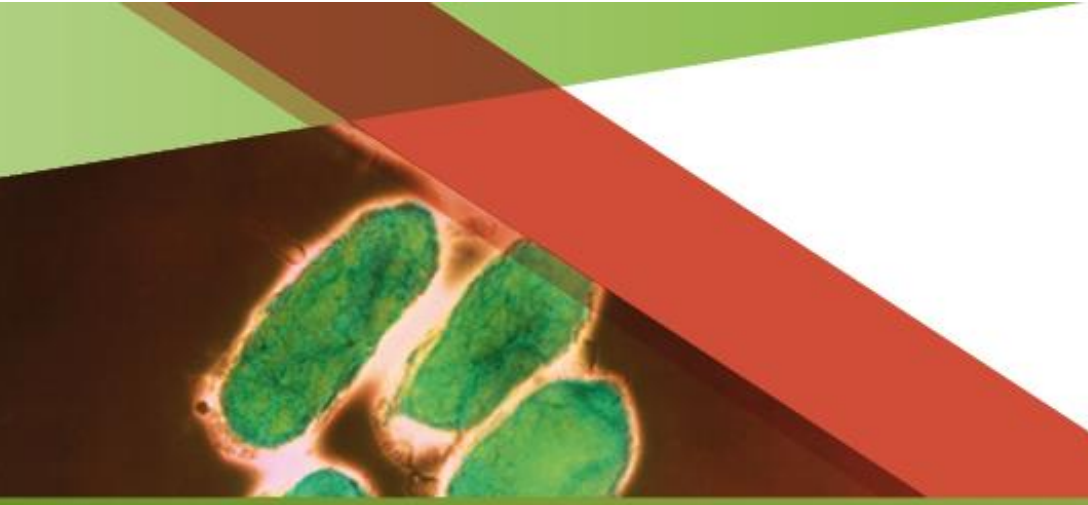


SURVEILLANCE REPORT

Yersiniosis

Annual Epidemiological Report for 2022

Key facts

- Yersiniosis was the fourth most commonly reported gastrointestinal infection in the EU/EEA after campylobacteriosis, salmonellosis and Shiga toxin-producing *Escherichia coli* (STEC) in 2022.
- For 2022, 27 countries reported 8 037 confirmed yersiniosis cases in the EU/EEA.
- The overall notification rate was 2.2 cases per 100 000 population, which was 22.2% higher than in 2021.
- The highest notification rates were reported by Denmark, Finland and Luxembourg.
- The highest notification rate was detected in 0–4-year-old children with 10.1 cases per 100 000 population for males and 9.0 cases per 100 000 population for females.

Introduction

Yersiniosis is an enteric infection caused primarily by *Yersinia enterocolitica* and rarely by *Yersinia pseudotuberculosis.* Pigs are the most common reservoir of *Y. enterocolitica*. Human infections are typically related to the consumption of undercooked pork or cross-contamination of other food items during the handling of raw pork.

Both domestic and wild animals are natural reservoirs of *Y. pseudotuberculosis*. Human infections are mostly caused by the consumption of contaminated vegetables. Symptoms of yersiniosis include fever and abdominal pain in the right lower part of the abdomen and may be confused with appendicitis. Children can also have (bloody) diarrhoea.

Methods

This report is based on data for 2022 retrieved from The European Surveillance System (TESSy) on 9 September 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 in the 'Introduction to the Annual Epidemiological Report' [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].

For 2022, yersiniosis data were reported by 27 EU/EEA countries. Croatia did not report data in 2022 and no yersiniosis surveillance system exists in Liechtenstein and in the Netherlands. Notification of yersiniosis was mandatory in 23 EU/EEA countries except for Belgium, France, Greece and Italy where notification is voluntary. The surveillance systems for yersiniosis infections had national coverage in all reporting countries except for three: France, Italy and Spain. No estimate for population coverage was provided for France and Italy, so notification

Suggested citation: European Centre for Disease Prevention and Control. Yersiniosis. In: ECDC. Annual Epidemiological Report for 2022. Stockholm: ECDC; 2024.

