

# EU level surveillance FWD domain

Cecilia Jernberg GenEpiBioTrain Inter disciplinary course - FWD, 27 May 2024

# The intended learning outcome and (hopefully) a trigger for discussion within and between country teams

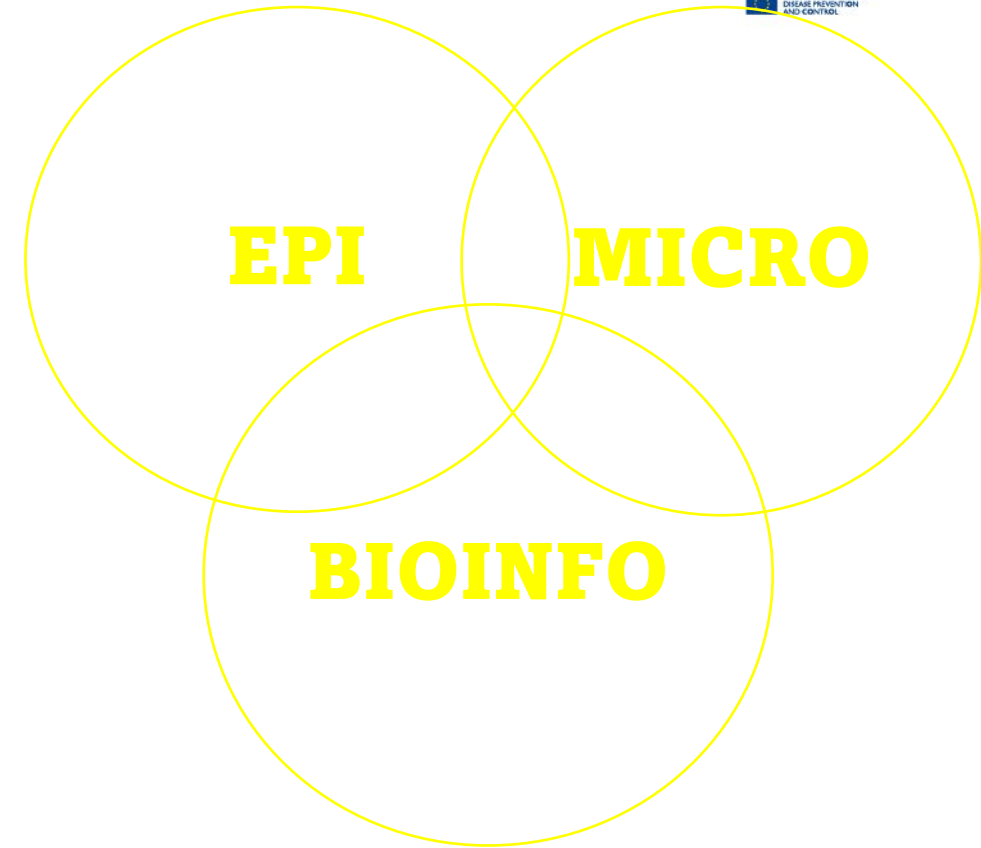


- Understand the principles and procedures of human surveillance at the EU level, including **data sharing** and **reporting** mechanisms to the ECDC and between member states.
- Explore the **functionalities of EpiPulse**, a platform for epidemiological and genomic data sharing and visualization, and its significance in EU-level surveillance efforts.
- Gain insights in **what the data reported to and collected by ECDC from countries are used for**, e. g. surveillance reports, risk assessments
- Understand why so many genepi projects, grants, are running and have been running, **financed on EU level.**

# How to strive for fit for purpose public health surveillance system?

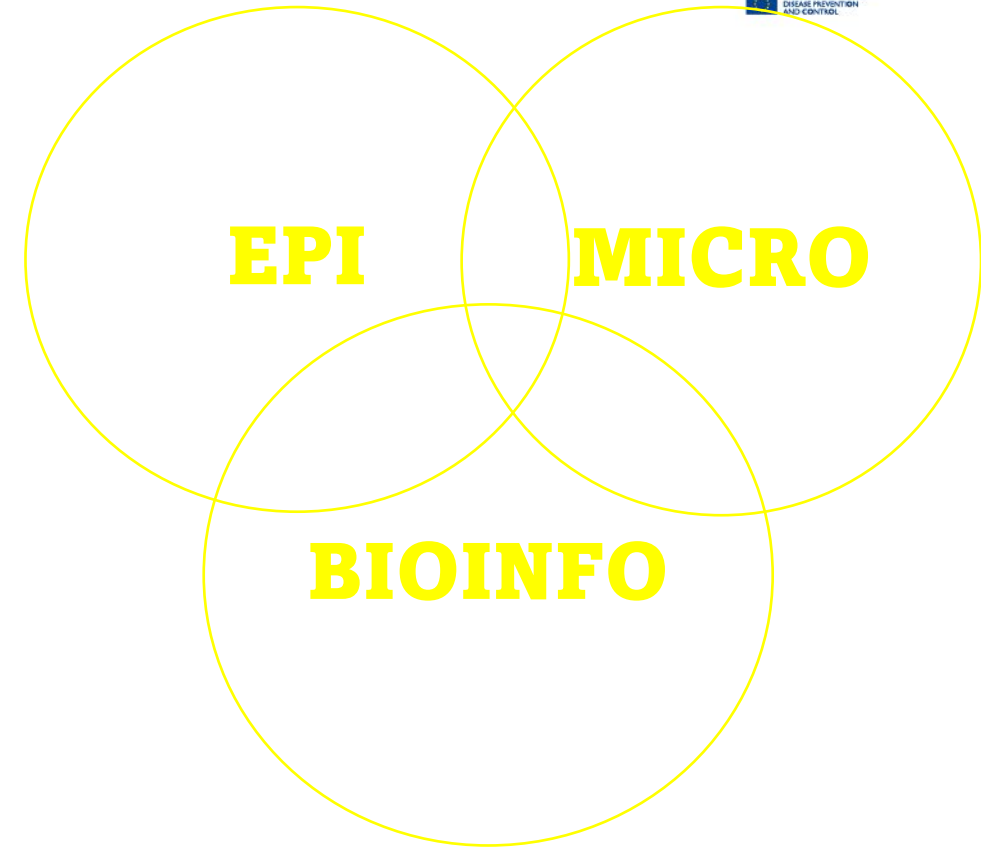
GenEpiBioTrain for capacity building  
Depending on your background ->  
increase in the general understanding of epidemiology,  
microbiology or bioinformatics.  
And primarily genetic epidemiology.

**Networking within countries and between countries !**



# How to strive for a fit for purpose public health surveillance system? Additional examples.

Good collaboration with IT, with legal  
Who is responsible for what  
Notification systems which can link lab and case data  
Relevant access rights to notification systems  
Form networks with regional labs/county medical offices  
Representative data collections  
Know your data – what does it represent



Keep each other informed, e.g. regular meetings, form outbreak teams  
Etc.

# Public health surveillance: reporting, collecting and sharing of data



- Detect outbreaks and epidemics of known or new pathogens
  - Measure the magnitude of health issues
  - Document the distribution and spread of health events
  - Evaluate control and prevention measures
  - Support epidemiological and laboratory research
- 
- Sharing public health surveillance data between countries improves disease detection and response capabilities. It can help identify outbreak sources when national-level data alone cannot.

# Why EU level surveillance?

The four (or possibly five?) freedoms in the EU internal (single) market

- Free movement of goods
- Free movements of services
- Free movement of capital
- Free movement of persons
- Free movement of pathogens

# ECDC surveillance outputs

# Annual reporting to TESSy of diseases under EU level surveillance



## Outputs:

- Surveillance atlas
- Annual Epidemiological Reports
- The European Union One Health 2022 Zoonoses Report
- The European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food



# Surveillance Atlas of Infectious Diseases



Campylobacteriosis ▼

Disease surveillance ▼

Confirmed cases ▼

Reported cases ▼

2022 ▼

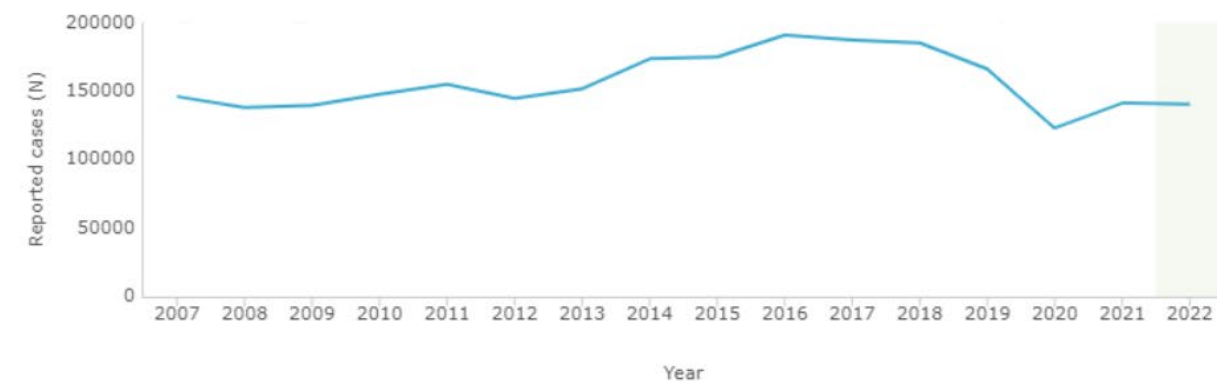


Region ▼	Reported cases (N)
EU (without UK)	137309
EU (with UK until 2019)	137309
EU/EEA (without UK)	140443
EU/EEA (with UK until 2019)	140443
Austria	6294
Belgium	5457
Bulgaria	107
Croatia	1467
Cyprus	82
Czechia	14412
Denmark	5143
Estonia	211

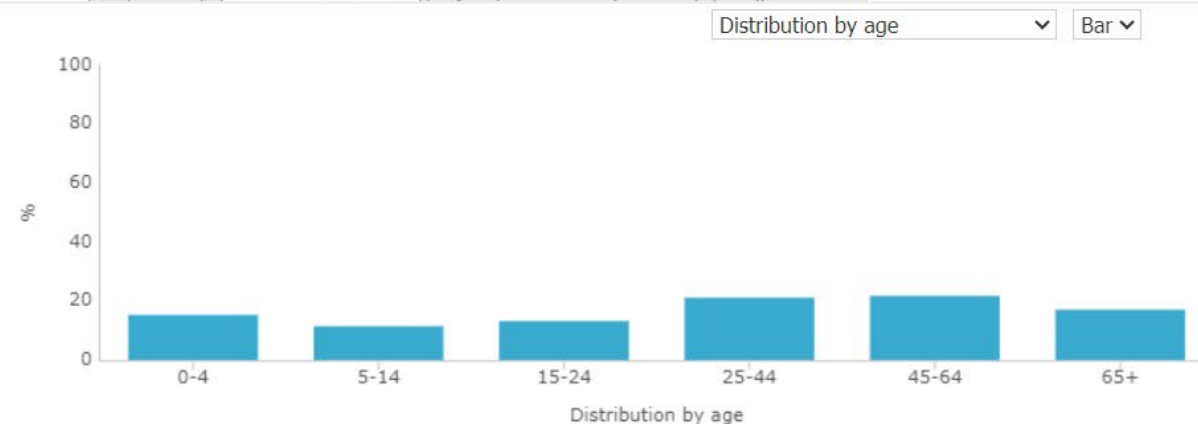


Reported cases (N)

