Yersiniosis

Annual Epidemiological Report for 2021

Key facts

- Yersiniosis is the third most commonly reported gastrointestinal infection in the EU/EEA after campylobacteriosis and salmonellosis.
- For 2021, 28 countries reported 6 876 confirmed yersiniosis cases in the EU/EEA.
- The overall notification rate was 1.9 cases per 100 000 population, which represents an 11.8% increase compared with 2020 and the pre-pandemic years from 2017 to 2019.
- The highest notification rates were reported by Denmark, Finland and Lithuania.
- The highest notification rate was detected in 0–4-year-old children, with 9.4 cases per 100 000 population for males and 8.0 cases per 100 000 population for females.

Introduction

Yersiniosis is an enteric infection caused primarily by *Yersinia enterocolitica*, and on rare occasions by *Yersinia pseudotuberculosis.* Pigs are the most common reservoir of *Y. enterocolitica*. Human infections are typically related to the consumption of under-cooked 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 2021 retrieved from The European Surveillance System (TESSy) on 9 October 2022. 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 2021, yersiniosis data were reported by 28 EU/EEA countries. The notification of yersiniosis is mandatory in 24 EU/EEA countries, and there are four where notification is voluntary (Belgium, France, Greece and Italy). No yersiniosis surveillance system exists in Liechtenstein and the Netherlands. The surveillance systems for yersiniosis infections have national coverage in all reporting countries except for three: France, Italy and Spain. No estimate for population coverage was provided, so no notification rates were calculated for these three countries. Greece reported data on laboratory-confirmed cases collected in public hospitals from 2018 onwards. For 2020−2021,

Spain did not receive data from all regions normally reporting and the case numbers are therefore lower than expected. Twelve countries used the latest (EU 2018) case definition, six countries used the one from 2012, five countries used the 2008 case definition, four countries reported using another case definition and one country did not specify the definition used. Most countries (24) undertook passive surveillance and in 18 countries cases were reported by both laboratories and physicians and/or hospitals. All countries provided case-based data except Belgium, Bulgaria and Greece, which reported aggregated data. No data were reported for 2020–2021 by the United Kingdom due to their withdrawal from the EU on 31 January 2020.

Epidemiology

For 2021, 6 876 confirmed cases of yersiniosis (caused by *Yersinia enterocolitica* and *Y. pseudotuberculosis*) were reported by 28 EU/EEA countries with an overall rate of 1.9 cases per 100 000 population. This represented an increase of 11.8% on 2020 and the pre-pandemic period (2017–2019). As in previous years, Germany accounted for the highest number of cases, followed by France. These two countries accounted for 49% of all confirmed yersiniosis cases in the EU/EEA. Denmark had the highest notification rate of 7.8 cases per 100 000 population, followed by Finland, Lithuania and Czechia (Table 1, Figure 1).

Thirty-three percent of 1 649 yersiniosis cases with known information were hospitalised. No deaths were reported among the 3 659 cases with known outcome.

Table 1. Distribution of confirmed yersiniosis cases and rates per 100 000 population by country and year, EU/EEA, 2017–2021

| Country	2017		2018		2019		2020		2021		
	Number	Rate	Number	Rate	Number	Rate	Number	Rate	Number	Rate	ASR
Austria	95	1.1	136	1.5	112	1.3	128	1.4	138	1.5	1.6
Belgium	317	2.8	392	3.4	406	3.5	260	2.3	418	3.6	3.5
Bulgaria	17	0.2	9	0.1	11	0.2	4	0.1	5	0.1	0.1
Croatia	29	0.7	20	0.5	12	0.3	11	0.3	12	0.3	0.3
Cyprus	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0.0
Czechia	611	5.8	622	5.9	618	5.8	437	4.1	456	4.3	4.4
Denmark	206	3.6	282	4.9	221	3.8	413	7.1	453	7.8	8.0
Estonia	43	3.3	63	4.8	42	3.2	44	3.3	45	3.4	3.5
Finland	423	7.7	529	9.6	406	7.4	386	7.0	331	6.0	6.3
France	738	NR	929	NR	1 135	NR	988	NR	1 451	NR	NR
Germany	2 581	3.1	2 193	2.6	2 164	2.6	1 860	2.2	1 912	2.3	2.6
Greece	19	0.2	21	0.2	13	0.1	3	0.0	7	0.1	NR
Hungary	30	0.3	36	0.4	38	0.4	25	0.3	50	0.5	0.6
Iceland	0	0.0	2	0.6	2	0.6	3	0.8	4	1.1	1.1
Ireland	6	0.1	8	0.2	9	0.2	13	0.3	19	0.4	0.4
Italy	8	NR	14	NR	12	NR	21	NR	35	NR	NR
Latvia	47	2.4	68	3.5	60	3.1	88	4.6	83	4.4	4.4
Liechtenstein	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Lithuania	174	6.1	139	4.9	181	6.5	123	4.4	153	5.5	5.7
Luxembourg	15	2.5	16	2.7	18	2.9	26	4.2	12	1.9	2.0
Malta	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0.0
Netherlands	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Norway	67	1.3	105	2.0	85	1.6	83	1.5	85	1.6	1.6
Poland	191	0.5	170	0.4	196	0.5	90	0.2	142	0.4	0.4
Portugal	35	0.3	30	0.3	29	0.3	25	0.2	34	0.3	0.4
Romania	36	0.2	22	0.1	36	0.2	6	0.0	15	0.1	0.1
Slovakia	242	4.5	259	4.8	255	4.7	168	3.1	213	3.9	4.0
Slovenia	18	0.9	32	1.5	28	1.3	26	1.2	49	2.3	2.6
Spain	585	NR	549	NR	409	NR	296	NR	444	NR	NR
Sweden	236	2.4	278	2.7	393	3.8	220	2.1	310	3.0	3.1
UK	142	0.2	198	0.3	163	0.2	NR	NR	NR	NR	NR
EU-EEA	**6 911**	**1.7**	**7 122**	**1.7**	**7 054**	**1.7**	**5 747**	**1.7**	**6 876**	**1.9**	**2.0**

