

# Outbreak of *Shigella sonnei* in the EU/EEA, the United Kingdom, and the United States among travellers returning from Cabo Verde

17 February 2023

## Summary

- An increased reporting of shigellosis cases, mainly caused by *Shigella sonnei*, among travellers returning from Cabo Verde has been ongoing in the European Union/European Economic Area (EU/EEA), the United Kingdom (UK), and the United States (US) since September 2022. This outbreak evolved rapidly during November and December 2022.
- As of 16 February 2023, 258 cases (221 confirmed *Shigella sonnei* infections and 37 possible cases) with a link to Cabo Verde have been reported in 10 EU/EEA countries, the UK, and the US: Belgium (14), Czechia (4), Denmark (4), Finland (9), France (31), Germany (5), the Netherlands (47), Norway (1), Portugal (2), Sweden (42), the United Kingdom (95), and the United States (4).
- The centralised sequencing analysis of 106 human isolates from Czechia, the Netherlands, Sweden, the UK, and the US shows a genetically compact cluster suggesting a common source.
- There is predominance of women among the cases, with a female-to-male ratio of 2.5:1.
- The *Shigella sonnei* strains among cases show predicted resistance to trimethoprim, streptomycin, and hydrogen peroxide.
- *Shigella* co-infections with other bacterial and parasitic gastrointestinal pathogens (e.g. *Salmonella* Mbandaka, *Campylobacter*, *Cryptosporidium*, and strains of diarrhoeagenic *Escherichia coli*) have been reported among cases.
- Information on possible vehicles of infection or common exposures have not yet been identified. Multiple modes of transmission are plausible, with the most likely being foodborne (including via infected food handlers), but person-to-person transmission is also possible.
- Based on the available information, many cases are reported to have stayed in the region of Santa Maria on the island Sal, including in all-inclusive hotels. The most recent cases were reported in Sweden on 19 January 2023, suggesting an ongoing moderate risk of new infections among travellers in Cabo Verde, particularly among those staying in the Santa Maria region of Sal.

## Event background

On 3 November 2022, the Netherlands opened an event in EpiPulse, a restricted communications platform managed by ECDC, about an unusual increase of cases with *Shigella sonnei* infection and with travel history to Cabo Verde ([2022-FWD-00088](#)). By the end of 2022, several EU/EEA countries, the UK, and the US had reported several cases with *Shigella sonnei* infections among travellers returning from Cabo Verde.

The first communication of an increased risk for travellers was published on 12 November 2022 in ECDC's weekly Communicable Disease Threats Report, [week 45](#), 6–12 November 2022. ECDC, the World Health Organization's Regional Office for Europe, and INFOSAN (the International Food Safety Authorities Network), including focal points from Cabo Verde, held meetings on 9 and 16 January 2023 to discuss the epidemiological situation in Cabo Verde, based on the cases notified in the EU/EEA and the UK in 2022. As cases continued to be reported in January 2023, ECDC decided to prepare this Rapid Risk Assessment.