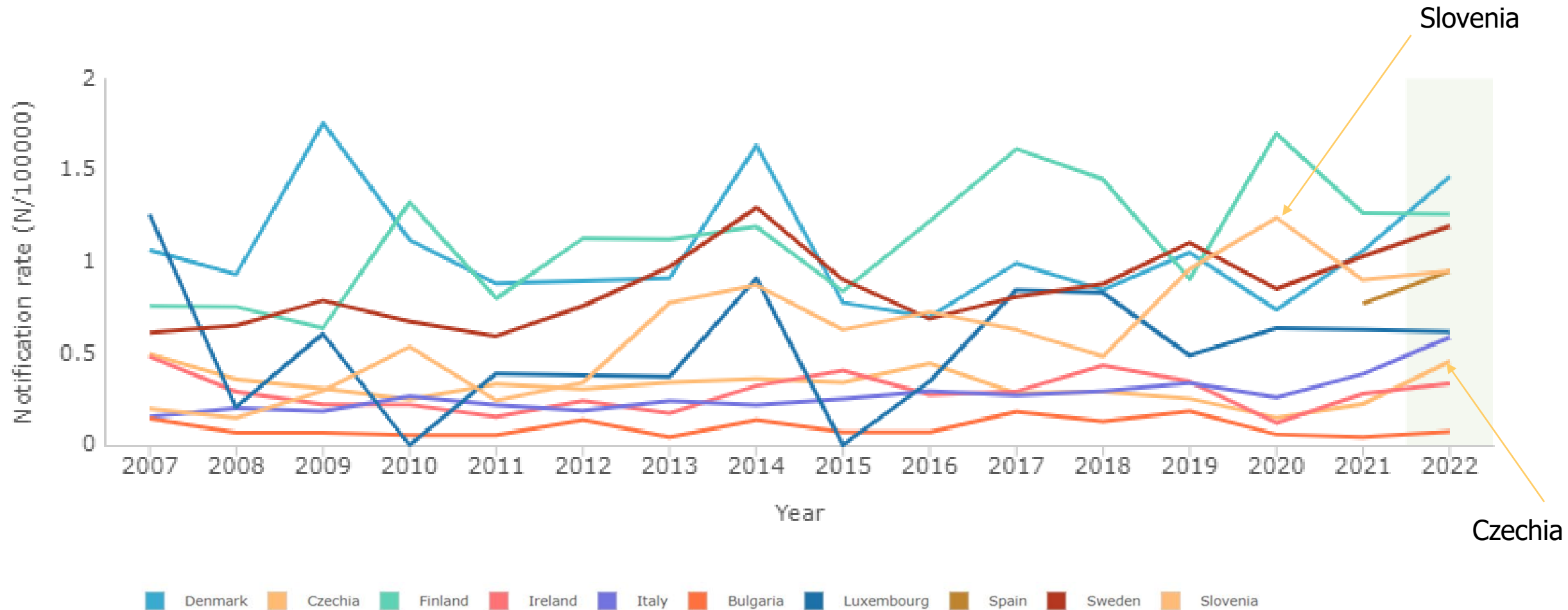
Value range: 1 - 73736



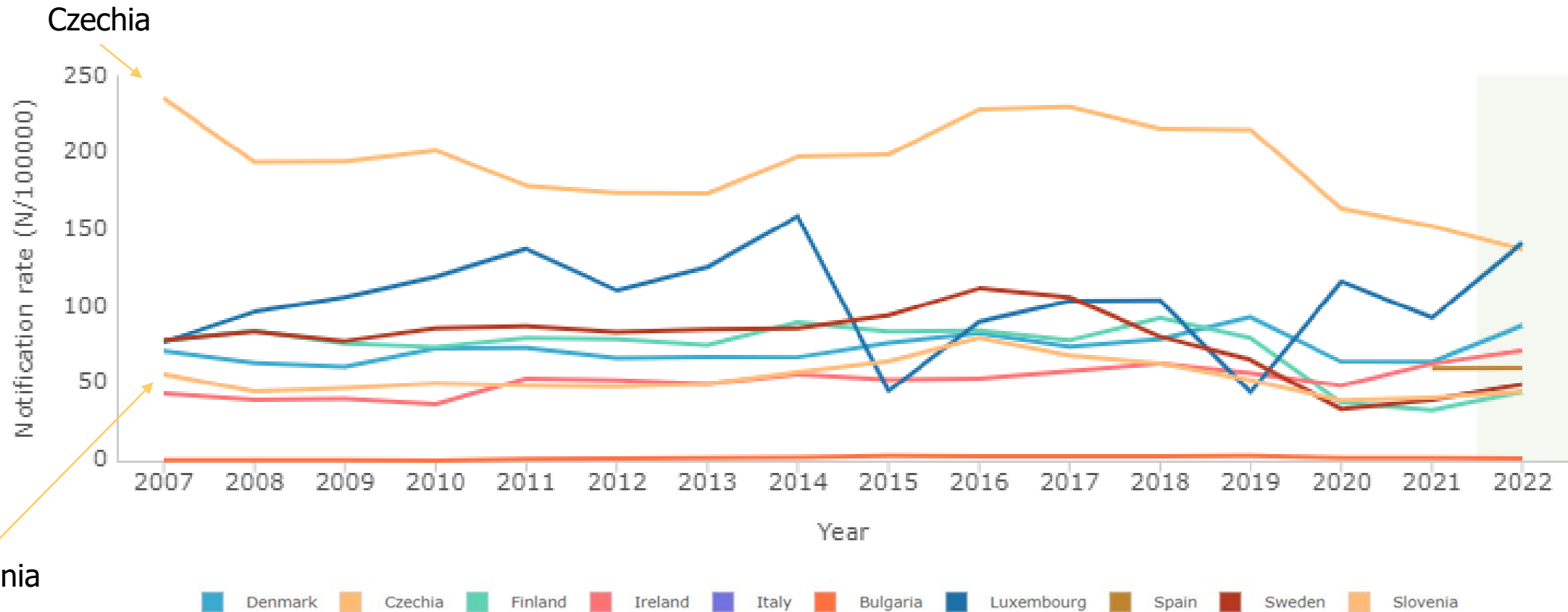
■ EU/EEA (without UK)



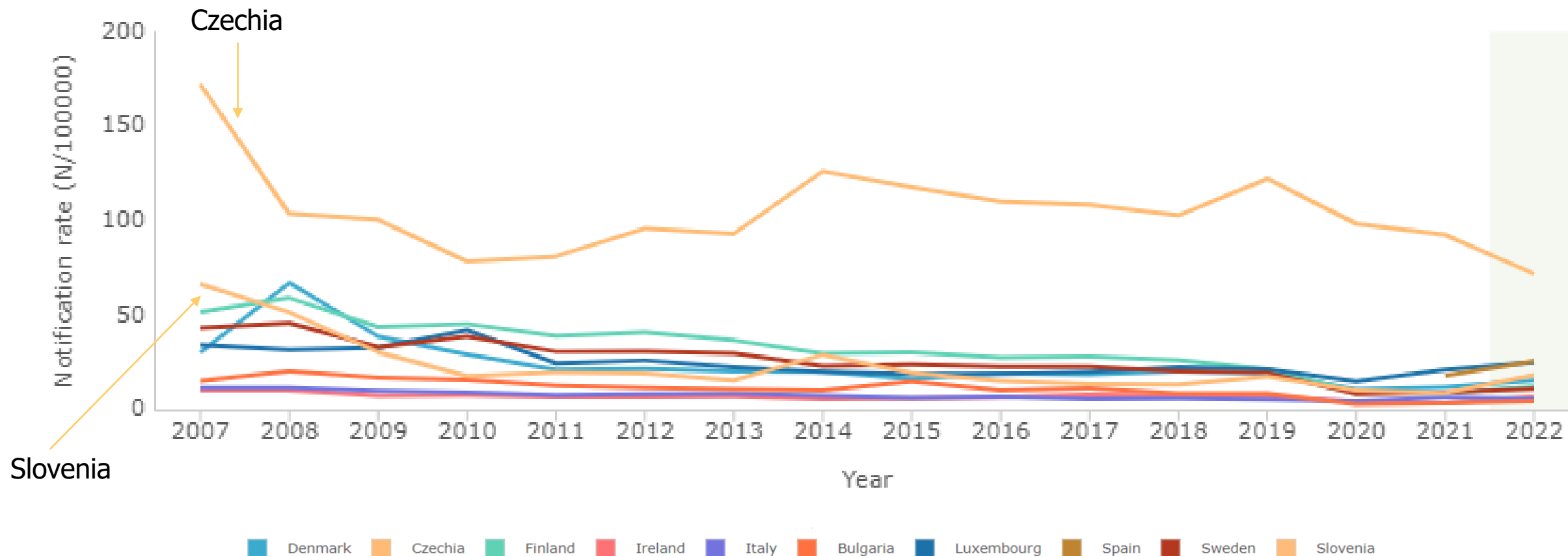
# Listeriosis. 2022 notification rate 0.62, 2770 cases in EU/EEA.



