

SURVEILLANCE OF INFECTIOUS DISEASES

IN ANIMALS AND HUMANS IN SWEDEN 2022

*Chapter excerpt:
Listeriosis*



Editor: Karl Ståhl

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

Authors: Emmi Andersson, Märit Andersson, Charlotte Axén, Anna Bonnevie, Ioana Bujila, Erika Chenais, Mariann Dahlquist, Leigh Davidsson, Rikard Dryselius, Helena Eriksson, Linda Ernholm, Charlotta Fasth, Malin Grant, Gittan Gröndahl, Gunilla Hallgren, Anette Hansen, Marika Hjertqvist, Mia Holmberg, Cecilia Hultén, Hampus Hällbom, Helena Höök, Karoline Jakobsson, Désirée Jansson, Tomas Jinnerot, Jonas Johansson Wensman, Jerker Jonsson, Oskar Karlsson Lindsjö, Sara Kjellsdotter, Ulrika König, Elina Lahti, Emelie Larsdotter, Neus Latorre-Margalef, Mats Lindblad, Anna Lundén, Anna Nilsson, Oskar Nilsson, Maria Nöremark, Anna Omazic, Anna Ordell, Ylva Persson, Emelie Pettersson, Ivana Rodriguez Ewerlöf, Thomas Rosendal, Marie Sjölund, Karl Ståhl, Lena Sundqvist, Robert Söderlund, Magnus Thelander, Karin Troell, Henrik Uhlhorn, Anders Wallensten, Stefan Widgren, Camilla Wikström, Ulrika Windahl, Beth Young, Nabil Yousef, Siamak Zohari, Erik Ågren, Estelle Ågren

Typesetting: Wiktor Gustafsson

Cover: A cultivation of *Salmonella* at the Public Health Agency of Sweden.
Photo: Nicklas Thegerström/DN/TT. Cover design by Rodrigo Ferrada Stoeהל.

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 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

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 2022, National Veterinary Institute (SVA), Uppsala, Sweden. SVA:s rapportserie 89 1654-7098

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

Listeriosis

BACKGROUND

The genus *Listeria* contains several species, but *Listeria monocytogenes* is the only zoonotic species and was first described in 1926. Previously, sporadic cases of listeriosis were reported, often in employees in contact with diseased animals but since the 1980s outbreaks and cases of listeriosis have been traced to food products.

Listeria bacteria are widely distributed in the environment, such as in soil, silage and water. They can survive for long periods in the environment and tolerate disinfection and also grow at refrigerator temperatures, in vacuum packed food and in modified atmospheres. These properties make elimination of *L. monocytogenes* difficult. *L. monocytogenes* and other *Listeria* species are often found as environmental contaminants in food producing establishments. However, it is only *L. monocytogenes* that is relevant regarding human health. The main sources of human listeriosis are contaminated food products, such as cold-smoked or gravad vacuum-packed fish products, meat products and soft and semi-soft cheeses or other ready-to-eat foods with a long shelf-life. *L. monocytogenes* is destroyed by heating (pasteurisation or cooking).

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

In Sweden, during the last ten years approximately 70–120 human cases have been reported annually. Outbreaks have been associated with vacuum-packed fish, with semi-soft cheese, cold cuts, frozen corn and with convenience meals.

DISEASE

Animals

L. monocytogenes can infect a wide range of animal species, both domestic and wild. The clinical picture of the infection in animals varies from an asymptomatic infection to severe. Especially in sheep and goats, listeriosis manifests as an encephalitis, abortion, mastitis or septicaemia.

Humans

Listeriosis can be manifested either as a milder non-invasive form or as a severe invasive disease. The non-invasive form is generally presented as a febrile gastroenteritis. The severe form most often occurs in immunocompromised persons, newborns, pregnant women and the elderly. Symptoms of invasive listeriosis are septicaemia, meningitis and meningoencephalitis. For those with severe infection, the case fatality rate is high (20–40%). The infection can lead to miscarriage, premature delivery or neonatal death.

LEGISLATION

Animals

Listeriosis is a notifiable disease in animals according to SJVFS 2021:10.

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 2022:1224).

SURVEILLANCE

Animals

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

Food

No official control programme exists for *L. monocytogenes*. National and local authorities may perform sampling as part of extended official controls or targeted projects. Producers of ready-to-eat foods are obliged to take samples for analysis of *L. monocytogenes* as part of their self-controls, but the results are not normally reported to the authorities.

Humans

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

RESULTS

Animals

In 2022, listeriosis was reported in 20 sheep, five cattle, one horse, one red deer and in one hare.

Food

In 2022, 266 samples from different types of food taken by national and local authorities were analysed for presence of *L. monocytogenes* in qualitative analysis (presence or no presence). *L. monocytogenes* was detected in 8 samples (Table 12). In addition, 18 samples were analysed in quantitative analysis (number of colony-forming units per gram (CFU/g)). The levels of *L. monocytogenes* in these samples were <10 CFU/g.

