

SURVEILLANCE OF INFECTIOUS DISEASES IN ANIMALS AND HUMANS IN SWEDEN 2020

Chapter excerpt -
Cryptosporidiosis



Editor: Karl Ståhl

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

Authors: Charlotte Axén, Mia Brytting, Ioana Bujila, Erika Chenais, Rikard Dryselius, Helena Eriksson, Eva Forsgren, Malin Grant, Gittan Gröndahl, Gunilla Hallgren, Kristina Hammarén Busch, Anette Hansen, Marika Hjertqvist, Mia Holmberg, Cecilia Hultén, Helena Höök, Cecilia Jernberg, Jerker Jonsson, Oskar Karlsson Lindsjö, Ulrika König, Elina Lahti, Emelie Larsdotter, Moa Lavander, Mats Lindblad, Anna Lundén, Margareta Löfdahl, Oskar Nilsson, Maria Nöremark, Anna Ohlson, Ylva Persson, Karin Persson-Waller, Thomas Rosendal, Karl Ståhl, Lena Sundqvist, Robert Söderlund, Magnus Thelander, Karin Troell, Henrik Uhlhorn, Anders Wallensten, Per Wallgren, Stefan Widgren, Ulrika Windahl, Joakim Wistedt, Beth Young, Nabil Yousef, Siamak Zohari, Erik Ågren, Estelle Ågren, Elina Åsbjer

Cover: Juvenile mink in hand. Photo: Elina Kähkönen

Copyright of map data: ©EuroGeographics for the administrative boundaries

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

Layout: The production of this report continues to be accomplished using a primarily open-source toolset. The method allows the source text, produced by authors, to be edited independently of the template for the layout which can be modified and reused for future reports. Specifically, the chapter texts, tables and captions are authored in Microsoft Word and then converted using pandoc and R to the LaTeX typesetting language. Most figures and maps are produced using the R software for statistical computing and the LaTeX library pgfplots. Development for 2020 has further improved the importing of content from Excel files to automatically build figures in the pgfplots LaTeX library. The tool is available as an R-package on GitHub (<https://github.com/SVA-SE/mill/>). The report generation R-package and process was designed by Thomas Rosendal, Wiktor Gustafsson and Stefan Widgren. In 2020, final typesetting was done primarily by Wiktor Gustafsson with contributions from the report authors.

Print: TMG Tabergs AB.

Except where otherwise noted, the reuse of this document is authorised under the Creative Commons Attribution 4.0 International (CC BY 4.0) licence. This means that reuse is allowed provided appropriate credit is given and any changes are indicated. For any use or reproduction of photos or other material that is not owned by SVA, permission must be sought directly from the copyright holders.

Suggestion citation: Surveillance of infectious diseases in animals and humans in Sweden 2020, National Veterinary Institute (SVA), Uppsala, Sweden. SVA:s rapportserie 68 1654-7098.

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

Cryptosporidiosis

BACKGROUND

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

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

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

DISEASE

Animals

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

Humans

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

IN FOCUS: *Cryptosporidium* chipmunk genotype I

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

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

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

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

SURVEILLANCE

Animals

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

Humans

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

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

LEGISLATION

Animals

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

Humans

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

RESULTS

Humans

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

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

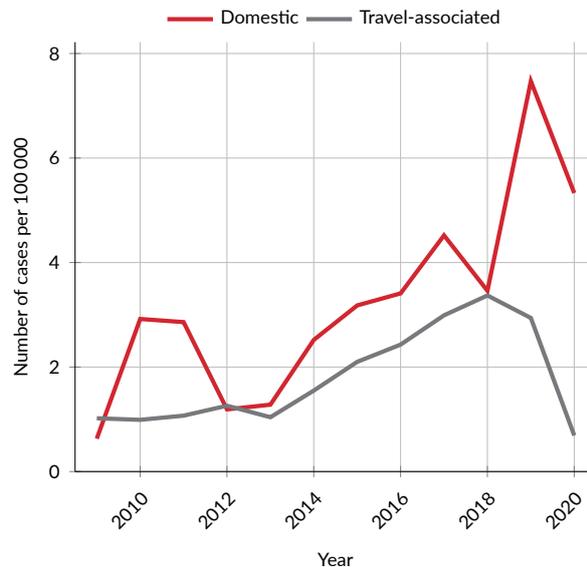


Figure 8: Number of notified human cases of cryptosporidiosis per 100 000 inhabitants from 2009 to 2020.

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

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

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

DISCUSSION

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

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

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