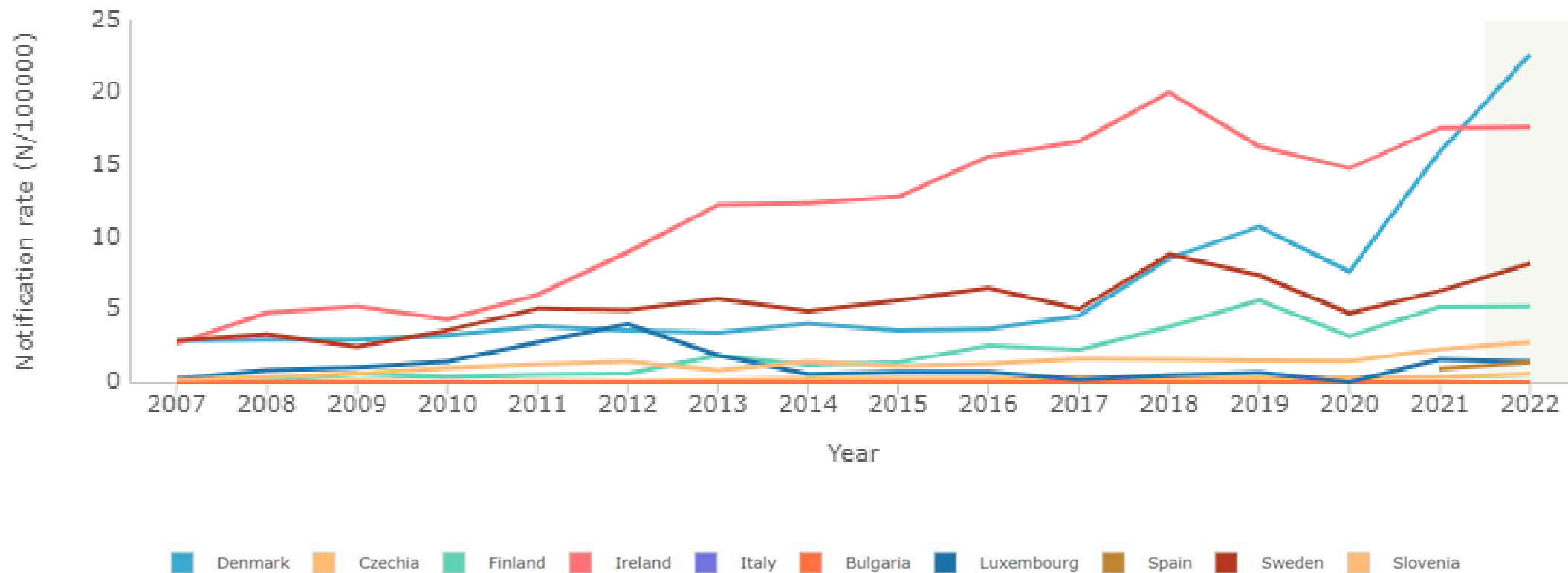
# Campylobacteriosis. 2022 notification rate 46.93, 140 241 cases in EU/EEA



# Salmonellosis. 2022 notification rate 15.52, 65 967 cases in EU/EEA

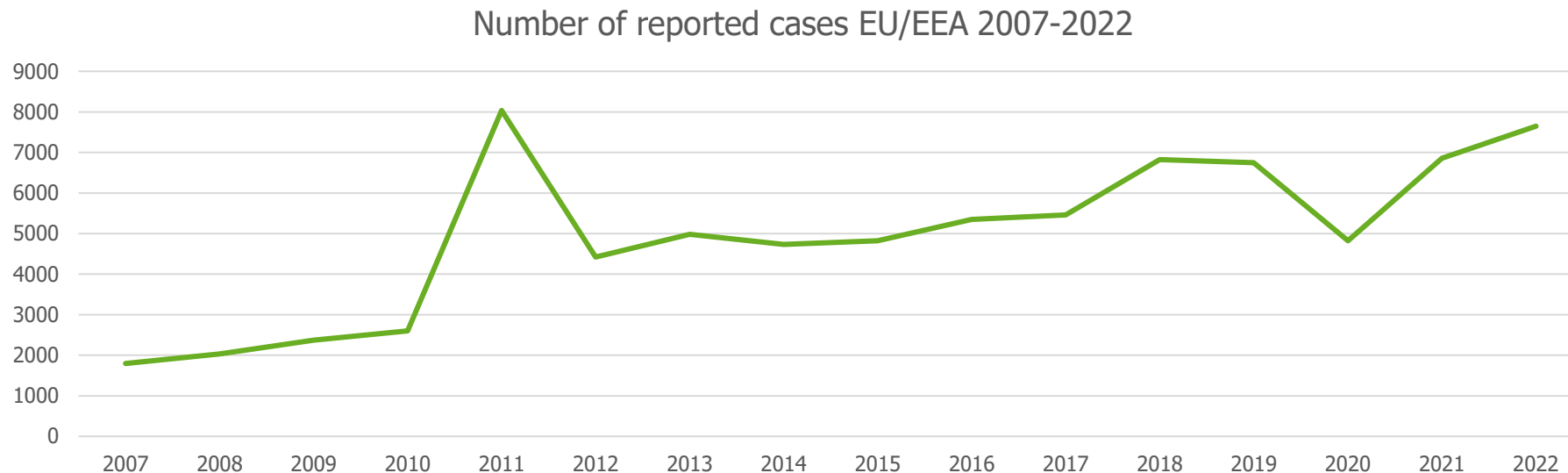


# STEC infection EU/EEA notification rate 2022 2.47, 8565 cases in EU/EEA



## Interpret surveillance data with care

- Increased awareness after 2011 outbreak to test for STEC
- PCR panels slowly introduced in clinical labs starting around 2012 in many countries
- "All" fecal samples from GI cases can easily be tested for STEC, no selection based on e. g. age, season



# Annual Epidemiological reports (AERs)



# Annual Epidemiological Reports

- 19 FWD diseases
- Key facts, Introduction, Methods



SURVEILLANCE REPORT

## STEC infection

Annual Epidemiological Report for 2022

### Key facts

- For 2022, 29 European Union/European Economic Area (EU/EEA) countries reported 8 565 confirmed cases of Shiga toxin-producing *Escherichia coli* (STEC) infection.
- The overall EU/EEA notification rate was 2.5 cases per 100 000 population, which exceeded the pre-pandemic level and represented a 25% increase compared to the notification rate in 2021.
- The STEC notification rate was highest in children under five years of age with 12.1 cases per 100 000 population for males and 11.3 cases per 100 000 population for females.
- The confirmed haemolytic-uremic syndrome (HUS) cases increased in 2022 after a stable trend of reported cases before and during the pandemic years in the EU/EEA. Among the 568 HUS cases reported, the majority were in the youngest age groups, from 0–4 years (60%) to 5–14 years (24%). However, the majority of the deceased cases with HUS were over 60 years old.

### Introduction

Shiga toxin-producing *Escherichia coli* (STEC) are strains of the bacterium *Escherichia coli* that can produce Shiga toxins. These toxins affect small blood vessels, such as those found in the digestive tract and the kidneys. The main reservoir of STEC is grass-feeding animals, cattle in particular. STEC infection is regularly associated with the consumption of undercooked beef which has been contaminated with animal faeces due to poor processing methods during slaughter, or other contaminated food e.g. unpasteurised milk and dairy products, vegetables, and water. Direct contact with infected animals, for example in petting farms and zoos, is considered an important risk of STEC infection, especially in young children. STEC infection often causes gastroenteritis, enterocolitis, and bloody diarrhoea, and sometimes a severe complication called haemolytic-uremic syndrome (HUS), a progressive kidney failure.

### 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].



# Annual Epidemiological Reports

- 19 FWD diseases
- Key facts, Introduction, Methods
- Epidemiology
  - Number of cases (5 years)
  - Notification rates (5 years)
  - Domestic vs. travel related cases
  - Hospitalisation, outcome
  - Transmission mode
- Species, serotype
- AMR (Shigellosis, Typhoid fever)

## Epidemiology

Of the 29 EU/EEA countries reporting for 2022, 25 countries reported 8 565 confirmed cases of STEC infection (Table 1). The EU/EEA notification rate was 2.5 cases per 100 000 population. This was a 25% increase compared with 2021 and the rate and number of cases were higher than before the pandemic years in 2018–2019. The EU/EEA rate was higher, even though the data from Spain were included for the first time in 2021 and 2022, which lowered the EU/EEA rate due to the country's large population. Data from Spain were included as the estimated population coverage of the surveillance system was provided for 2021–2021.

The increase in 2022 was mainly due to a high increase in reported cases by one country (Denmark), which reported the highest numbers of confirmed cases in 2022, followed by Germany and Ireland. Together, these three countries accounted for 47.8% of all reported cases in the EU/EEA. The highest country-specific notification rates were observed in Denmark, Ireland, Malta, and Liechtenstein, with 22.6, 17.6, 15.0, and 10.2, cases per 100 000 population, respectively. A total of 12 southern and eastern EU/EEA countries reported  $\leq 0.4$  cases per 100 000 population (Table 1, Figure 1).

Thirty-seven percent of 3 462 STEC cases with known information were hospitalised. Twenty-eight of 6 044 cases with known outcome were reported to have died, resulting in a case fatality of 0.5%. Most of the deceased cases were over 60 years old (54%; 15/28) and the majority of them (71%; 20/28) had HUS.

**Table 1. Confirmed cases of STEC infection and rates per 100 000 population by country and year, EU/EEA, 2018–2022**

Country	2018		2019		2020		2021		2022	
	Number	Rate	Number	Rate	Number	Rate	Number	Rate	Number	Rate
Austria	305	3.5	284	3.2	288	3.2	383	4.3	469	5.2
Belgium	112	1.0	131	1.1	84	0.7	124	1.1	187	1.6
Bulgaria	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
Croatia	10	0.2	22	0.5	8	0.2	12	0.3	16	0.4
Cyprus	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0
Czechia	26	0.2	33	0.3	32	0.3	36	0.3	58	0.6
Denmark	493	8.5	623	10.7	445	7.6	928	15.9	1 329	22.6
Estonia	7	0.5	6	0.5	10	0.8	7	0.5	11	0.8
Finland	210	3.8	311	5.6	175	3.2	288	5.2	291	5.2
France	259	NRC	335	NRC	262	NRC	298	NRC	473	NRC

# Annual Epidemiological Reports

- Figures
  - EU/EEA Map
  - Trend graph
  - Seasonality
  - Age/gender distribution