## Characteristics of the *Shigella sonnei* strain

- Sequence type (ST) 152.
- The Enterobase cgMLST hierarchical cluster designation is HC5\_181425.
- Genotype 3.7.17 according to the genotyping method by Hawkey et al. [1]
- In the Netherlands, genes predicting resistance against trimethoprim (*dfiA1*), streptomycin (*aadA1*), and hydrogen peroxide (*siABC*) were detected. One of the Dutch isolates also carries *aph(6)*-Id, *aph(3'')*-Ib (both predicting streptomycin resistance), *su2* (predicting sulfamethoxazole resistance), and *dfiA14* (predicting trimethoprim resistance), indicative for the acquirement of the pCERC1 plasmid.
- In the UK, all *S. sonnei* isolates from cases notified since September 2022 have had genes predicting resistance to trimethoprim (*dfiA1*) and streptomycin (*aadA1b*). Two isolates from cases notified in February and November 2022, respectively, were multidrug-resistant. One isolate had *blaTEM-1*, *aadA1b*, *aph6*-Id, *dfiA1*, *dfiA14*, *tetA1* and *su2*, predicting resistance to ampicillin, streptomycin, trimethoprim, tetracycline, and sulfamethoxazole, and one had *blaTEM-1*, *aph6*-Id, *dfiA1*, *dfiA14* and *su2*, predicting resistance to ampicillin, streptomycin, trimethoprim, and sulfamethoxazole. The isolates have not been tested phenotypically.
- In Sweden, genes predicting resistance against trimethoprim (*dfiA1*) and streptomycin (*aadA1*) were detected. One isolate had the additional markers for ampicillin (*blaTEM-1*) and sulfamethoxazole (*su2*).
- In Portugal, genes predicting resistance against trimethoprim (*dfiA1*), streptomycin (*aadA1*), and hydrogen peroxide (*siABC*) were detected.
- In the US, the predicted resistance profile includes streptomycin and trimethoprim (AMR genes *aadA1* *dfiA1*).
- SRA numbers for the representative sequences in European Nucleotide Archive (ENA) from the *S. sonnei* cluster in the UK are: SRR22099609, SRR18143656, SRR22085217.

## European outbreak case definition for *Shigella sonnei*

The European outbreak case definition is as follows:

### A confirmed outbreak case:

- A laboratory-confirmed *Shigella sonnei* case with gastrointestinal symptoms on or after 1 November 2021 (date of sampling or date of receipt by the reference laboratory if date of onset is not available).

AND

- Fulfilling at least one of the following laboratory criteria:
  - clustering by the national cgMLST pipeline within eight cg-allelic differences (AD) from the representative Dutch outbreak strain, OR
  - clustering in a centralised whole genome sequencing (WGS) analysis within eight cg-allelic differences in a single linkage analysis, OR
  - belonging to the same cgMLST HC5\_181425 cluster (Enterobase scheme), OR
  - belonging to a 10-SNP single linkage cluster with SNP designation 1.3.496.1102.2052.% (t10.2052) according to the UK Health Security Agency pipeline in the UK.

OR

- linked with recent travel history to Cabo Verde at the time of diagnosis.

### A possible outbreak case:

- A laboratory-confirmed *Shigella* sp. with gastrointestinal symptoms on or after 1 September 2022 (date of sampling or date of receipt by the reference laboratory if date of onset is not available).

AND

- Linked with recent travel history to Cabo Verde at the time of diagnosis.

**Exclusion criterion:** A case with laboratory-confirmed infection by other *Shigella* species than *S. sonnei*.

## Epidemiological and microbiological investigations of human cases

As of 16 February 2023, 258 shigellosis cases have been reported in 10 EU/EEA countries, the UK, and the US with a link to recent travel to Cabo Verde and/or clustering by WGS with the representative Dutch *S. sonnei* outbreak strain: Belgium (14), Czechia (4), Denmark (4), Finland (9), France (31), Germany (5), the Netherlands (47), Norway (1), Portugal (2), Sweden (42), the UK (95), and the US (4) (Table 1). Of these, 221 are confirmed *Shigella sonnei* and 37 possible outbreak cases. The majority of isolates harbour resistance markers for streptomycin and trimethoprim. There is a predominance of females with almost three times (female-to-male ratio 2.5:1) more women than men and most cases have been infected in the last quarter of 2022 (Table 1). Most cases have stayed in five-star, all-inclusive hotels in the Santa Maria region of the island Sal.

**Table 1. Number of cases, demographic information, and temporal occurrence of 258 confirmed and possible *Shigella sonnei* cases in 10 EU/EEA countries, the UK, and the US, as of 16 February 2023**

