Listeriosis

Annual Epidemiological Report for 2022

Key facts

- In 2022, 30 countries reported 2 770 confirmed listeriosis cases in the EU/EEA.
- The age-standardised EU/EEA notification rate was 0.52 cases per 100 000 population.
- The highest rate was detected among people over 64 years old (2.1 cases per 100 000 population).
- The number of confirmed listeriosis cases reported per year is increasing in the EU/EEA.

Introduction

Listeriosis is a disease caused by *Listeria monocytogenes*. The disease primarily causes problems in pregnant women, newborns, and adults with a weakened immune system. After exposure, most healthy adults do not develop any symptoms, except in the case of pregnant women. After an incubation period of about three weeks pregnant women may suffer from a self-limiting influenza-like illness which may affect the uterus. In addition, listeriosis in adults with weakened immune system and the elderly may lead to meningitis, brain infection, and severe blood infection.

Methods

This report is based on data for 2022 retrieved from The European Surveillance System (TESSy) on 11 October 2023. TESSy is a system for the collection, analysis and dissemination of data on communicable diseases.

For a detailed description of methods used to produce this report, please refer to the 'Methods' chapter [1]. An overview of the national surveillance systems is available online [2].

A subset of the data used for this report is available through ECDC's online Surveillance atlas of infectious diseases [3].

The notification of listeriosis in humans is mandatory in all European Union/European Economic Area (EU/EEA) countries except Belgium. The surveillance systems for listeriosis have full national coverage in all reporting countries except in Belgium and Spain. The population coverage is estimated to be 80% in Belgium since 2015 and 97% in Spain in 2021–2022. These proportions were used when calculating the national notification rates for these two countries. For 2020, Spain did not receive data from all regions, so the case numbers were therefore lower than expected. No estimate of population coverage in Spain was provided prior to 2021, so notification rates were not calculated. All countries provide case-based data except Bulgaria, which reported aggregate data. Both

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reporting formats were included to calculate numbers of cases, notification rates, disease trends, and distributions by age and gender. For pregnancy-associated cases, only the mother is reported to the EU/EEA-level surveillance.

Subtyping of *L. monocytogenes* is either performed by phenotypic methods where serotypes are assigned or by PCR where corresponding serogroups are assigned or can be derived from WGS data. These data are compiled in the EU surveillance reporting system, where for example serotype 1/2a is combined with data reported as serogroup IIa. EU/EEA countries have the possibility to report the seven-gene multi-locus sequence type (ST) via case-based data collection. ST for *L. monocytogenes* has a higher discriminatory power than serogroup/serotype. In addition, ST was derived *in silico* from whole genome sequencing (WGS) data for countries that routinely submit sequences for WGS-enhanced listeriosis surveillance but did not report STs via case-based data collection.

During 2022, ECDC continued EU/EEA-wide WGS-enhanced surveillance of listeriosis through isolate-based data collection, which started in March 2019.

For cluster detection, raw reads or assemblies were submitted by the participating countries. Sequences were analysed at ECDC with BioNumerics version 7.6.3 (Applied-Maths, Sint-Martens-Latem, Belgium). The analysis of raw reads included trimming using the default Bionumerics 7.6.3 settings; *de novo* assembly using SPAdes version 3.7.1; post-assembly optimisation by mapping reads back onto the assembly and keeping the consensus (using MismatchCorrector implemented in SPAdes version 3.7.1). The default settings of BLAST parameters for allele calling were used. Core genome multi-locus sequence typing (cgMLST) analysis was performed using assembly-based allele calling according to the Institut Pasteur scheme [4] in BioNumerics. Isolates were retained in the analysis if at least 1 574 (90%) of the 1 748 core loci were detected.

A multi-country core cluster of *L. monocytogenes* was assigned when at least two different EU/EEA countries reported one or more isolates each with a maximum of four differing alleles in cgMLST in single-linkage analysis. To further investigate the core clusters, a threshold of seven core genome alleles was used to search for isolates that were possibly epidemiologically linked.