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

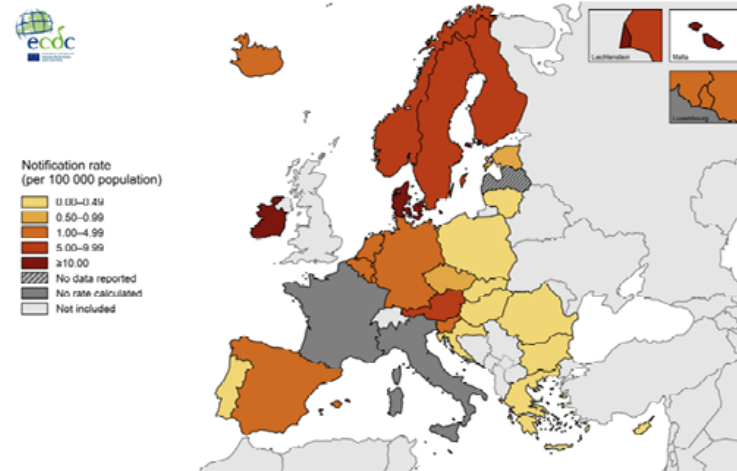


Figure 2. Confirmed cases of STEC infection by month, EU/EEA, 2018–2022

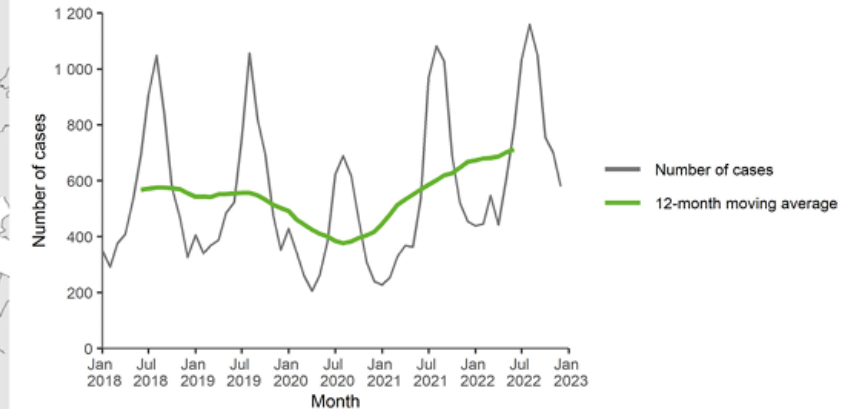


Figure 4. Confirmed cases of STEC infection by month, EU/EEA, 2022 and 2018–2021

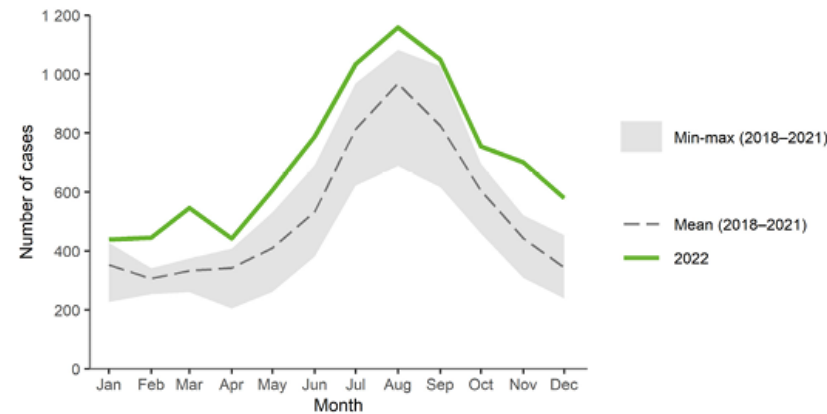
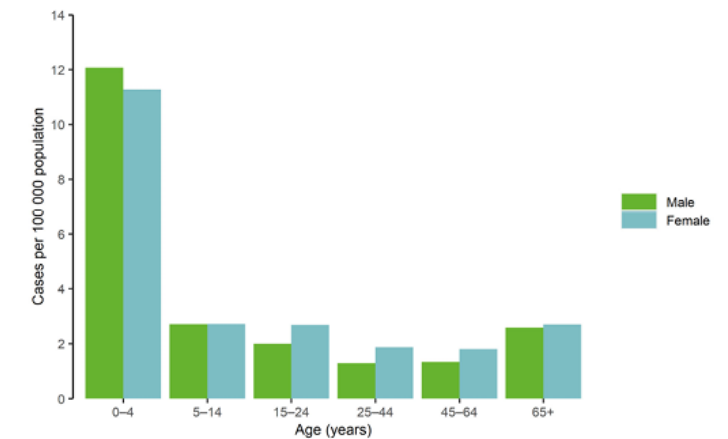


Figure 5. Confirmed cases of STEC infection per 100 000 population, by age and gender, EU/EEA, 2022



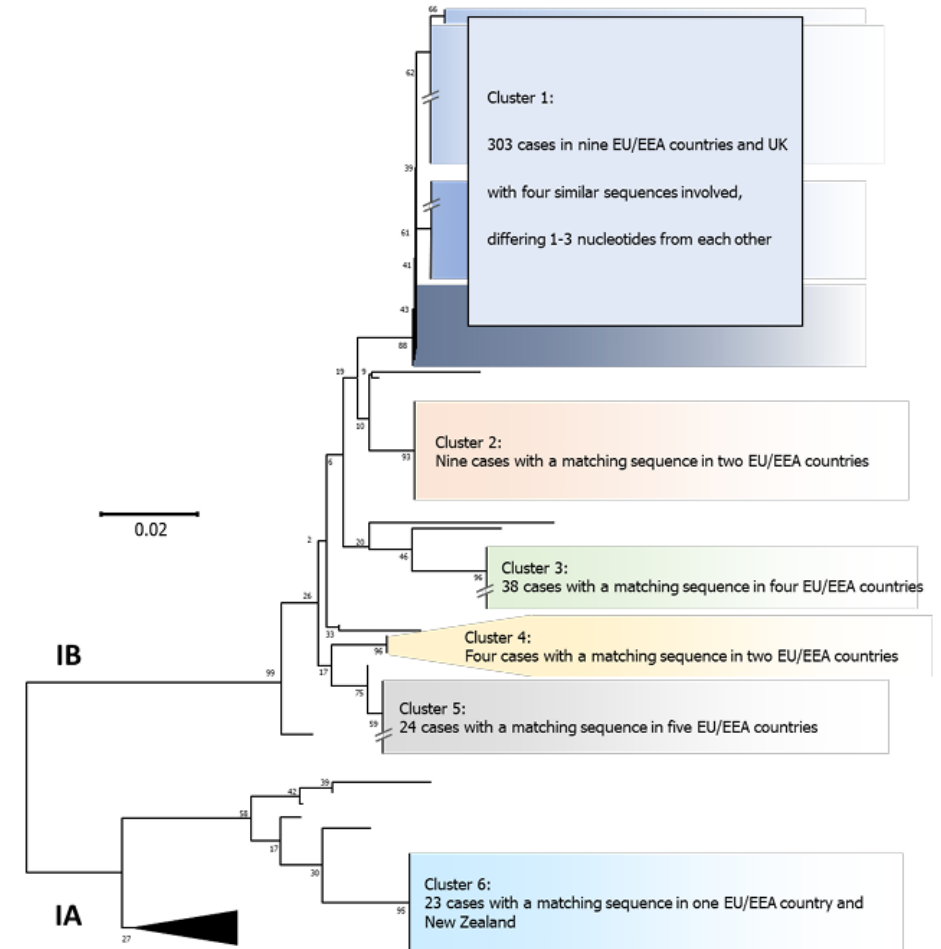
# Annual Epidemiological Reports

## *Priority disease reports*

- **Microbial surveillance**

- STEC infection: serogroup, virulence genes
- Salmonellosis: serovars, serogroups, AMR
- Campylobacteriosis: species, AMR
- Listeriosis: serotype, sequence type
- Yersiniosis: species, serotype, bioserotype
- Shigellosis: species, serotype, AMR
- Hepatitis A: sub-genotypes

**Figure 5.** Phylogenetic analysis of hepatitis A sub-genotype IA- and IB virus clusters reported in EpiPulse during 2022



The phylogenetic tree was constructed using information reported by countries in EpiPulse during 2022 on sequences matching the VP1/2A outbreak sequences with the Neighbour-joining method in MEGA11, using the Tamura Nei as evolutionary model, and a bootstrapping approach for the statistical analysis (1 000 replicates). The scale bar indicates the number of nucleotide substitutions per site.

## *Priority disease* report example STEC 2022, third most commonly reported.

### Microbial surveillance

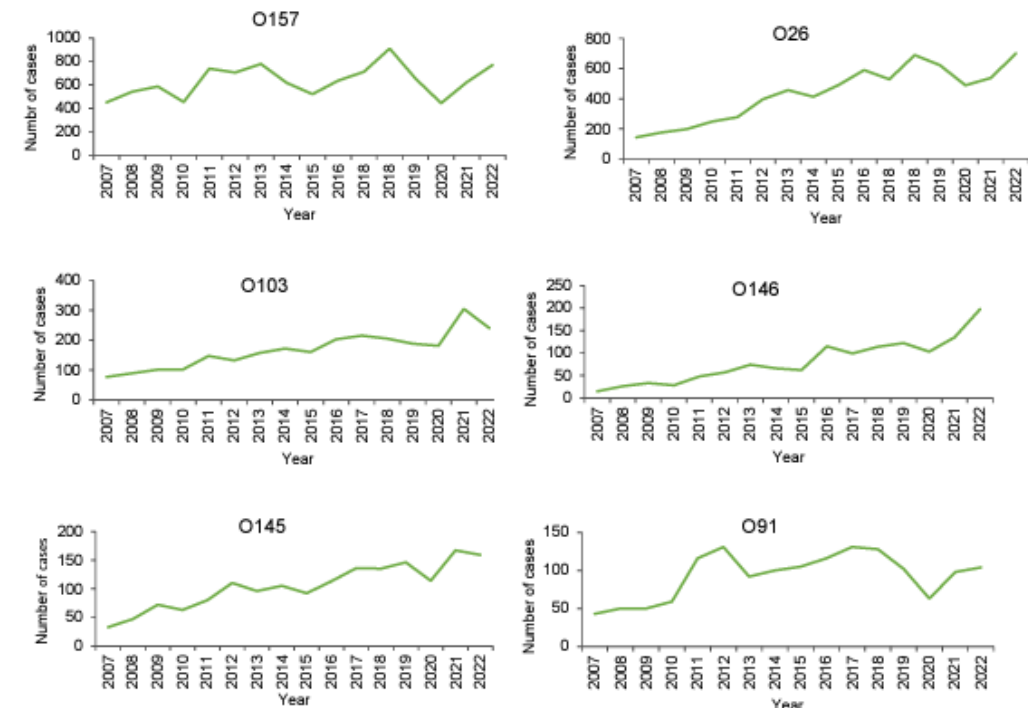
Serogroups (types) reported over time

Some serotypes more common in certain countries

### Microbial surveillance

Information on STEC serogroups was reported by 22 countries for 3 617 confirmed cases (42.2%) in the EU/EEA in 2022. The numbers reported are affected by outbreaks and countries' possibility for characterisation of STEC isolates. The six most frequently reported serogroups were O157 (21.3%), O26 (19.4%), O103 (6.6%), O146 (5.5%), O145 (4.4%), and O91 (2.9%) (Figure 6). These serogroups together accounted for over 60% of the total number of confirmed STEC cases with known serogroups in 2022. During the last 15 years, since the start of EU-level surveillance of STEC, a continuous increase had been seen, especially for four of the most common serogroups reported: O26, O146, O145, and O103. For 2022, the highest number ever reported could be seen for O146 and O26 (Figure 6). For 2 414 cases (28.2%) the full serotype was reported, i.e. both the O type and the H type. The most common serotype was O157:H7 (18.4%) followed by O26:H11 (18.1%) and O103:H2 (7.6%). For cases with STEC-associated HUS, serogroup was reported for 393 cases; O26 was most frequently reported (51.4%) followed by O157 (14.5%), O80 (6.0%) and O145 (5.8%).