Source: country reports.
ASR: age-standardised rate
ND: no data reported
NR: no rate calculated.

Figure 1. **Distribution of confirmed yersiniosis cases per 100 000 population by country, EU/EEA, 2021**
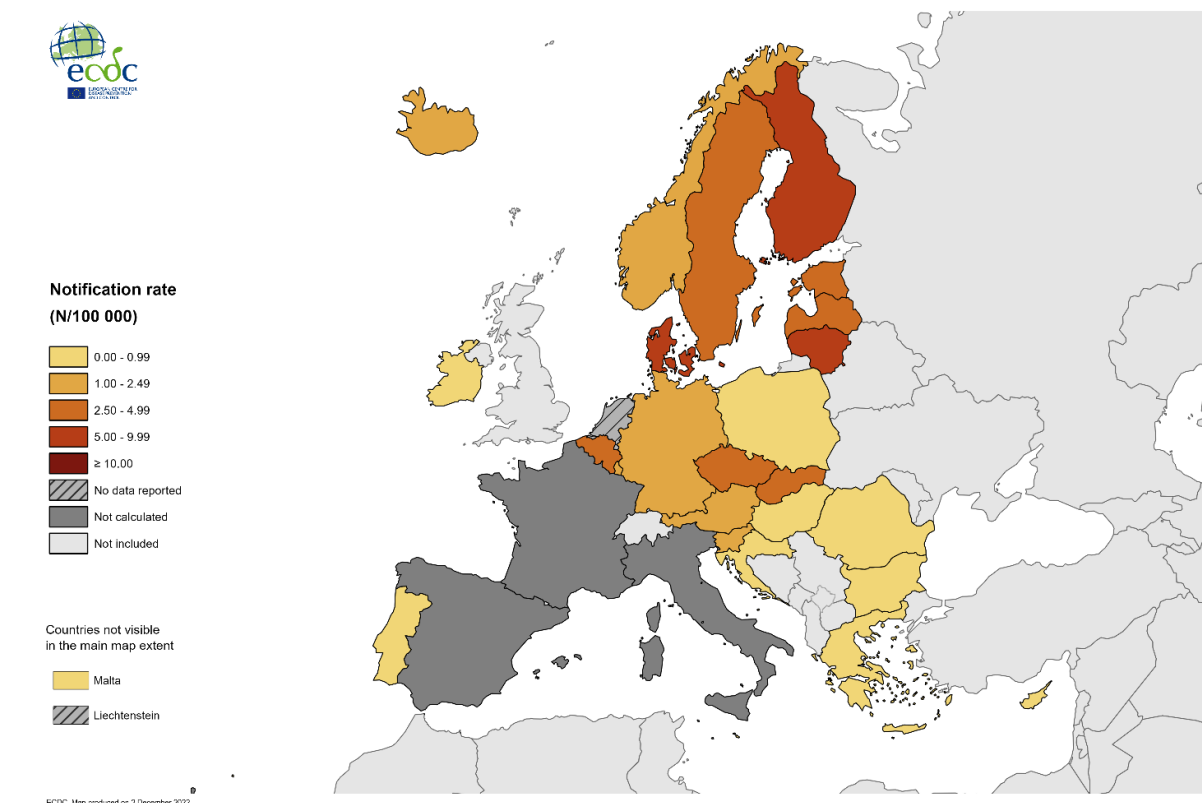
Following a decrease in 2020 due to the COVID-19 pandemic, the EU/EEA trend for confirmed yersiniosis cases increased again in 2021 (Figure 2).
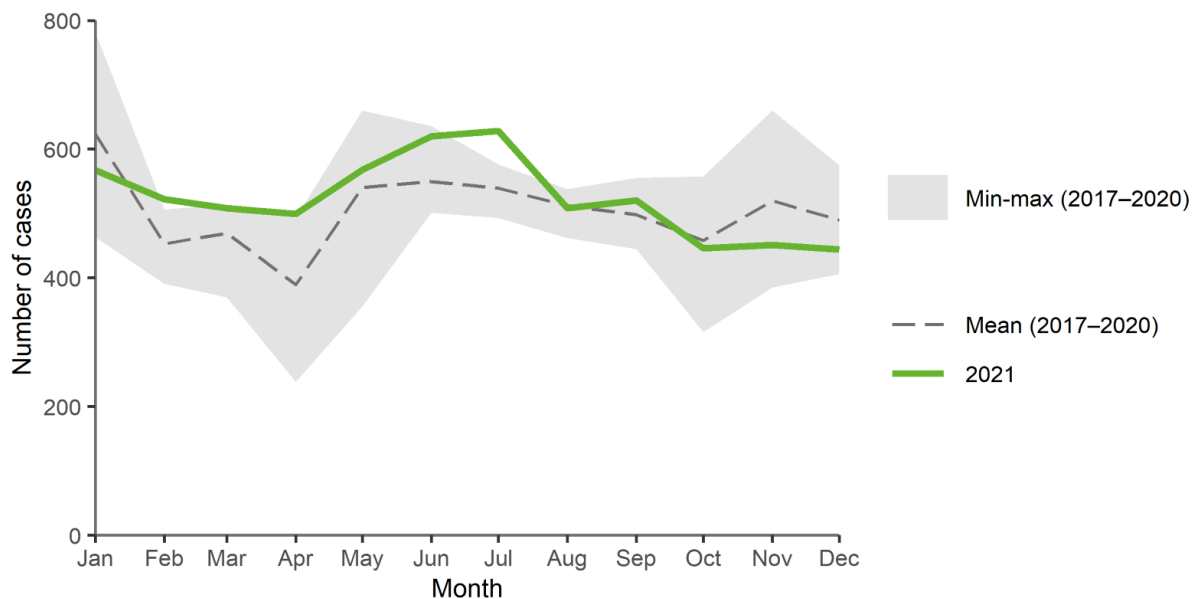
Figure 2. **Distribution of confirmed yersiniosis cases by month, EU/EEA, 2017−2021**

