

STEC infection

Annual Epidemiological Report for 2021

Key facts

- For 2021, 30 EU/EEA countries reported 6 534 confirmed cases of Shiga toxin-producing *Escherichia coli* (STEC) infection.
- The overall notification rate was 2.2 cases per 100 000 population. The highest notification rates were reported in Ireland, Denmark, Malta and Norway.
- After a significant decline in notification rates in 2020, primarily as a result of the COVID-19 pandemic, the EU/EEA notification rate increased to the pre-pandemic level in 2021.
- The highest notification rate of confirmed cases was observed in children aged 0–4 years, with 12.7 cases per 100 000 population for males and 10.8 cases per 100 000 population for females.

Introduction

Shigatoxigenic *Escherichia coli* (STEC) are strains of the bacterium *Escherichia coli* that can produce Shiga toxins. The main reservoir of STEC is grass-feeding animals, cattle in particular. STEC infection is regularly linked to the consumption of under-cooked beef, contaminated due to poor processing methods during slaughter, and to other contaminated foods, such as unpasteurised milk and dairy products, vegetables and water. Direct contact with infected animals (e.g. in petting farms/zoos) is considered to pose a considerable risk of STEC infection, especially in young children. STEC infection often causes gastroenteritis, enterocolitis, and bloody diarrhoea and sometimes a severe complication called haemolytic-uremic syndrome (HUS), particularly in children.

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 [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, data on STEC infections were reported by 30 EU/EEA Member States. Liechtenstein reported for the first time since 2008. The notification of STEC infections is mandatory in all but EU/EEA countries, where notification is either voluntary (Belgium and France) or based on another type of system (Italy). Eleven countries used the latest case definition (EU 2018), also including a PCR-positive find as a laboratory confirmed case; eight used the previous case definition from 2012; four reported in accordance with the 2008 definition and seven reported using other or unspecified case definitions. The surveillance systems for STEC infections have national coverage in all EU/EEA countries except for three: France, Italy, and Spain. As no estimate for population coverage was provided, notification rates could not be calculated for these three countries. In France, STEC surveillance is based on paediatric haemolytic-uraemic syndrome (HUS) surveillance, and similarly in Italy, the surveillance is primarily

based on the national registry for HUS [2]. For 2020–2021, Spain did not receive data from all the regions that normally report and the case numbers are therefore lower than expected. All countries except Bulgaria reported case-based data. No data was reported by the United Kingdom for 2020–2021 due to its withdrawal from the EU on 31 January 2020.

In addition to case-based surveillance, ECDC coordinates centralised analysis of whole genome sequencing (WGS) data where necessary to support multi-country outbreak investigations.

Epidemiology

For 2021, 6 534 confirmed cases of STEC infection were reported by 30 EU/EEA countries (Table 1). Twenty-seven countries reported at least two confirmed cases, and three countries reported no cases. The EU/EEA notification rate was 2.2 cases per 100 000 population, representing a 37.5% increase compared with the previous year.

The highest numbers of confirmed cases were reported by Germany and Ireland, which together accounted for 38% of all reported cases in the EU/EEA. The highest country-specific notification rates were observed in Ireland, Denmark, Malta and Norway with 17.5, 15.9, 13.2, and 8.1 cases per 100 000 population, respectively. A total of 11 southern and eastern EU/EEA countries reported ≤ 0.3 cases per 100 000 population (Table 1, Figure 1).