In addition to the WGS data submitted by the EU/EEA countries for the listeriosis cluster detection, ECDC also collects and analyses sequence data in relation to ongoing multi-country outbreak investigations.

The One Health WGS System hosted by ECDC and the European Food Safety Authority (EFSA) [5] allows searching for genetically close non-human isolates matching clusters of human isolates. The non-human data constitutes sequence data submitted to EFSA by national food authorities in the EU as well as data from public sequence repositories. For all isolates, genome profiles are calculated from assembled genomes using BSR-Based Allele Calling Algorithm (chewBBACA) version 2.8.5 (https://github.com/B-UMMI/chewBBACA) Institut Pasteur scheme [4] made available by chewie Nomenclature Server at https://chewbbaca.online/species/6. Since the end of 2022, all human isolate clusters detected by ECDC are used to query the EFSA One Health WGS system on a weekly basis using a cut-off of seven differing alleles in cgMLST to at least one isolate in the human cluster.

Epidemiology

In 2022, 2 770 confirmed cases of listeriosis were reported by 30 EU/EEA countries, which was the highest annual number of cases since the start of EU/EEA-level surveillance. The EU/EEA notification rate was 0.62 per 100 000 population (Table 1). Germany, France, and Spain had the highest numbers of reported cases (548, 451, and 437, respectively), corresponding to 51.8% of all cases reported in the EU/EEA. The highest incidence rates were observed in Denmark, Finland, and Sweden (Table 1). Figure 1 illustrates the country-specific rates per 100 000 population.

Table 1. Confirmed listeriosis cases and rates per 100 000 population by country and year, EU/EEA, 2018–2022

| Country	2018		2019		2020		2021		2022	
	Number	Rate	Number	Rate	Number	Rate	Number	Rate	Number	Rate
Austria	27	0.31	38	0.43	41	0.46	38	0.43	47	0.52
Belgium	74	0.81	66	0.72	54	0.59	68	0.74	87	0.94
Bulgaria	9	0.13	13	0.19	4	0.06	3	0.04	5	0.07
Croatia	4	0.10	6	0.15	5	0.12	8	0.20	5	0.13
Cyprus	1	0.12	1	0.11	2	0.23	1	0.11	1	0.11
Czechia	31	0.29	27	0.25	16	0.15	24	0.22	48	0.46
Denmark	49	0.85	61	1.05	43	0.74	62	1.06	86	1.46
Estonia	27	2.05	21	1.59	3	0.23	5	0.38	11	0.83
Finland	80	1.45	50	0.91	94	1.70	70	1.26	70	1.26
France	338	0.50	373	0.56	334	0.50	435	0.64	451	0.66
Germany	678	0.82	571	0.69	546	0.66	562	0.68	548	0.66
Greece	19	0.18	10	0.09	20	0.19	21	0.20	7	0.07
Hungary	24	0.25	39	0.40	32	0.33	35	0.36	64	0.66
Iceland	2	0.57	4	1.12	4	1.10	5	1.36	2	0.53
Ireland	21	0.43	17	0.35	6	0.12	14	0.28	17	0.34
Italy	178	0.29	202	0.34	155	0.26	230	0.39	345	0.58
Latvia	15	0.78	6	0.31	8	0.42	10	0.53	8	0.43
Liechtenstein	NDR	NRC	NDR	NRC	NDR	NRC	0	0.00	0	0.00
Lithuania	20	0.71	6	0.21	7	0.25	7	0.25	13	0.46
Luxembourg	5	0.83	3	0.49	4	0.64	4	0.63	4	0.62
Malta	1	0.21	5	1.01	5	0.97	0	0.00	1	0.19
Netherlands	69	0.40	103	0.60	90	0.52	86	0.49	94	0.53
Norway	24	0.45	27	0.51	37	0.69	20	0.37	30	0.55
Poland	128	0.34	121	0.32	57	0.15	120	0.32	142	0.38
Portugal	64	0.62	56	0.54	47	0.46	57	0.55	63	0.61
Romania	28	0.14	17	0.09	2	0.01	11	0.06	14	0.07
Slovakia	17	0.31	18	0.33	7	0.13	13	0.24	25	0.46
Slovenia	10	0.48	20	0.96	26	1.24	19	0.90	20	0.95
Spain	370	NRC	504	NRC	191	NRC	355	0.77	437	0.95
Sweden	89	0.88	113	1.10	88	0.85	107	1.03	125	1.20
EU/EEA (30 countries)	**2 402**	**0.51**	**2 498**	**0.50**	**1 928**	**0.43**	**2 390**	**0.53**	**2 770**	**0.62**
United Kingdom	168	0.25	154	0.23	NDR	NRC	NA	NA	NA	NA
EU/EEA (31 countries)	**2 570**	**0.47**	**2 652**	**0.46**	**1 928**	**0.43**	**NA**	**NA**	**NA**	**NA**

