



Update on the annual reporting of STEC in the EU and on EFSA activities for molecular typing data collection for food and animal isolates

Mirko Rossi
Scientific officer

Trusted science for safe food

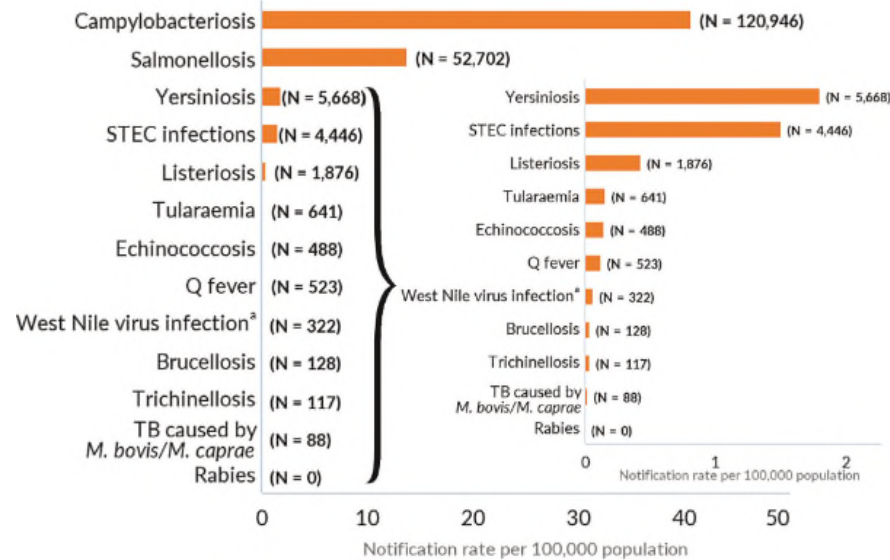
EU One Health Summary Report 2020

Challenging data analyses

Withdrawal of UK
COVID-19 pandemic



Reported numbers and notification rates of confirmed human zoonoses in the EU, 2020



Note: The total number of confirmed cases is indicated in parentheses at the end of each bar.
 (a): Regarding West Nile virus infection, the total number of cases was used (includes probable and confirmed cases).

Main findings (EUOHZ 2020 report)

- Drop in reported zoonotic diseases** in humans and foodborne outbreaks in 2020, due to impact of the COVID-19 pandemic in Europe, ranging from 7% to 53% depending on the reported disease in question. For STEC the relative reduction in notification rate was 22%.
- The number of reported foodborne outbreaks also fell by 47%.
- Campylobacteriosis** was the most reported zoonosis in the EU in 2020 followed by **salmonellosis**
- Listeriosis** and **West Nile virus** infections: the most severe zoonotic disease, with high rates of hospitalisation (97% and 92% resp.) and fatality (13% and 12% resp.)

STEC infections in humans, EU 2020



STEC is the fourth most commonly reported foodborne gastrointestinal infection in humans in the EU and the fourth most commonly reported bacterial agent detected in foodborne outbreaks in the EU

Shiga toxin-producing *Escherichia coli* (STEC)

Human cases

Notification rate (per 100,000 population) **1.49** Trend (2016–2020)

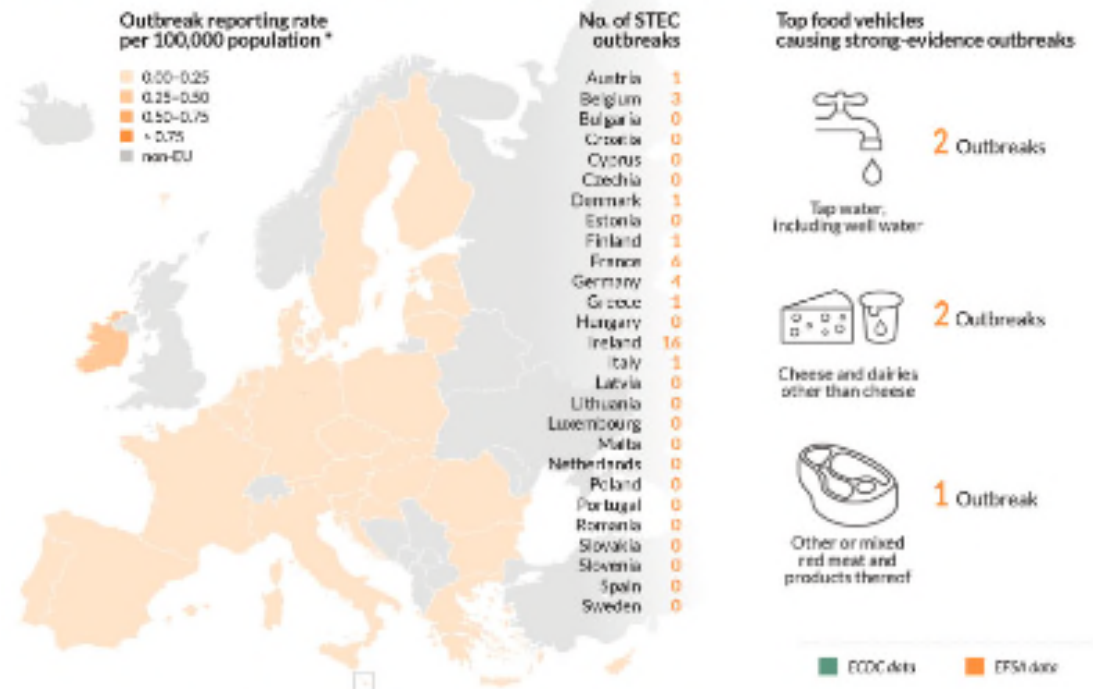
4,446 Cases of illness

3,327	Infections acquired in the EU	652	Hospitalisations
148	Infections acquired outside the EU	13	Deaths
971	Unknown travel status or unknown country of infection		