Stockholm, February 2024

rates for these two countries were not calculated. From 2018 onwards, Greece reported data on laboratory-confirmed cases collected from public hospitals. For 2020, Spain did not receive data from all regions which normally report cases so the notification rates and case numbers are lower than expected. Notification rates are therefore not calculated for Spain in 2020. Fifteen countries used the latest (EU 2018) case definition, two countries used the one from 2012, five countries used the 2008 case definition, five countries reported using another case definition and one country did not specify the case definition used. Most countries (24) undertook passive surveillance and cases were reported by both laboratories and physicians and/or hospitals for 18 countries. All countries provided case-based data except for Bulgaria and Greece, which reported aggregated data.

Epidemiology

For 2022, 8 037 confirmed cases of yersiniosis (caused by *Yersinia enterocolitica* and *Y. pseudotuberculosis*) were reported by 27 EU/EEA countries with an overall rate of 2.2 cases per 100 000 population. This was an increase by 22.2% compared with 2021. The rate and number of cases reported in 2022 were higher than the years prior to the COVID-19 pandemic (2018-2019). Denmark had the highest notification rate of 12.7 cases per 100 000 population, followed by Finland (7.4), Luxembourg (5.4) and Slovakia (5.3) - Table 1, Figure 1. As in previous years, Germany accounted for the highest number of cases followed by France and Spain. These three countries accounted for 56.4% of all confirmed yersiniosis cases in the EU/EEA.

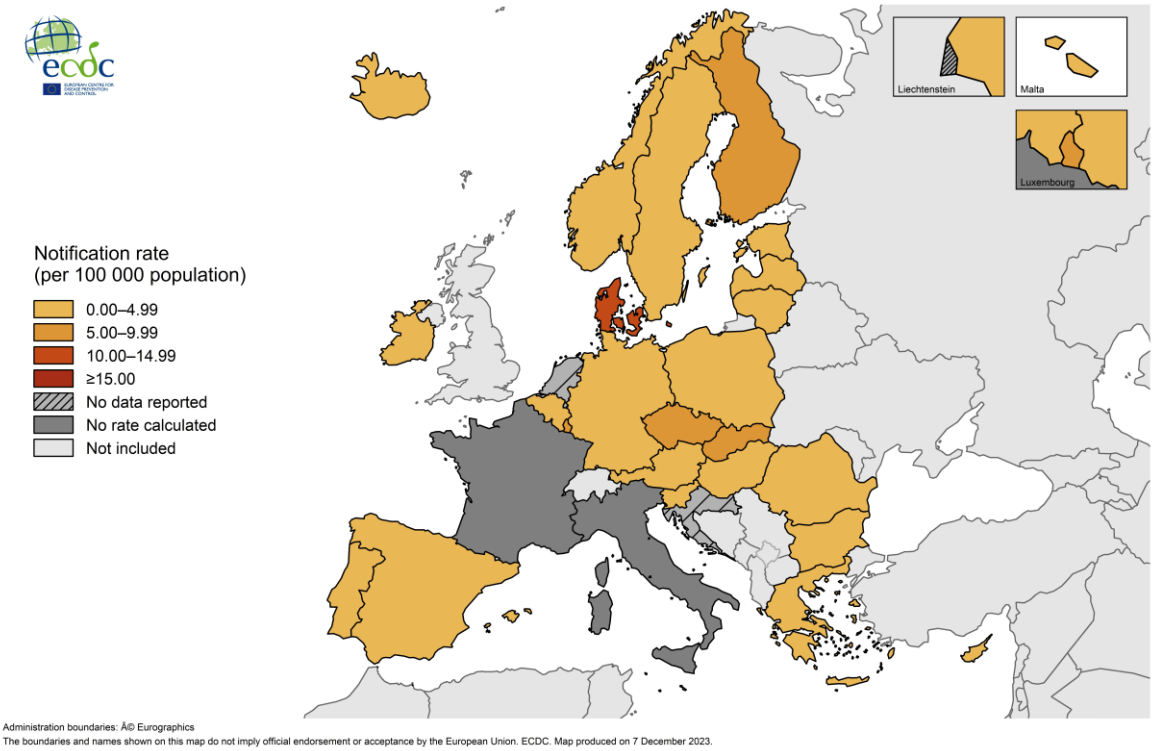
Thirty percent of 2 230 yersiniosis cases with known information were hospitalised. No deaths were reported among 3 659 cases with known outcome.