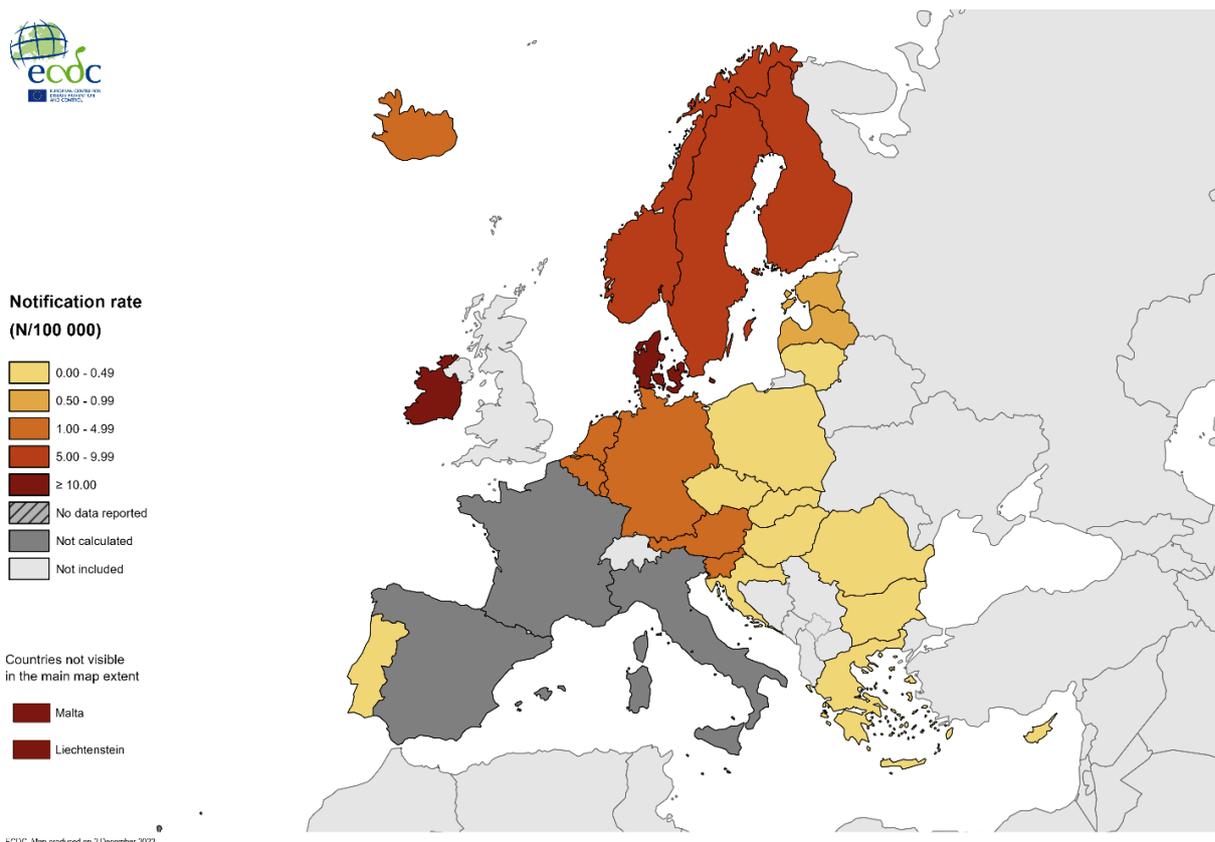
Forty-one percent of 2 575 STEC cases with known information were hospitalised. Eighteen of 4 625 cases with known outcome were reported to have died, resulting in a case fatality rate of 0.4%. Most of the deceased were over 65 years (61%). From a total of 365 HUS cases, the majority were in the youngest age groups from 0–4 years (64%), to 5–14 years (20%), with a case fatality rate of 2.4%. All four fatal cases with HUS were in the youngest age group (0–4 years).

