

SURVEILLANCE REPORT

Shigellosis

Annual Epidemiological Report for 2022

Key facts

- In 2022, 30 EU/EEA countries reported 4 149 confirmed cases of shigellosis. Of those cases with information available on travel history, 48% were associated with travel.
- The overall notification rate was 1.5 cases per 100 000 population. This represents an increase in the notification rate compared to 2020 and 2021, but is consistent with the notification rates reported before the COVID-19 pandemic (2019 and preceding years).
- The highest notification rate was observed in children under five years of age, followed by male adults aged 25–44 years. Sexual transmission of shigellosis among gay, bisexual and other men who have sex with men (gbMSM) is thought to have contributed to the gender imbalance in the latter group.
- In 2022, two multi-country shigellosis outbreaks were reported to EpiPulse. Both involved *S. sonnei* ST152 and had links to international travel.
- The rise in resistance to first- and second line antimicrobials in *Shigella* isolates observed in recent years is of concern.

Introduction

Shigellosis is a gastrointestinal infection caused by one of four species of *Shigella* bacteria: *Shigella sonnei*, *S. flexneri*, *S. boydii* and *S. dysenteriae*. Humans are the only primary reservoir and thus, infection with *Shigella* can occur if a person ingests material, food or water contaminated by human faeces, either via contaminated hands or objects which have been in contact with infected faeces. Secondary infections are common due to the low infectious dose. The incubation period is 1–2 days and symptoms can range from mild to severe. Shigellosis symptoms include diarrhoea that may be bloody or prolonged (more than three days' duration), fever, abdominal pain and discomfort and having a frequent urge to pass stools, without being able to do so (tenesmus). In low-income settings, shigellosis is typically a disease affecting children, although in high-income settings, international travellers and gay, bisexual and other men who have sex with men (gbMSM) are considered the main groups at risk. In recent years, increasing resistance of *Shigella* to first- and second line antimicrobials has been a concern.

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].

Stockholm, February 2024

© European Centre for Disease Prevention and Control, 2024. Reproduction is authorised, provided the source is acknowledged.

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

Thirty countries reported data for 2022. Twenty-five countries used various versions of the EU case definition for shigellosis (from 2002, 2008, 2012 or 2018). Compared with previous EU case definitions, the 2018 EU case definition allows genotypic tests for laboratory confirmation of a probable case. Denmark, France, Germany, Italy and Liechtenstein used a case definition described as 'other' and Belgium did not specify the definition used [2].

The notification of shigellosis is mandatory in 27 EU/EEA countries. Three countries have a voluntary notification system (Belgium, France and Italy). The surveillance systems for shigellosis had full national coverage in all reporting countries except in France and Italy. In France, the coverage of the surveillance system was estimated to be 44% of the population; this estimate was used when calculating notification rates for France. No estimate was provided for the coverage of the surveillance system in Italy; rates are therefore not calculated. For 2020, Spain had not received data from all regions so rates were not displayed for this year. All countries provide case-based data except Bulgaria which reports aggregate data. Both reporting formats were included to calculate number of cases, notification rates, disease trends, and distributions by age and gender.

In addition to TESSy reporting, information was collected from event-based surveillance for shigellosis clusters or outbreaks with a potential EU dimension through the European surveillance portal for infectious diseases, EpiPulse.

Epidemiology

For 2022, 30 EU/EEA countries reported 4 149 confirmed cases of shigellosis (Table 1). Three countries accounted for 50.6% of all cases: France, the Netherlands and Spain, with France alone accounting for 31.7% of all cases. Two countries, Iceland and Lichtenstein, reported zero cases.

The overall EU/EEA notification rate for shigellosis cases was 1.5 cases per 100 000 population for 2022. France reported the highest notification rate of all EU/EEA countries, with 4.3 cases per 100 000 population, followed by Luxembourg and Slovakia at 4.2 and 3.3 cases per 100 000 population, respectively (Table 1, Figure 1).

Information on travel history was available for 2 492 cases (60.1%) and 1 198 of these (48.0%) were related to travel. Among travel-related cases, the probable country of infection was reported for 1 104 cases: Egypt (13.9%; 153 cases), Morocco (11.5%; 127 cases) and Tunisia (10.7%; 118 cases) were those most frequently mentioned as probable country of infection.