Human cases in foodborne outbreaks

34	Foodborne outbreaks	208	Cases of illness
5	Strong-evidence outbreaks	30	Hospitalisations
29	Weak-evidence outbreaks	1	Death

Foodborne outbreaks in the EU

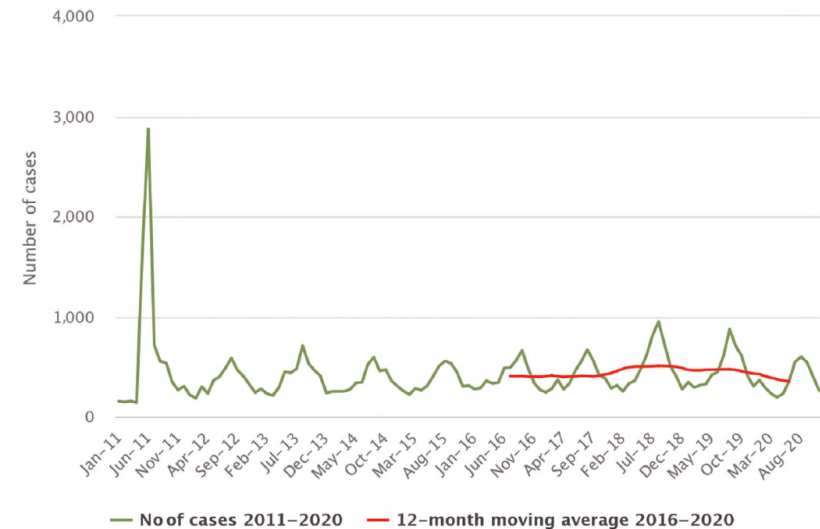


* Differences among countries shall be interpreted with caution as this indicator depends on several factors including the type of outbreaks under surveillance and does not necessarily reflect the level of food safety in each country.

STEC infections in humans, EU, 2016-2020



- EU 2020 **notification rate was 1.5** per 100,000 population.
- The highest country-specific notification rates were observed in Ireland and Denmark, (14.8 and 7.6 cases per 100,000 population, respectively).
- At EU level the overall trend for STEC in 2016–2020 did not show any statistically significant increase or decrease
- At the MS level, a statistically significant increasing trend ($p < 0.01$) was observed in years 2016–2020 in Denmark and Finland



Source: Austria, Czechia, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Lithuania, Luxembourg, the Netherlands, Poland, Romania, Slovakia, Slovenia, Sweden.

Country	2020		2019		2018		2017		2016			
	National coverage ^(a)	Data format ^(a)	Confirmed cases and rates		Confirmed cases and rates		Confirmed cases and rates		Confirmed cases and rates			
			Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate		
EU Total 27	–	–	4,446	1.5	6,214	1.8	6,327	1.9	5,078	1.7	5,107	1.7
United Kingdom	–	–	–	–	1,587	2.4	1,840	2.8	993	1.5	1,367	2.1
EU Total^(e)	–	–	4,446	1.5	7,801	1.9	8,167	2.0	6,071	1.7	6,474	1.8

- In 2020, 22 MS reported the **presence of STEC in 2.4%** of 19,036 **food sample units** taken according an 'objective sampling' strategy (compared with 2.8% in 2019)
- STEC was most commonly found in '**meat of different types**' derived from different animal species (3.4% STEC-positive), followed by 'milk and dairy products' (2.1%), while 'fruits and vegetables' was the least contaminated category (0.1%)
- '**Sprouted seeds**' were tested by 6 MS in the context of Regulation (EC) No 2073/2005 with **no positive STEC units** in 323 official samples

- Seventeen MS tested 7,924 **ready-to-eat (RTE) food samples** for STEC of which 105 (1.3%) were found to be STEC-positive
 - 28 (1.7%) 'meat and meat product samples'
 - 33 (1.5%) 'milk and milk product samples'
 - four STEC-positive samples from 'fruits, vegetables and juices' (0.2%)
 - two (0.5%) samples from 'spices and herbs'
- Testing of animal samples was still not widely carried out in the EU (2,112 animal samples reported taken by six MS in 2020)

- 17.7% of isolates from food* were typed as 'top five' serogroups (O157, O26, O103, O111 and O145) majority of the remaining strains belong to top 20 serogroups reported in human infections to ECDC in 2016–2019
- 39.3% of the isolates from food were reported together with information on the *stx* gene type (*stx1* or *stx2*), 8% on *stx* subtype and 48.2% on intimin-coding gene *eae*
- Most of the virulotypes of STEC isolates from food and animals were also identified in severe STEC infections in humans

*detected with the reference method ISO TS 13136:2012 and provided with information on the serogroup

EU One Health Zoonoses report → new communication tools published in 2020



EFSA's story map on foodborne outbreaks

Foodborne Outbreaks
Updated last on 11.30.2021

List of Contents

- What foodborne outbreaks are and how they are classified
 - How foods may cause foodborne outbreaks
 - How organisms and symptoms
 - How, why and where food contamination may occur
- Who investigates foodborne outbreaks
- How many foodborne outbreaks in 2020
- What is the real burden on public health
- How to protect yourself from foodborne illness
- EU regulatory framework and the role of EFSA
- References and further reading on this topic



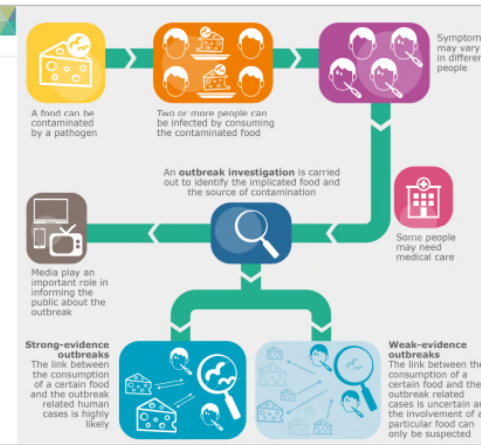
Foodborne Outbreaks

What foodborne outbreaks are and how they are classified

A foodborne outbreak can be defined as "an incident in which two or more people develop the same disease or infection following the consumption of a common contaminated food". Most of the agents implicated in foodborne outbreaks are **zoonotic agents**. The severity of the disease varies in humans, with effects ranging from mild to serious illness and even death (WHO, food safety).