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

Country	2017		2018		2019		2020		2021		
	Number	Rate	ASR								
Austria	250	2.8	305	3.5	284	3.2	288	3.2	383	4.3	4.4
Belgium	123	1.1	112	1.0	131	1.1	84	0.7	124	1.1	1.0
Bulgaria	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0.0
Croatia	7	0.2	10	0.2	22	0.5	8	0.2	12	0.3	0.3
Cyprus	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0.0
Czechia	37	0.3	26	0.2	33	0.3	32	0.3	36	0.3	0.3
Denmark	263	4.6	493	8.5	623	10.7	445	7.6	927	15.9	15.5
Estonia	3	0.2	7	0.5	6	0.5	10	0.8	7	0.5	0.5
Finland	123	2.2	210	3.8	311	5.6	175	3.2	288	5.2	5.2
France	260	NR	259	NR	335	NR	262	NR	298	NR	NR
Germany	2 065	2.5	2 226	2.7	1 907	2.3	1 409	1.7	1 635	2.0	2.0
Greece	3	0.0	1	0.0	5	0.0	3	0.0	10	0.1	0.1
Hungary	12	0.1	14	0.1	23	0.2	8	0.1	24	0.2	0.3
Iceland	3	0.9	3	0.9	27	7.6	4	1.1	7	1.9	1.7
Ireland	795	16.6	966	20.0	798	16.3	734	14.8	878	17.5	16.8
Italy	92	NR	73	NR	62	NR	45	NR	65	NR	NR
Latvia	1	0.1	3	0.2	48	2.5	2	0.1	13	0.7	0.7
Liechtenstein	NR	NR	NR	NR	NR	NR	NR	NR	6	15.4	14.3
Lithuania	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0.0
Luxembourg	1	0.2	3	0.5	4	0.7	0	0.0	10	1.6	1.6
Malta	9	2.0	41	8.6	53	10.7	43	8.4	68	13.2	13.3
Netherlands	392	2.3	488	2.8	459	2.7	323	1.9	484	2.8	2.8
Norway	381	7.2	494	9.3	511	9.6	331	6.2	437	8.1	8.0
Poland	4	0.0	6	0.0	14	0.0	3	0.0	7	0.0	0.0
Portugal	1	0.0	2	0.0	1	0.0	5	0.0	2	0.0	0.0
Romania	11	0.1	20	0.1	36	0.2	14	0.1	6	0.0	0.0
Slovakia	3	0.1	12	0.2	3	0.1	1	0.0	5	0.1	0.1
Slovenia	33	1.6	32	1.5	31	1.5	30	1.4	48	2.3	2.4
Spain	86	NR	126	NR	269	NR	74	NR	101	NR	NR
Sweden	504	5.0	892	8.8	756	7.4	491	4.8	653	6.3	6.2
UK	993	1.5	1 840	2.8	1 587	2.4	NR	NR	NR	NR	NR
EU-EEA	6 455	1.8	8 664	2.4	8 339	2.2	4 824	1.6	6 534	2.2	2.2

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

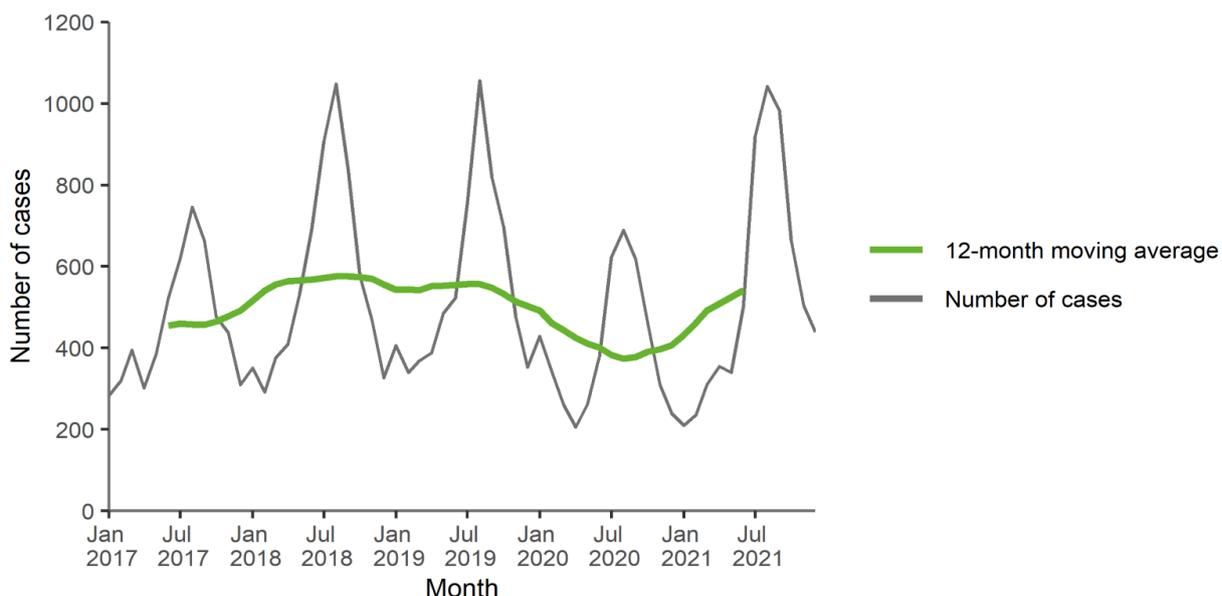
Figure 1. Distribution of confirmed STEC infection cases per 100 000 population by country, EU/EEA, 2021



Following a decrease in 2020 due to the COVID-19 pandemic, the EU/EEA trend in confirmed STEC cases increased in 2021 (Figure 2).