Figure 6. The six most common STEC serogroups in the EU/EEA, 2007–2022



# Annual Epidemiological Reports

## Priority disease report STEC 2022, cont.

### Microbial surveillance

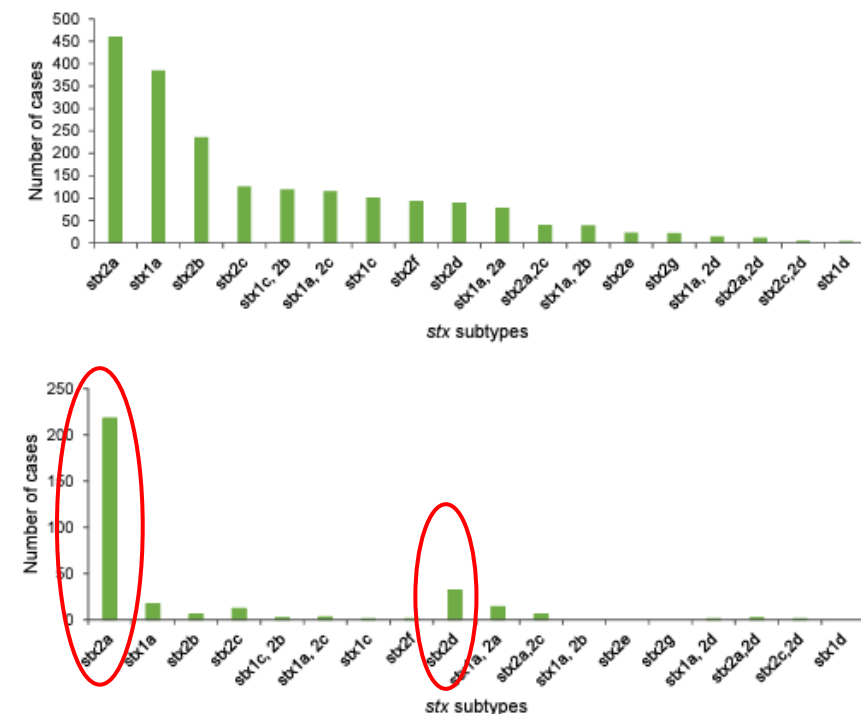
Which are the most common *stx* subtypes.

Which *stx* subtypes could cause more severe diseases (HUS)

### Microbial surveillance

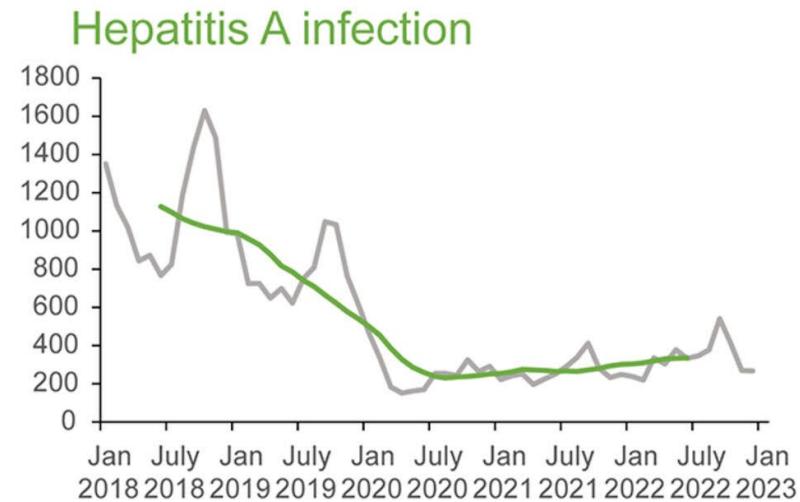
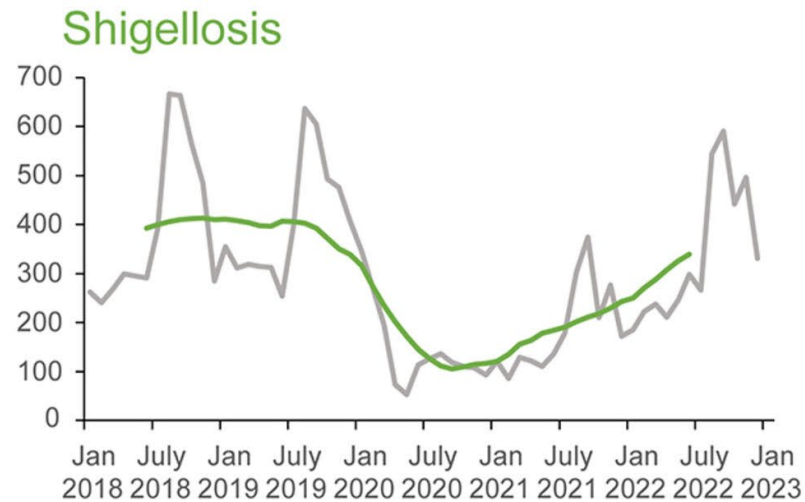
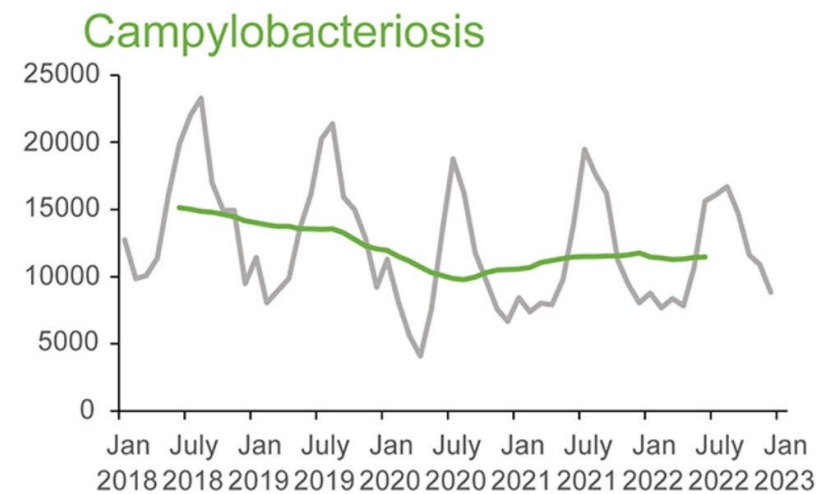
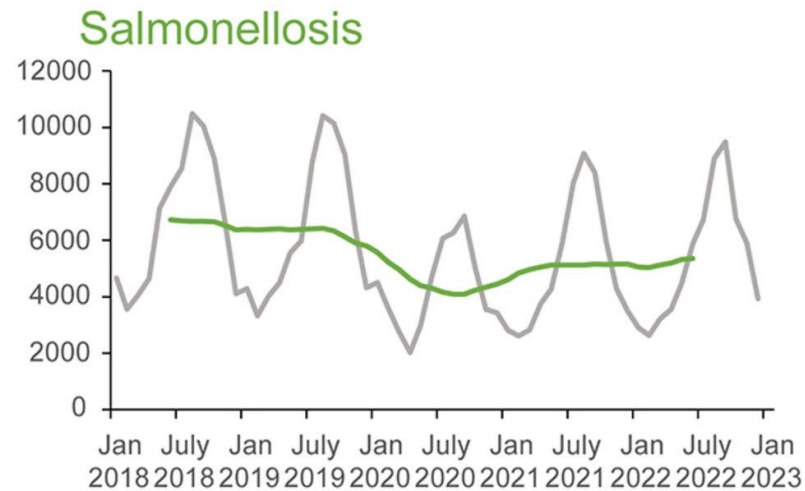
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**Figure 7.** *Stx* gene subtypes for confirmed STEC cases with complete subtyping data (n=1 968) (top panel) and for STEC associated HUS cases (n=316) (bottom panel), in EU/EEA, 2022



