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Integration of AMR into surveillance and outbreak investigation

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Today’s presentation

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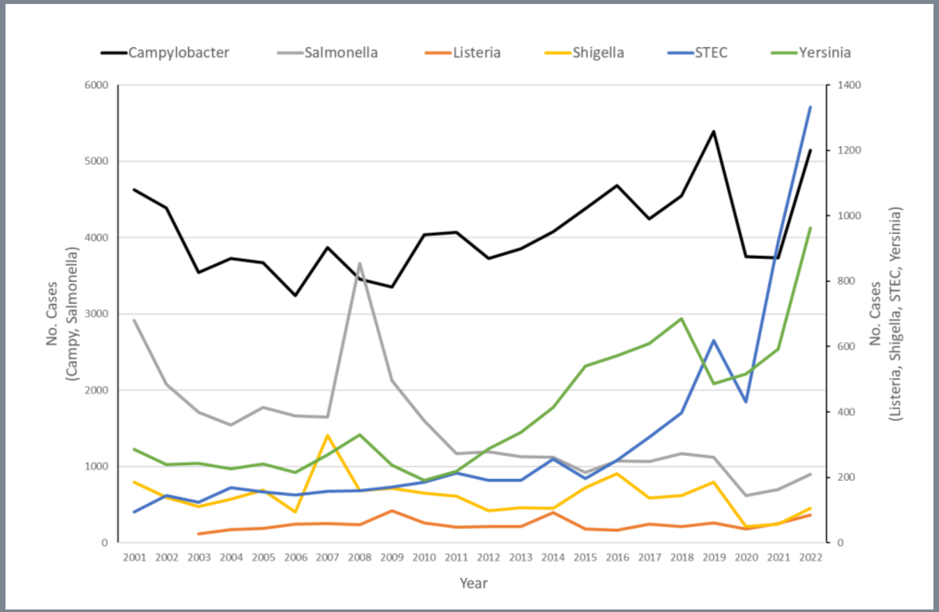
Danish AMR surveillance of *Salmonella* and *Campylobacter* from human infection

- Routine surveillance including AMR testing
- Integrated (OH) AMR surveillance in Denmark
- EU level surveillance
- Genotypic AMR

Surveillance of human *Salmonella and Campylobacter* infections

Clinical Microbiological Department (CMD)

Case-based surveillance
Isolate based surveillance



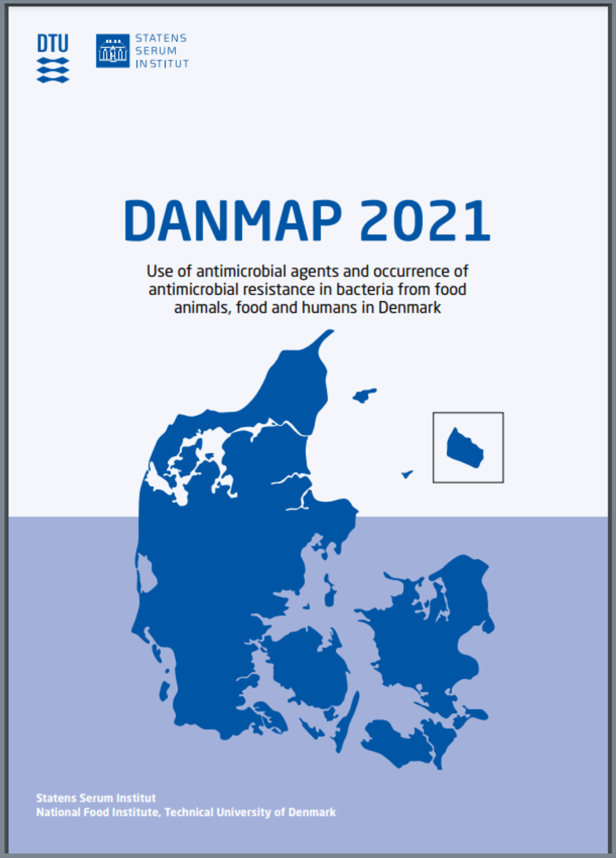
Isolate based surveillance

- Phenotypic AMR testing of all *Salmonella* except *S*. Enteritidis
- Phenotypic AMR testing on a subset of *Campylobacter*
  - at SSI for surveillance following the EU protocol for harmonised monitoring of antimicrobial resistance in human *Salmonella* and *Campylobacter* isolates – June 2016 (Stockholm: ECDC; 2016).