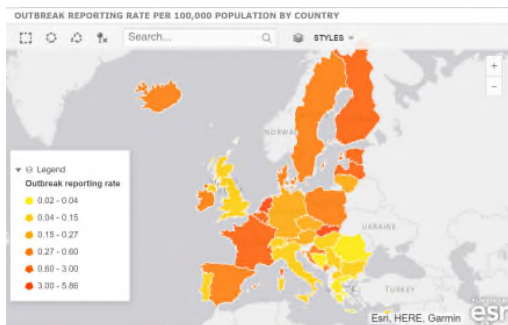
The EU collects data on outbreaks caused by the consumption of food and water contaminated by bacteria, viruses, parasites, algae, fungi, or their products (e.g. toxins and biological amines, such as histamine). Reporting also includes the agents for which foodborne transmission is possible but usually accidental.

The EU Foodborne Outbreak Reporting System (EU-FORS: EFSA, 2014) categorises foodborne outbreaks as **strong-evidence outbreaks** and **weak-evidence**



<https://multimedia.efsa.europa.eu/fbo-storymaps/index.html>

EFSA's dashboard on foodborne outbreaks



Foodborne outbreaks - dashboard

CAUSATIVE AGENTS

Reporting year: 2020 | Strength of evidence: (All) | Type of outbreak: (All) | EU and non EU: (All) | Reporting country: (All)

Number of countries	Outbreaks	Cases	Hospitalisations	Deaths
33	3,143	21,513	1,830	48

each graph can be maximized with the icon that appears to the right corner of the titlebar.

NUMBER OF OUTBREAKS BY CAUSATIVE AGENT

Causative agent	Number of outbreaks
Unknown / Unspecified	1,244
Salmonella	708
Bacterial toxins unspecified	372
Campylobacter	222
norovirus and other Calicivirus	132
Bacillus toxin	72
Staphylococcus aureus toxin	44
Histamine and Scombrotoxin	43
STEC	41
Clostridium perfringens	39
Haemolytic E. coli	29
Listeria monocytogenes	20
Other viruses	18
Yersinia	16
Other bacterial agents	15
Clostridium botulinum	9
Trichinella	8
Hepatitis A	7
Other parasites	5
Cryptosporidium	4
Other agents	3
Brucella	1

NUMBER OF HUMAN CASES AND HOSPITALISATIONS BY CAUSATIVE AGENT

Causative agent	Human cases	Hospitalisations
Salmonella	6,280	4,527
Bacterial toxins unspecified	2,061	2,041
Bacillus toxin	1,326	1,204
Staphylococcus aureus toxin	412	172
Yersinia	351	172
Other bacterial agents	292	172
Trichinella	252	172
Other parasites	252	172
Other agents	252	172
Brucella	252	172

DISTRIBUTION (%) OF DEATHS BY CAUSATIVE AGENTS

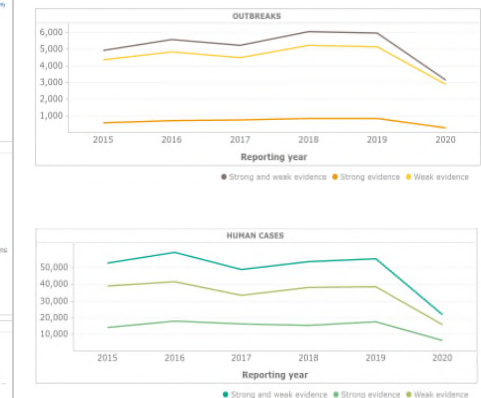
Causative agent	Percentage of deaths
STEC	2.08%
Salmonella	16.07%
Bacillus toxin	2.08%
Histamine and Scombrotoxin	2.08%
norovirus and other Calicivirus	2.08%
Listeria monocytogenes	62.50%

Legend: Causative agent (Salmonella, Bacillus toxin, Bacterial toxins, Brucella, Campylobacter, Clostridium botul.)

Legend: Metrics (Human cases, Hospitalisations)

Legend: Reporting year (2015-2020) (Strong and weak evidence, Strong evidence, Weak evidence)

Footer: <https://www.efsa.europa.eu/en/microstrategy/FBO-dashboard>



<https://www.efsa.europa.eu/en/microstrategy/FBO-dashboard>

Acknowledgements



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Therese Wrestrel



Consortium ZOE: Consortium ZOE: Istituto Superiore di Sanità staff; Istituto Zooprofilattico delle Venezie staff; the French Agency for Food, Environmental and Occupational Health & Safety staff; Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale" staff; Istituto Zooprofilattico Sperimentale della Lombardia ed Emilia Romagna B. Ubertini – IZSLER staff

Data Providers

EFSA: Scientific Networks for Zoonoses Monitoring Data and AMR

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

Contact in EFSA

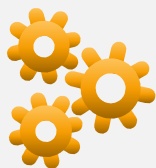
□ zoonoses@efsa.europa.eu

www.efsa.europa.eu

EFSA One Health WGS System



Main objectives



Two interoperating systems (EFSA & ECDC)

Each system collects and stores the data (i.e. allelic profiles and descriptive data) of the respective data domain



Cross-sector matches

Databases will be queried, and comparison will be performed live to the data stored, returning any matches (according to business rules)



Machine-to-machine

Automatic exchanging of allelic profiles and descriptive data as established in the Collaboration Agreement

Why two interoperable systems?

