# UPDATE ON STEC MONITORING DATA IN THE EU AND ON EFSA MOLECULAR TYPING DATA COLLECTION

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### MONITORING OF ZOONOSES AND FOODBORNE OUTBREAKS IN EU

- Mandatory monitoring of zoonoses and foodborne outbreaks in accordance with Directive 2003/99/EC
- Data collected
  - in the context of Regulation (EC) No 2073/2005
  - All the other food and animal testing data originate from the reporting obligations of MSs under **Directive 2003/99/EC**
- STEC monitoring data are non-harmonized and not comparable between MS; not possible assessing temporal and spatial trends at EU level.



# **EFSA RESOURCES FOR STEC**

#### https://www.efsa.europa.eu/en/topics/topic/foodborne-zoonotic-diseases



# **STEC, 2022 HUMAN DATA**







# **STEC, MONITORING OF FOODBORNE OUTBREAKS IN EU, 2022**



Strong-evidence outbreak

Foodborne outbreaks

Weak-evidence outbreaks 📒

408 Cases of illness63 Hospitalisations

Number of foodborne outbreaks by causative agent, reported to the EU by MSs, 2013–2022



#### **STEC, MONITORING OF FOODBORNE OUTBREAKS IN EU, 2022**

Country	Shiga	Shiga toxin-producing <i>E.coli</i>		
	N	variation (%)		
European Union (27 MS + XI)	71	129%		
Austria	1	-75%		
Belgium	5	0%		
Bulgaria	0			
Croatia	0	.=		
Cyprus	0	12		
Czechia	0	-		
Denmark	3	-50%		
Estonia	0	-		
Finland	0	-100%		
France	37			
Germany	3	50%		
Greece	0			
Hungary	0			
Ireland	8	100%		
Italy	3	-		
Latvia	0	5		
Lithuania	0	14		
Luxembourg	0	100275		
Malta	1	-50%		
Netherlands	3	200%		
Poland	2	· · · · · · · · · · · · · · · · · · ·		
Portugal	0	5		
Romania	0	-		
Slovakia	0	12		
Slovenia	0			
Spain	3	50%		
Sweden	1	-67%		
United Kingdom (Northern Ireland)	1	-		
Bosnia and Herzegovina	0	17		
Iceland	0	-		
Montenegro	0	19403		
Norway	1	-50%		
Rep. North Macedonia	0	-		
Serbia	0	12		
Switzerland	0	-100%		

#### Implicated food vehicles (Strong-evidence outbreaks)

Bovine meat and Top food products thereof vehicles Outbreak



# **STEC - MAIN FINDINGS IN FOOD AND ANIMALS**, 2022



#### Units tested by food and animal categories

- 20 MSs reported the presence of STEC in 1.8% of 18,815 food samples taken according to an 'objective sampling' strategy
  - No significant changes in units tested across years
  - No positivity reported in sprouted seeds
  - 15 MSs tested 8,556 RTE food sampling units: 1.1% STEC-positive
  - 18 MSs tested 10,259 non-RTE food sampling units: 2.5% STEC-positive
- Half of animal (1916) tested compared with 2021 data from 4 MSs
  - Highest STEC prevalence: cattle, 41.5%.
  - Sheep testing increased



# **STEC - MAIN FINDINGS IN RTE FOOD, 2022**





# **STEC - MAIN FINDINGS IN NON-RTE FOOD, 2022**



### **SEROGROUPS AND VIRULENCE GENE TYPING, 2022**

- Of the food isolates, 47.6% were provided with information, many belonging to the top STEC serogroups reported in human
- 89.4% (N = 396) of the STEC isolated from food in 2022 were reported with information on virulence gene typing (stx1 or stx2 and eae)

 TABLE 37
 Virulotypes (stx type and presence of eae) identified in food, animal and human STEC isolates causing severe infection (haemolytic-uraemic syndrome (HUS), hospitalisation and bloody diarrhoea) in 2022.

 Relative frequency of the virulotype in<sup>b</sup>

Virulence gene profile	N of animal isolates in 2022 <sup>a</sup>	N of food isolates	N of human isolates in 2022 (%)	Relative frequency of the virulotype in"		
				HUS	Hospitalisation	Bloody diarrhoea
stx2; eae+	14	37	410 (47.8)	17.7	42.0	40.2
stx1; stx2; eae+	9	32	142 (16.6)	5.9	35.7	64.8
stx2; eae-	5	154	110 (12.8)	2.7	24.3	14.8
stx1; eae+	24	61	84 (9.8)	1.2	27.4	27.3
stx1; eae-	4	50	59 (6.9)	0.3	20.3	14.1
stx1; stx2, eae-	3	62	52 (6.1)	1.4	15.3	19.4
Total	59	396	857 (100)	2	2	1

Abbreviations: STEC, Shiga toxin-producing Escherichia coli; HUS, haemolytic-uraemic syndrome. The stx genes were characterised at the type level (stx1 and stx2). \*Due to the low number of isolates virulotyped for food and animals, only the number of isolates is shown.

<sup>b</sup>Relative frequencies (%) of the different combinations of stx gene types with or without the eae gene in STEC isolated from severe disease (TESSy data, 2012–2017) (EFSA BIOHAZ Panel, Koutsoumanis, Allende, Alvarez-Ordonez, et al., 2020).



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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



www.efsa.europa.eu





# EFSA ONE HEALTH WGS SYSTEM



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### **DATA SHARING TO EFSA** OVERVIEW EFSA DATABASE – SEPTEMBER 2024



### **DATA SHARING TO EFSA** MEMBER STATES CONTRIBUTION



EFSA system: 3,088 genome sequences shared since July 2022 (approx. 100/month)



#### DATA SHARING TO EFSA MEMBER STATES CONTRIBUTION



#### **DATA SHARING TO EFSA MEMBER STATES CONTRIBUTION – E.COLI**

Total 189 (80% with EpiData submitted)





by sample matrix



#### DATA SHARING TO EFSA MEMBER STATES CONTRIBUTION – E.COLI



Very different population with 1650 AD distance as average

			Cluster size			
Threshold	Total	Singleton	Average	Median	Max	
AD15	144	118	3	2	9	
AD115	74	51	6	3	61	
AD800	41	20	8	3	68	



## **IN SUMMARY**

- Successful example of cross-sectoral collaboration at EU level
- EFSA system: 174 users across 27 EU MS and 2 EEA countries
- EFSA system: > 3,000 profiles shared by 26 EU MS and EEA countries since July 2022 (approx. 100/month) + over 5,000 profiles generated from public data (including Salmonella and Listeria and E. coli)
- So far, ECDC sent ~1,100 of Salmonella and Listeria clusters weekly for a total 60k queries
- Hundreds of clusters of *Salmonella* and *Listeria* containing human and food data detected; *E. coli* cross-sectoral analysis is not started yet, but we are ready in case of ROA requests

The One Health WGS system supported the collection and analysis of WGS data for the assessment of many EU multi-countries foodborne outbreaks involving several hundreds of human cases across EU

