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Update on STEC in the EU, based on the EU One Health Zoonoses 2019 report

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Trusted science for safe food



EU One Health 2019 Zoonoses report



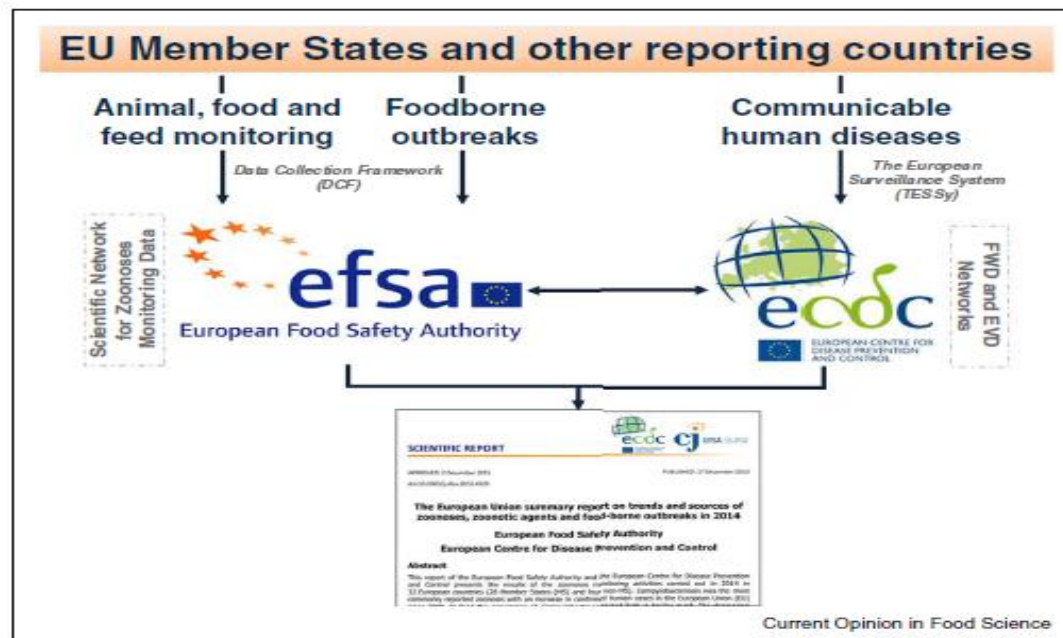
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The European Union One Health 2019 Zoonoses Report