A small proportion of cases (13.9%; 578 cases) had information on the suspected mode of transmission; transmission via food was the most commonly reported (68.2%; 394 cases), followed by sexual transmission (20.6%; 119 cases) and person-to-person (10.0%; 58 cases; excluding mother-to-child and sexual transmission). It is worth noting that among cases where the suspected mode of transmission was sexual, all were male (119 cases). Four cases were associated with transmission from recreational water, three cases had unspecified 'other' mode of transmission.

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

Countral	2018		2019		2020		2021		2022	
Country	Number	Rate								
Austria	69	0.8	72	0.8	25	0.3	39	0.4	60	0.7
Belgium	427	3.7	423	3.7	115	1.0	199	1.7	307	2.6
Bulgaria	235	3.3	219	3.1	47	0.7	27	0.4	52	0.8
Croatia	29	0.7	17	0.4	1	0.0	3	0.1	2	0.1
Cyprus	4	0.5	2	0.2	0	0.0	0	0.0	1	0.1
Czechia	142	1.3	127	1.2	72	0.7	41	0.4	104	1.0
Denmark	146	2.5	192	3.3	51	0.9	57	1.0	107	1.8
Estonia	17	1.3	29	2.2	4	0.3	2	0.2	10	0.8
Finland	111	2.0	154	2.8	41	0.7	30	0.5	56	1.0
France	1 132	3.8	1 167	3.9	564	1.9	769	2.6	1 290	4.3
Germany	655	0.8	614	0.7	140	0.2	142	0.2	339	0.4
Greece	78	0.7	104	1.0	61	0.6	23	0.2	60	0.6
Hungary	13	0.1	45	0.5	61	0.6	30	0.3	18	0.2
Iceland	4	1.1	4	1.1	1	0.3	1	0.3	0	0.0
Ireland	101	2.1	121	2.5	66	1.3	59	1.2	130	2.6
Italy	32	NRC	40	NRC	14	NRC	14	NRC	21	NRC
Latvia	17	0.9	14	0.7	3	0.2	1	0.1	3	0.2
Liechtenstein	NDR	NRC	NDR	NRC	NDR	NRC	0	0.0	0	0.0
Lithuania	21	0.7	17	0.6	2	0.1	2	0.1	6	0.2
Luxembourg	11	1.8	13	2.1	13	2.1	8	1.3	27	4.2
Malta	4	0.8	9	1.8	0	0.0	0	0.0	5	1.0
Netherlands	484	2.8	516	3.0	187	1.1	202	1.2	419	2.4
Norway	102	1.9	133	2.5	37	0.7	33	0.6	80	1.5
Poland	89	0.2	34	0.1	12	0.0	18	0.0	38	0.1
Portugal	24	0.2	8	0.1	5	0.0	11	0.1	20	0.2
Romania	147	0.8	117	0.6	15	0.1	17	0.1	25	0.1
Slovakia	195	3.6	146	2.7	103	1.9	131	2.4	182	3.3
Slovenia	26	1.3	24	1.2	14	0.7	18	0.9	16	0.8
Spain	455	1.0	512	1.1	72	NRC	309	0.7	598	1.3
Sweden	259	2.6	305	3.0	81	0.8	77	0.7	173	1.7
EU/EEA (30 countries)	5 029	1.6	5 178	1.7	1 807	0.7	2 263	0.8	4 149	1.5
United Kingdom	2 617	3.9	3 270	4.9	NDR	NRC	NA	NA	NA	NA
EU/EEA (31 countries)	7 646	2.0	8 448	2.2	1 807	0.7	NA	NA	NA	NA

Source: country reports. NDR: no data reported.

NRC: no rate calculated.

NA: not applicable.

No data for 2020–2022 were reported by the United Kingdom, due to its withdrawal from the EU on 31 January 2020. Rates are not calculated for Italy (2017–2022) or Spain (2020) as data are not nationally representative.