1

EFSA and ECDC has different architectural constrains and IT policies

2

EFSA and ECDC has different way to manage identities and different legal frameworks

3

The cross-sectorial exchange of data should happen under specific circumstances (i.e. *when matches have been found*)

EFSA – ECDC collaboration agreement



- The EFSA – ECDC interaction is described in the collaboration agreement and its Annex

<https://www.efsa.europa.eu/sites/default/files/2022-06/collaboration-agreement-molecular-typing-EFSA-ECDC-WGS-DataCollection.pdf>

Both parties agreed on the following main points:

- Use **comparable analytical pipelines** for generation and quality assurance of WGS data (chewBBACA version > 2.8.0 with schema for *Salmonella*, *E. coli* and *Listeria* from chewieNS)
- Use **CRC32 integer for allele designation**
- Use **harmonized procedure and agreed thresholds** for searching for clusters and matches between profiles and for the communication of the results
- Automatic exchange of **cgMLST profiles and metadata (Date, Country, Sample category, Cluster ID)** upon a match is found
- The exchanged data can be stored in the respective databases and specific visibility rules for respective data providers

Detection of joint microbiological clusters of food-borne pathogens isolates

The trigger is a public health signal or event

Indicator-based surveillance

- Recurring weekly querying
- Weekly clustering at ECDC side
- Submission to EFSA queries based on the cluster definition at ECDC
- Fixed agreed threshold

Event-based surveillance

- *Ad hoc* querying
- Usually linked to event in EpiPulse
- Multiple thresholds (up to a maximum agreed value)

Every time ECDC finds matches in EFSA database, EFSA system sends to ECDC automatically a query based on the found matches

Data collection during multi-country event



When a ROA or JNS is requested EFSA initiates a data call from food sector at Member State level

The Country Officer communicate the request to the national data providers and alert the Food authority

The Data Providers submit the data if available to the EFSA One Health WGS System

Added value at EU

■ Accelerate multi-country outbreak detection and investigation

8096

Queries Received

613

EFSA Entries Matched

651

Clusters

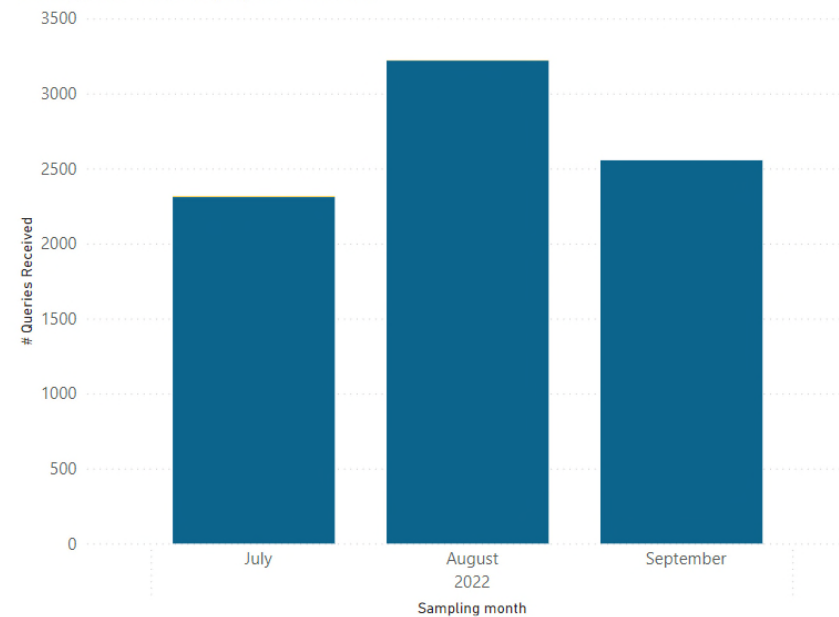
Last Month

isolate_species_code	Numbers Of Clusters ECDC sent	Numbers Of Clusters matching EFSA
L. monocytogenes	635	80

Total

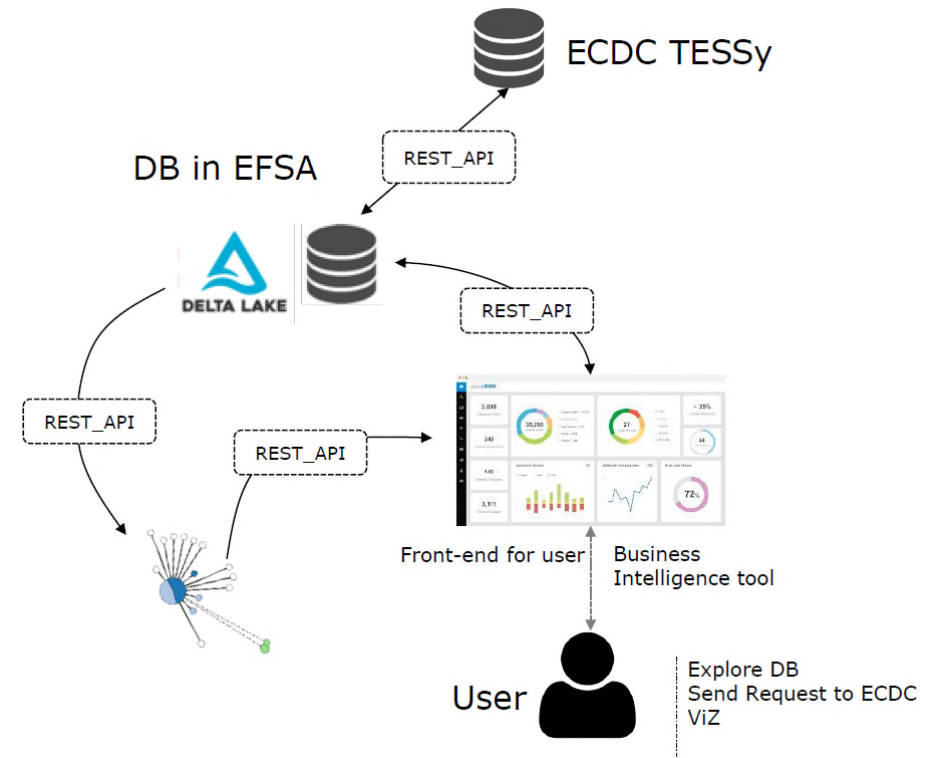
isolate_species_code	Numbers Of Clusters ECDC sent	Numbers Of Clusters matching EFSA
L. monocytogenes	645	85
S. enterica	6	3