Country	Total number of cases	Confirmed cases (since 1 November 2021)	Possible cases (since 1 September 2022)	Sex			Date of onset/sampling/isolation
				M	F	Unk	
Belgium	14	14	0	0	0	14	Nov 2021 (n=1), Feb 2022 (n=2), Oct–Nov 2022 (n=11)
Czechia	4	4	0	1	3	0	Oct (n=2), Nov (n=2) 2022
Denmark	4	2	2	0	4	0	17 Nov 2021 – 28 Dec 2022
Finland	9	8	1	7	2	0	30 Oct – 30 Dec 2022
France	31	31	0	12	19	0	Feb 2022 – Jan 2023
Germany	5	4	1	1	4	0	5 Sep – 1 Dec 2022
Netherlands	47	34	13	12	32	3	13 Aug – 23 Nov 2022
Norway	1	1	0	Unk	Unk	Unk	5 Dec 2022
Portugal	2	2	0	1	1	0	Aug and Oct 2022
Sweden	42	22	20	12	30	0	1 Nov 2021 – 19 Jan 2023
<b>Total EU/EEA</b>	<b>159</b>	<b>122</b>	<b>37</b>	<b>46</b>	<b>95</b>	<b>17</b>	
United Kingdom	95	95	0	22	73	0	22 Nov 2021 – 9 Dec 2022
United States	4	4	0	1	3	0	2 Nov 2021 – 2 Oct 2022
<b>Total</b>	<b>258</b>	<b>221</b>	<b>37</b>	<b>69</b>	<b>171</b>	<b>17</b>	

M: Male; F: Female; Unk: Unknown.

**Belgium** reports **11** *S. sonnei* isolates from cases with a travel history to Cabo Verde in October–November 2022. WGS analysis of three isolates showed close relatedness to the reference sequence; no WGS data on the other isolates are yet available. Furthermore, **three** isolates identical to the Dutch reference sequence were isolated in November 2021 (n=1) and February 2022 (n=2).

**Czechia** reports **four** *S. sonnei* cases with a travel history to Cabo Verde in 2022; two in October and two in November 2022. One female case confirmed by WGS (aged 25–44 years) stayed at a hotel on the island Sal. The case is reported to have only eaten in the hotel (all-inclusive), including consuming ice in drinks, fruit, and vegetables. The second case, a male aged 44–64 years, stayed at a hotel on Sal in mid-October for seven days.

Separately, two further cases, a mother (aged 15–24 years) and a child (aged 5–14 years), also stayed at a hotel on Sal in November 2022. After their return to Czechia, they infected the father of the child.

**Denmark** reports **four** *S. sonnei* cases with a travel history to Cabo Verde between 17 November 2021 and 28 December 2022; two confirmed cases matching the Dutch reference strain sequenced as part of a large enteroinvasive *Escherichia coli* (EIEC)/*Shigella* outbreak between December 2021 and February 2022. An additional two possible cases from December 2022 reported travel to Cabo Verde; these isolates have not been sequenced.

**Finland** reports **eight** *Shigella sonnei* cases with travel history to Cabo Verde in 2022; six cases' *Shigella* strains have been sequenced and cluster together. In addition, **one** *Shigella* sp. case has been reported to the infectious disease register with sampling date on 30 October 2022; the case had stayed at a hotel on Sal. The cases include seven males and two females (age range 9–63 years, median 41). The sampling dates were between 30 October and 30 December 2022.

**France** reports **31** cases with isolates matching the Dutch reference strain and belonging to the cluster HC5\_181425 (EnteroBase cgMLST scheme), and genotype 3.7.17 (new genotyping nomenclature of Hawkey et al. [1]) during the period February 2022 to January 2023; 12 cases are male and 19 female. Ten cases reported travel to Cabo Verde and one case mentioned a trip to Africa (strain isolated in August 2022).

**Germany** reports **five** *Shigella* cases with history to Cabo Verde. The cases include four females and one male (age range 26–63 years, median 61) and have disease onsets between 5 September and 1 December 2022. Four cases were infected by *S. sonnei*, the *Shigella* species of the fifth case was not determined. One of the cases (disease onset 23 November 2022) stayed at a hotel in Santa Maria on Sal. Detailed information on travel (island, hotel, restaurants visited) of the other cases is not available. In pre-pandemic years (2014–2019), 0–5 *S. sonnei* cases with travel history to Cabo Verde were reported per year in Germany.