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

During the period 2018 and 2022, the 12-month moving average of the reported number of cases was lowest in 2020 (Figure 2). Since 2020, the number of cases has steadily increased towards pre-pandemic figures in 2022. In 2020 and 2021, a considerable decrease in the number of reported cases was observed compared to previous years. This is mainly attributed to the COVID-19 pandemic and restrictions, including reduced international travel, fewer social interactions, and improved hygiene measures (hand washing, etc.). In fact, the lowest number of cases ever reported since 2007 (which is when EU-level surveillance began) was in 2020.





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

Administration boundaries: © Eurographics The boundaries and names shown on this map do not imply official endorsement or acceptance by the European Union. ECDC. Map produced on 17 January 2024.

Shigellosis typically has a seasonal pattern of transmission in EU/EEA countries, with cases frequently peaking in the summer and autumn months (Figure 3). In 2022, this peak was mainly driven by an increase in shigellosis cases in France, Germany, and the Netherlands, linked to two multi-country shigellosis outbreaks (see section 'Outbreaks and other threats' below for further information).



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

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

For 2022, the highest notification rate of shigellosis was reported in children under five years at 3.0 cases per 100 000 population (Figure 4). Male cases aged 25–44 years had a notification rate of 2.7 cases per 100 000 population. The overall male-to-female ratio was 1.8:1 and in the age group 25–44 years, 1.7:1.



Figure 4. Confirmed shigellosis 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

Species information was available for 3 434 cases (82.8%) (Table 2). Among these, *Shigella sonnei* was the most frequent species identified, followed by *Shigella flexneri*. Together they accounted for 95.8% of confirmed cases. *S. sonnei* was the most frequently identified species among both travel-related cases (n=749; 69.7%) and domestically acquired cases (n=552; 54.8%). *S. sonnei* has been the most frequently reported *Shigella* species since 2007. *S. flexneri* serotype 2a (154 cases), 1b (153 cases) and 3a (98 cases) were the most common serotypes reported for *S. flexneri* (among 467 cases with serotype information provided). The most common serotype reported for *S. boydii* was serotype 2 (11 of 27 cases with available information) and for *S. dysenteriae*, serotype 16 (one of the newly defined serotypes) and serotype 3 were most common (three cases each from 12 cases with available information). *S. sonnei* is a clonal species and is not divided into different serotypes. A small number of sequence types (STs) were reported through event-based surveillance via EpiPulse in 2022 (see section 'Outbreaks and other threats' below); ST152 was the ST most frequently reported for *S. sonnei*.

Pathogen	Number of cases	Percentage
Shigella sonnei	2 139	62.3%
Shigella flexneri	1 151	33.5%
Shigella boydii	99	2.9%
Shigella dysenteriae	45	1.3%
Total	3 434	100%

	Table 2. Number	of confirmed	shigellosis	cases by	species,	EU/EEA,	2022
--	-----------------	--------------	-------------	----------	----------	---------	------

Source: TESSy data extracted 10 November 2023

Six EU/EEA countries reported antimicrobial resistance data for *S. sonnei* and *S. flexneri* cases for 2022. Table 3 provides an overview of antimicrobial resistance in isolates from confirmed shigellosis cases, stratified by species (only *S. sonnei* and *S. flexneri* presented). Isolates were predominantly tested for ampicillin, ceftazidime and ciprofloxacin resistance. In both species, more than 80% of isolates were resistant to ampicillin. Resistance to third-generation cephalosporins was generally low in *S. flexneri*, but in *S. sonnei*, at least half of isolates were either resistant or susceptible with increased exposure. This resistance pattern in *S. sonnei* isolates is related to an outbreak of extended-spectrum beta-lactamase (ESBL)-producing *S. sonnei* ST152 infections with travel links to Tunisia (see section 'Outbreaks and other threats' below). Resistance to ciprofloxacin was also notable at 31.9% and 40.2% in *S. sonnei* and *S. flexneri* isolates, respectively. A smaller number of isolates were tested for susceptibility to trimethoprim-sulfamethoxazole (STX) than other antibiotics. Of these the majority the of *S. sonnei* isolates. No isolates were reported to have been tested for azithromycin, the reasons for this are unknown.