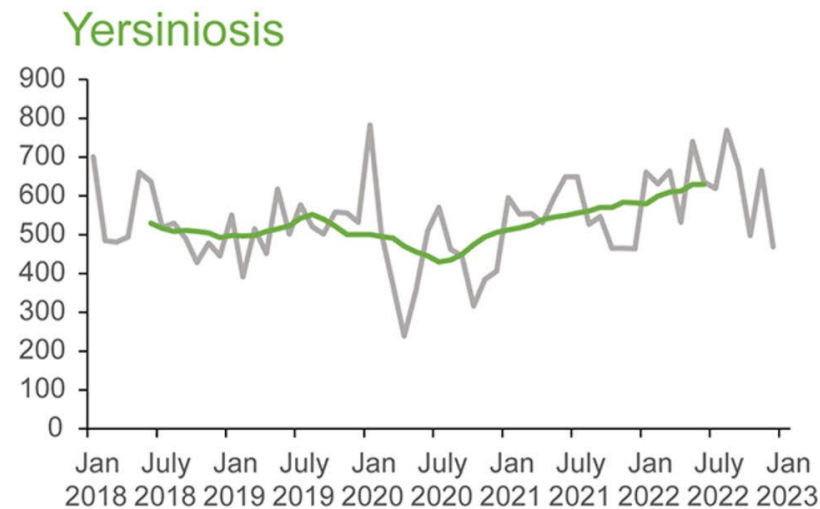
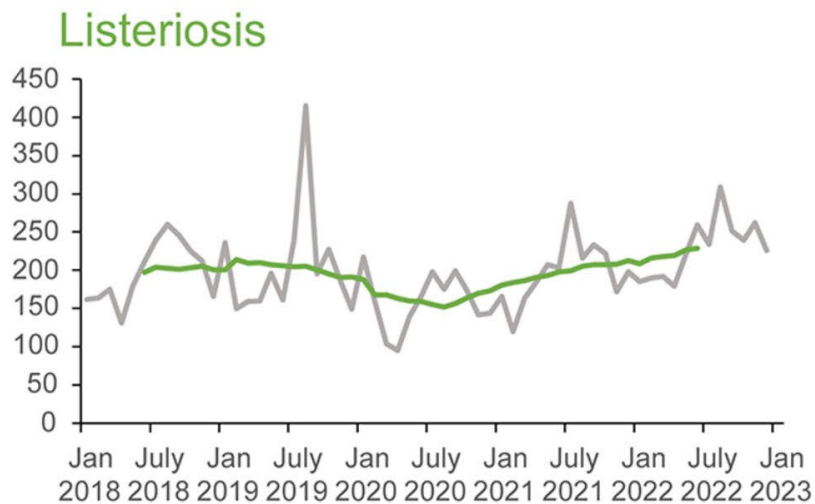
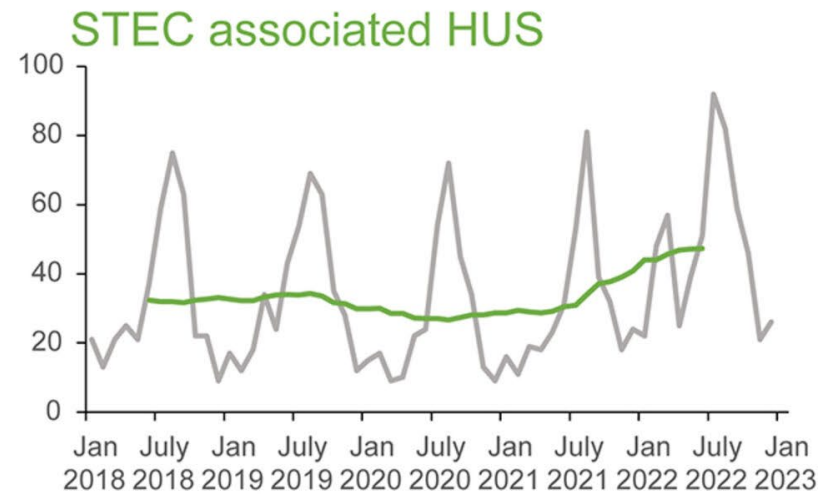
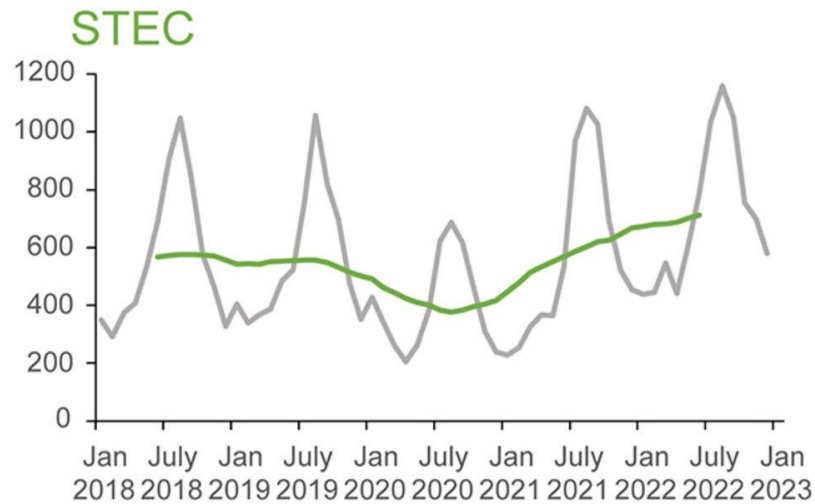


# Compare trends between diseases, 2022 data.



— Number of cases — 12 month moving average

# Compare trends between diseases, 2022



— Number of cases — 12 month moving average

# EU/EEA genomic surveillance



# EU legal framework for molecular pathogen data sharing



ECDC is mandated to collect ‘pathogen data, including at molecular level, if required for epidemiological surveillance and for detecting or investigating serious cross-border threats to health.

Link: [\*EUR-Lex - 32022R2370 - EN - EUR-Lex \(europa.eu\)\*](#)

The National competent Authorities shall communicate, to the ECDC, the Commission and to participating authorities within the disease networks, molecular pathogen data based on agreed indicators and standards, if required for detecting or investigating serious cross-border threats to health.

Link: [\*Regulation \(EU\) 2022/2371 on serious cross-border threats to health\*](#)

# Support to EU/EEA countries to capacity build for genomic surveillance to strengthen public health surveillance, nationally -> EU level



- EC HERA sequencing and bioinformatics capacity building grants
  - GenEpiBioTrain (ECDC, FWD wave Institut Pasteur)
  - Sequencing support projects – *Salmonella* and *Campylobacter* AMR sequencing capacity building project (ECDC)
  - Sequencing support for events and outbreaks (ECDC)
  - EC HaDEA FWD AMR-RefLabCap (SSI)
- 
- Development of EpiPulse Molecular Typing Tool – analysis and visualisation of your data

# EpiPulse

# EpiPulse - The ECDC platform for nominated users



Events, Forum & News  
Notification and discussion platform

Molecular Typing Tool  
A tool for visualising WGS based results integrated with epidemiological data

The screenshot displays the EpiPulse web application interface. At the top left is the ECDC EpiPulse logo. Below it, a navigation bar contains five tabs: 'Report', 'Manage', 'Explore', 'Collaborate', and a user profile section on the right with a menu icon, a user icon, and a notification icon. A large green menu area is open below the tabs, listing various functions. In the 'Report' column, 'Events, Forum & News' is circled in red. In the 'Manage' column, 'Atlas', 'Validate COVID-19', and 'Dataset Manager' are listed. In the 'Explore' column, 'Public Atlas', 'Surveillance Dashboards/Reports', 'Events, Forum & News' (circled in red), 'Download data', 'Signal detection tool', 'Molecular typing tool' (circled in red), 'Documents Overview', and 'EQA Lab Reports' are listed. In the 'Collaborate' column, 'CCB contacts', 'Domain Contacts', 'Extranets', 'Duty Schedule', and 'TESSy Help & Docs' are listed. A vertical 'Help' button is on the far right. Below the menu, a welcome message reads: 'Welcome to EpiPulse - the European surveillance portal for infectious diseases!'. A paragraph follows: 'Through this portal you can report and share information on cases or events of infectious diseases/pathogens, explore European data or exchange information with other nominated users.' A final note states: 'Note: EPIS ELDSNet continues to work as usual, migration will occur on a later stage. The function and use of EWRS remain unaffected.'

ecdc EpiPulse

Report Manage Explore Collaborate

Events, Forum & News

Cases

Sequence Data

Determinant Data

Surveillance system

descriptors

COVID-19

Edit case/Case validation

Atlas

TALD cases

TALD sites

Validate COVID-19

Dataset Manager

Public Atlas

Surveillance Dashboards/Reports

Events, Forum & News

Download data

Signal detection tool

Molecular typing tool

Documents Overview

EQA Lab Reports

CCB contacts

Domain Contacts

Extranets

Duty Schedule

TESSy Help & Docs

Help

Welcome to **EpiPulse** - the European surveillance portal for infectious diseases!

Through this portal you can report and share information on cases or events of infectious diseases/pathogens, explore European data or exchange information with other nominated users.

Note: **EPIS ELDSNet continues to work as usual**, migration will occur on a later stage. The function and use of EWRS remain unaffected.

# Report an event in EpiPulse



Please treat the data in the platform as sensitive non-classified unless specifically indicated as public.

**Title\***

**Domain\*** Please select

**Country/Organisation\*** ECDC

**Sector\*** Public Health

**Type\*** Please select

**Topic\*** Please select

**Pathogens\*** Please select

**Diseases\*** Please select

**First source of information** Please select

## Initial comment

**Countries with reported cases** Please select

**Countries of possible exposure - Type\*** Please select

**Number of confirmed human cases\***  ☐ Unknown

**Number of non-confirmed human cases\***  ☐ Unknown

**Number of confirmed deaths**  ☐ Unknown

## Epidemiological information

Normal **A** **B** **I** **U**   

## Microbiological information

Normal **A** **B** **I** **U**   

Add attachment

E.g. FASTA file

Help

# EpiPulse - The ECDC platform for nominated users



Events, Forum & News  
Notification and discussion platform

Molecular Typing Tool  
A tool for visualising WGS based results integrated with epidemiological data

**EpiPulse**

**Report** **Manage** **Explore** **Collaborate** (0)

Report	Manage	Explore	Collaborate
Cases	Edit case/Case validation	Public Atlas	CCB contacts
Events, Forum & News	<a href="#">Atlas</a> ▶	<a href="#">Surveillance Dashboards/Reports</a> ▶	<a href="#">Domain Contacts</a> ▶
Sequence Data	TALD cases	Events, Forum & News	Extranets
Determinant Data	TALD sites	Download data	Duty Schedule
Surveillance system	<a href="#">Validate COVID-19</a> ▶	Signal detection tool	TESSy Help & Docs
descriptors	<a href="#">Dataset Manager</a> ▶	<u><a href="#">Molecular typing tool</a></u>	
COVID-19		Documents Overview	
		EQA Lab Reports	

**Help**

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# EpiPulse Molecular Typing Tool search function

> Explore > Molecular typing tool

Please, select a Pathogen to review and analyse its data.