**The Netherlands** report **47** shigellosis cases with a travel history to Cabo Verde since mid-August 2022, with a sharp increase in the number of cases in mid-September 2022. Thirty-four cases are confirmed *S. sonnei* cases by WGS. A further 13 cases without WGS are considered part of the outbreak as they reported travel to Cabo Verde since mid-September. Among the 47 cases, the age range is 9–69 years (median 46 years); 32 are females and 12 males. Cases are reported to have stayed in different hotels of the same chain in Santa Maria on Sal. The most recent illness onset date for a case is 23 November 2022. Among nine cases with WGS data, genes predicting resistance against trimethoprim (*dhfrA1*), streptomycin (*aadA1*), and hydrogen peroxide (*shiABC*) are detected. One isolate had *aph(6)*-Id, *aph(3'')*-Ib (both predicting streptomycin resistance), *sul2* (predicting sulfamethoxazole resistance), and *dhfrA14* (predicting trimethoprim resistance), indicative for the acquirement of the pCERC1 plasmid.

**Norway** reports **one** case with *S. sonnei* infection matching the Dutch outbreak sequence (3 AD) with travel history to Cabo Verde in November 2022. The sampling date was 5 December 2022. The case had stayed at a five-star hotel in the Santa Maria region of Sal.

**Portugal** reports **two** *S. sonnei* cases; the first was a female aged 25–44 years from October 2022 with a clustering isolate (6 AD) to the Dutch reference strain. The case reported recent travel to Cabo Verde. The case was hospitalised with gastrointestinal infection and possible haemolytic-uraemic syndrome (HUS). Based on WGS data, the isolate belongs to ST152 and also has resistance genes for trimethoprim (*dhfrA1*) and streptomycin (*aadA1*) as evidenced in the Dutch and UK isolates. The second case was a male aged <5 years in August 2022, who was reported hospitalised with gastrointestinal symptoms. The case had a travel history of one month to Cabo Verde (city of Praia, Santiago island) between the beginning of July and the beginning of August 2022. Based on WGS data, this isolate, also belonging to ST152, has genes predicting resistance against trimethoprim (*dhfrA1*), streptomycin (*aadA1*), and hydrogen peroxide (*shiABC*).

**Sweden** reports **42** cases between 1 November 2021 and 19 January 2023, with 22 of these cases reported since 1 December 2022. All cases are linked to travel to Cabo Verde. Of 42 cases, 22 are confirmed *S. sonnei* cases and 20 are possible cases (PCR). The patients were predominantly females (30 cases). The median age was 51 years (range 1–80 years). Some of the patients reported having stayed at hotels in the Santa Maria region of Sal. The majority reported eating at restaurants in all-inclusive hotels. A large variety of foods were consumed: fresh salads/vegetables, grilled and cooked meat and fish, sushi, fruit, ice creams, juice, drinks with ice, etc. Two cases were co-infected with other gastrointestinal pathogens, including *Campylobacter* and *Cryptosporidium*.

Earlier in 2022, 11 cases were reported with a travel history to Cabo Verde and one case with a secondary infection from a household member with travel history to Cabo Verde. Seven of these were confirmed as *S. sonnei* cases. In November and December 2021, four cases of *S. sonnei* were reported. Isolates from six cases of *S. sonnei*, notified since January 2022, have been sequenced and genes predicting resistance against trimethoprim (*dhfrA1*) and streptomycin (*aadA1*) were detected. One isolate had additional resistance markers, ampicillin (*blaTEM-1*) and sulfamethoxazole (*sul2*).

**The United Kingdom** reports **95** confirmed *S. sonnei* cases, nationally distributed across England, Scotland, Wales, and Northern Ireland. Case sample dates range between 22 November and 9 December 2022, with 88 cases (94%) with sample dates reported since 7 September 2022. The majority of cases (72/94) have been female. In total, **63** cases report travel to Cabo Verde, among which 48 reported illness onset between 25

September and 1 December 2022. A further six cases reported travel to the African continent (country unspecified and destination not verified but the destination being Cabo Verde cannot be ruled out). Information on travel is not always routinely available for all cases. Eight cases have had *S. sonnei* co-infections with the following pathogens: three cases with *Salmonella* Mbandaka, one case with *Campylobacter* sp., and four cases with strains of diarrhoeagenic *E. coli*. For *S. Mbandaka*, the 5-SNP designation using the UKHSA pipeline is 1.1.3.458.643.739.% (t5.739). The Enterobase cgMLST hierarchical cluster designation is HC5\_77532 and the SRA number for representative sequence is SRR22197065.