		Ampicillin (6 countries)		Azithromycin (0 countries)		Cefotaxime (5 countries)		Ceftazidime (6 countries)		Ciprofloxacin (6 countries)		SXT (3 countries)	
	Susceptibility	N	%	N	%	N	%	N	%	N	%	N	%
S. sonnei	R	541	80.6	NA	NA	134	49.5	18	2.7	208	31.9	41	97.6
	I/NWT	0	0.0	NDR	NA	1	0.4	388	57.9	187	28.7	0	0.0
	S/WT	130	19.4	NDR	NA	136	50.2	264	39.4	257	39.4	1	2.2
	Total	671	NA	NA	NA	271	NA	670	NA	652	NA	42	NA
S. flexneri	R	124	91.2	NA	NA	6	6.7	7	5.2	51	40.2	6	30
	I/NWT	0	0.0	NDR	NA	0	0.0	38	27.9	7	5.5	0	0.0
	S/WT	12	8.8	NDR	NA	84	93.3	91	66.9	69	54.3	14	70.0
	Total	136	NA	NA	NA	90	NA	136	NA	127	NA	20	NA

Table 3	Antimicrohial	resistance in	isolates f	from confirmed	l chinellocic	cases by	nathogen	2022
Table J.	Anumiciobiai	i constante in	isulates i		i siliyeliosis	cases by	paulogen,	2022

Source: country Reports from Austria, Belgium, Estonia, France, Italy, and Lithuania. TESSy data extracted 10 November 2023.

N – Number of isolates; NA – Not applicable; NDR – Not reported.

% - percent of tested isolates; R - resistant; I/NWT - Susceptible, increased exposure or non-wild type.

S/WT – Susceptible, standard dosing regimen or wild type; SXT – Trimethoprim-sulfamethoxazole.

* Azithromycin classification is based on epidemiological cut-off values and therefore the terminology wild type and non-wild type is used.

In 2022, thirteen countries reported 512 cases with 'probable' case classification, among which three-quarters (76%) were reported by Sweden (261 cases; 51%), Luxembourg (91 cases; 18%) and Spain (38 cases; 7%). This is most probably explained by the current EU case definition (2018) where the detection of *Shigella spp*. nucleic acid in a clinical specimen without bacterial isolation is classified as a probable case. Clinical laboratories in many EU/EEA countries have gradually switched from culture-based diagnostic tests to PCR-based methods as the primary diagnostic tool for detection of gastrointestinal bacterial pathogens. The target gene used in PCR panels for *Shigella*/enteroinvasive E. *coli (EIEC)* is the *ipaH* gene which cannot distinguish between *Shigella* and EIEC. The outcome of the PCR analysis is therefore positive or negative for *Shigella*/EIEC. To be able to confirm a case of shigellosis, culture is required. However, *Shigella* is challenging to culture, which in part is because it may not survive transport to the laboratory or storage due to pH changes in the stool sample. It is important to consider that while a specimen may be negative for bacterial isolation, a positive PCR can yield important information for specific events – e.g. investigation of a shigellosis outbreak.

Outbreaks and other threats

During 2022, two shigellosis outbreaks were reported in EpiPulse. In November 2022, France reported a rapid and unusual increase in cases of ESBL-producing S. sonnei ST152 infections with travel links to Tunisia. In this outbreak a rapid and unusual increase in cases of ESBL-producing S. sonnei ST152 infections was reported. Between July and October 2022, 152 cases (64% female) were identified in France, among which 36.5% reported travel to Tunisia [4]. Information from interviewed cases who travelled to Tunisia did not identify a common exposure or likely mode of transmission (different cities visited, different types of housing, no common restaurant identified) [4]. All French strains were part of the hierarchical cluster HC10_20662 according to the Enterobase cqMLST scheme (different HC5 profiles) and belonged to genotype 3.6.3 using Hawkey et al. (2021) genotyping nomenclature [4]. By early-December 2022, over 100 cases from Czechia, France, the Netherlands, and Norway had been identified, either as part of cluster HC10 20662 and/or as cases with travel history to Tunisia [4]. It is worrying that several isolates among the cases identified were ESBL-producers, resulting in reduced susceptibility or resistance to third-generation cephalosporins [4]. Resistance markers for azithromycin resistance, and decreased susceptibility to ciprofloxacin were also detected [4]. As with other bacterial gastrointestinal pathogens, whole genome sequencing (WGS) is becoming more common for Shigella to assess markers of antibiotic resistance, primarily for surveillance purposes and as a typing marker for outbreak strains. Subtyping using WGS is also an efficient tool to identify clusters of Shigella spp.