Source: Country reports.
NDR: No data reported.
NRC: No rate calculated.
NA: Not applicable.
No data for 2020 and 2021 were reported by the United Kingdom, due to its withdrawal from the EU on 31 January 2020.

Figure 1. Confirmed listeriosis cases per 100 000 population by country, EU/EEA, 2022
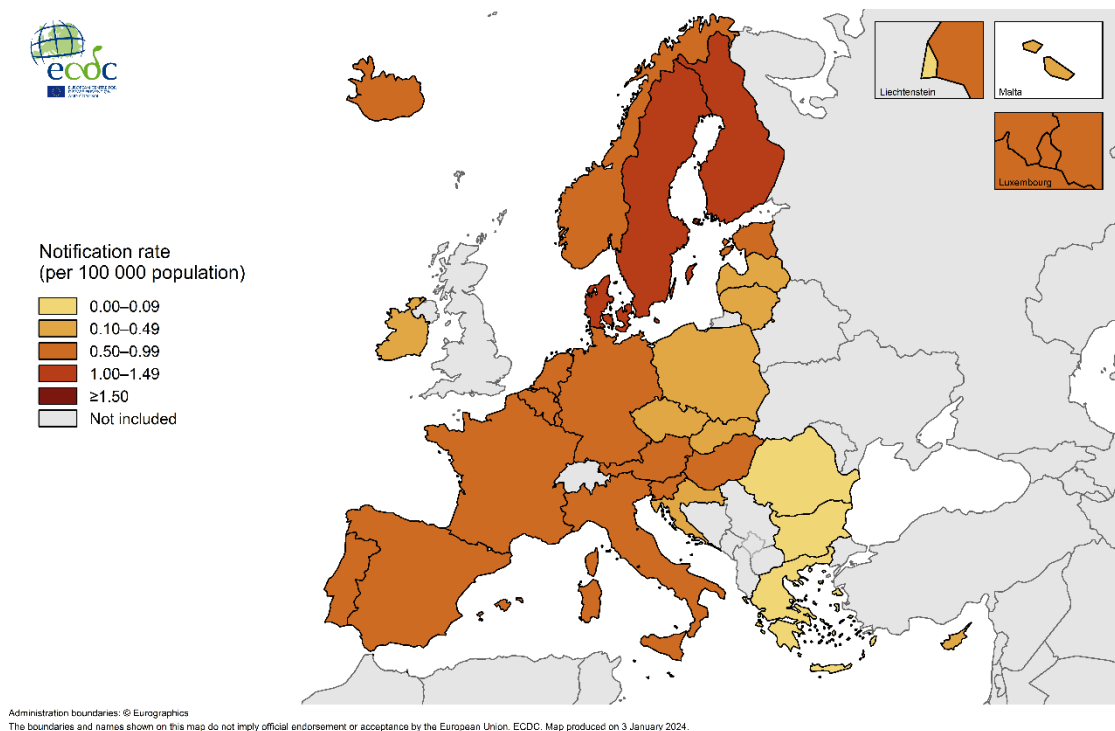
Listeriosis cases from EU/EEA countries reporting consistently from 2018 to 2022 showed a decrease in 2018 to 2020, followed by an increase (Figure 2).