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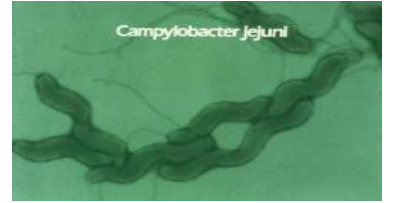
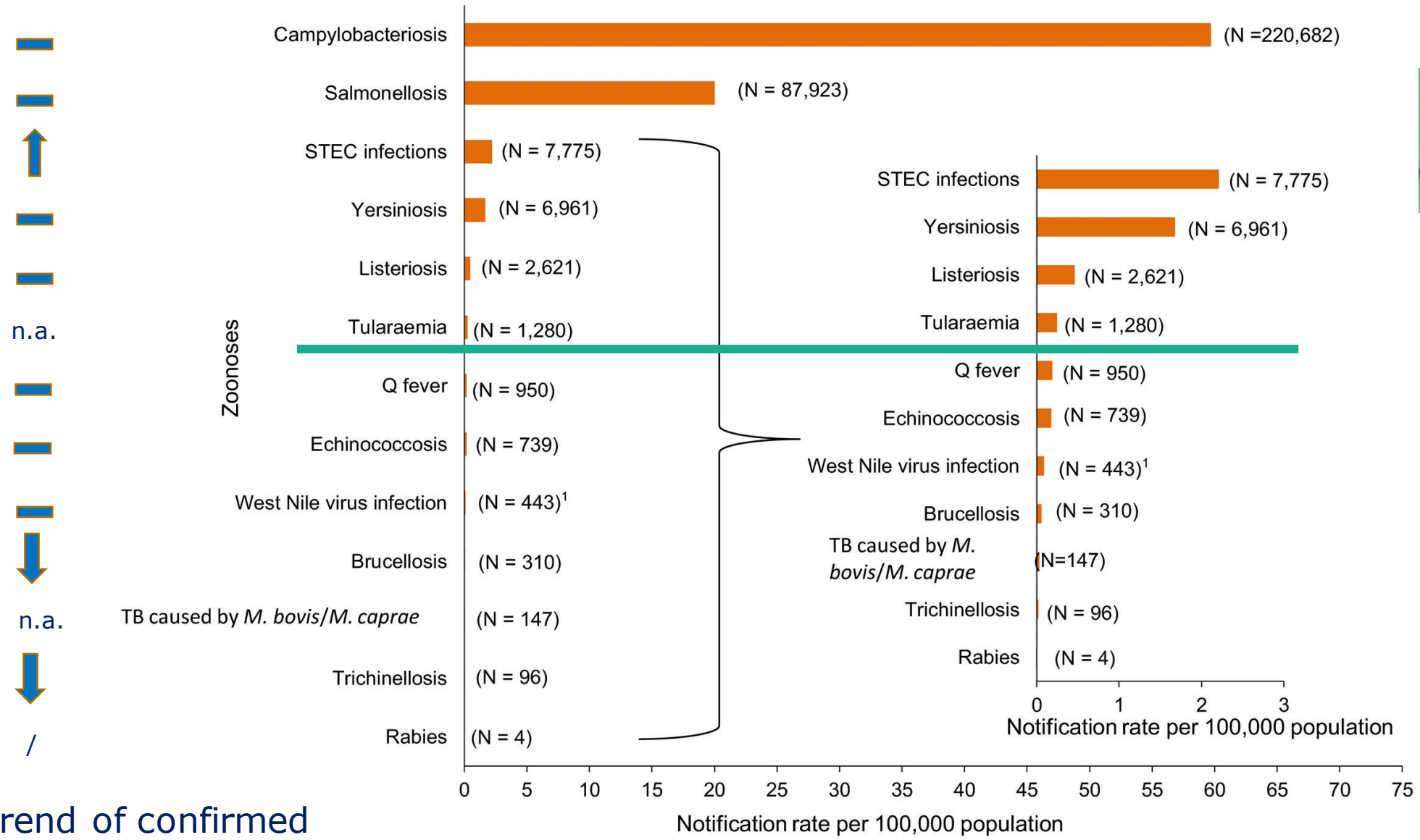


The EUOHZ:

- a joint scientific report by EFSA and ECDC, and
- the product of intensive collaboration with MS and EC DG SANTE (D4, G2 and G4)

Data flow and EFSA's integrated approach for the production of the joint EFSA-ECDC EU Summary Report on zoonoses and food-borne outbreaks in the EU. Note: FWD Network: European Food and Waterborne Diseases and Zoonoses Network; EVD Network: European Emerging and Vector-borne Diseases Network.

Reported numbers and notification rates of confirmed human zoonoses in the EU, 2019



EU trend of confirmed cases in 2015–2019

-
-
- ↑
-
-
- n.a.
-
-
-
- ↓
- n.a.
- ↓
- /

Reported hospitalisations and case fatalities due to zoonoses in confirmed human cases in the EU, 2019