Salmonella

▼ Search & Refine Selection

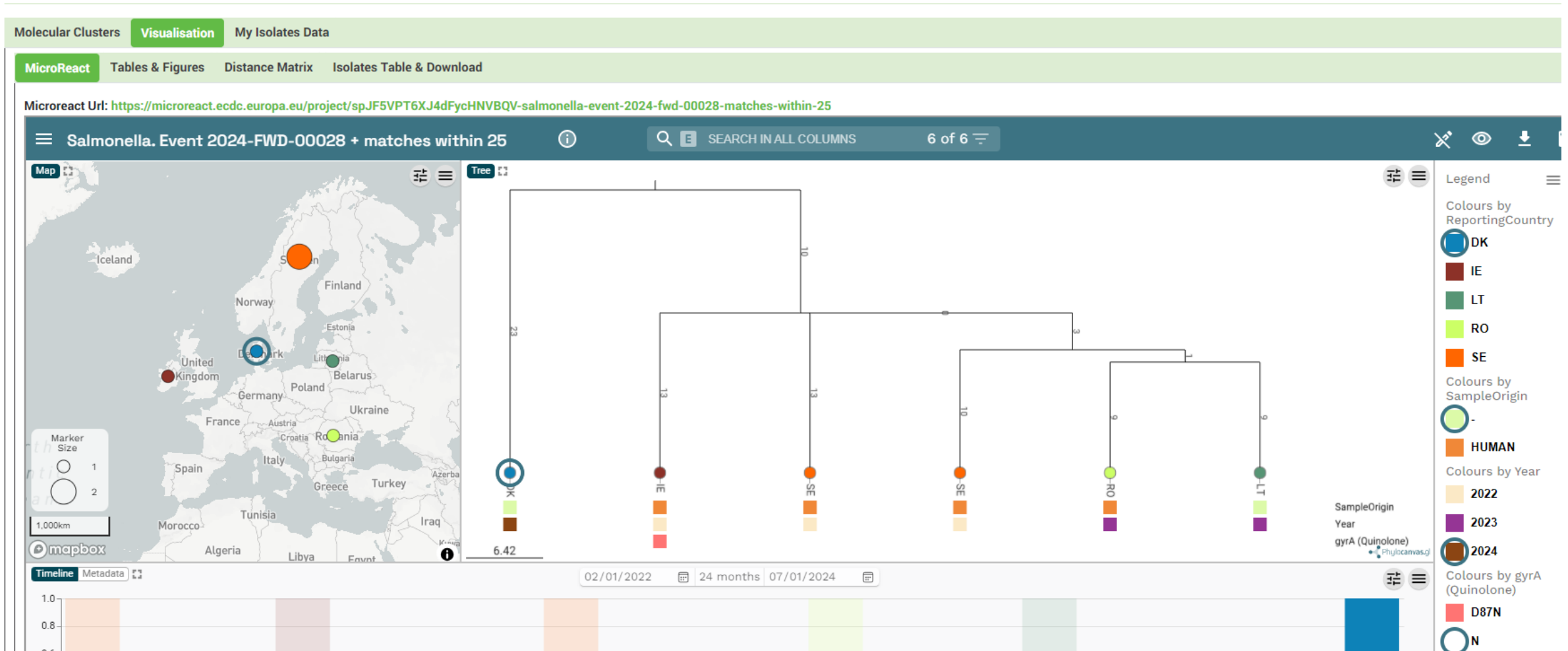
Serotype Please, select one Serotype	Cluster Please, select one or more clusters <small>If empty, all the clusters will be selected.</small>	Events 2024-FWD-00028	Isolates Isolates
Countries Please, select one or more countries <small>If empty, all the countries will be selected.</small>	Date used for statistics dd/mm/yyyy	Submission Date dd/mm/yyyy	Distance metric to match Default
Match Distance 25	Cluster Method Default	Epidemiological Data BN_Cluster, PB_DateUsedForStatistics, PB_ReportingCountry	

Reset form Search

Single linkage  
Complete linkage  
Neighbor joining

# Example no matching isolates in the system.

Publicly available sequence data shared by the UK show many matching isolates





# Tuesday 4 June – WGS system for One Health

Priyanka Nannapaneni (ECDC)

Mirko Rossi (EFSA)

12:40 – 14:00
<b>MODULE 5. SURVEILLANCE</b>
<b>WGS systems for One Health (14:00 – 15:00)</b>
<b>Mirko Rossi and Priyanka Nannapaneni</b>

# Let's discuss cluster cut-offs

# Regular automatic cluster detection of all sequences uploaded to the ECDC database



- Automatic cluster detection once a week for *Listeria* and *Salmonella*.
- Clusters including two or more human isolates are queried to EFSA database.
- Matching non-human isolates from EFSA db are integrated and visualised in the MTT

# Species specific cluster criteria for automatic cluster detection



- *L. monocytogenes*: core cluster within 4 AD, extended cluster 7 AD
- *Salmonella* spp.: core cluster within 5 AD, extended cluster 10 AD. For certain serotypes/subtypes, for example *S. Enteritidis*, a tighter core cluster could be needed for outbreak investigations. In addition, the single linkage clustering approach possibly needs to be replaced with a Neighbour joining clustering approach for endemic clones.
- STEC: core cluster within 5 AD, extended cluster 10 AD. For certain subtypes a tighter core cluster cut-off could be needed for outbreak investigations.
- *Campylobacter* spp.: core cluster within 5 AD, extended cluster 10 AD.
- *Shigella* spp./EIEC: core cluster within 5 AD, extended cluster 10 AD. For certain species/subtypes a tighter core cluster cut-off could be needed for outbreak investigations.

N.B Specific cluster cut-offs could be applied for multi country outbreak case definitions.

## Note!

In the centralised WGS analysis (at ECDC) a wider cut-off (AD) for clusters than national criteria is expected.

WGS data from different platforms can generate some artefactual differences. EQAs have shown approximal 2 AD can be seen between the EQA participants.

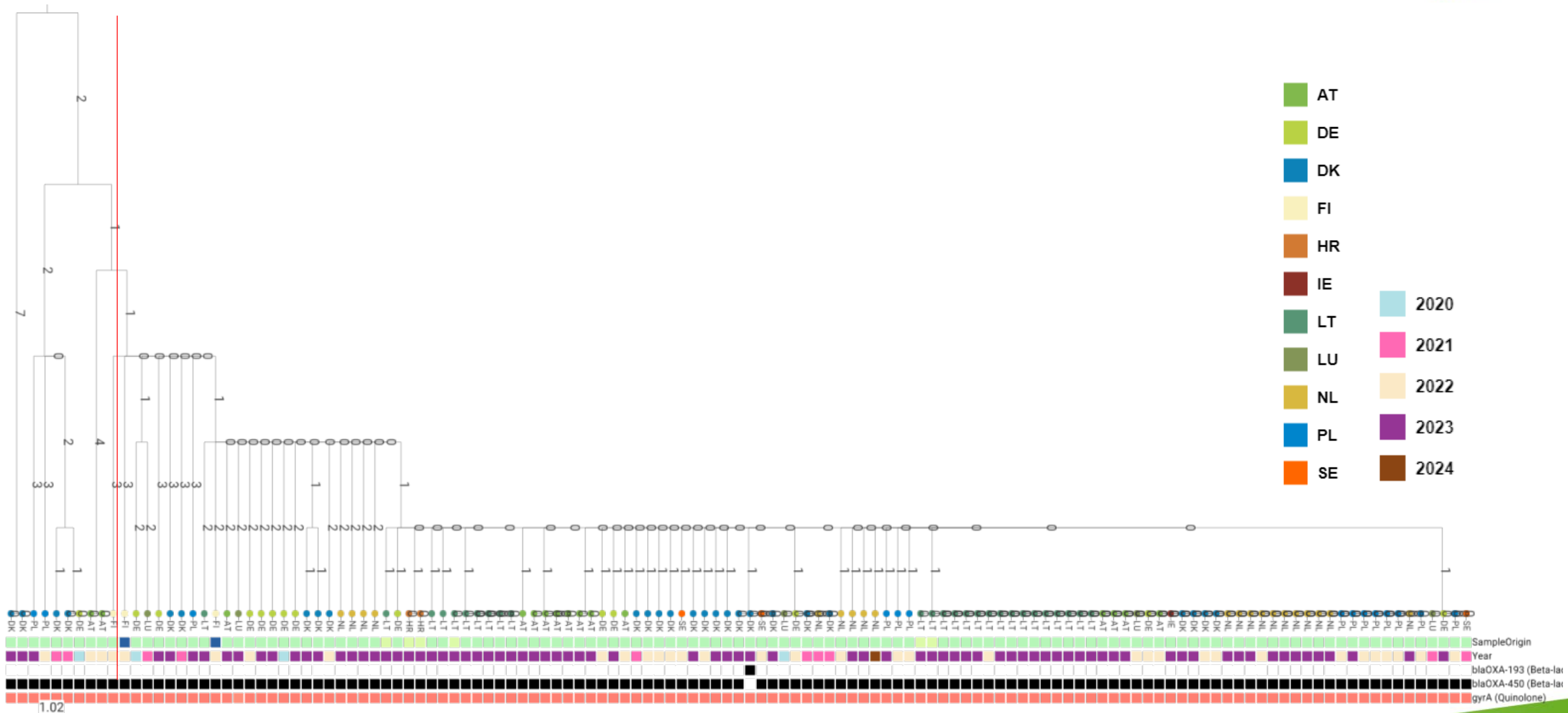
# Example *Campylobacter* cluster connected to an EpiPulse event, ST-464.

5 AD, 11 countries, 120 isolates. Single linkage.

Cluster with imported chicken meat



# 10 AD cut-off, 129 isolates, 11 countries



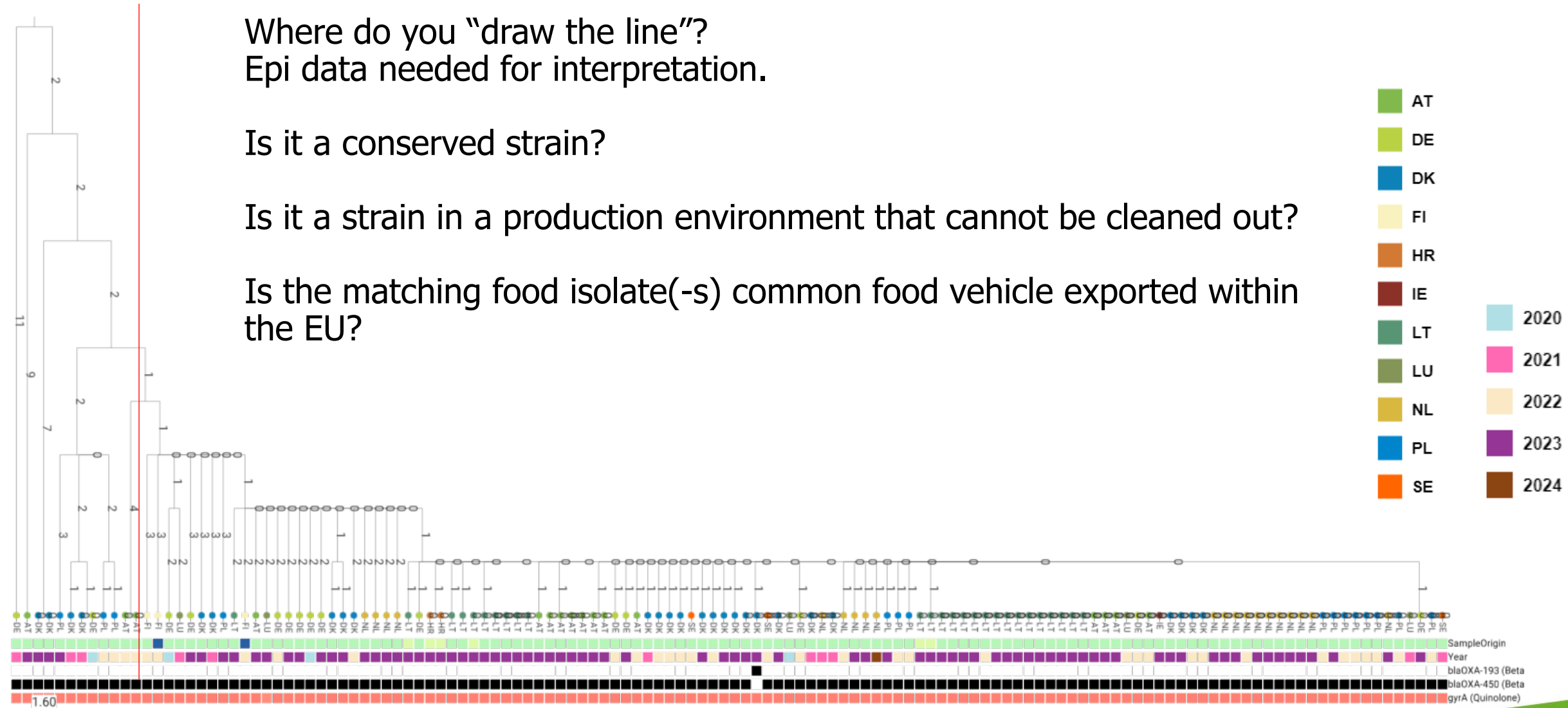
# The clade has a maximum of 13 AD, 132 isolates, 11 countries

Where do you “draw the line”?  
Epi data needed for interpretation.