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.

As in previous years, cases of yersiniosis did not show a clear seasonal pattern in 2021. The highest number of cases were reported in June−July (Figure 3). From February to July 2021, reported cases were higher than average compared to the same month in 2017−2020 (Figure 3).

Figure 3. **Distribution of confirmed yersiniosis cases by month, EU/EEA, 2021 and 2017−2020**

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 6 853 (99.7%) yersiniosis cases for which gender was reported, 52% were males and 48% were females, with a male-to-female ratio of 1.1:1. The highest notification rate per 100 000 population was detected in the age group 0−4-years, with 9.4 for males and 8.0 for females. This age group accounted for 1 676 (24%) of the 6 853 cases with information on age. The notification rate decreased with age and was lowest in the 45−64 years age group: 0.7 cases in males and 0.8 cases in females per 100 000 population (Figure 4).

Figure 4. **Distribution of confirmed yersiniosis cases per 100 000 population, by age and gender, EU/EEA, 2021**
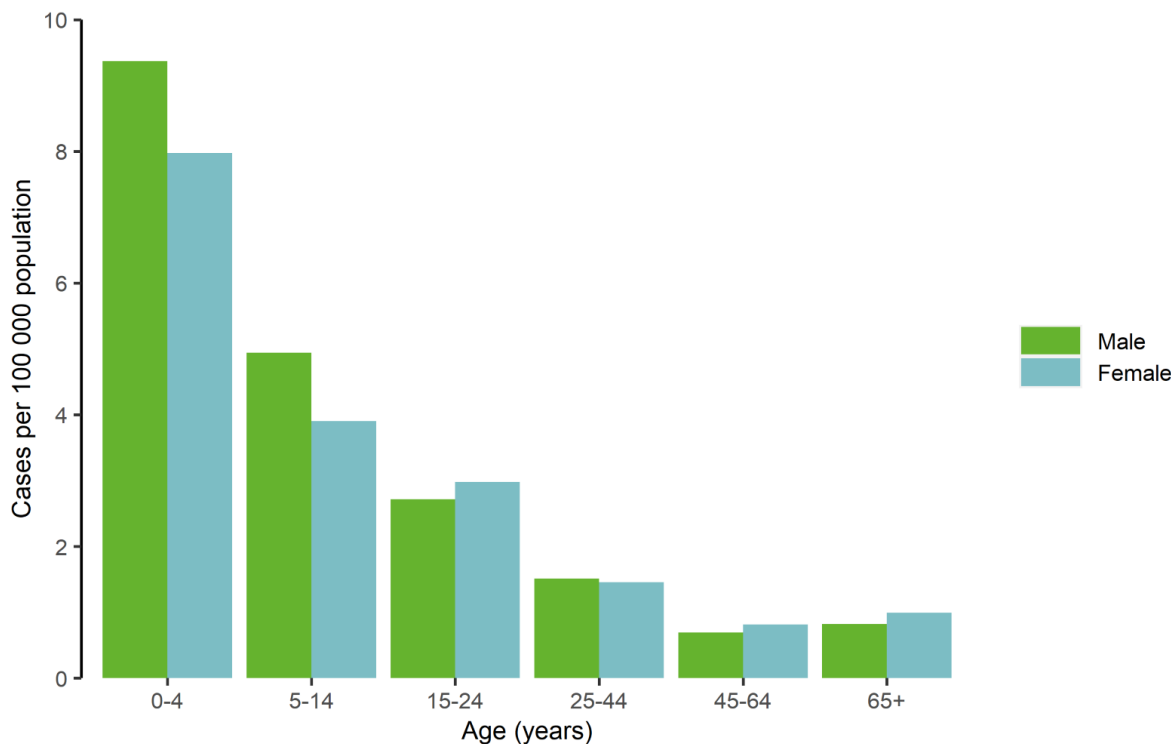
Source: Country reports from Austria, Belgium, Bulgaria, Croatia, Cyprus, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Latvia, Lithuania, Luxembourg, Malta, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain and Sweden.

Microbial surveillance

Information on species was reported by 23 countries for 6 150 cases (89.4%) in the EU/EEA in 2021. *Y. enterocolitica* was the most commonly reported species in all countries, with 6 035 confirmed cases representing 98.1% of all cases with species information available. *Y. enterocolitica* serotype information was provided for 3 066 (50.8%) confirmed cases. The most commonly reported serotype was O:3, representing 83.3% of cases for which information was available on serotype, followed by O:9 (12.3%). Altogether, the other