Table 1. Confirmed yersiniosis 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	136	1.5	112	1.3	128	1.4	138	1.5	131	1.5
Belgium	392	3.4	406	3.5	336	2.9	329	2.8	357	3.1
Bulgaria	9	0.1	11	0.2	4	0.1	5	0.1	8	0.1
Croatia	20	0.5	12	0.3	11	0.3	12	0.3	NDR	NRC
Cyprus	0	0.0	0	0.0	0	0.0	0	0.0	1	0.1
Czechia	622	5.9	618	5.8	437	4.1	456	4.3	525	5.0
Denmark	282	4.9	221	3.8	413	7.1	453	7.8	746	12.7
Estonia	63	4.8	42	3.2	44	3.3	45	3.4	53	4.0
Finland	529	9.6	406	7.4	386	7.0	331	6.0	408	7.4
France	929	NRC	1 135	NRC	988	NRC	1 451	NRC	1 558	NRC
Germany	2 193	2.6	2 164	2.6	1 860	2.2	1 912	2.3	1 814	2.2
Greece	21	0.2	13	0.1	3	0.0	7	0.1	9	0.1
Hungary	36	0.4	38	0.4	25	0.3	50	0.5	60	0.6
Iceland	2	0.6	2	0.6	3	0.8	4	1.1	1	0.3
Ireland	8	0.2	9	0.2	13	0.3	19	0.4	17	0.3
Italy	14	NRC	12	NRC	21	NRC	35	NRC	36	NRC
Latvia	68	3.5	60	3.1	88	4.6	83	4.4	76	4.1
Liechtenstein	NDR	NRC	NDR	NRC	NDR	NRC	NDR	NRC	NDR	NRC
Lithuania	139	4.9	181	6.5	123	4.4	153	5.5	114	4.1
Luxembourg	16	2.7	18	2.9	26	4.2	12	1.9	35	5.4
Malta	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
Netherlands	NDR	NRC	NDR	NRC	NDR	NRC	NDR	NRC	NDR	NRC
Norway	105	2.0	85	1.6	83	1.5	85	1.6	117	2.2
Poland	170	0.4	196	0.5	90	0.2	142	0.4	180	0.5
Portugal	30	0.3	29	0.3	25	0.2	34	0.3	36	0.3
Romania	22	0.1	36	0.2	6	0.0	15	0.1	14	0.1
Slovakia	259	4.8	255	4.7	168	3.1	213	3.9	287	5.3
Slovenia	32	1.5	28	1.3	26	1.2	50	2.4	54	2.6
Spain	549	NRC	409	NRC	296	NRC	754	1.7	1 162	2.7
Sweden	278	2.7	393	3.8	220	2.1	310	3.0	238	2.3
EU/EEA (30 countries)	**6 924**	**2.1**	**6 891**	**2.0**	**5 823**	**1.7**	**7 098**	**1.8**	**8 037**	**2.2**
United Kingdom	198	0.3	163	0.2	NDR	NRC	NA	NA	NA	NA
EU/EEA (31 countries)	**7 122**	**1.7**	**7 054**	**1.7**	**5 823**	**1.7**	**NA**	**NA**	**NA**	**NA**

Source: Country reports.
NDR: No data reported.
NRC: No rate calculated.
NA: Not applicable.
No data for 2020, 2021 and 2022 were reported by the United Kingdom, due to its withdrawal from the EU on 31 January 2020.