Listeriosis cases typically peak during the summer months and have a smaller increase during the winter. In 2022, the monthly listeriosis case numbers followed the usual pattern but were mainly higher than the mean of previous years (Figure 3).

Figure 2. Confirmed listeriosis cases by month, EU/EEA, 2018–2022
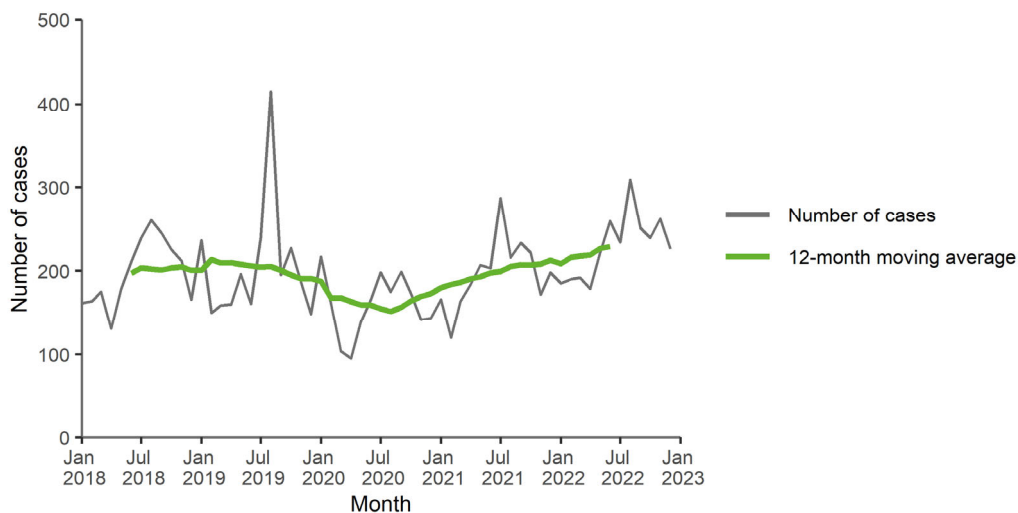
Source: Country reports from Austria, Belgium, Cyprus, Czechia, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Luxembourg, Malta, the