| Disease | Number of confirmed human cases | Hospitalisation | | | | Deaths | | | |
|--|---------------------------------|----------------------|---------------------------------------|-----------------------------|-----------------------------|-----------------------|---------------------------------------|-----------------|-------------------|
| | | Status available (%) | Number of reporting MS ^(b) | Reported hospitalised cases | Proportion hospitalised (%) | Outcome available (%) | Number of reporting MS ^(b) | Reported deaths | Case fatality (%) |
| Campylobacteriosis | 220,682 | 29.1 | 16 | 20,432 | 31.8 | 78.0 | 17 | 47 | 0.03 |
| Salmonellosis | 87,923 | 44.5 | 15 | 16,628 | 42.5 | 71.8 | 17 | 140 | 0.22 |
| STEC infections | 7,775 | 37.3 | 18 | 1,100 | 37.9 | 61.0 | 20 | 10 | 0.21 |
| Yersiniosis | 6,961 | 27.4 | 15 | 648 | 33.9 | 57.0 | 14 | 2 | 0.05 |
| Listeriosis | 2,621 | 51.1 | 19 | 1,234 | 92.1 | 65.1 | 20 | 300 | 17.6 |
| Tularaemia | 1,280 | 22.8 | 12 | 149 | 51.0 | 21.6 | 13 | 1 | 0.36 |
| Echinococcosis | 739 | 33.3 | 14 | 109 | 44.3 | 31.4 | 14 | 2 | 0.86 |
| Q fever | 950 | NA ^(c) | NA | NA | NA | 67.3 | 13 | 4 | 0.63 |
| West Nile virus infection^(a) | 443 | 83.7 | 9 | 347 | 93.5 | 99.3 | 11 | 52 | 11.8 |
| Brucellosis | 310 | 44.5 | 11 | 98 | 71.0 | 36.8 | 12 | 2 | 1.75 |
| Trichinellosis | 96 | 16.7 | 5 | 6 | 37.5 | 25.0 | 7 | 1 | 4.20 |
| Rabies | 4 | NA ^(c) | NA | NA | NA | 75.0 | 3 | 3 | 100.0 |

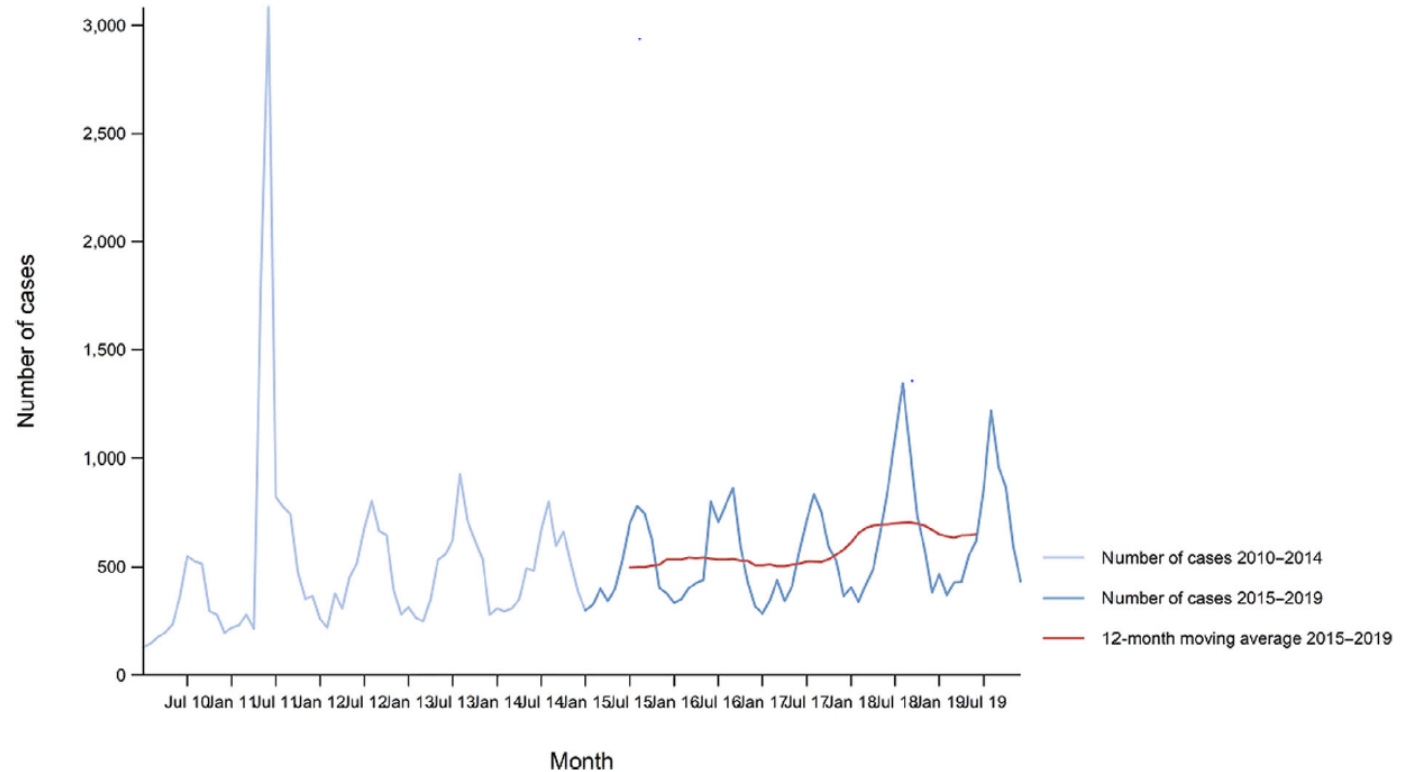
Severity of the diseases was analysed based on hospitalisation and outcome of the reported cases. Based on data on severity, **listeriosis** and **West Nile virus infection** were the two most severe diseases with the highest case fatality (listeriosis, 17.6%) and the highest hospitalisation (West Nile virus infection, 93.5%). Almost all confirmed cases with data available on hospitalisation for these two diseases were hospitalised. About one out of every fifth and one out of 10 confirmed listeriosis and WNV cases, respectively, with known data were fatal.