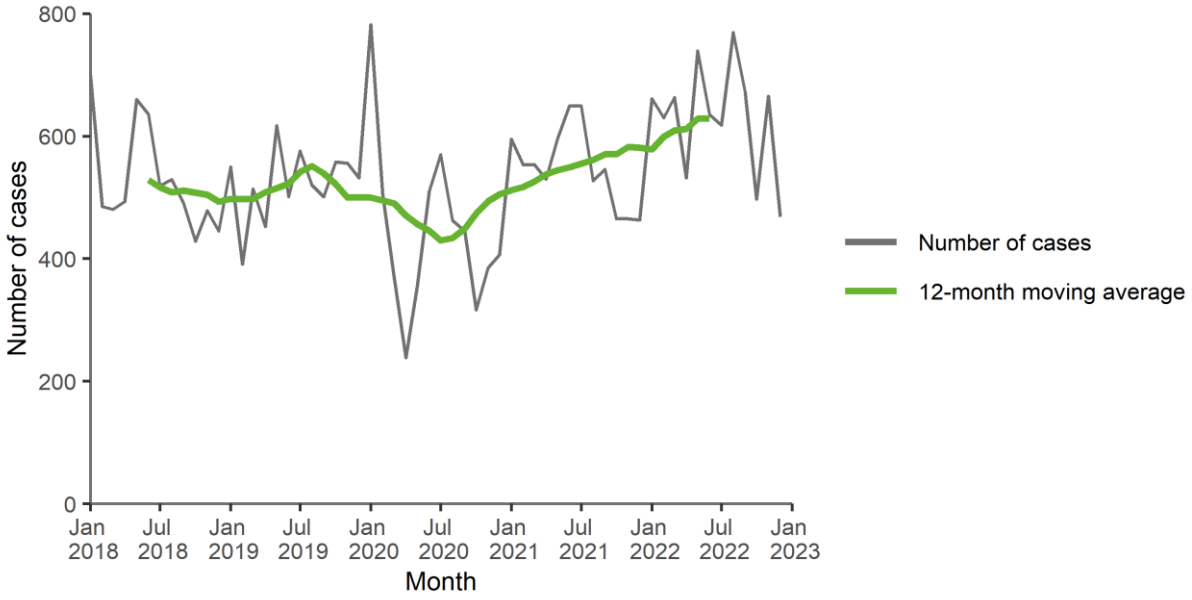
Figure 1. Confirmed yersiniosis cases per 100 000 population by country, EU/EEA, 2022



Source: Country reports.

The number of confirmed yersiniosis cases in the EU/EEA continued to increase in 2022 after a drop of cases in 2020 - likely due to COVID-19 pandemic (Figure 2). The trend of human yersiniosis cases in the EU for 2018–2022 showed no statistically significant increase or decrease [4]. Four Member States (Germany, Poland, Slovakia, and Sweden) reported significantly decreasing ($p<0.05$) trends during the period 2018–2022. Eight countries (Denmark, France, Ireland, Italy, Latvia, Portugal, Slovenia, and Spain) reported a significantly increasing trend over the same period.

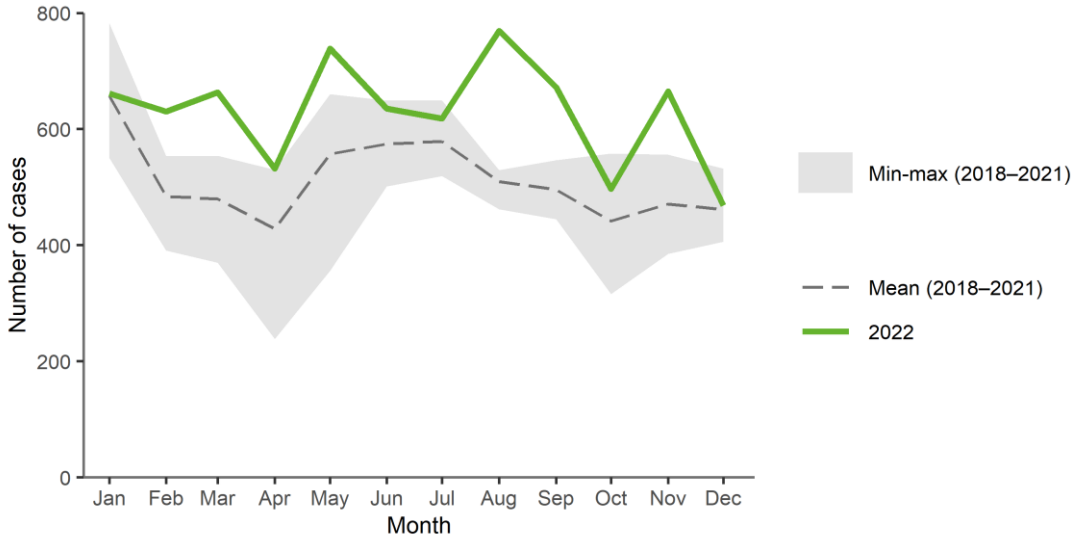
Figure 2. Confirmed yersiniosis cases by month, EU/EEA, 2018–2022



Source: Country reports from Austria, Cyprus, Czechia, Denmark, Estonia, Finland, France, Germany, Hungary, Iceland, Ireland, Italy, Latvia, Luxembourg, Malta, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden.