Humans

During 2022 the incidence of listeriosis (incidence 1.2 cases per 100 000 inhabitants) increased slightly compared to 2021 and the overall picture shows an increasing trend of listeriosis cases in Sweden (Figure 26). In total, 125 cases were reported compared to 107 cases in 2021 (incidence 1.0 cases per 100 000 inhabitants) (Figure 26). The majority of the cases reported with listeriosis belong to the older age groups. The median age was 79 years and as in previous years, most cases were reported in the age group over 80 years (Figure 27). Sixty-seven cases were females and 57 were males. In total, 45 cases (36 percent of reported cases) died within one month from diagnosis. Listeriosis is most often a domestic infection and for 92 percent of the reported cases in 2022 Sweden was noted as the country of infection. In 2022 all but nine (93 percent) of the human isolates were sent to the Public Health Agency of Sweden for typing. The most common molecular serotypes were as in previous years IIa (n=83), IVb (n=22) and IIb (n=9) while only two cases of IIc were reported. In addition to serotype, sequence type (ST) is also identified by WGS. During 2022 the most common STs were ST37 (n=17) and ST8 (n=15). A more in-depth cluster analysis showed that the proportion of isolates belonging to a cluster was 45 percent (n=52), which was higher than in 2021 (33 percent). In total, 23 different clusters were identified of which 21 contained identical or closely related isolates identified already before 2022. Five cases with a rare strain of *L. monocytogenes* in Sweden, ST1593, were included in a larger cluster with cases from 2019–2022. All cases were notified during the Autumn period and the source of infection could not be identified.

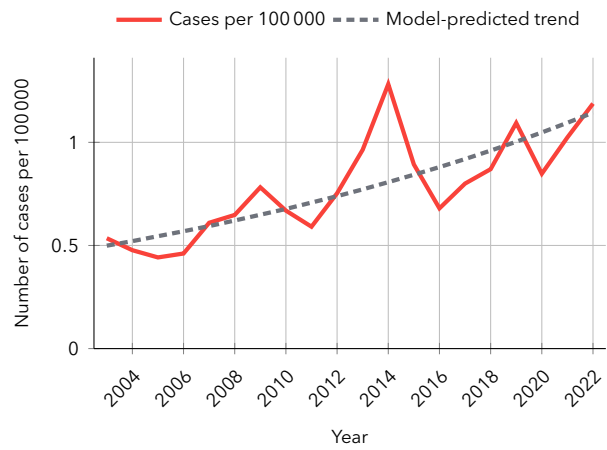


Figure 26: Notified incidence per 100 000 inhabitants of human cases of listeriosis in Sweden 2003–2022 and a model-predicted trend (negative binomial regression). The higher incidence in 2013–2014 is due to two larger outbreaks with in total 49 and 28 cases, respectively.

Investigations of outbreaks and single cases of listeriosis

Vacuum-packed salmon was sampled at retail level in a local investigation of a case of *L. monocytogenes* ST37. Isolates that clustered with isolates from the human case were found in two samples of gravad and gravad/cold smoked salmon, respectively. During further investigation, three additional human cases in Sweden 2022 with the same strain were identified and two of these stated that they had eaten salmon. WGS data from one food isolate was uploaded into the GenBank database at the National Center for Biotechnology Information (NCBI) in the USA. The isolate clustered with several previous isolates from salmon processing equipment and environment in Norway, indicating that salmon raw material that had become contaminated during processing in Norway was the source of the outbreak.

WGS analysis of an isolate of *L. monocytogenes* from a sample of an opened package of a pre-cooked minced meat product taken at home of a case with *L. monocytogenes* ST8 showed that the food isolate clustered with the human isolate. The human case belonged to a cluster of 16 cases with the same strain from 2020 – 2022, of which seven were from the second half of 2022. Early in 2023, a clustering isolate was found in an environmental sample taken by the competent authority at the meat processing plant (a large company with national distribution of various pre-cooked minced meat products), indicating that products from this plant was the source of the outbreak.

Table 12: Results of analyses in 2022 for presence of *L. monocytogenes* in food samples taken by authorities.

Reason for sampling	No. of samples	No. of positive samples	Food in which <i>L. monocytogenes</i> was detected
Survey	8	0	
Routine control	225	2	1 meat preparation, 1 ready meal
Suspected food poisoning or complaint	33	6	1 cheese, 2 vacuum-packed salmon, 3 meat preparation
Total	266	8	

Similarly, WGS analysis of an isolate of *L. monocytogenes* from a sample of an opened package of a washed rind cheese taken at home of a case with *L. monocytogenes* ST155 showed that the food isolate clustered with the human isolate. Also, four additional human cases in Sweden from 2018 through 2022 with the same strain were identified. However, after the Public Health Authority of Sweden reported the outbreak in EpiPulse, it became clear that the likely source of the outbreak was salmon and not cheese. The five cases in Sweden could be linked to 11 cases in five other countries 2017 – 2022. At the beginning of 2023, the European Food Safety Authority (EFSA) invited EU Member States to submit genomic data regarding food isolates of *L. monocytogenes* ST155 to the EFSA One Health WGS system. The results show that many isolates from salmon and salmon products clustered with the human cases, indicating that this type of products is the source of the international outbreak.