isolate_specie ● L. monocytogenes ● S. enterica



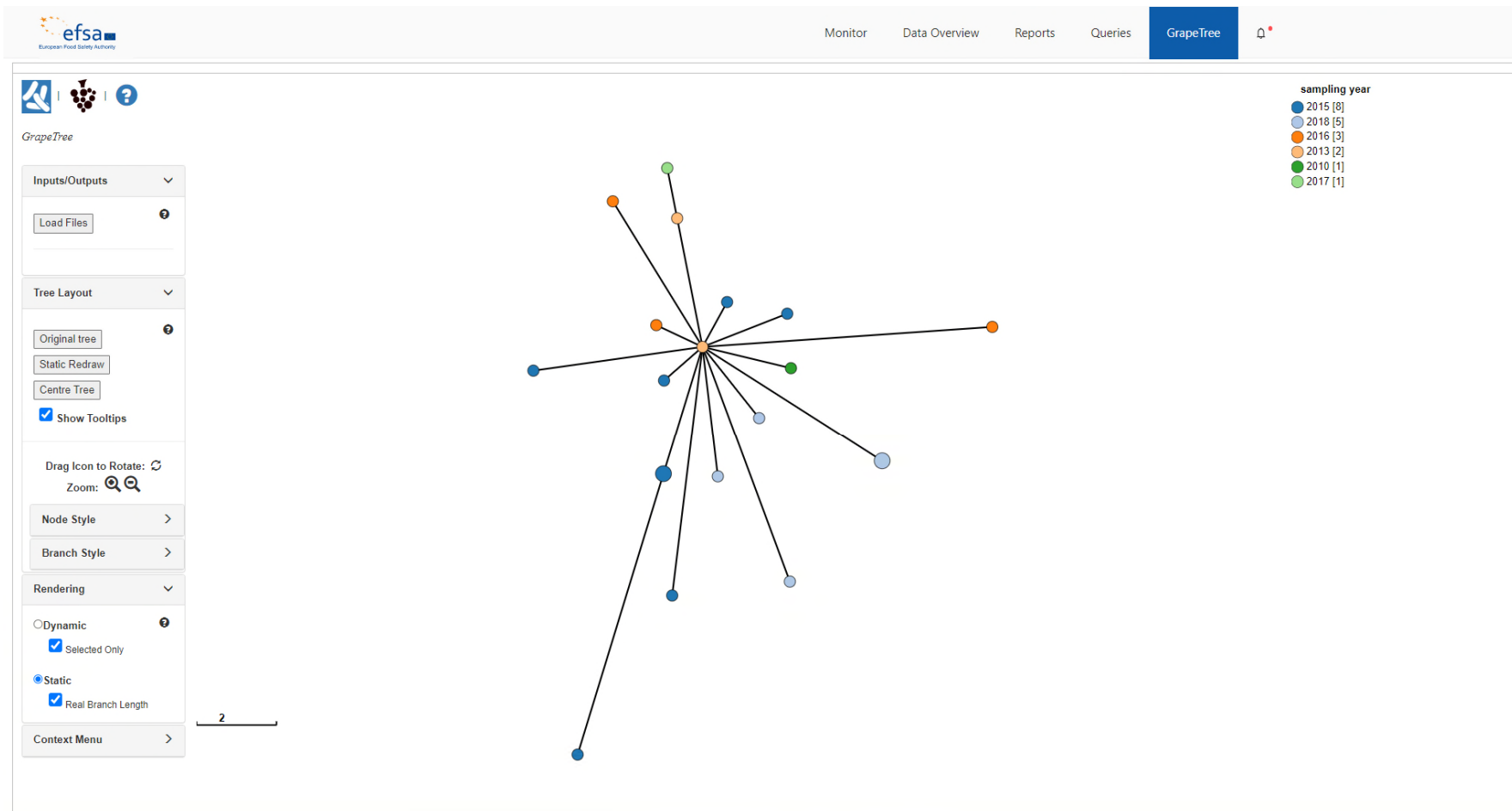
Added values at MS level

1. Support foodborne outbreak investigation
2. One-stop-shop for bioinformatic analysis
3. Compare own data with EU data



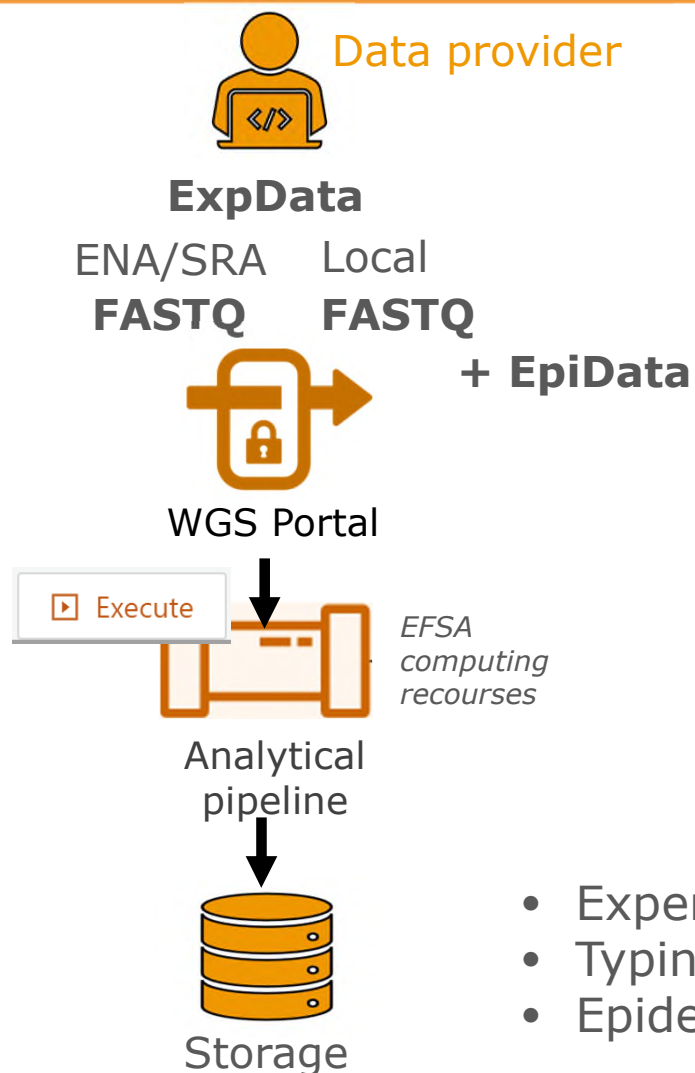
1 - Added values at MS level

Support foodborne outbreak investigation



2 - Added values at MS level

One-stop-shop for bioinformatic analysis



- Use EFSA computing resources for generating large set of typing information in a standardised manner
- No bioinformatic skills needed

- Experimental Data
- Typing Data (inc. Allelic profiles)
- Epidemiological Data