Interviews have been conducted with 50 cases in this UK cluster; 49 cases reported foreign travel, 48 of which reported travel to Cabo Verde. Forty-seven cases reported visiting the same resort in Santa Maria on Sal. Cases travelled from at least four different airports in the UK, and 29 cases reported using the same tour operator.

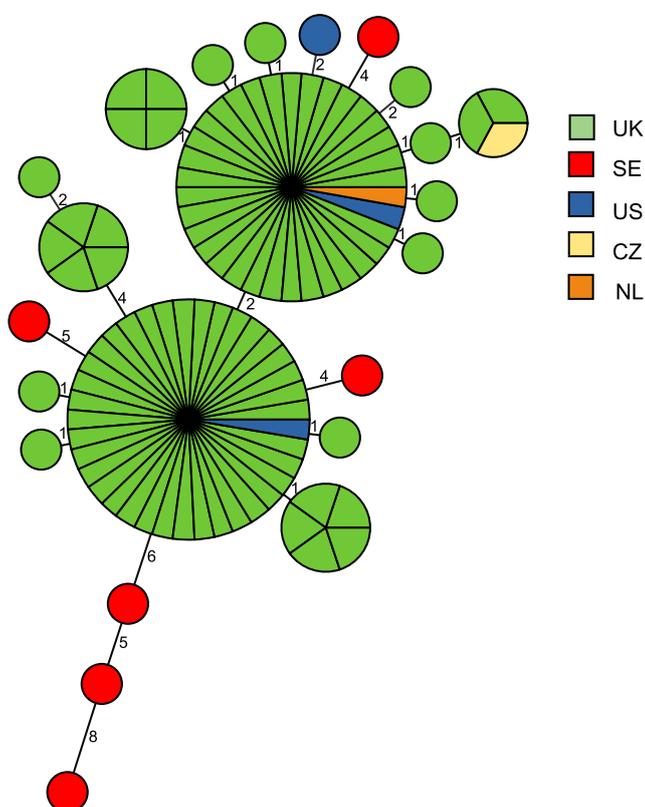
The majority of UK cases have indicated that all food was consumed within the resort as part of an all-inclusive holiday package. Cases reported a variety of foods available from restaurants and buffets in the resort, including: fresh salads/fruit/vegetables, seafood/sushi, eggs, cooked meats, poultry, milk, cheese, dairy, ice cream, etc.

**The United States** reports four *S. sonnei* cases highly related within 0 and 8 alleles by cgMLST. One case reports travel to Cabo Verde; travel history for the remaining cases is unknown. The cases include three females and one male (age range 3–88 years, median 29). Collection dates ranged from 2 November 2021 to 2 October 2022. An older case related by sequencing but lost to follow-up has been excluded from this report as travel history could not be confirmed. The overall predicted resistance profile includes streptomycin and trimethoprim (AMR genes *aadA1* *dfiA1*).

## Centralised whole genome sequencing cluster analysis

Representative sequences from countries, including public repository data (SRA, Sequence Read Archive), were analysed by ECDC using BioNumerics version 7.6.3 (Applied-Maths, Sint-Martens-Latem, Belgium), which included raw sequence trimming using the default settings; de novo assembly including mismatch correction using SPAdes v.3.7.1. Allele calling was performed on assemblies using Enterobase core genome scheme and isolates were excluded from further analysis if less than 2 702 (90%) of the 3 002 core loci were detected. A minimum spanning tree was generated to visualise the results (Figure 1).