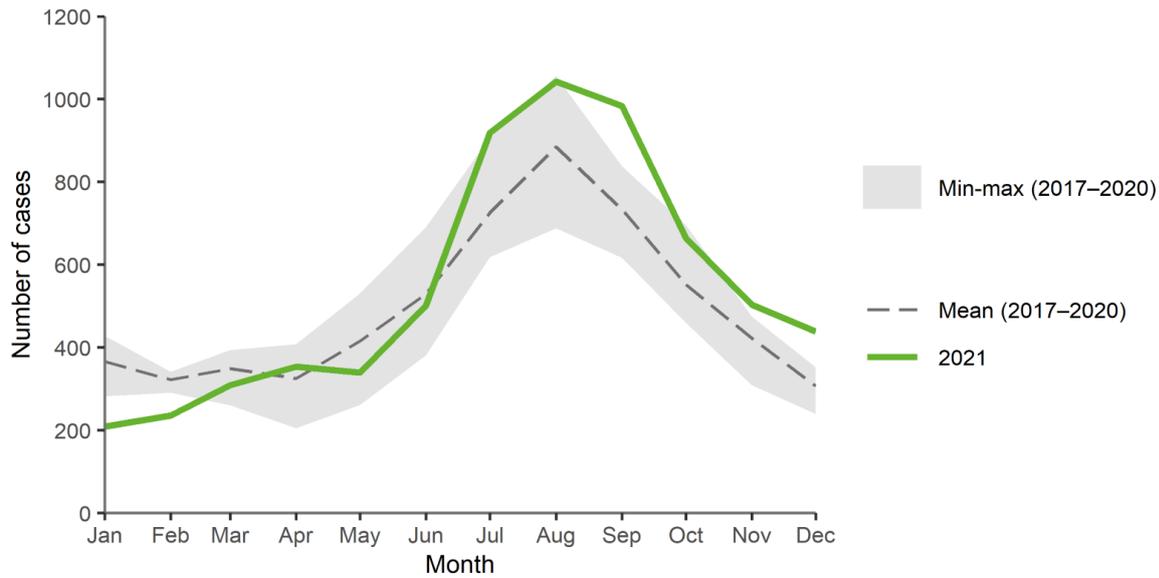
A clear seasonal trend in the number of confirmed STEC cases was observed between 2017 and 2021, with more cases reported during the summer months from June to September. In 2021, the number of reported cases was higher than the average compared to the same month in 2017–2020 for all months except January–February and May (Figure 3).

Figure 2. Distribution of confirmed STEC infection cases by month, EU/EEA, 2017–2021



