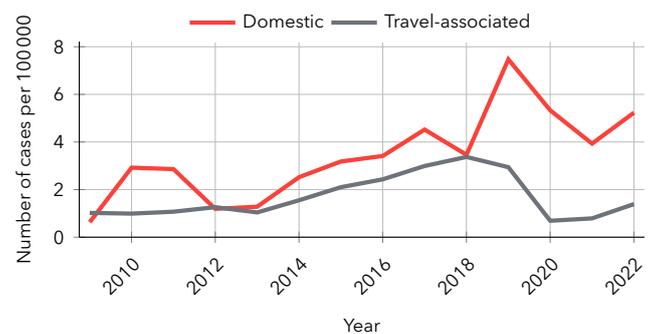


Figure 17: Number of notified human cases of cryptosporidiosis per 100 000 inhabitants from 2009 to 2022

A peak in reported cases is usually seen in late summer and autumn. In 2022 most domestic cases were reported in August (n=64), and in October (n=206) due to a national outbreak (see “In focus”). Out of the 146 cases infected abroad, 75 percent (n=106) were reported July–October. The most common destination was Somalia (n=14) followed by Turkey (n=9) and Portugal (n=8).

As part of the microbiological surveillance programme, 364 *Cryptosporidium* positive samples were further analysed for species and subtype. The majority of samples were *C. parvum* (n=297). The second most common cause of cryptosporidiosis was *C. hominis* (n=20) followed by *Cryptosporidium* chipmunk genotype I (n=9). The most common *C. parvum* subtypes were IIAA15G2R1 (n=138), IIAA16G1R1b (n=19), IIDA22G1c (n=19) and IIDA20G1e (n=14). Two samples of *Cryptosporidium erinacei* and one sample of *Cryptosporidium* horse genotype were also detected. For 35 samples, the molecular typing was unsuccessful.

During the spring and early summer there were several cases with suspected zoonotic transmission. One cluster was reported late January from a school in the region of Uppsala. Several students reported illness and four had confirmed cryptosporidiosis and were diagnosed with *C. parvum* subtype IIAA14R1. The school has an agricultural profile and has several animals on the school farm, including cattle, sheep and horses. All cases had had contact with cattle and the calves were the suspected source. The sampled calves were positive for *C. parvum* subtype IIAA14R1.

In May, three cases of cryptosporidiosis were detected in personal at an assisted living in the region of Södermanland. They had all been in contact with a lamb due to bottle feeding. Samples from two human cases were analysed

and found positive for *C. parvum* subtype IIAA14G1R1r1. Lambs were sampled but the samples were negative for *Cryptosporidium* spp. However, the lamb that was the suspected source of infection was not sampled.

In June, four cases of cryptosporidiosis were detected in students and a teacher after a farm visit with calves in the region of Jönköping. Two cases were sent for typing and *C. parvum* subtype IIAA15G2R1 was detected. No calves were sampled.

In December four cases, all students at a school with agricultural profile were reported ill with cryptosporidiosis in the region of Västra Götaland. Samples sent for typing were all positive for *C. parvum* subtype IIDA19G1. The students had been in contact with several different animals including calves the week before disease onset. No animals were sampled.

DISCUSSION

The incidence of human cases of cryptosporidiosis increased compared to 2021 partly as a result of a national outbreak during autumn and also an increase of imported cases as a result of increased travelling.

The increase of reported cases of cryptosporidiosis over time is primarily a result of altered laboratory methods and increased awareness of the disease in primary care. Vegetables as vehicles for *Cryptosporidium* spp. warrants further investigation. This route of transmission is complex as it may involve animals, irrigation water, contaminated water and natural fertilisers. Not seldom are these outbreaks widespread, as the distribution of vegetables can be nationwide, and they require national coordination and collaboration between various agencies and regional disease prevention offices.

IN FOCUS: Nationwide *C. parvum* outbreak linked to contaminated lettuce

In September 2022, there was an increase in the number of cases of cryptosporidiosis. Several regions reported cases and a national outbreak investigation was initiated. Between 25 September and 15 October, 107 cases with *C. parvum* subtype IIAA15G2R1 were detected in 15 different regions. The median age was 40 years and more females (67%) than males (36%) were infected. Most cases were detected in the region of Jönköping (n=22), Halland (n=18), Västra Götaland (n=13) and Östergötland (n=13). IIAA15G2R1 is a common *C. parvum* subtype and has been reported to cause outbreaks in other European countries, but not previously in Sweden. Epidemiological investigations pointed towards contaminated frisée lettuce in ready-to-eat green leaf-mixes as the probable cause of infection. The origin of the frisée lettuce was never confirmed.

Since the outbreak involved several regions and was quite prolonged over time, it was suspected that there might be several contaminated sources and hence more than one outbreak. A panel of samples were analysed with a higher resolution molecular typing method in order to investigate this. The analysis confirmed that all the samples shared the same profile which strengthened the hypothesis that all the cases belonged to one outbreak and this one source of contamination.