DISCUSSION

During 2022 the incidence of listeriosis increased compared to the year before and the overall picture shows an increasing trend of listeriosis. (Figure 26). The same trend has been observed in other European countries. The reasons for the increase remain unclear but are most likely related to the increased population size of the elderly and an increased proportion of susceptible persons within different age groups,

possibly in combination with other factors such as preference changes to more ready-to-eat foods. The ECDC collaborates with the member states to strengthen the molecular surveillance and thereby facilitate detection of cross-border clusters and outbreaks of *L. monocytogenes*. This collaboration includes the EFSA and is essential for investigation of foodborne cross-border outbreaks in Europe.

Surveillance of *L. monocytogenes* in humans and in food and food processing environments is essential for understanding the sources for human infection and providing tools for prevention. For detection of outbreak clusters of *L. monocytogenes* and for identifying possible links between human cases and food products, subtyping of isolates using WGS is essential. Also, uploading genomic data from food, animals, environment and humans into international databases such as GenBank (hosted by NCBI in the USA) and The European Surveillance System (TESSy, hosted by ECDC) increases the possibility to detect sources of infection in both national and international outbreaks. In addition to the previously existing databases, the EFSA One Health WGS system opened to final users in 2022 and has become fully operational in January 2023.

REFERENCES

EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2018. Scientific Opinion on the *Listeria monocytogenes* contamination of ready-to-eat foods and the risk for human health in the EU. EFSA Journal 2018;16(1):5134, 173 pp.

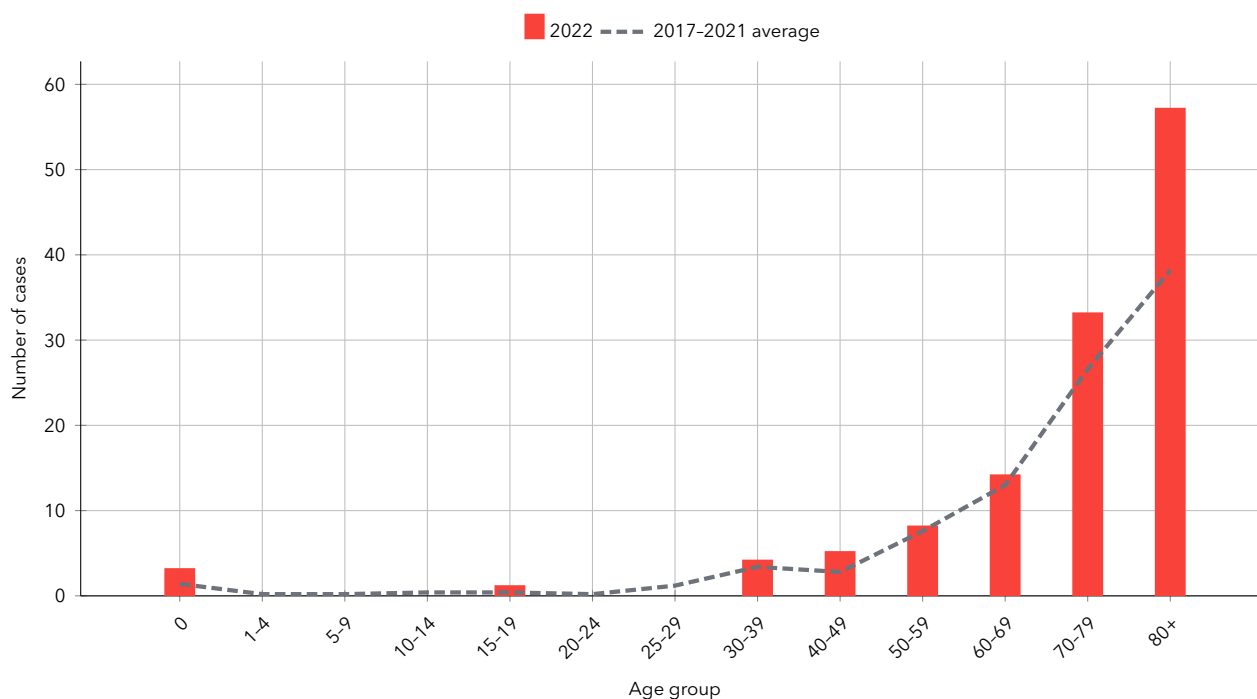


Figure 27: Number of notified human cases of listeriosis per age group in 2022 and annual average for 2017-2021.