3 - Added values at MS level

Compare own data vs EU aggregated data

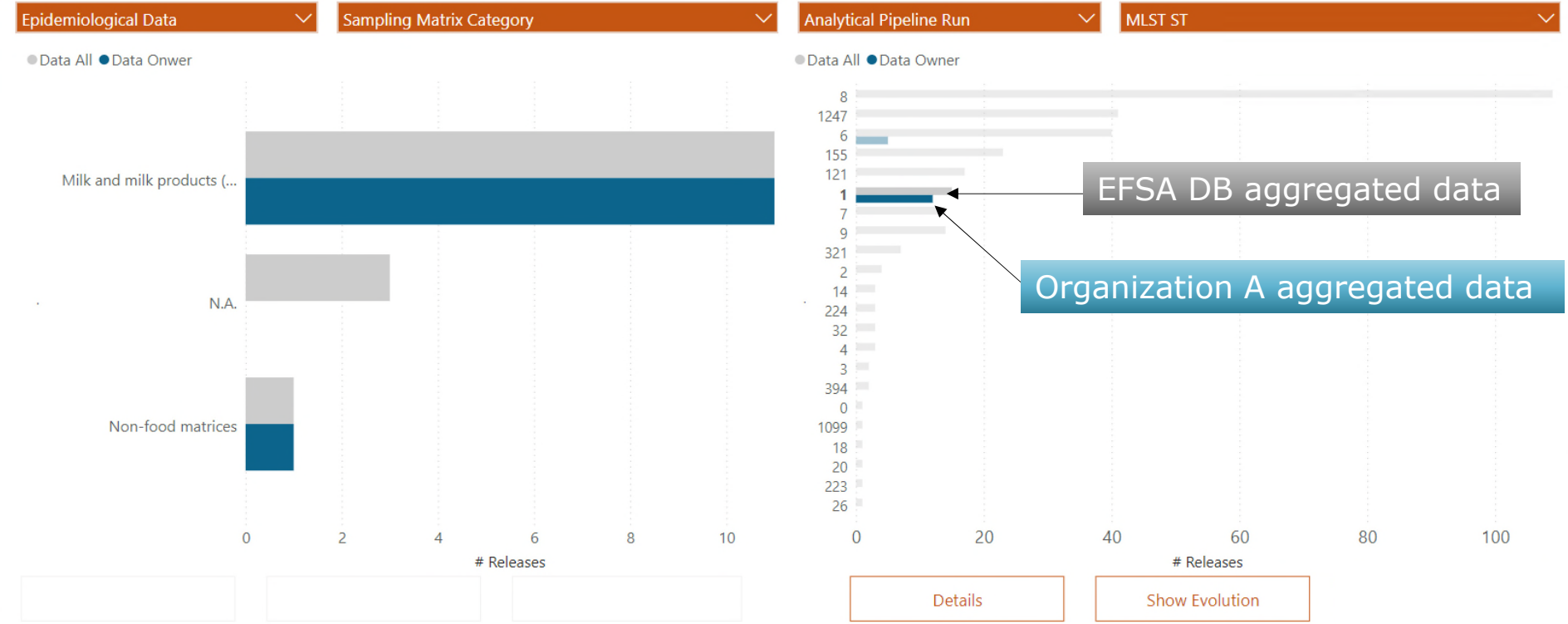
*How many countries reported ST 1 of Listeria monocytogenes?
 How many profiles are available in the EFSA DB?
 From which sampling matrix categories have been sampled?
 ...*

5%
1
 # Reporting countries

4%
12
 # Released profiles with EpiData

8%
3
 # Sampling matrixes reported

5%
15
 # Released profiles



Visibility of submitted data

Country A
Org A



Entry	Exp. Data	Epi. Data	Typing Data
ENTRY1	RawReadsID, Organization, country, MDS checksum ...	SampleID, Sample Matrixes, sampling country ...	MLST, serovar, cgMLST profile...