Is it a conserved strain?

Is it a strain in a production environment that cannot be cleaned out?

Is the matching food isolate(-s) common food vehicle exported within the EU?





# When events are escalated to EU level risk assessments

# ECDC tools for risk assessment outputs of an EU/EEA-wide foodborne events with or without EFSA



## ECDC Rapid Risk Assessment

- **Aim:** to assess a cross-border health risk
- **Food information:** no
- **Main use** to inform public of risks (often travel-related) where specific foodborne risks are not specified
- **Published** on ECDC website

## ECDC Notification Summary

- **Aim:** immediate notification of a cross-border foodborne risk
- **Food information:** only based on patient interviews or epidemiological studies (hypothesis on suspected vehicle)
- **Main use** to inform risk managers and to trigger food and epi investigations
- **Restricted** distribution to risk managers:  
ECDC => EC/EWRS, FWD-Net  
EFSA => EC/RASFF

## ECDC-EFSA Joint Notification Summary

- **Aim:** immediate notification of a cross-border foodborne risk
- **Food information:** from EFSA database and public repository for sequences, RASFF information included if available
- **Main use** to inform risk managers and to trigger targeted food and epi investigations
- **Restricted** distribution to risk managers:  
ECDC => EC/EWRS, FWD-Net  
EFSA => EC/RASFF

## ECDC-EFSA Joint Rapid Outbreak Assessment

- **Aim:** assess a cross-border foodborne public health threat
- **Food information:** from EFSA database and public repository for sequences, RASFF information for trace back and forward analysis
- **Main use** to inform public, public health professionals, and risk managers
- **Published** on ECDC and EFSA web sites

# Reporting and analysis of AMR in *Salmonella* and *Campylobacter*

# EU case definitions

## Example

### *Campylobacter*

#### Laboratory Criteria

At least one of the following two:

- Isolation of human pathogenic *Campylobacter* spp. from a clinical specimen;
- Detection of *Campylobacter* spp. nucleic acid in a clinical specimen.

Note: Antimicrobial susceptibility testing of *Campylobacter* spp. should be performed on a representative subset of isolates

#### Epidemiological Criteria

At least one of the following five epidemiological links:

- Animal to human transmission;
- Human to human transmission;
- Exposure to a common source;
- Exposure to contaminated food/drinking water;
- Environmental exposure.

#### Case Classification

A. Possible case NA

B. Probable case

Any person meeting the clinical criteria with an epidemiological link

C. Confirmed case

Any person meeting the clinical and the laboratory criteria

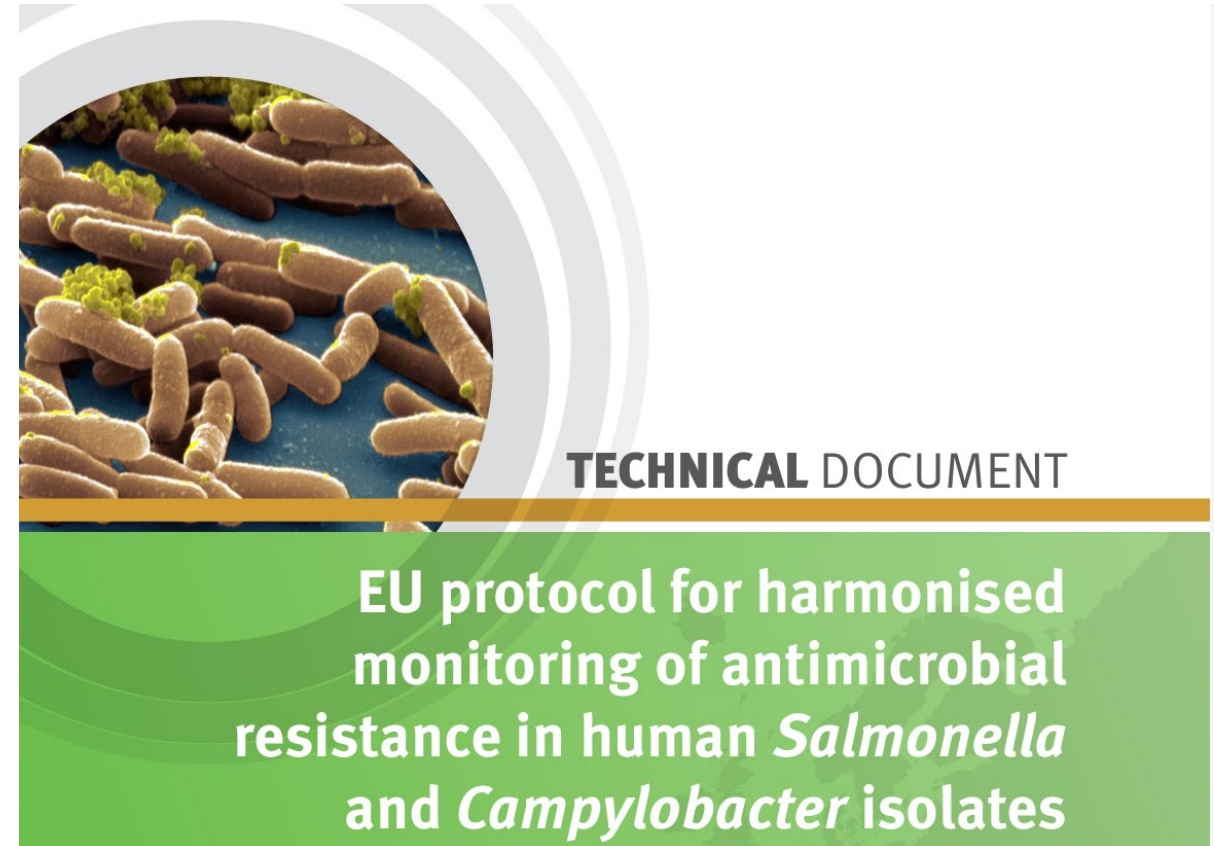
Note: If the national surveillance system is not capturing clinical symptoms, all laboratory-confirmed individuals should be reported as confirmed cases.

#### Antimicrobial resistance

The results of antimicrobial susceptibility tests must be reported according to the methods and criteria agreed between ECDC and Member States as specified in the EU protocol for harmonised monitoring of antimicrobial resistance in human *Salmonella* and *Campylobacter* isolates <sup>(1)</sup>.

Q campylobacter

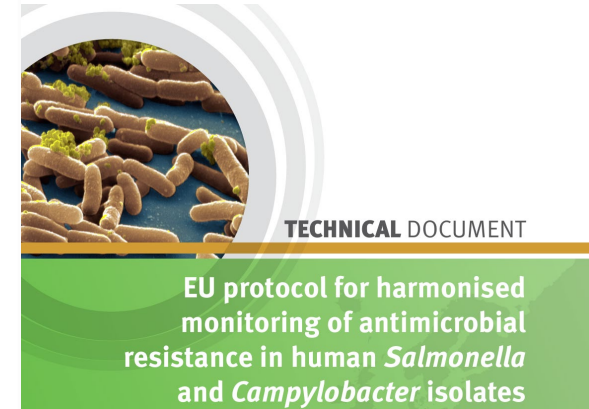
In the EU protocol objectives for the surveillance are listed and antibiotics to be tested for.



## 2 EU surveillance objectives

The proposed surveillance objectives for antimicrobial resistance in zoonotic bacteria, specifically *Salmonella* spp. and *Campylobacter* spp. are:

- a) To monitor, in human clinical isolates, trends in the occurrence of resistance to antimicrobial agents relevant for treatment of human *Salmonella* and *Campylobacter* infections, including comparison with food/animal isolates
- b) To monitor, in human clinical isolates, trends in the occurrence of resistance to other antimicrobial agents of public and animal health importance, including comparison with food/animal isolates
- c) To monitor, in human clinical isolates, the prevalence of ESBL, plasmid-encoded Ambler class C  $\beta$ -lactamases (pAmpC) and carbapenemase phenotypes
- d) To use antimicrobial resistance patterns to characterise human clinical isolates, i.e. as an epidemiological marker, to support identification of outbreaks and related cases
- e) To identify and monitor, in human clinical isolates, genetic determinants of resistance that are important for public health e.g. to aid recognition of epidemic cross-border spread of multi-drug resistant *Salmonella* strains
- f) To monitor, in human clinical isolates, trends in the occurrence of resistance to antimicrobial agents that may be needed for future therapeutic use.



# Harmonised and simplified EU level AMR monitoring using WGS predicted resistance.



- Agreed panel of priority antimicrobials to test and report to EU level is large – 13 antimicrobials for *Salmonella*, 4 for *Campylobacter*
- Expanding list on food safety side to try to identify resistance mechanisms of concern via combinations of phenotypic resistance. Uses a pre-defined microdilution plate
- Difficult to motivate public health laboratories to test the full panel when not required for treatment

## By using genomics

- Phenotypic resistance can be predicted to all antimicrobial agents of interest
- Resistance mechanisms of particular concern can be identified directly without using phenotypic “proxies”
- Predicted resistance primarily for surveillance purposes, still phenotypic resistance important for treatment purposes.

# ECDC's vision for EU-level FWD AMR surveillance



- WGS should be the method for EU level *Salmonella* and *Campylobacter* AMR surveillance
- All countries are reporting a representative subset of *Campylobacter* and *Salmonella* isolates with sequencing data each year
- Transition period, report both phenotypic and genotypic data for the same isolates for validation, when possible



# Thank you for your attention!

Please let us know how we can support you with data sharing, reporting, using EpiPulse tools etc!  
[ECDC.Microbiology@ecdc.europa.eu](mailto:ECDC.Microbiology@ecdc.europa.eu)