As in previous years, cases of yersiniosis did not show a clear seasonal pattern in 2022. Although case numbers peaked in May, August and November, the monthly number of cases reported were consistently higher for each month than the mean number of cases reported between 2018-2021 (Figure 3).

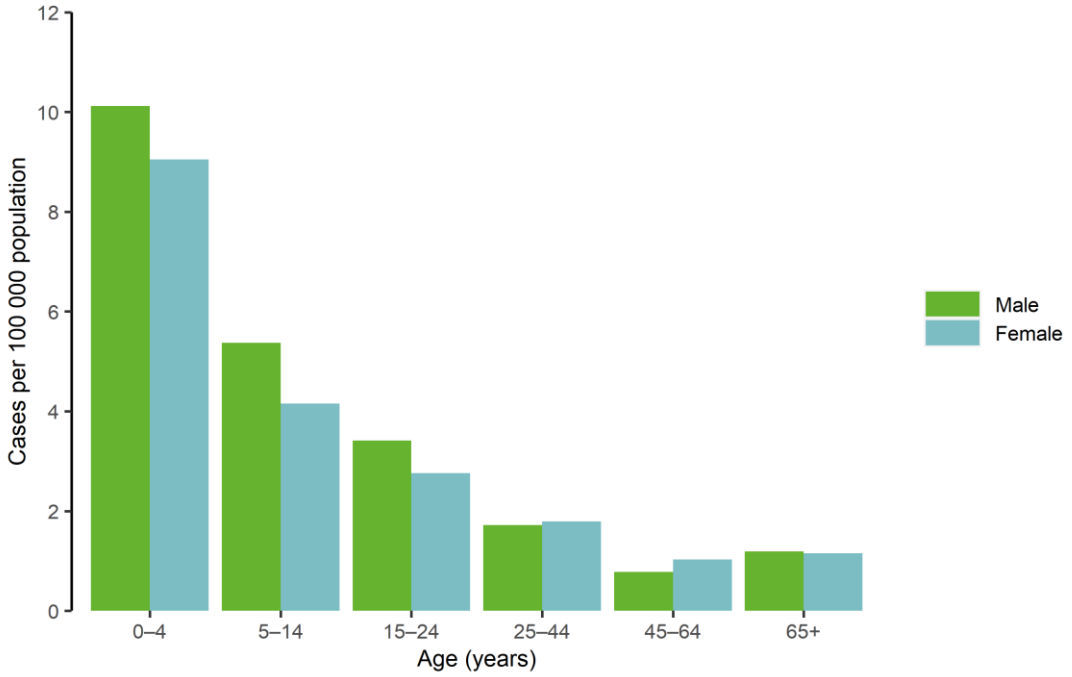
Figure 3. Confirmed yersiniosis cases by month, EU/EEA, 2022 and 2018–2021



Source: Country reports from Austria, Cyprus, Czechia, Denmark, Estonia, Finland, France, Germany, Hungary, Iceland, Ireland, Italy, Latvia, Luxembourg, Malta, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden.

Among the 8 009 (99.7%) yersiniosis cases for which gender was reported, 53% were males and 47% were females, with a male-to-female ratio of 1.1:1. The highest notification rate was detected in the age group 0-4-years with 10.1 cases per 100 000 population for males and 9.0 per 100 000 population for females. This age group accounted for 1 732 (22%) of the 8 002 cases with information on age. The notification rate decreased with age and was the lowest in the 45–64 years age group: 0.8 cases in males and 1.0 cases in females per 100 000 population (Figure 4).

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



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

Microbial surveillance

Information on species was reported by 23 countries for 7 663 cases (95.3%) in the EU/EEA in 2022. *Y. enterocolitica* was the most commonly reported species in all countries, with 7 563 confirmed cases representing 98.7% of all cases with species information available. Eleven countries reported a total of 100 *Y. pseudotuberculosis* cases. Belgium, Finland, France, Germany and Sweden accounted for 91% of these cases.

