SURVEILLANCE OF INFECTIOUS DISEASES IN ANIMALS AND HUMANS IN SWEDEN 2019

Chapter excerpt -
Cryptosporidiosis

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

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

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

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

DISEASE

Animals

Cryptosporidiosis in animals is of veterinary importance and may result in clinical morbidity, mortality, and associated production losses. However, different *Cryptosporidium* species infect different host species of animals and may 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.

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

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

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

There was a national increase in the number of reported cases of cryptosporidiosis in the autumn of 2019. 58 percent (n=450/771) of annual domestic cases were reported from 1 October-31 December. Reported cases peaked during three weeks in November (Figure 9). An outbreak investigation was initiated and 300 isolates from cases were typed as part of that investigation. Five foodborne outbreaks were identified during this period, all attributed to infection with *C. parvum* (n=285). Dominating subtypes were IIaA22G1c (n=122) and IIdA24G1 (n= 65). Both these subtypes have been detected both earlier in 2019 and in the previous years. During the outbreak period, 122 cases in ten different regions were caused by subtype IIdA22G1c. The county of Stockholm had the most cases (n=58) followed by Västra Götaland (n=16) and Halland (n=16) counties. The median age of the cases was 39 years (2–83 years) with no significant gender difference (52% women, 48% men). Using surveys in collaboration with other authorities, unpasteurised juice with spinach was identified as the source of infection with subtype IIdA22G1c.

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

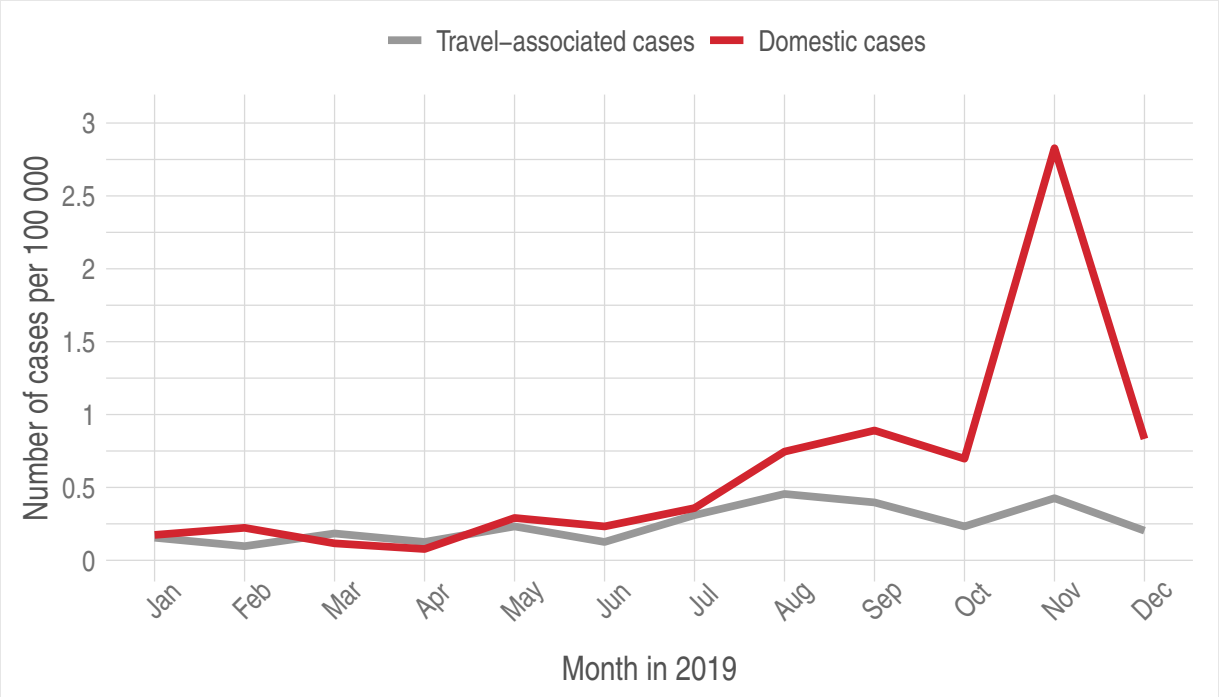

Figure 9: Number of notified human cases of cryptosporidiosis during 2019.

Humans

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

SURVEILLANCE

Animals

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

Humans

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

In 2018, the Public Health Agency of Sweden initiated a microbiological surveillance programme with the aim of determining species and subtypes of all domestic cryptosporidiosis cases in order to better understand the national epidemiology.

LEGISLATION

Animals

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

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

Up until the start of the investigation initiated by the increase of reported cases, 299 samples were analysed as part of the microbiological surveillance programme. The majority of samples, 80 percent were *C. parvum* (n=239) and 9.2 percent were *Cryptosporidium hominis* (n=22), where the most common *C. hominis* subtype was IbA10G2 (n=14). The most common *C. parvum* subtypes were IIaA16G1R1b (n=40), IIdA24G1 (n= 26) and IIdA22G1c (n=23). The latter two subtypes were also the two dominating subtypes in the autumn of 2019 (see In Focus Box). The following species were also detected in 2019: *Cryptosporidium* chipmunk genotype I (n=12), *Cryptosporidium cuniculus* (n=3), *Cryptosporidium erinacei* (n=2), *Cryptosporidium felis* (n=1) and *Cryptosporidium* horse genotype (n=1).

In May, one patient sought care for abdominal symptoms in Jönköping county. The patient had been attending a confirmation reception where 11–12 others also were reported to have abdominal symptoms. Four samples were analysed and they were all positive for *C. parvum* subtype IIdA22G1. Through surveys, green salad was identified as the probable cause of infection. A smaller outbreak of *Cryptosporidium* chipmunk genotype I was detected at a pre-school in Stockholm in the end of September. The suspected source of infection was a culture of peas in the yard of the pre-school where red squirrels had been spotted. Three samples from cases were typed and they were all *Cryptosporidium* chipmunk genotype I, but the source of infection could not be confirmed. Attempts were made to collect environmental samples and squirrel faeces on site but none of the samples could be confirmed to originate from squirrels.

DISCUSSION

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

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

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

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