**Figure 1. Minimum spanning tree based on number of differing alleles (cgMLST, Enterobase scheme), including *S. sonnei* from 106 human isolates from the UK (n=95), Sweden (n=6), Czechia (n=1), the Netherlands (n=1), and the US (n=3), November 2021 to December 2022**



## ECDC public health risk assessment

As of 16 February 2023, 258 *Shigella sonnei* outbreak cases (221 confirmed and 37 possible) have been reported in 10 EU/EEA countries, the UK, and the US with a link to recent travel to Cabo Verde and/or clustering by WGS with the representative Dutch *S. sonnei* outbreak strain: Belgium (14), Czechia (4), Denmark (4), Finland (9), France (31), Germany (5), the Netherlands (47), Norway (1), Portugal (2), Sweden (42), the UK (95), and the US (4). This outbreak evolved rapidly during November and December 2022. In Sweden and the UK, co-infections with other bacterial and parasitic gastrointestinal pathogens have also been reported. The centralised sequencing analysis of 106 human isolates from Czechia, the Netherlands, Sweden, the UK, and the US show genetically compact cluster suggesting a common source.

There is a predominance of women among cases, with a female-to-male ratio of 2.5:1 ( $p < 0.001$ ). This is unusual for shigellosis outbreaks, which are often reported among men who have sex with men (MSM) [2]. In foodborne shigellosis outbreaks however, a slightly larger proportion of females can be observed among cases, with infected food handlers and the bare-handed preparation of ready-to-eat food identified as major risk factors [3]. In the current outbreak, information on possible vehicles of infection or common exposures have not yet been identified but investigations are ongoing in Cabo Verde. Multiple modes of transmission are plausible, with the most likely one being foodborne (including via infected food handlers) but person-to-person transmission is also possible. The *S. sonnei* strain in the current outbreak indicates predicted resistance to trimethoprim and streptomycin, but single isolates with multidrug resistance profile have also been detected. The detection of a resistance gene against hydrogen peroxide indicates *S. sonnei* isolates' regular exposure to this disinfectant.

Based on available information, many cases are reported to have stayed in the Santa Maria region of the island Sal in all-inclusive hotels. The most recent cases were reported in Sweden on 19 January 2023, suggesting an ongoing moderate risk of new infections among travellers in Cabo Verde, particularly among those staying in the Santa Maria region of Sal.

## Recommendations and options for response

ECDC encourages public health authorities in the EU/EEA to increase awareness among healthcare professionals on an increased possibility of *Shigella* infections in people with recent travel to Cabo Verde. In addition, interviews of these cases are recommended to narrow down the high-risk areas/sites in Cabo Verde. Countries are encouraged to update the public health data in EpiPulse [2022-FWD-00088](#) should new information come available.

Together with the WHO Regional Office for Europe, ECDC is in regular contact with authorities in Cabo Verde to strengthen investigations of possible sources, as this is the key for controlling the outbreak, and to increase awareness among healthcare professionals in Cabo Verde of an increased possibility of *Shigella* infections, particularly in the Santa Maria region of Sal.

ECDC can offer sequencing and coordination support to EU/EEA countries as well as facilitate analytical epidemiological studies at national or EU/EEA level.

## Source and date of request

ECDC internal decision on 26 January 2023.

## Consulted experts and national contact points

**ECDC experts (in alphabetical order):** Áine Collins, Cecilia Jernberg, Johanna Takkinen.

### Public health experts consulted for data and facts validation:

**Belgium:** Dieter Van Cauteren, Wesley Mattheus, Pieter-Jan Ceyssens (Sciensano);

**Czechia:** Ondřej Daniel (National Reference Laboratory for Salmonella, National Institute of Public Health), Michaela Špačková (Department of Infectious Diseases Epidemiology, National Institute of Public Health);

**Denmark:** Luise Müller and Susanne Schjørring (Statens Serum Institute);

**Finland:** Ruska Rimhanen-Finne and Saara Salmenlinna (Finnish Institute for Health and Welfare);

**France:** Sophie Lefèvre and François-Xavier Weill (French National Reference Centre for *Escherichia coli*, *Shigella* and *Salmonella*), Mathieu Tourdjman (Santé publique France);

**Germany:** Angelika Fruth (National Reference Centre for Salmonella and Other Bacterial Enterics, Robert Koch Institute) and Bettina Rosner (Department of Infectious Disease Epidemiology, Robert Koch Institute);