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

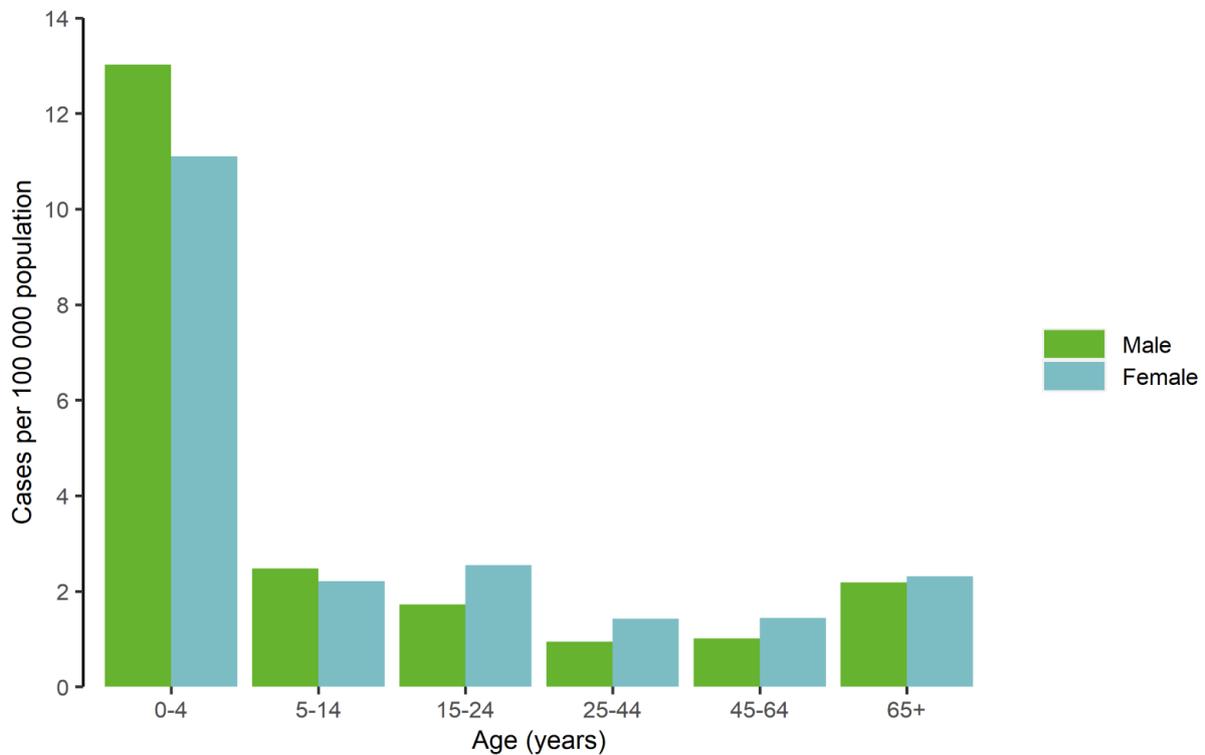
Figure 3. Distribution of confirmed STEC infection cases by month, EU/EEA, 2021 and 2017–2020



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

Among the 6 509 (99.6%) confirmed STEC cases for which gender was reported, 47% were males and 53% were females, with a male-to-female ratio of 0.9:1. The highest notification rate per 100 000 population was observed in the age group 0–4-years (12.7 for males and 10.8 for females). This age group accounted for 1 894 (29%) of the 6 532 cases for whom information on age was available. The notification rate decreased with age and was lowest (0.9) in the 25-44 and 45-64-years age groups for males. For females, the lowest notification rate (1.3) was in the same age groups as for males (Figure 4).

Figure 4. Distribution of confirmed STEC infection cases per 100 000 population, by age and gender, EU/EEA, 2021