STEC infections in humans, EU/EEA, 2008-2019



There was a significantly increasing trend ($p < 0.01$) for STEC in the EU/EEA in 2015–2019.

Five MS (Austria, Denmark, Finland, Malta and Poland) reported significantly increasing trends ($p < 0.01$). One MS (the Netherlands) had a significantly decreasing ($p < 0.01$) trend over the same time period.



Source: Austria, Cyprus, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, the Netherlands, Norway, Poland, Romania, Slovakia, Slovenia, Sweden and the United Kingdom. Belgium, Bulgaria, Czechia, Croatia, Portugal and Spain did not report data to the level of detail required for the analysis.

- In 2019, 7,775 confirmed cases of Shiga toxin-producing *E. coli* (STEC) infections in humans were reported at the EU level by 27 EU countries.
- The EU notification rate was 2.2 cases per 100,000 population, which was similar to 2018.
- The highest notification rates were reported in Ireland, Malta, Denmark and Sweden.
- The EU/EEA **trend has been increasing** from 2015 to 2019.
- STEC was the third most frequent bacterial agent detected in food-borne outbreaks in the EU, with 42 outbreaks, 273 cases, 50 hospitalisations and 1 death reported in 2019.
- The sources in the four strong-evidence STEC food-borne outbreaks during 2019 were 'bovine meat and products thereof' (two outbreaks), 'milk' and 'tap water, including well water' (one outbreak each). During 2010–2018, strong-evidence STEC outbreaks were mostly caused by 'bovine meat and products thereof' (18), 'tap water, including well water' (16), 'vegetables and juices and other products thereof' (10) and milk (8) and cheese (8).
- In 2019, 21 MS reported the presence of STEC in **2.8% of 20,395 food samples**, compared with 2.4% in 2018.

- Sprouted seeds were tested by six MS with no positive STEC results from 331 official samples. An EU regulation with a microbiological criterion for the presence of STEC in this food commodity has been in force since 2013.
- Overall, STEC was most commonly found in meat of different types derived from different animal species (4.1% STEC-positive), followed by 'milk and dairy products' (2.1%) while 'fruits and vegetables' was the least contaminated category (0.1%). Sixteen MS tested **6,297 'ready-to-eat' food samples for STEC of which 37 (0.6%) were found to be STEC-positive**, including 17 meat and meat product samples, 16 milk and milk product samples with 10 from cheese, two samples from spices and herbs, and one STEC-positive sample from salads and 'fruits, vegetables and juices' each.