**The Netherlands:** Roan Pijnacker and Maaïke van den Beld (National Institute for Public Health and the Environment);

**Norway:** Lin T. Brandal and Silje B. Lavoll (Norwegian Institute of Public Health);

**Portugal:** Pedro Pinto Leite and João Vieira Martins (Directorate of Information and Analysis, Directorate-General of Health), Paula Vasconcelos and Mariana Ferreira (Public Health Emergencies Operations Centre, Directorate-General of Health), Ângela Pista and Miguel Pinto (National Institute of Health Doutor Ricardo Jorge);

**Sweden:** Nadja Karamemedovic and Barbro Mäkitalo (Public Health Agency of Sweden);

**The United Kingdom:** Derek Brown (Public Health Scotland); Lesley Larkin, Ann Hoban, Parisha Katwa and Iman Mohamed (United Kingdom Health Security Agency);

**The United States:** Morgan Schroeder, Sharla McDonald, and Naeemah Logan (Centers for Disease Control and Prevention).

## Disclaimer

ECDC issues this risk assessment document based on an internal decision and in accordance with Article 20(1)(a) of Regulation (EU) 2022/2371 on serious cross-border threats to health of Decision No 1082/13/EC and Article 7(1) and 8a of Regulation (EC) No 853/2004 as amended establishing a European centre for disease prevention and control (ECDC). In the framework of ECDC's mandate, the specific purpose of an ECDC risk assessment is to present science-based recommendations and options for response different options on a certain matter. The responsibility on the choice of which option to pursue and which actions to take, including the adoption of mandatory rules or guidelines, lies exclusively with the EU/EEA Member States. In its activities, ECDC strives to ensure its independence, high scientific quality, transparency, and efficiency.

This report was written with the coordination and assistance of an Internal Response Team at the European Centre for Disease Prevention and Control. All data published in this risk assessment are correct to the best of our knowledge at the time of publication. Maps and figures published do not represent a statement on the part of ECDC or its partners on the legal or border status of the countries and territories shown.

# Annex 1. Disease background

## Disease characteristics

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, shigellosis is caught by swallowing material contaminated by human faeces, either via the hands or on objects which have been in contact with faeces. Infection can also be caught from contaminated food and water. It is largely a disease of children in low-income settings, although within high-income settings, travellers and MSM (men who have sex with men) are identified as the main risk groups. Increasing resistance to first and second line antimicrobials is of concern. Further information about shigellosis can be found on the websites of ECDC and US CDC [4,5].

## Disease surveillance for shigellosis in the EU/EEA

In EU/EEA countries, a total of 18 426 confirmed shigellosis cases were reported between 2017 and 2021, with an annual average of 3 685 cases (UK data not included).

For 2021, 30 EU/EEA countries reported 2 405 cases of shigellosis to ECDC, 2 115 (87.9%) of which were confirmed. This represents a drop of shigellosis cases by 75.0% compared to 2019. While in 2020, 78.6% fewer cases were reported compared to 2019. The drop in the number of cases reported in 2021 and 2020 is largely due to the COVID-19 pandemic and the fact that the UK, which accounted for a large proportion of the reported cases in previous years, no longer reported to The European Surveillance System (TESSy) following its exit from the EU. The number of cases reported in 2019 is therefore considered a better reflection the pre-pandemic epidemiological situation in the EU/EEA and the UK.

In 2019, 8 448 confirmed cases of shigellosis were reported by 30 EU/EEA countries, including the UK, with an overall EU/EEA notification rate of 2.2 cases per 100 000 population. Three countries accounted for 59.8% of confirmed cases: Germany, France, and the UK, with the UK alone accounting for 38.7% of confirmed cases. The overall male-to-female ratio was 1.4:1. In 2019, 65.3% of male cases were between 25 and 64 years and the respective proportion for females was 56.6%. Travel information was available for 51.4% of the confirmed cases in 2019 and, of these, 48.2% were related to travel, mostly to Egypt, India, Morocco, and Pakistan.