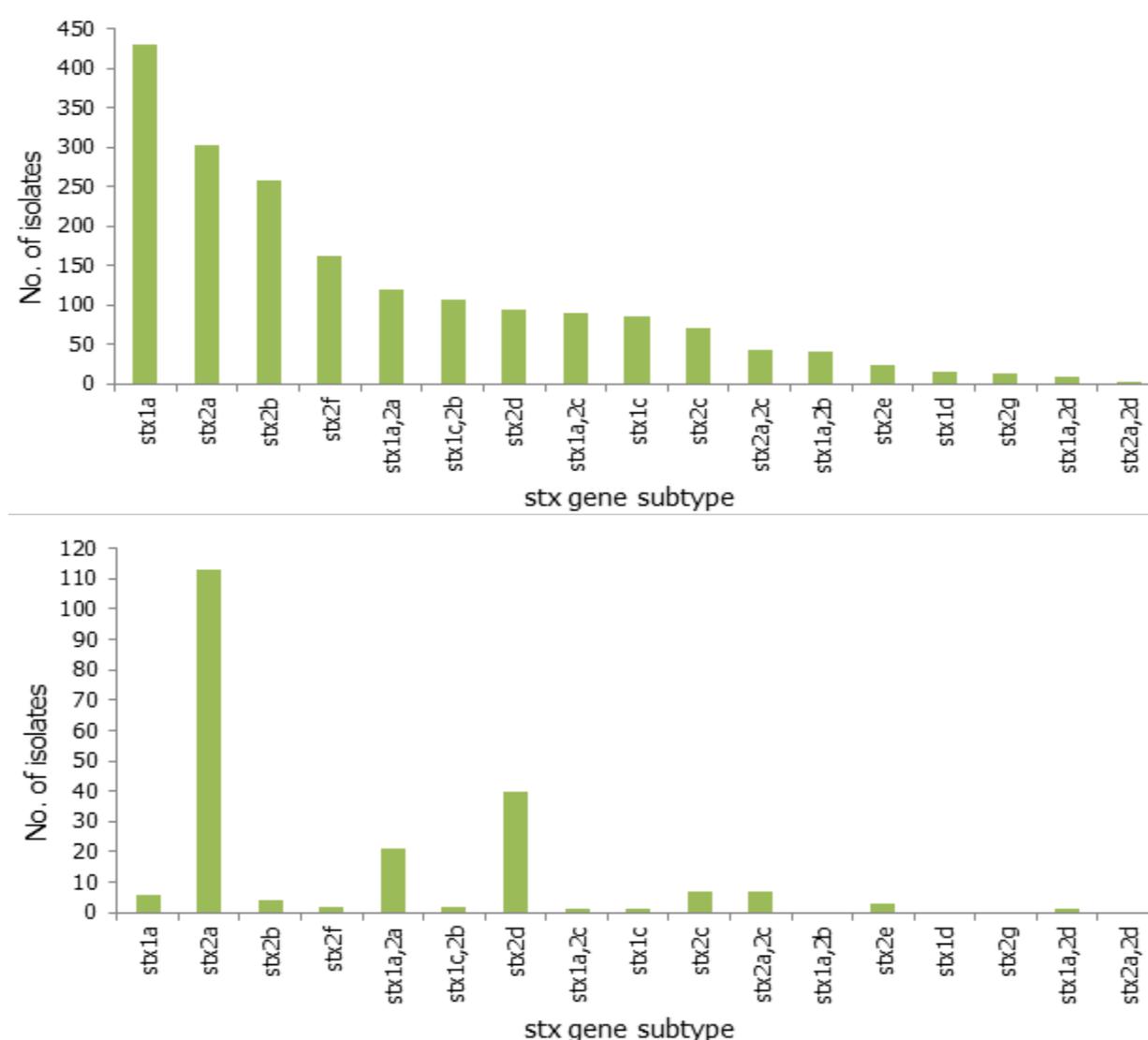
Source: Country reports from Austria, Belgium, Bulgaria, Croatia, Cyprus, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, Norway, the Netherlands, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden.

Microbial surveillance

Information on STEC serogroups was reported by 23 countries for 3 642 cases (55.7%) in the EU/EEA in 2021. The five most frequently reported serogroups were O157 (15.1%), O26 (14.7%), O103 (8.4%), O145 (4.6%) and O146 (3.7%). These serogroups together accounted for 46.5% of the total confirmed STEC cases with known serogroups in 2021. Among HUS cases, serogroup O26 was most commonly reported (34%) followed by O157 (19.8%). The proportion of cases where no serotype could be retrieved was 25.9%, which was an increase on previous years. Antigen H was reported for 2 496 confirmed cases (38.2%). The most common serotypes were O157:H7 (13.3%), followed by O26:H11 (10.4%) and O103:H2 (10.0%).

Data on virulence gene combinations (based on Shiga toxin-coding genes *stx1*, *stx2* and intimin-coding gene *eae*) was provided for 2 650 (40.6%) STEC cases. The most frequently reported virulence gene combination was *stx2* and *eae* -positive (25.5%) and *stx2* positive and *eae* negative (20.1%). In strains isolated from severe cases (HUS, bloody diarrhoea and/or hospitalised cases), 31.5% were positive *stx2* and *eae*. Almost half of the isolates with reported *stx1* and *stx2* were provided with information on *stx* gene subtypes (40.7% and 48.5%, respectively). Among isolates with reported subtyping data the most common *stx* subtypes were *stx1a* (23.1%), *stx2a* (16.3%), *stx2b* (13.8%) and *stx2f* (8.7%). The subtype *stx2f* has been an emerging variant with the highest number of isolates reported since 2009 (163 cases in 2021). The most common serotype associated with *stx2f* was O63:H6 (47.0%). In severe human infections *stx2a* (32.9%) was most commonly reported, followed by *stx1a* (24.9%), *stx2c* (9.7%) and *stx1a,2c* (8.7%). For cases with HUS where subtype was reported (57.0%), 92% had one of the subtypes *stx2a*, *stx2d* or *stx1a,2a*, showing the potential for these variants to cause more severe disease (Fig.5).