serotypes (O:8, O:5,27 and others) accounted for 4.5% of the cases with known serotype. Information on *Y. enterocolitica* bioserotypes was provided for 1 682 (27.9%) confirmed cases. The most common bioserotypes were 4/O:3 (83.2%) and 2/O:9 (15.3%). Eleven countries reported a total of 115 *Y. pseudotuberculosis* cases. Finland, France, Germany and Sweden accounted for 89% of these cases.

Outbreaks and other threats

EpiPulse, a new ECDC portal integrating several former ECDC applications, including the Epidemic Intelligence Information System (EPIS) platform, was launched on 22 June 2021. The portal facilitates collection, analysis and dissemination of indicator- and event-based surveillance data on infectious diseases and associated health issues. In 2021, four events on *Y. enterocolitica* infection were launched through EpiPulse. For all four events WGS was used to identify the clusters. One of the outbreaks was considered multi-country based on WGS analysis of clustering isolates.

Discussion

In 2021, yersiniosis was the third most commonly reported foodborne zoonotic disease in the EU/EEA after campylobacteriosis and salmonellosis [3,4]. From 2017 to 2019, the overall EU/EEA trend of reported cases of yersiniosis remained stable before decreasing considerably in 2020, most probably as a result of the COVID-19 pandemic, and to a lesser extent, the withdrawal of the United Kingdom from the EU. In 2021, the trend increased, and the number of reported cases was comparable to the situation before the pandemic. The yersiniosis notification rate increased in 2021 compared to both 2020 and to the pre-pandemic period (2017–2019). Although the COVID-19 pandemic was still ongoing, the gradual reduction of COVID-19 restriction measures and the return to daily activities (social events, doctor's visits, travel, reopening of bars, restaurants and catering facilities - i.e. schools, workplaces) may explain this increase.