In 2019, *Shigella* species were reported for 76.7% of confirmed cases, among which 45.5% were *S. sonnei* followed by *S. flexneri* with 27.1%. For *S. sonnei*, the number of travel-associated cases decreased by 88.4% and 88.2% between 2019 and 2020, and 2019 and 2021, respectively. In 2021, among *S. sonnei* cases with known travel country (n=195), the five travel destinations most frequently reported by cases were the Republic of Madagascar (n=41), Egypt (n=32), Spain (n=15), Tanzania (n=12), and Cabo Verde (n=10). For comparison, in 2019, among *S. sonnei* cases with known travel destination (n=1 071), the five travel destinations most frequently reported for *S. sonnei* cases were Egypt (n=168), Indonesia (n=104), the Republic of Madagascar (n=81), Pakistan (n=40), and Mexico (n=33).

For the period 2017–2021, slightly more *S. sonnei* cases were reported among males than females (54.6% male, 44.5% female and <1% missing sex). One third (30.8%) of cases were travel associated, 32.5% were considered domestically acquired and 36.7% lacked information on travel status. Information on transmission mode was available for 14.2% (1 535 out of 11 086) of *S. sonnei* cases infected within the EU/EEA (including the UK) in 2009–2021. Among these 1 535 *S. sonnei* cases, 710 cases (46.2%) were considered foodborne, 404 (26.3%) sexually transmitted, 397 (25.9%) person-to-person transmission, and 24 (1.6%) were considered other types of transmission.

For the period 2017–2020, data on antimicrobial resistance was reported to TESSy for 41% (5 216/12 695) of the laboratory-confirmed cases of *S. sonnei* in the EU/EEA. Among the 2 394 isolates tested for penicillins, quinolones and third generation cephalosporins, 174 isolates (7.3%) were resistant to all three classes. Twelve out of 20 isolates tested were classified as non-wild-type to azithromycin.

Further information can be found in ECDC's Annual epidemiological report [6] and the online *Surveillance atlas of infectious diseases* [7].

## References

1. Hawkey J, Paranagama K, Baker KS, Bengtsson RJ, Weill FX, Thomson NR, et al. Global population structure and genotyping framework for genomic surveillance of the major dysentery pathogen, *Shigella sonnei*. *Nat Commun* 2021 May 11;12(1):2684. Available from: <https://www.ncbi.nlm.nih.gov/pubmed/33976138>
2. European Centre for Disease Prevention and Control. Increase in extensively-drug resistant *Shigella sonnei* infections in men who have sex with men in the EU/EEA and the UK - 23 February 2022. Stockholm: ECDC; 2022. Available from: <https://www.ecdc.europa.eu/en/publications-data/rapid-risk-assessment-increase-extensively-drug-resistant-shigella-sonnei>
3. Nygren BL, Schilling KA, Blanton EM, Silk BJ, Cole DJ, Mintz ED. Foodborne outbreaks of shigellosis in the USA, 1998-2008. *Epidemiol Infect.* 2013 Feb;141(2):233-41. Available from: <https://www.ncbi.nlm.nih.gov/pubmed/22361246>
4. Centers for Disease Control and Prevention. Shigella - Shigellosis. General information [Internet]. Atlanta: CDC; 2020 [updated 7 October 2020; cited 9 February 2023]. Available from: <http://www.cdc.gov/shigella/index.html>
5. European Centre for Disease Prevention and Control. Shigellosis [Internet]. Available from: <https://www.ecdc.europa.eu/en/shigellosis>
6. European Centre for Disease Prevention and Control. Shigellosis. In: ECDC. Annual epidemiological report for 2020. Stockholm: ECDC; 2022. Available from: <https://www.ecdc.europa.eu/en/publications-data/shigellosis-annual-epidemiological-report-2020>
7. European Centre for Disease Prevention and Control. Surveillance atlas of infectious diseases [Internet]. Stockholm: ECDC; 2021 [cited 9 February 2023]. Available from: <https://atlas.ecdc.europa.eu/public/index.aspx?Dataset=27&HealthTopic=48>