Distribution of the 20 most frequent serogroups reported in confirmed cases of human STEC infections in EU/EEA, 2017–2019



Confirmed cases in humans: data on STEC serogroups (based on the O antigen) were reported in 2019 by 24 MS. Serogroup data were available for 57.9% of the human confirmed cases, which was a slight decrease compared with in 2018 (61.6%).

| Serogroup | 2019 | | | 2018 | | | 2017 | | |
|---------------------|--------------|-----------|--------------|--------------|-----------|--------------|--------------|-----------|--------------|
| | Cases | MS | % | Cases | MS | % | Cases | MS | % |
| O157 | 1,195 | 22 | 26.6 | 1,735 | 21 | 34.5 | 1,299 | 22 | 31.9 |
| O26 | 722 | 16 | 16.0 | 833 | 18 | 16.6 | 577 | 17 | 14.2 |
| NT ⁽¹⁾ | 572 | 11 | 12.7 | 497 | 9 | 9.9 | 493 | 10 | 12.1 |
| O146 | 220 | 11 | 4.9 | 179 | 9 | 3.6 | 139 | 8 | 3.4 |
| O103 | 213 | 13 | 4.7 | 233 | 14 | 4.6 | 245 | 13 | 6.0 |
| O91 | 181 | 12 | 4.0 | 192 | 10 | 3.8 | 178 | 12 | 4.4 |
| O145 | 162 | 11 | 3.6 | 158 | 12 | 3.1 | 147 | 12 | 3.6 |
| O128 ⁽²⁾ | 113 | 12 | 2.5 | 107 | 10 | 2.1 | 79 | 11 | 1.9 |
| O80 | 80 | 9 | 1.8 | 64 | 8 | 1.3 | 42 | 7 | 1.0 |
| O111 | 63 | 12 | 1.4 | 79 | 15 | 1.6 | 92 | 17 | 2.3 |
| O63 | 62 | 8 | 1.4 | 24 | 6 | 0.5 | 30 | 6 | 0.7 |
| O113 | 60 | 10 | 1.3 | 63 | 7 | 1.3 | 56 | 7 | 1.4 |
| O117 | 52 | 6 | 1.2 | 52 | 7 | 1.0 | 29 | 3 | 0.7 |
| O76 | 48 | 9 | 1.1 | 52 | 9 | 1.0 | 31 | 6 | 0.8 |
| O27 | 44 | 6 | 1.0 | 23 | 5 | 0.5 | 15 | 5 | 0.4 |
| O55 | 36 | 10 | 0.8 | 35 | 9 | 0.7 | 30 | 8 | 0.7 |
| O8 | 36 | 7 | 0.8 | 48 | 8 | 1.0 | 28 | 6 | 0.7 |
| O78 | 30 | 8 | 0.7 | 21 | 7 | 0.4 | 23 | 5 | 0.6 |
| O121 | 29 | 8 | 0.6 | 45 | 6 | 0.9 | 30 | 6 | 0.7 |
| O182 | 28 | 7 | 0.6 | 20 | 6 | 0.4 | 16 | 4 | 0.4 |
| Other | 554 | – | 12.3 | 573 | – | 11.4 | 488 | – | 12.0 |
| Total | 4,500 | 22 | 100.0 | 5,033 | 23 | 100.0 | 4,067 | 23 | 100.0 |

(1): Non-typable STEC include those strains in which the laboratory tried but was not able to define the O-serogroup. This depends on how many sera/molecular tools are included in the typing panel.

(2): Including O128ab.

Source: 24 MS and two non-MS: Austria, Belgium, Croatia, Czechia, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Luxembourg, Malta, the Netherlands, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden, the United Kingdom and Iceland and Norway.