Among the two pathogenic *Yersinia* species that were notified at EU/EEA level, *Y. enterocolitica* caused the majority of human infections, followed by *Y. pseudotuberculosis*. The main reservoir for *Y. enterocolitica* is the domestic pig, and the pathogenic *Y. enterocolitica* bioserotypes 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 the *Yersinia* bacteria to survive and grow at low temperatures is of considerable significance for food hygiene. Refrigeration temperatures are generally not sufficient to efficiently suppress the growth of these bacteria.

Y. pseudotuberculosis is a rare cause of human foodborne infections, but when cases occur these typically take the form of outbreaks. Contaminated vegetables have been the major vehicle of infection in these outbreaks, particularly root vegetables with a long period of cold storage [5]. In recent years, outbreaks of *Y. enterocolitica* linked to vegetables have also been reported [4, 6, 7], suggesting that sources other than pork may play a role. In 2021, 25 yersiniosis outbreaks were reported to the European Food Safety Authority (EFSA) annual zoonoses data collection. The number of outbreaks reported in 2021 was relatively stable compared with 2020 and the pre-pandemic years. These outbreaks involved 125 cases in 11 countries. *Y. enterocolitica* was the species identified as the causative agent in all the outbreaks. The serotype most commonly involved was O:3, but this was only reported for three outbreaks. Four 'strong-evidence outbreaks' with a known vehicle of infection were notified involving fruit/berries, vegetables or iceberg lettuce as a vehicle in three outbreaks, and pig meat in one outbreak [4].

There has been a transition process in clinical microbiological laboratories from culture-based detection methods to molecular-based using PCR panels, and this is still ongoing. According to the EU case definition for yersiniosis, PCR findings of *Y. enterocolitica* and *Y. pseudotuberculosis* have been notifiable since 2018. The subtypes of *Y. enterocolitica* detected varies depending on the choice of PCR panel and target genes used. Examples of marker genes used for the detection of *Yersinia* are *ail* and *vir*F which both exclude apathogenic *Y. enterocolitica* biotype (BT)1A, and this is also excluded in the EU case definition. Other target genes used in PCR panels are *inv*A and *y*stB. However, these target genes are also present in *Y. enterocolitica* BT1A. With regard to *Y. pseudotuberculosis*, all subtypes are considered pathogenic for humans. In 2021, biotype information, which traditionally has been crucial for evaluating the pathogenicity of *Y. enterocolitica* isolates, was only provided by six countries for less than one-third of the reported *Y. enterocolitica* cases. This might be partly due to the use of PCR panels for detection in countries where no isolates have been retrieved for typing. At EU level, there is no evidence so far that the number of reported cases or the proportion of isolates with serotype-biotype information would have been affected, which could be a marker for a higher proportion of notifications based on PCR [3].

As for the majority of food- and waterborne pathogens, whole genome sequencing (WGS) is also increasingly being used to subtype and to investigate clusters 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 seven gene Multi Locus Sequence Typing (MLST) schema. Cluster analysis of isolate sequences in outbreak and source tracing investigations can be performed by identifying the core genome MLST (cgMLST) allelic profiles of the isolates and assessing the allelic distances between them. Overall, the use of WGS for the typing of *Yersinia* isolates in animals and humans facilitates the monitoring of 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 in many cases these infections are related to the consumption of under-cooked, contaminated pork or cross-contamination of other food items during the handling and preparation of raw pork. Pork should only be consumed after adequate cooking, especially when being served to young children. Proper kitchen hygiene is required to avoid cross-contamination. It is also important to bear in mind that the 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, as well as 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 fresh produce becoming contaminated, thereby preventing 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 and Control (ECDC). European Union One Health 2021 Zoonoses Report. EFSA Journal 2022. Available at: https://www.efsa.europa.eu/en/efsajournal/pub/7666

5. Vasala M, Hallanvuo S, Ruuska P, Suokas R, Siitonen A, Hakala M. High frequency of reactive arthritis in adults after *Yersinia pseudotuberculosis* O:1 outbreak caused by contaminated grated carrots. Ann Rheum Dis. 2014 Oct;73(10):1793-6

6. Espenhain L, Riess M, Müller L, Colombe S, Ethelberg S, Litrup E, et al. Cross-border outbreak of *Yersinia enterocolitica* O3 associated with imported fresh spinach, Sweden and Denmark, March 2019. Euro Surveill. 2019 Jun 13; 24(24)

7. *Yersinia* outbreak linked to imported iceberg lettuce. Food Safety News. 20 March 2021. Available at: https://www.foodsafetynews.com/2021/03/yersinia-outbreak-linked-to-imported-iceberg-lettuce/

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, et al. 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.