Netherlands, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, and Sweden.
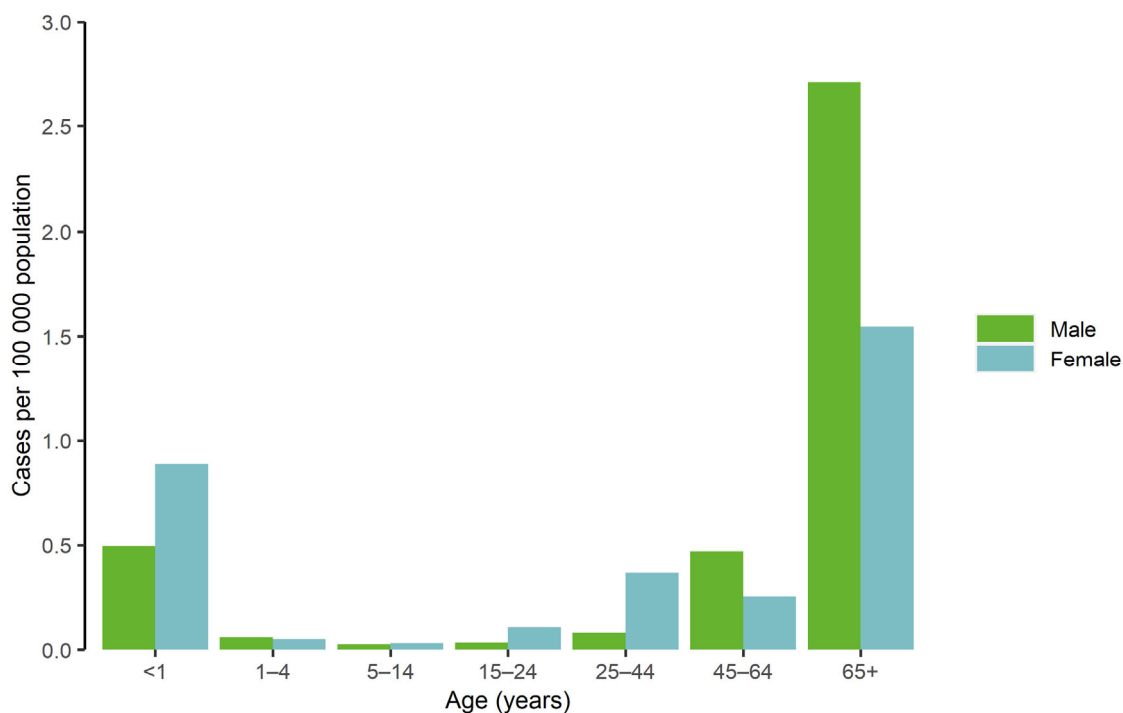
Figure 3. Confirmed listeriosis cases by month, EU/EEA, 2018–2021 and 2022
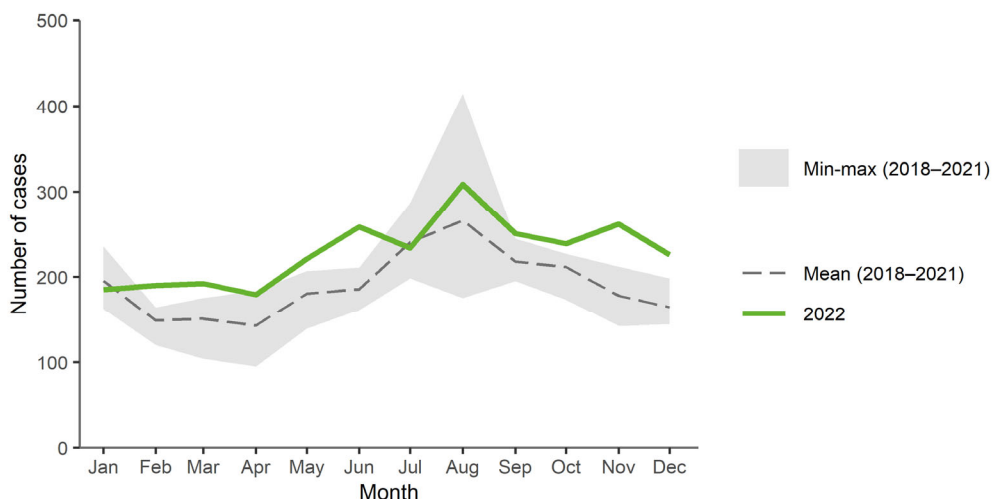
Source: Country reports from Austria, Belgium, Cyprus, Czechia, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Luxembourg, Malta, the Netherlands, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, and Sweden.