In November 2022, the Netherlands opened a separate event in EpiPulse about an unusual increase in cases of *S. sonnei* infections with travel history to Cabo Verde. This outbreak evolved rapidly in the latter half of 2022. By mid-February 2023, over 250 cases with *S. sonnei* ST152 infections had been identified in ten EU/EEA countries (Belgium, Czechia, Denmark, Finland, France, Germany, the Netherlands, Norway, Portugal and Sweden), the UK, and the US among international travellers returning from Cabo Verde. The centralised sequencing analysis of more than 100 human isolates from five counties showed a genetically compact cluster, suggesting a common source. The cases were predominantly women, with a female-to-male ratio of 2.5:1. The *S. sonnei* strains among cases showed predicted resistance to trimethoprim, streptomycin, and hydrogen peroxide. Co-infections with other bacterial and parasitic gastrointestinal pathogens (e.g. *Salmonella, Campylobacter, Cryptosporidium*, and strains of diarrhoeagenic *Escherichia coli*) were also reported among cases. While the exact source of the infections could not be identified, multiple modes of transmission were considered, including foodborne transmission (e.g. via infected food handlers) and possibly also person-to-person transmission. Based on the available information, many cases reported staying in the same region on one of the islands, in all-inclusive hotels. A rapid risk assessment was published in February 2023 [5].

According to data collected by the European Food Safety Authority (EFSA) and reported in the European Union One Health 2022 Zoonoses report [6], 27 foodborne shigellosis outbreaks (16 more than the number of foodborne outbreaks reported in 2021) were reported by 11 EU/EEA countries (Austria, Belgium, France, Germany, Greece, Ireland, Malta, the Netherlands, Slovakia, Spain, and Sweden)¹. Among 14 food-borne outbreaks with available information, 12 were caused by *S. sonnei* and two by *S. flexneri*.

Discussion

A total of 4 149 confirmed shigellosis cases were reported by 30 EU/EEA countries in 2022. This corresponds to an EU/EEA notification rate of 1.5 cases per 100 000 population, which is higher than the notification rate reported during the COVID-19 pandemic years of 2020 and 2021, but consistent with the rates reported in the years preceding the COVID-19 pandemic. In 2022, the number of shigellosis cases and notification rates increased in the majority of countries (25 of 30 countries), indicating a rise in shigellosis transmission in EU/EEA countries. This may be linked to increased international travel, more social interaction and less social distancing, and reduced adherence to hygiene measures such as hand washing and disinfection, which were presumably more common during the COVID-19 pandemic.

¹ These data were collected by EFSA.

In 2022, the majority (55.6%) of shigellosis cases were reported by France (31.1%), Spain (14.4%) and the Netherlands (10.1%). In 2022, France reported the highest number of shigellosis cases ever since 2007. A large proportion of the 2022 cases (775 of 1 290 cases; 60.1%) were reported between August and November and relate to the multicounty shigellosis outbreak reported in EpiPulse by France (see section 'Outbreaks and other threats'). Similarly, the Netherlands reported a large proportion of their cases (250 of 419 cases; 48.4%) between August and December 2022. This relates to the multi-country outbreak of *S. sonnei* infections and involved some with travel history to Cabo Verde (see section 'Outbreaks and other threats'). This outbreak evolved rapidly in several EU/EEA countries during the latter half of 2022.

In 2022, Spain reported the highest number of shigellosis cases since 2007. If the data from the pandemic years of 2020 and 2021 is excluded, both the number of cases and the annual notification rates for shigellosis have been increasing in Spain since 2016 [3]. Among cases with available information, a large proportion of cases reported by Spain since 2016 were male (72.3%; 1 768 of 2 446 cases), in those aged 25–44 years (50.2%; 1 228 of 2 446 cases), infected with either *S. sonnei* or *S. flexneri* (96.7%; 1 264 of 1 307 cases) or domestically acquired infections (81.5%; 1 654 of 2 029 cases). A study of shigellosis cases diagnosed between 1988 and 2012 in Barcelona reported a change in the epidemiology of the disease, involving a transition from both genders being equally affected to a higher incidence being reported in men, especially since 2009 [7].