Y. enterocolitica serotype information was provided for 3 696 (48.9%) cases by 18 countries. The most commonly reported serotype was O:3 representing 83.3% of cases with information on serotype available, followed by O:9 (12.7%). Altogether, the other serotypes (O1A, O:5, O:5,27, O:8 and others) accounted for 4.0% of the cases with known serotype. Information about *Y. enterocolitica* bioserotypes was provided for 2 191 (29.0%) cases by seven countries. The most common bioserotypes were 4/O:3 (83.2%) and 2/O:9 (15.1%).

Outbreaks and other threats

No events on *Yersinia* infection were launched through EpiPulse in 2022.

In 2022, 14 yersiniosis outbreaks were reported in the annual zoonoses data collection to the European Food Safety Authority (EFSA) [4]. This was a decrease in outbreaks (25) compared with 2021. These outbreaks involved 96 cases in seven EU countries (Belgium, Denmark, Finland, France, Germany, Poland and Spain). *Y. enterocolitica* was the species identified as the causative agent in the majority (86%; 12/14) of the outbreaks. Three strong evidence outbreaks of *Y. enterocolitica* O:3 with a known vehicle of infection were notified, all of which were reported by Norway. Two were caused by salad and one was caused by pork [5].

Discussion

In 2022, yersiniosis was the fourth most commonly reported foodborne zoonotic disease in the EU/EEA after campylobacteriosis, salmonellosis and Shiga toxin -producing *Escherichia coli* (STEC) [3]. Before the COVID-19 pandemic, the overall EU/EEA trend of reported cases of yersiniosis in the last decade was stable , before case numbers decreased notably in 2020, as a likely effect of the pandemic. In 2021-2022, the number of cases increased, and were among the highest number of confirmed cases reported since the beginning of yersiniosis surveillance in the EU/EEA in 2007. This can be due to changes in laboratory techniques, such as the increasing use of diagnostic PCR panels and MALDI-TOF in clinical laboratories as reported by some countries with increased number of cases in the recent years.

Among the two pathogenic *Yersinia* species that are notified at the EU/EEA level, *Y. enterocolitica* caused the majority of human infections followed by *Y. pseudotuberculosis,* which is a rare cause of foodborne infections. The main reservoir for *Y. enterocolitica* is the domestic pig, and the pathogenic *Y. enterocolitica* bioserotypes, which are most commonly reported in human infections, are frequently found in pork products. The *Y. pseudotuberculosis* reservoir comprises both domestic and wild animals (e.g. pigs, deer, wild birds and rodents). The ability of *Yersinia* bacteria to survive and grow at low temperatures has considerable importance in food hygiene. Refrigeration temperatures are generally not sufficient to efficiently suppress the growth of these bacteria. Contaminated vegetables have been the major vehicle of *Y. pseudotuberculosis* infections, particularly root vegetables with a long period of cold storage. In recent years, *Y. enterocolitica* outbreaks linked to vegetables have also been reported [4, 5], suggesting that sources other than pork may play a role.

In the last decade, there has been a transition process in clinical microbiological laboratories from culture-based detection methods to molecular-based methods using PCR panels, a process that is still ongoing. PCR findings of *Y. enterocolitica* and *Y. pseudotuberculosis* virulence genes have been notifiable according to the EU case definition for yersiniosis since 2018. Depending on the choice of PCR panel and target genes used, the outcome of which subtypes of *Y. enterocolitica* are detected varies [6]. Examples of virulence genes used for the detection of *Yersinia* are *ail* and *vir*F. The latter entirely excludes apathogenic *Y. enterocolitica* biotype (BT)1A, which is also excluded from the EU case definition. The *ail* gene has been sporadically found in *Y. enterocolitica* BT1A and apathogenic *Yersinia* spp. which can give a false-positive result in PCR testing [7]. Other target genes used in PCR panels are *inv*A and *yst*B. These target genes are however also present in *Y. enterocolitica* BT1A. Regarding *Y. pseudotuberculosis*, all subtypes are considered pathogenic in humans. Biotype information, which is important to evaluate the pathogenicity of *Y. enterocolitica* isolates, was only provided by seven countries for less than one-third of the reported *Y. enterocolitica* cases in 2022, similar to previous years. This might be partly due to the use of PCR panels in other countries where no isolates have been retrieved for typing. At the EU-level, the proportion of yersiniosis cases with reported serotype-biotype information has not been affected in recent years, which could be a marker for a higher proportion of notifications based on PCR.