Distribution of the 20 most frequent serogroups reported in confirmed cases of human STEC infections and of STEC in food and in animals in EU/EEA, 2019



- Food : 25,238 sample units tested of which 2.5% (641) were STEC-positives.
- Animals : 2,588 animal sample units tested of which 14.1% (366) were STEC-positive.

| Serogroup | Human | | | Food | | | Animals | | |
|---------------------|--------------|-----------|--------------|---------------|-----------|--------------|---------------|----------|--------------|
| | STEC cases | MS | % | STEC-positive | MS | % | STEC-positive | MS | % |
| O157 | 1,195 | 22 | 26.6 | 43 | 7 | 6.7 | 45 | 5 | 12.3 |
| O26 | 722 | 16 | 16.0 | 14 | 6 | 2.2 | 1 | 1 | 0.3 |
| NT ⁽¹⁾ | 572 | 11 | 12.7 | 316 | 10 | 49.1 | 253 | 4 | 69.1 |
| O146 | 220 | 11 | 4.9 | 13 | 2 | 2.0 | 2 | 1 | 0.5 |
| O103 | 213 | 13 | 4.7 | 8 | 6 | 1.2 | 1 | 1 | 0.3 |
| O91 | 181 | 12 | 4.0 | 10 | 4 | 1.6 | ND | | 0.0 |
| O145 | 162 | 11 | 3.6 | 4 | 1 | 0.6 | 1 | 1 | 0.3 |
| O128 ⁽²⁾ | 113 | 12 | 2.5 | 2 | 1 | 0.3 | ND | | 0.0 |
| O80 | 80 | 9 | 1.8 | ND | | 0.0 | ND | | 0.0 |
| O111 | 63 | 12 | 1.4 | 1 | 1 | 0.2 | 1 | 1 | 0.3 |
| O63 | 62 | 8 | 1.4 | ND | | 0.0 | ND | | 0.0 |
| O113 | 60 | 10 | 1.3 | 17 | 5 | 2.7 | 2 | 1 | 0.5 |
| O117 | 52 | 6 | 1.2 | 2 | 1 | 0.3 | ND | | 0.0 |
| O76 | 48 | 9 | 1.1 | ND | | 0.0 | ND | | 0.0 |
| O27 | 44 | 6 | 1.0 | ND | | 0.0 | ND | | 0.0 |
| O55 | 36 | 10 | 0.8 | 10 | 1 | 1.6 | ND | | 0.0 |
| O8 | 36 | 7 | 0.8 | 7 | 2 | 1.1 | 14 | 1 | 3.8 |
| O78 | 30 | 8 | 0.7 | ND | | 0.0 | ND | | 0.0 |
| O121 | 29 | 8 | 0.6 | 1 | 1 | 0.2 | 1 | 1 | 0.3 |
| O174 | ND | | 0.0 | 8 | 2 | 1.2 | 1 | 1 | 0.3 |
| O182 | 28 | 7 | 0.6 | ND | ND | ND | ND | ND | ND |
| Other | 554 | – | 12.3 | 97 | 6 | 15.1 | 43 | 3 | 11.7 |
| Total | 4,500 | 22 | 100.0 | 641 | 20 | 100.0 | 366 | 8 | 100.0 |

ND: not detected.

(1): Non-typable STEC include those strains in which the laboratory tried but was not able to define the O-serogroup. This depends on how many sera/molecular tools are included in the typing panel.

(2): Including O128ab.

Proportion of positive samples for any STEC and STEC belonging to the 'top-five' serogroups in food categories, in reporting MS, 2019

Food : of 212 isolates 45 (21.2%) belonged to the top five serogroups (O157, O26, O103, O111 and O145) while the remaining 167 isolates (78.8%) belonged to 53 different O-groups. All the top 20 STEC serogroups isolated from human infections were also found in the STEC isolated from food in 2019, except for serogroups O80, O5 and O76 only found in food.

| Food category ^(a) | Samples positive for | | | | | |
|--|----------------------|-----------|-----------|----------|----------|----------|
| | Any STEC | O157 | O26 | O145 | O103 | O111 |
| | N | N | N | N | N | N |
| Bovine meat | 315 | 14 | 7 | 4 | 4 | 1 |
| Ovine and goat meat | 102 | 3 | 3 | 0 | 2 | 0 |
| Other ruminants meat ^(b) | 10 | 0 | 0 | 0 | 0 | 0 |
| Pig meat | 54 | 0 | 0 | 0 | 0 | 0 |
| Other meat ^(c) | 21 | 0 | 0 | 0 | 1 | 0 |
| Mixed meat | 16 | 0 | 0 | 0 | 1 | 0 |
| Milk and dairy products ^(d) | 39 | 0 | 3 | 0 | 0 | 0 |
| Raw milk ^(e) | 52 | 1 | 1 | 0 | 0 | 0 |
| Fruit and vegetable seeds ^(f) | 2 | 0 | 0 | 0 | 0 | 0 |
| Other food | 5 | 0 | 0 | 0 | 0 | 0 |
| Total | 616 | 18 | 14 | 4 | 8 | 1 |

MS: Member State; N: number of samples; STEC: Shiga toxin-producing *Escherichia coli*.