In recent years, an increase in sexual transmission of multi-drug and extensively drug resistant *Shigella* strains, particularly *S. sonnei* and *S. flexneri*, has been observed in several countries, particularly among gbMSM [8, 9]. In late 2021 and early 2022, the UK Security Agency (UKHSA) reported a rise in cases of extremely antibiotic-resistant *S. sonnei* infections, mainly in gbMSM [10]. This was also highlighted in Epipulse where nine countries reported having detected genetically similar strains, with cases predominantly identified among adult males and gbMSM. The high prevalence of antimicrobial resistant infections in adult males and gbMSM is of particular concern. Information on sexual orientation is not available in the EU-level surveillance data for shigellosis. However, 20.7% of those with known transmission mode in 2022 (119 of 576 cases) were classified as sexually transmitted, of which all cases were male.

Unfortunately, the EU-level surveillance data for shigellosis do not allow for inference regarding the presence of antimicrobial resistance in the EU/EEA. However, of the isolates tested in 2022, a substantial proportion were resistant to ampicillin and ciprofloxacin. In addition, almost all of the *S. sonnei* isolates were resistant to trimethoprim-sulfamethoxazole and half were resistant or had decreased susceptibility to third-generation cephalosporins. Given that these drugs are recommended as first or second-line therapy, concerns have been raised about the risk of therapeutic failure [11]. Fluoroquinolone-resistant *Shigella* spp. was listed as a priority for antibiotic development by the World Health Organization in 2017 [12].

Public health implications

Humans are the primary reservoir for *Shigella* species, although non-human primates also can be infected. Transmission occurs either through person-to-person contact or ingestion of contaminated food or water [12]. On a global scale, the burden of shigellosis is highest in low- and middle-income settings [12]. In recent decades, sexually transmitted *Shigella* has been increasingly reported [12]. In high-income settings, international travellers and gbMSM have been identified as the main risk groups for shigellosis [12, 14]. Collaboration and information sharing is recommended between experts in food- and waterborne diseases, sexually transmitted diseases and antimicrobial resistance. In general, prevention of infection and control of outbreaks relies on good personal and environmental hygiene practices to prevent faecal-oral transmission, including during sexual activities.

With regard to gbMSM, it is important to increase awareness among clinicians and microbiology laboratories of the international spread of multidrug-resistant *Shigella* bacteria among gbMSM and to ensure antimicrobial susceptibility testing of *Shigella* for cases of gastroenteritis in gbMSM. It is recommended that public health authorities collaborate with civil society organisations working with MSM in order to increase awareness in this population.

Individuals who travel to endemic areas are encouraged to follow advice on how to avoid food and water-borne infections (e.g. frequent washing of hands with soap and warm water, avoid eating and drinking raw/unpasteurised foods such as fruit, vegetables, milk or dairy products, tap water - including ice made from tap water - and items purchased from street vendors). Targeted information campaigns to increase awareness of shigellosis may help reduce the spread of infection among at-risk groups. Despite extensive vaccine research in recent decades, there is no approved vaccine against shigellosis.

Even though the main therapy for shigella infection is conservative, antibiotics may be used in the event of dysentery (multiple scanty, bloody, mucoid stools) to shorten the duration of symptoms and pathogen shedding [11]. However, prescribing clinicians are reminded of the increasing resistance in commonly-prescribed antibiotics, especially among high-risk groups.