Figure 5. Distribution of *stx* gene subtypes for all confirmed cases with complete subtyping data (n=1 865) (top panel) and for STEC-associated HUS cases (n=208) (bottom panel), in EU/EEA, 2021



Note: cases with isolates ≤1 not included.

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, nine events on STEC infection were launched through EpiPulse. One genetically-related multi-country cluster of STEC serogroup O103:H2, *stx1a* was detected between June and August in three countries, with 75 cases.

Discussion

In 2021, STEC was the fourth most commonly reported foodborne zoonotic disease in the EU/EEA [3,4]. The overall EU/EEA trend of reported STEC cases in 2017–2019 was increasing. Contributing factors probably include changes in laboratory techniques, such as the increasing use of multiplexed PCR assays PCR with DNA extraction from specimens as a template, followed by isolation and further strain characterisation if possible. In 2020, the trend in reported cases of STEC infection decreased considerably due to the COVID-19 pandemic, although it increased to the pre-pandemic (2017–2019) level again in 2021. The withdrawal of the United Kingdom from the EU resulted in a lower EU/EEA notification rate for STEC, related to a recurring high number of cases previously reported by the United Kingdom relative to population size.

STEC was the third most frequent bacterial agent detected in food- and waterborne outbreaks in the EU reported to the European Food Safety Authority (EFSA) annual zoonoses data collection in 2021. STEC outbreaks involved 275 cases in 36 outbreaks across 11 Member States. Information on the STEC serogroup was available for 22 outbreaks. Overall, the serogroups identified in STEC outbreaks were O157 (nine outbreaks), O26 (six outbreaks), O103 (five outbreaks) and O12, O145, O146, O91 (one outbreak each). A food vehicle was reported in five strong-evidence foodborne outbreaks; an outbreak of STEC O26 was caused by raw cow milk, pre-cut vegetables caused an outbreak of STEC O103, in two O157 outbreaks the incriminated vehicle was bovine meat (minced meat and carpaccio), and in one outbreak caused by 'meat and meat products' the serotype was not specified. The majority of STEC isolates from food came from the top-20 STEC serogroups reported in human infections in EU [4].

In 2021, the most frequently reported serogroup identified in human STEC cases was O157, followed by O26, although the two proportions diverged by only 0.4%. In recent years, there has been an increasing trend in the number of STEC O26 cases observed, while the number of STEC O157 cases has decreased during the same period. This inversion in relative frequency can be explained by the increasing number of laboratories that are testing for serogroups other than O157. There has also been a shift in diagnostic methods, with PCR amplification of Shiga toxin-coding genes (*stx*) being more commonly used to detect STEC cases in several countries instead of diagnosis being primarily based on cultivation and serogroup determination for detection of O157. The change in diagnostics could also result in more samples being screened for STEC, where the phenotypic methods required different selective plates to isolate different STEC serotypes, which is a more demanding process than isolating *Salmonella*, for example. Over the past five years, the proportion of STEC cases with no information on serogroup has been steadily increasing at EU-level, which could be a marker for a higher proportion of notifications based on PCR. In 2021, STEC O26 was the most reported serogroup among HUS cases, as has been the case since 2016. Most of the HUS cases caused by this serogroup were reported by three countries (France, Italy and Belgium), two of which base their STEC infection surveillance mainly on the detection of HUS cases. A high proportion of HUS cases due to non-O157 serogroups points towards an emerging risk of severe infections caused by serogroups other than O157 [5,6].