Note: Only results from samples tested by the ISO TS 13136:2012 method were included.

(a): The different meat categories presented in this table include all types of meat (not only fresh).

(b): Includes meat from deer.

(c): Includes meat from other animals (other than ruminants).

(d): Includes any type of dairy product, cheese and milk other than raw milk.

(e): Includes raw milk from different species, but most tested and all the positive samples were from cows.

(f): Includes only sprouted seeds.

Virulotypes of the food, animal and human isolates causing severe infection (HUS, hospitalisation and bloody diarrhoea) in 2019 and comparison with those associated with severe disease in humans in 2012–2017, in EU



| Virulence genes profile | No of animal isolates in 2019 [^] | No of food isolates in 2019 [^] | No of human isolates in 2019 (%) | Relative frequency of the virulotype in* | | |
|-------------------------|--|--|----------------------------------|--|-----------------|------------------|
| | | | | HUS | Hospitalisation | Bloody diarrhoea |
| <i>stx2; eae+</i> | 8 | 13 | 399 (42.1) | 17.7 | 42.0 | 40.2 |
| <i>stx2; stx1; eae+</i> | 26 | 3 | 285 (30.1) | 5.9 | 35.7 | 64.8 |
| <i>stx2; eae-</i> | ND | 42 | 90 (9.5) | 2.7 | 24.3 | 14.8 |
| <i>stx1; eae+</i> | 1 | 25 | 88 (9.3) | 1.2 | 27.4 | 27.3 |
| <i>stx1; eae-</i> | ND | 25 | 44 (4.6) | 0.3 | 20.3 | 14.1 |
| <i>stx2; stx1; eae-</i> | 1 | 30 | 42 (4.4) | 1.4 | 15.3 | 19.4 |
| Total | 36 | 138 | 948 | | | |

ND: Not detected.

*: Relative frequencies (%) of the different combinations of *stx* gene subtypes with or without the *eae* gene in STEC isolated from severe disease (TESSy data, 2012–2017). Data from: EFSA Journal 2020;18(1):5967.

[^]: Due to the low number of isolates virulotyped for food and animals only the number of isolates is displayed.

The most commonly reported virulence gene combination was *stx1-/stx2+/eae+*, accounting for 42.1% (399/948) of the severe human cases with known virulotypes. The proportion of the second most common virulotype *stx1+/stx2+/eae+* accounted for 30.1% (285/948) of the cases. Together these two virulotypes represented 72.2% of the total number of severe human cases with known virulotypes in 2019.

Stx-coding genes profiles of the food and human isolates causing severe infection (HUS, hospitalisation and bloody diarrhoea) in 2019 and comparison with those associated with severe disease in humans in the 2012–2017, in EU



The most common *stx* gene subtypes (human isolates) were *stx1a* (261/865; 30.2%), *stx2a* (222/865; 25.7%), *stx2c* (182/865; 21.0%) and *stx2a;stx2c* (100/865; 11.6%), representing 88.5% of the total number of subtypes in severe human cases.