As for the majority of food- and waterborne pathogens, whole genome sequencing (WGS) is increasingly also used to subtype and for cluster investigations of pathogenic *Yersinia* isolates in outbreaks [8, 9]. WGS analysis can provide information on species and virulence genes, in addition to sequence type (ST) using the 7 gene Multi Locus Sequence Typing (MLST) schema. Cluster analysis of sequences in outbreaks, and source tracing investigations can be done by identifying the core genome MLST (cgMLST) allelic profiles of the isolates and assess the allelic distances between them. Overall, the use of WGS for typing of *Yersinia* isolates in animals and humans facilitates monitoring animal-to-human and food-to-human transmission of these pathogens and improves public health surveillance of the pathogenic lineages [10].

Public health implications

Pigs are the most common source of *Y. enterocolitica* infections and many cases are related to the consumption of undercooked contaminated pork or cross-contamination of other food items during the handling and preparation of raw pork. Pork should only be consumed after thorough cooking, especially when given to young children. Proper kitchen hygiene is required to avoid cross-contamination. Prolonged cold storage of contaminated food allows the survival and growth of *Yersinia*.

Outbreaks of *Y. pseudotuberculosis* have almost exclusively been linked to raw vegetables and ready-to-eat vegetable products such as lettuce and carrots with long periods of cold storage. In recent years, increasing numbers of *Y. enterocolitica* outbreaks have also been linked to vegetables in addition to pork products. Good agricultural and hygiene practices in food storage and processing as well as proper washing and peeling of vegetables in home kitchens can decrease the risk of contamination of fresh produce and prevent further infections.

References

1. European Centre for Disease Prevention and Control (ECDC). Introduction to the Annual Epidemiological Report. Stockholm: ECDC. Available at: http://ecdc.europa.eu/annual-epidemiological-reports/methods
2. European Centre for Disease Prevention and Control (ECDC). Surveillance systems overview for 2021. Stockholm: ECDC. Available at: Surveillance systems overview for 2021 (europa.eu)
3. European Centre for Disease Prevention and Control (ECDC). Surveillance Atlas of Infectious Diseases. Stockholm: ECDC. Available at: http://atlas.ecdc.europa.eu/public/index.aspx?Dataset=27&HealthTopic=62.
4. European Food Safety Authority (EFSA) and European Centre for Disease Prevention (ECDC) and Control. European Union One Health 2022 Zoonoses Report. EFSA Journal 2023. Available at: https://www.ecdc.europa.eu/sites/default/files/documents/EFS2_8442.pdf
5. Norway records rise in outbreaks in 2022. Food Safety News 2022 May 11. Available at: https://www.foodsafetynews.com/2023/05/norway-records-rise-in-outbreaks-in-2022/
6. Berenger B.M, Chui L, Ferrato C, Loyd T, Li V, Pillai D.R. Performance of four commercial real-time PCR assays for the detection of bacterial enteric pathogens in clinical samples. IJID.2022 Jan;114:195-201.
7. Joutsen S, Johansson P, Laukkanen-Ninios R, Björkroth J, Fredriksson-Ahomaa M. Two copies of the ail gene found in *Yersinia enterocolitica* and *Yersinia kristensenii*. Vet Microbiol. 2020. Aug:247:108798
8. Strydom H, Wang J, Paine S, Dyet K, Cullen K, Wright J. Evaluating sub-typing methods for pathogenic *Yersinia enterocolitica* to support outbreak investigations in New Zealand. Epidemiol Infect. 2019; 147: e186.
9. Inns T, Flanagan S, Greig DR, Jenkins C, Seddon K, Chin T, et al. First use of whole-genome sequencing to investigate a cluster of *Yersinia enterocolitica*, Liverpool, United Kingdom, 2017. J Med Microbiol. 2018 Dec; 67(12):1747-1752
10. Hunter E, Greig D, Schaefer U, Wright M, Dallman T, McNally A, Jenkins C. Identification and typing of *Yersinia enterocolitica* and *Yersinia pseudotuberculosis* isolated from human clinical specimens in England between 2004 and 2018. J Med Microbiol. 2019 March; 68:538–548