Of those confirmed listeriosis cases with available information regarding sex (N=2 766), 54.2% were males and 45.8% females, corresponding to a male-to-female ratio of 1.2:1. The most affected age group was those over 64 years (1 903 cases; 71.0%, notification rate: 2.1 per 100 000 population). In 2022, 117 pregnancy-associated listeriosis cases were reported. Of these, 23 resulted in miscarriage or a fatal outcome for the newborn (pregnancy outcome reported for 56.4% of pregnancy-associated cases).

Figure 4. Confirmed listeriosis cases per 100 000 population, by age and gender, EU/EEA, 2022

Source: Country reports from Austria, Belgium, Bulgaria, Croatia, Cyprus, Czechia, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Liechtenstein, Lithuania, Luxembourg, Malta, the Netherlands, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, and Sweden.

Microbial surveillance

In 2022, 14 EU/EEA countries reported serotype and serogroup data (Austria, Belgium, Czechia, France, Germany, Hungary, Ireland, Lithuania, Luxembourg, Norway, Slovakia, Spain, Sweden, and Slovenia). The most common serogroup was IIa (45.5%), followed by IVb (44.4%), IIb (7.7%), and IIc (2.3%) of the cases with available data of serotype or serogroup (23.3%; 646/2 770 cases).

In 2022, seven EU/EEA countries (Austria, Estonia, Ireland, the Netherlands, Norway, Sweden, and Slovenia) reported ST data for 440 isolates through TESSy case-based reporting. In addition to these, the ST could be determined *in silico* from WGS data submitted by Belgium and Portugal for a total of 137 isolates. In total, 20.8% (577 isolates) of the confirmed cases had information on ST. The most common ST was ST1 (n=66), followed by ST4 (n=37) and ST37 or ST451 (both with n=29).

WGS-enhanced surveillance

The objectives of EU/EEA-wide WGS-enhanced surveillance of listeriosis are:

In the short term:

- early detection and delineation of multi-country listeriosis outbreaks and/or dispersed clusters to trigger outbreak investigations and contribute to food trace back and forward investigations so that appropriate control and preventive measures can be implemented in the food chain.

In the medium term:

- detection of (re-)emergence and monitoring the spread of *Listeria monocytogenes* strains;
- identification of persistent *L. monocytogenes* strains causing human infections in EU/EEA and likely originating from continuous sources;
- identification of transmission chains, new risk factors for infection and severity of disease.

In the long term:

- monitoring of EU/EEA trends by selected indicators.

Five EU/EEA countries (Belgium, Finland, Portugal, Slovenia, and Spain) submitted *L. monocytogenes* WGS data to TESSy for 175 isolates during 2022. In addition, eight countries (Austria, Denmark, Germany, Italy, the Netherlands, Norway, the United Kingdom, and the United States) submitted sequence data to contribute to ongoing multi-country outbreak investigations from 22 isolates. When analysed against all sequences available in TESSy, no new multi-country clusters were detected during the year. However, 26 isolates matched with multi-country clusters that were detected before 2022.

By the end of 2022, among all sequences available in TESSy there were 132 multi-country clusters, including 1 034 isolates with median four isolates per cluster (range 2–88), and median two involved EU/EEA countries (range 2–10). The median cluster duration (time from oldest to newest isolate) was 2.7 years (range from 0 days to 14.8 years) for the 117 clusters with date information available for the first and the last isolate.

In the first query made in the ECDC-EFSA One Health WGS System at the end of 2022, matching non-human isolates were found for 49 of the 132 multi-country clusters (37.1%). Of these, 189 isolates derived from national food safety authorities and 451 from public sequence repositories.

Figure 5. Number of *Listeria monocytogenes* isolates in genomic multi-country clusters* detected by end of 2022
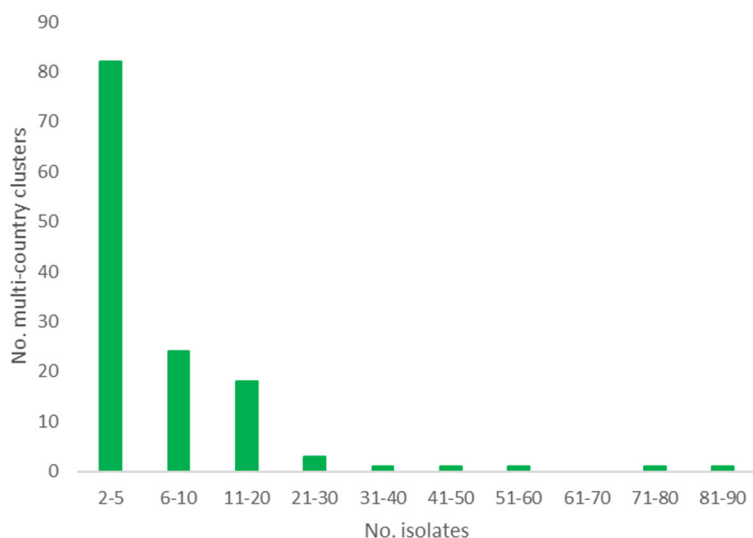
*All isolates within four alleles from at least one other isolate in the cluster by cgMLST.