Although the recent pathogenicity assessment of STEC confirms that serogroup is not a marker of pathogenicity, it still has some importance as an epidemiological marker, and is still useful for observing the circulation of the different STEC types in food and human cases of disease [7]. Analysis of the virulence gene combinations (*stx* and *eae*), particularly the subtyping of the *stx* genes, enables STEC virulotypes to be identified which have a higher frequency of association with severe disease in humans (hospitalised cases, bloody diarrhoea and HUS cases). Since 2012, there has been a steady increase in the reporting of *stx* and *eae* virulence genes to TESSy. The majority (>90%) of severe human cases were reported with information on *stx* gene subtypes and *stx2a* and *stx2d* are clearly associated with more severe disease and HUS specifically, as was also seen in 2021. An increase in reporting of *stx2f* was seen in 2021, with the highest level of reporting for this subtype. This variant is genetically more distant from the other subtypes within *stx2*. The general PCR primers targeting the *stx2* genes in primary diagnostics could therefore leave *stx2f* undetected. In recent years, an increase in awareness of this subtype could have resulted in more clinical laboratories complementing their PCR panels to also target this variant [9]. In general, the subtyping of Shiga toxin genes is still insufficiently comprehensive for food and animal isolates to enable an assessment of the risk of STEC circulating in the vehicles of infection.

Ruminants are the main natural reservoir of STEC. Over the years, several STEC outbreaks among children have been reported in petting farms/zoos due to direct contact with STEC-positive animals. Under-cooked ground beef or other meats have been found to be a significant risk factor for acquiring sporadic foodborne STEC infection, most often caused by serogroup O157 [8]. Beef and fresh produce (fruit and vegetables) have been incriminated as the most important sources of STEC infections in Europe, each estimated to be associated with 30% of illnesses [10]. Reported outbreaks also highlight a risk of STEC infections associated with raw milk and cheese made from unpasteurised milk [4,6].

Public health implications

STEC infection is mainly acquired through consumption of contaminated food or water and contact with animals and/or their faeces. Good hygiene practices in food processing and good handling practices at premises dealing with animals, as well as guidance on hand hygiene for visitors to petting farms/zoos can decrease the risk of infections and further outbreaks. Adequate cooking of food at home, particularly beef, and the use of pasteurised milk may reduce the risk of foodborne STEC infections. The STEC serogroups most frequently found in food samples are also those most commonly reported in human infections, highlighting the role of contaminated food as a source of human infections. Under-cooked meat and unpasteurised milk and dairy products, as well as fresh produce, are well known potential sources of STEC infections and outbreaks.

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 \(europa.eu\)](https://surveillance.ecdc.europa.eu/2021/01/surveillance-systems-overview-for-2021)
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=59>
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 from: <https://www.efsa.europa.eu/en/efsajournal/pub/7666>
5. Valilis E, Ramsey A, Sidiq S, DuPont HL. Non-O157 Shiga toxin-producing *Escherichia coli*-A poorly appreciated enteric pathogen: Systematic review. Int J Infect Dis. 2018 Nov; 76:82-87.
6. Jones G, Lefèvre S, Donguy MP, Nisavanh A, Terpant G, Fougère En et al. Outbreak of Shiga toxin-producing *Escherichia coli* (STEC) O26 paediatric haemolytic uraemic syndrome (HUS) cases associated with the consumption of soft raw cow's milk cheeses, France, March to May 2019. Euro Surveill. 2019 May; 30:24(22).
7. EFSA Panel on Biological Hazards, 2020. Pathogenicity assessment of Shiga toxin-producing *Escherichia coli* (STEC) and the public health risk posed by contamination of food with STEC. EFSA Journal 2020; 18(1):5967.
8. Kintz E, Brainard J, Hooper L, Hunter P. Transmission pathways for sporadic Shiga-toxin producing *E. coli* infections: A systematic review and meta-analysis. Int J Hyg Environ Health. 2017 Jan; 220(1):57-67.
9. 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. International Journal of Infectious Diseases. 2022 Jan; 114:195-201.
10. Pires SM, Majowicz S, Gill A, Devleeschauwer B. Global and regional source attribution of Shiga toxin-producing *Escherichia coli* infections using analysis of outbreak surveillance data. Epidemiology and Infection. 2019 Jan; 147.