References

- 1. European Centre for Disease Prevention and Control (ECDC). Introduction to the Annual epidemiological report. Stockholm: ECDC; 2023. Available at: <u>https://www.ecdc.europa.eu/en/surveillance-and-disease-data/annual-epidemiological-reports/introduction-annual</u>
- 2. European Centre for Disease Prevention and Control (ECDC). Surveillance systems overview for 2022. Stockholm: ECDC; 2022. Available at: <u>https://www.ecdc.europa.eu/en/publications-data/surveillance-systems-overview-2022</u>
- 3. European Centre for Disease Prevention and Control (ECDC). Surveillance Atlas of Infectious Diseases. Stockholm: ECDC; 2022. Available at: <u>https://atlas.ecdc.europa.eu/public/index.aspx?Dataset=27&HealthTopic=48</u>
- European Centre for Disease Prevention and Control (ECDC). *Shigella sonnei* ST152 multidrug resistant Multi-country – 2022. Weekly Communicable Disease Threats Report, Week 48, 27 November–3 December 2022. Stockholm: ECDC; 2022. Available from: <u>https://www.ecdc.europa.eu/sites/default/files/documents/CDTR-2022w48.pdf</u>
- European Centre for Disease Prevention and Control (ECDC). Outbreak of *Shigella sonnei* in the EU/EEA, the United Kingdom, and the United States among travellers returning from Cabo Verde – 17 February 2023. Stockholm: ECDC; 2023. Available from: <u>https://www.ecdc.europa.eu/sites/default/files/documents/shigella-sonnei-risk-assessment-february-2023.pdf</u>
- EFSA and ECDC (European Food Safety Authority and European Centre for Disease Prevention and Control). The European Union One Health 2022 Zoonoses Report. EFSA Journal. Available from: <u>https://www.ecdc.europa.eu/sites/default/files/documents/EFS2_8442.pdf</u>
- Culqui DR, García-de-Olalla-Rizo P, Alva-Chavez KP, Lafuente S, Rius C, de Simón M, et al. Analysis of the epidemiological pattern of Shigellosis in Barcelona between 1988 and 2012: Is it an emerging sexually transmitted infection?. Enferm Infecc Microbiol Clin. julio de 2015;33(6):379-84.
- 8. European Centre for Disease Prevention and Control (ECDC). 23 February 2022. Stockholm: ECDC; 2023. Rapid risk assessment: Increase in extensively-drug resistant *Shigella sonnei* infections in men who have sex with men in the EU/EEA and the UK. Available from: <u>https://www.ecdc.europa.eu/en/publicationsdata/rapid-risk-assessment-increase-extensively-drug-resistant-shigella-sonnei</u>
- 9. European Centre for Disease Prevention and Control (ECDC). Spread of multidrug-resistant *Shigella* in EU/EEA among gay, bisexual and other men who have sex with men 18 July 2023. Stockholm: ECDC; 2023. Available from: <u>https://www.ecdc.europa.eu/en/news-events/spread-multidrug-resistant-shigella-eueea-among-gay-bisexual-and-other-men-who-have-sex</u>
- 10. UK Health Security Agency (UKHSA). Rise in extremely drug-resistant *Shigella* in gay and bisexual men. 2022. Available at: <u>https://www.gov.uk/government/news/rise-in-extremely-drug-resistant-shigella-in-gay-and-bisexual-men</u>
- 11. Kotloff KL, Riddle MS, Platts-Mills JA, Pavlinac P, Zaidi AKM. Shigellosis. Lancet. 2018 Feb 24;391(10122):801-12. Available at: <u>https://www.ncbi.nlm.nih.gov/pubmed/29254859</u>
- 12. World Health Organization (WHO). Global priority list of antibiotic-resistant bacteria to guide research, discovery, and development of new antibiotics. 2017. Available at: <u>https://www.who.int/medicines/publications/WHO-PPL-Short_Summary_25Feb-ET_NM_WHO.pdf</u>
- 13. Kotloff KL, Riddle MS, Platts-Mills JA, Pavlinac P, Zaidi AKM. Shigellosis. Lancet. 2018 Feb 24;391(10122):801-12. Available at: <u>https://www.ncbi.nlm.nih.gov/pubmed/29254859</u>
- 14. Moreno-Mingorance A, Espinal P, Rodriguez V, Goterris L, Fabrega A, Serra-Pladevall J, et al. Circulation of multi-drug-resistant *Shigella sonnei* and *Shigella flexneri* among men who have sex with men in Barcelona, Spain, 2015-2019. Int J Antimicrob Agents. 2021 Sep;58(3):106378. Available at: https://www.ncbi.nlm.nih.gov/pubmed/34157402