| Stx genes subtypes combinations | No of food isolates in 2019 [^] | No of human isolates in 2019 (%) | Relative frequency of the <i>stx</i> genes subtypes combinations in* | | | | | |
|---------------------------------|--|----------------------------------|--|-------------|-----------------|-------------|-----------------|-------------|
| | | | HUS | | Hospitalization | | Bloody Diarrhea | |
| | | | <i>eae+</i> | <i>eae-</i> | <i>eae+</i> | <i>eae-</i> | <i>eae+</i> | <i>eae-</i> |
| <i>Stx1a</i> | 10 | 261 (30.2) | 1.2 | 0.0 | 27.6 | 20.7 | 27.3 | 8.0 |
| <i>Stx2a</i> | 3 | 222 (25.7) | 27.4 | 10.4 | 56.4 | 32 | 58.4 | 26.3 |
| <i>Stx2c</i> | 2 | 182 (21.0) | 4.3 | 5.0 | 19.8 | NR | 23.9 | NR |
| <i>Stx2c;Stx2a</i> | 1 | 100 (11.6) | 29.0 | NR | 57.1 | NR | 65.5 | NR |
| <i>Stx2d;Stx2a</i> | 1 | ND | – | – | – | – | – | – |
| <i>Stx2g;Stx2a</i> | 2 | ND | – | – | – | – | – | – |
| <i>Stx2b</i> | 1 | 39 (4.5) | NR | 0.5 | NR | 21.3 | NR | 10.5 |
| <i>stx1c</i> | ND | 30 (3.5) | NR | 0.6 | NR | 18.9 | NR | 19.5 |
| <i>Stx2d</i> | 4 | 16 (1.8) | NR | 10.3 | NR | 33.3 | NR | 16.0 |
| <i>Stx2f</i> | ND | 8 (0.9) | 3.8 | NR | 21.0 | NR | 8.7 | NR |
| <i>Stx1d</i> | 1 | 3 (0.3) | – | – | – | – | – | – |
| <i>Stx2c;Stx2a;Stx1a</i> § | 1 | ND | 20.8 | 4.5 | 59.3 | NR | 56.6 | NR |
| <i>Stx2a;Stx1a</i> | 8 | ND | 20.8 | 4.5 | 59.3 | NR | 56.6 | NR |
| <i>Stx1a;Stx1c</i> | ND | 1 (0.1) | – | – | – | – | – | – |
| <i>Stx2e</i> | ND | 1 (0.1) | – | NR | NR | NR | NR | 31.8 |
| <i>Stx2a;Stx2e</i> | ND | 1 (0.1) | – | – | – | – | – | – |
| <i>Stx2c;Stx2d</i> | ND | 1 (0.1) | – | – | – | – | – | – |
| <i>Stx2d;Stx2b</i> | 2 | ND | – | – | – | – | – | – |
| <i>Stx2d;Stx1a</i> | 1 | ND | – | – | – | – | – | – |
| <i>Stx2d;Stx2a;Stx1a</i> | 2 | ND | – | – | – | – | – | – |
| Total | 39 | 865 | | | | | | |

NR: data present in the TESSy data set used, with less than 20 isolates.

ND: Not detected.

– : not present in the TESSy database in the 2012–2017 period.

*: Relative frequencies (%) of the different combinations of *stx* gene subtypes in STEC isolated from severe disease (TESSy data, 2012–2017). Human data from: EFSA Journal 2020;18(1):5967.

[^]: Due to the low number of isolates virulotyped for food only the number of isolates is displayed. Only six animal isolates were provided with the information on the *stx* gene subtypes and have not been included in this table.

- Of the isolates from **food** with the reported information on the serogroup **21.2% belonged to the 'top-five' serogroups (O157, O26, O103, O111 and O145)** in 2019 and more than half of all the remaining STEC belonged to the top-20 STEC serogroups reported in human infections to ECDC in 2015–2018.
- Most of the virulotypes of STEC isolates from food and animal were also identified in severe STEC infections in humans. This identification, however, was only carried out on 52.9% of the food isolates for the stx gene typing (stx1 and stx2) and stx gene subtyping was only done for 6.1% of the food isolates, and even less for animal isolates.
- Testing of animal samples was still not widely carried out in the EU with 2,588 animal samples tested for STEC by nine MS in 2019.

Thank you for your attention

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Data Providers

| | |
|------|--|
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| ECDC | Food and Waterborne Diseases and Zoonoses Network, Emerging and Vector-borne Diseases Network and the Tuberculosis Network |

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