Source: data from Austria, Belgium, Bulgaria, Czechia, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Lithuania, Luxembourg, Malta, the Netherlands, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, and Sweden.

Outbreaks and other threats

In 2022, 22 listeriosis events were launched in EpiPulse by eight different EU/EEA countries and two non-EU/EEA countries. For 18 of these, no EU/EEA multi-country aspect was identified. A probable source was found for all four multi-country events, involving *L. monocytogenes* ST8, ST155, and ST504. The strain involved in one multi-country event had a seven-gene allelic profile for which a ST had not yet been assigned. The probable sources were processed meat products for two events, and salmon and almond milk cheese for one event each.

Discussion

Listeriosis is one of the food- and waterborne diseases under EU surveillance with the highest number of hospitalisations and fatal cases [6]. The EU surveillance of listeriosis focuses on severe, invasive forms of the disease, for which the risk groups are mainly older and immunocompromised people as well as pregnant women and infants. Listeriosis can also manifest in milder forms causing gastrointestinal symptoms, but these cases are usually not diagnosed and notified in EU/EEA countries.

Although the overall trend for listeriosis between 2018 and 2022 did not show a significant decrease or increase [6], the listeriosis case number and rate were the highest ever at the EU/EEA level in 2022. At national level, a significantly increasing trend was detected in four EU/EEA countries (Austria, Denmark, France and Hungary), whereas a significantly decreasing trend was detected Estonia [6].

In 2022, *L. monocytogenes* was identified as a causative agent in 17 strong-evidence and 18 weak-evidence foodborne outbreaks that together affected 296 people in the EU, with 242 hospitalised cases and 28 deaths, as reported to EFSA [6]. The number of foodborne outbreaks reported for 2022, including the associated number of hospitalisations and deaths, was the highest since EFSA first started collecting data.

In 2022, five countries reported sequence data for the EU/EEA-wide WGS-enhanced listeriosis surveillance. Since the beginning of WGS data reporting to TESSy, altogether 27 EU/EEA countries and the United Kingdom have provided sequence data by end of 2022. Microbiological clusters detected from these data show that although the multi-country clusters tend to be small and affect only a few countries (skewed by the low number of countries submitting data), they also often persist for several years, even decades. This indicates that microbiological cluster detection efforts combined with other relevant data, such as sequences from food isolates and exposure data from trawling interviews of case/relatives, could help locating sources of the pathogen and allow for implementation of control measures to reduce the EU/EEA burden of this notably severe disease. The launch of the ECDC-EFSA One Health WGS System in July 2022 facilitates hypothesis formation from microbiological comparisons during multi-country outbreaks. The inclusion of non-human WGS data from public sequence repositories gives global context to the analyses. By the end of 2022, already more than one third of the multi-country human clusters had matches with non-human data, despite limited number of countries reporting WGS data routinely.

Public health implications

Due to the high severity of listeriosis among vulnerable people (i.e. those who are immunosuppressed, infants and the elderly) and the increasing proportion of older people, the highest ever case number and population-adjusted notification rate at the EU/EEA level are concerning and call for more attention to the prevention and control of the disease and outbreaks. Raising awareness of listeriosis and risky foods for risk groups is important, both among the elderly and pregnant women. It is important to consider that even ready-to-eat foods that comply with the EU food safety criteria for *L. monocytogenes* can cause disease in immune-compromised people. Furthermore, supranational cross-sectorial collaboration, including sequence data-sharing, is essential for addressing the occurrence of persistent *L. monocytogenes* strains in humans.

References

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