Country B
Org C



Entry	Exp. Data	Epi. Data	Typing Data
ENTRY3	RawReadsID, Organization, country, MDS checksum ...	SampleID, Sample Matrixes, sampling country ...	MLST, serovar, cgMLST profile...

Country A
Org B




Entry	Exp. Data	Epi. Data	Typing Data
ENTRY2	RawReadsID, Organization, country, MDS checksum ...	SampleID, Sample Matrixes, sampling country ...	MLST, serovar, cgMLST profile...

Country B




Entry	Exp. Data	Epi. Data	Typing Data
ENTRY3	RawReadsID, Organization, country, MDS checksum ...	SampleID, Sample Matrixes, sampling country ...	MLST, serovar, cgMLST profile...

Country A






Entry	Exp. Data	Epi. Data	Typing Data
ENTRY1	RawReadsID, Organization, country, MDS checksum ...	SampleID, Sample Matrixes, sampling country ...	MLST, serovar, cgMLST profile...
ENTRY2	RawReadsID, Organization, country, MDS checksum ...	SampleID, Sample Matrixes, sampling country ...	MLST, serovar, cgMLST profile...



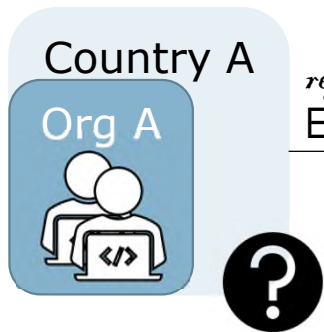
Entry	Exp. Data	Epi. Data	Typing Data
ENTRY1	RawReadsID, Organization, country, MDS checksum ...	SampleID, Sample Matrixes, sampling country ...	MLST, serovar, cgMLST profile...
ENTRY2	RawReadsID, Organization, country, MDS checksum ...	SampleID, Sample Matrixes, sampling country ...	MLST, serovar, cgMLST profile...
ENTRY3	RawReadsID, Organization, country, MDS checksum ...	SampleID, Sample Matrixes, sampling country ...	MLST, serovar, cgMLST profile...

EURL

species

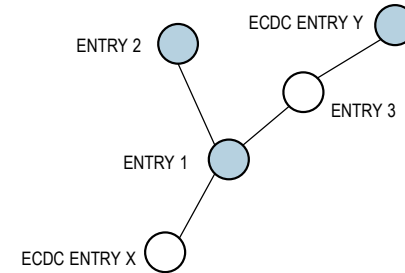
Visibility of data linked to query



ref
ENTRY 1

Query	Ref	Matches	Country	Date	Sample Matrix category	Sample Matrix details
OrgA-query1	ENTRY 1		A	DD-MM-YYYY	FOOD category A	Batch X Product Y
		ENTRY 2	A	DD-MM-YYYY	FOOD category B	-
		ENTRY 3	-	DD-MM-YYYY	FOOD category C	-
		ECDC ENTRY X	-	DD-MM-YYYY	HUMAN	-
		ECDC ENTRY Y	A	DD-MM-YYYY	HUMAN	-

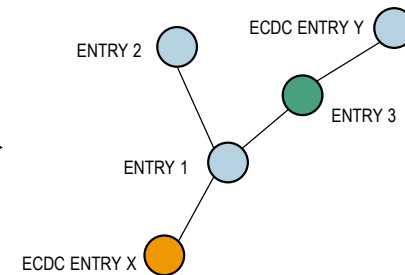
Country A



ref
ENTRY 1

Query	Ref	Matches	Country	Date	Sample Matrix category	Sample Matrix details
EFSA-query1	ENTRY 1		A	DD-MM-YYYY	FOOD category A	Batch X Product Y
		ENTRY 2	A	DD-MM-YYYY	FOOD category B	Batch Z Product Y
		ENTRY 3	B	DD-MM-YYYY	FOOD category C	Batch H Product Y
		ECDC ENTRY X	C	DD-MM-YYYY	HUMAN	-
		ECDC ENTRY Y	A	DD-MM-YYYY	HUMAN	-

Country A Country B Country C

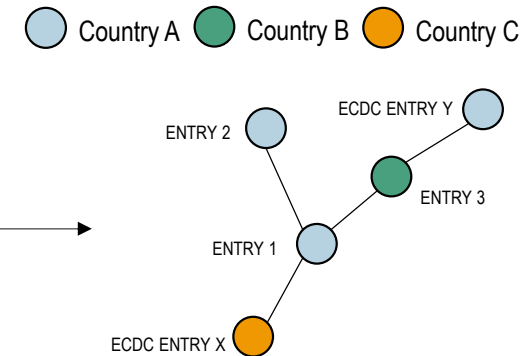


Visibility of data linked to query



ref
ECDC ENTRY X

Query	Ref	Matches	Country	Date	Sample Matrix category
ECDC-query1	ECDC ENTRY X		C	DD-MM-YYYY	FOOD category A
		ENTRY 1	A	DD-MM-YYYY	FOOD category B
		ENTRY 2	A	DD-MM-YYYY	FOOD category C
		ENTRY 3	B	DD-MM-YYYY	HUMAN
		ECDC ENTRY Y	A	DD-MM-YYYY	HUMAN



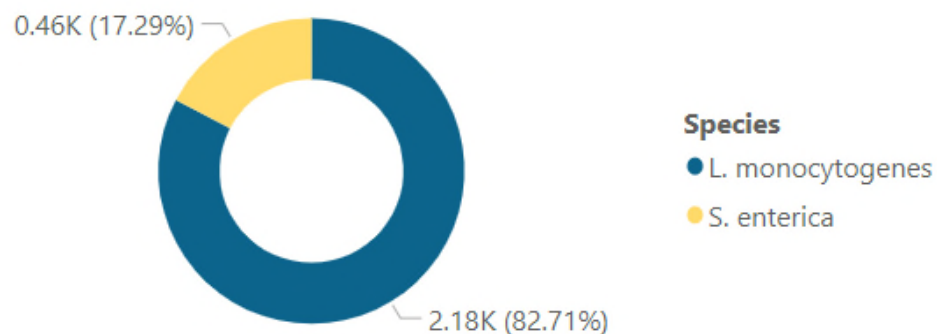
- The visibility of country info of food data follow similar implementation for MS level
- Country info is shared to ECDC on discretion of EFSA data providers

**EFSA One Health
WGS system:
statistics**



Statistics submissions

Released profiles by species



22
Reporting countries

74
Sampling matrixes reported

378 14%
Released profiles with EpiData

2638
Released profiles

469 profiles uploaded by appointed users → 452 formally submitted

2186 profiles imported from public repository

- Why?: a single query ECDC can search for matches in public data and data submitted by MS
- Regular import: 2022 focus on *Listeria* (few hundreds/week)
 - NCBI pathogen detection
https://www.ncbi.nlm.nih.gov/pathogens/isolates/#taxgroup_name:%22Listeria%20monocytogenes%22
 - Run accession number = yes
 - Isolation type = environmental/other
 - Location = any EU/EEA+CH+UK
- On demand: *Salmonella* and *Listeria* depending on event of interest (weekly discussion with ECDC)
 - Isolation type = environmental/other
 - Any countries
 - Filtered based on MLST or serovar

Sample matrixes

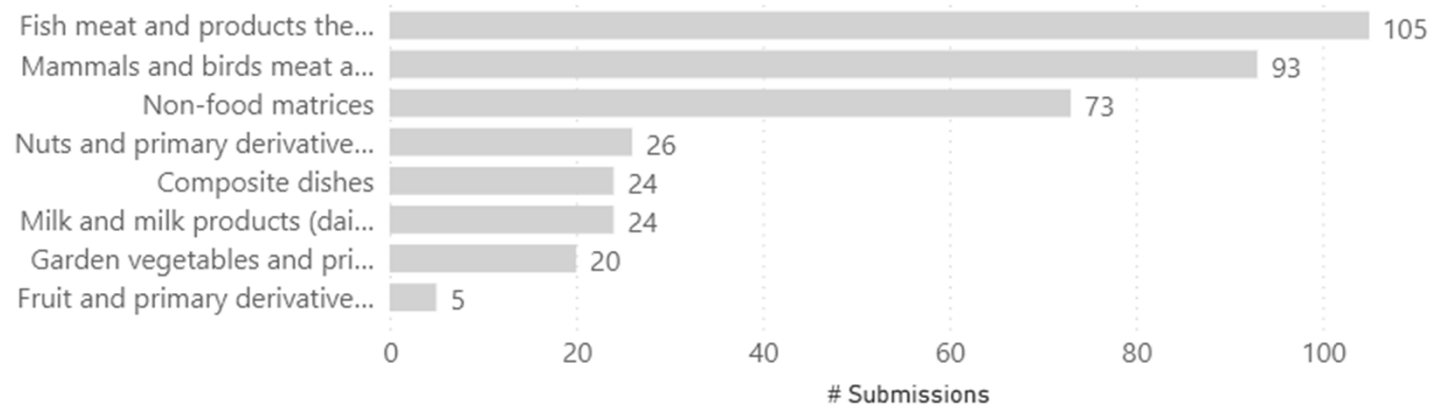
14%

378

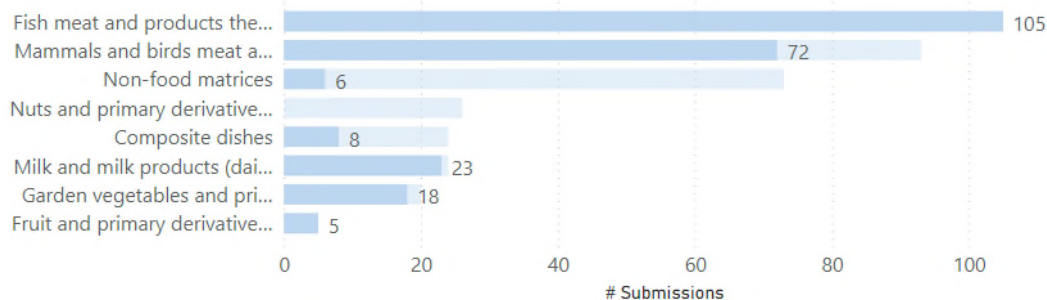
Released profiles with EpiData

74

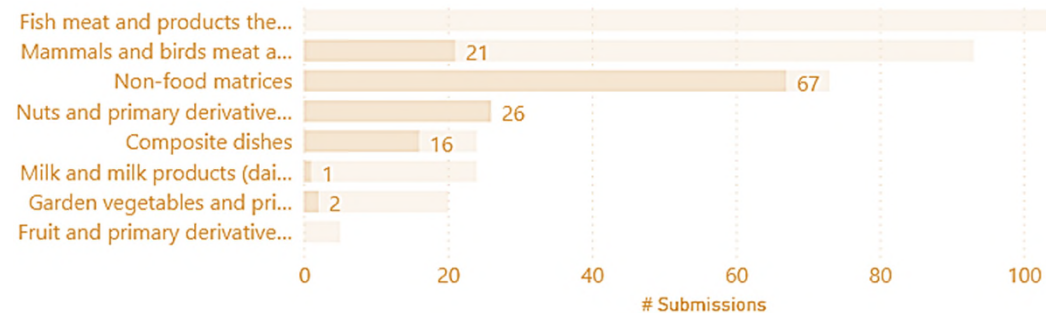
Sampling matrixes reported



Listeria



Salmonella



As of 30th September 2022

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