- Real-time WGS on all *Salmonella*
- Real-Time WGS on a subset of *Campylobacter*
  - In-house sequencing that includes a QC output with predicted serotypes, ST and **resistance genes** detected.
  - Cluster analyses done using cgMLST (Enterobase).

DANMAP

The Danish Integrated Antimicrobial Resistance Monitoring and Research Programme



DTU

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DANMAP 2021

Use of antimicrobial agents and occurrence of
antimicrobial resistance in bacteria from food
animals, food and humans in Denmark

Statens Serum Institut
National Food Institute, Technical University of Denmark

- Including AMR data on *Salmonella* Typhimurium/monophasic variant and a subset of *Campylobacter* from human infection
- Currently developed including more serotypes of *Salmonella* and WGS-derived AMR genes.

DANMAP

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Reporting use of antimicrobial agents and occurrence of antimicrobial resistance in bacteria from food animals, food and humans in Denmark

Visionary national programme

- Started in 1995
- By both the human and animal sector
- In a One Health perspective
- Research to fill knowledge gaps
- Providing data needed for action

Campylobacter

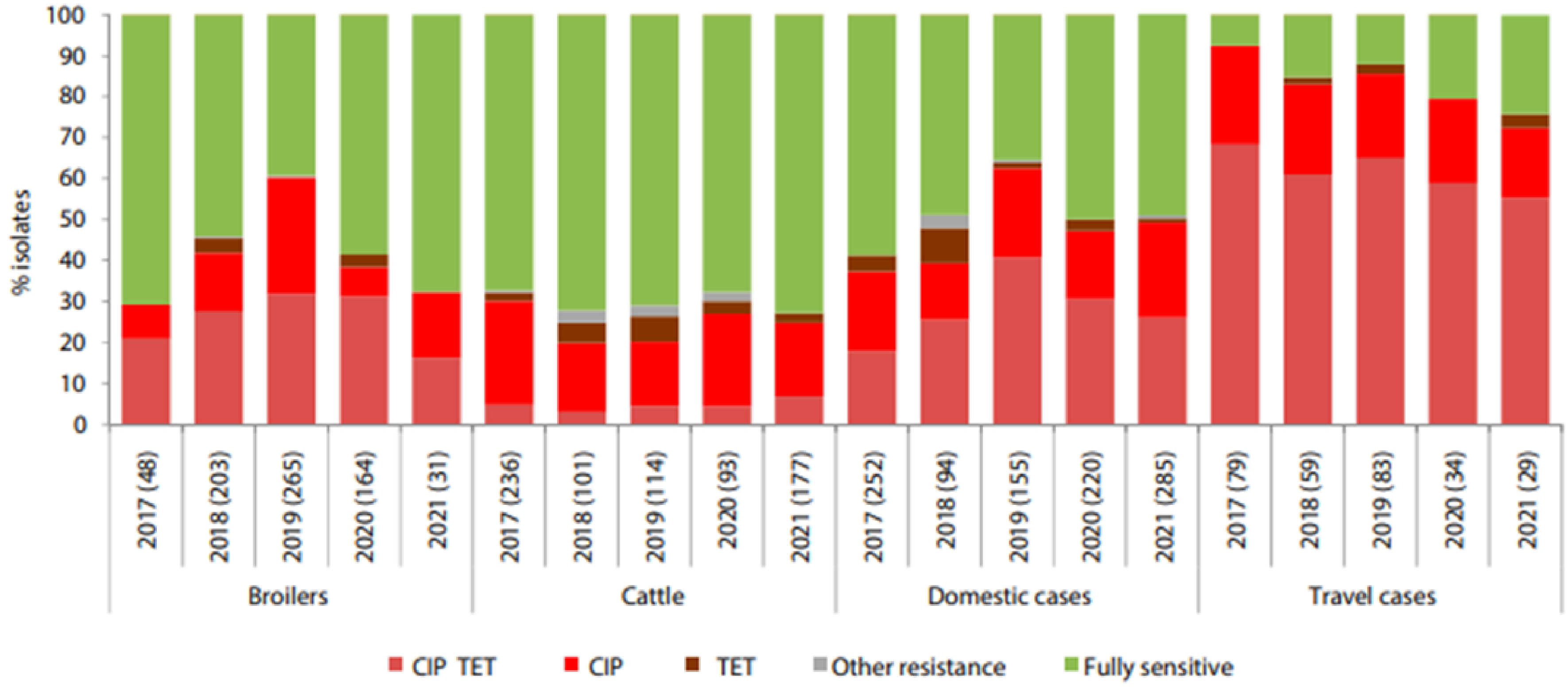
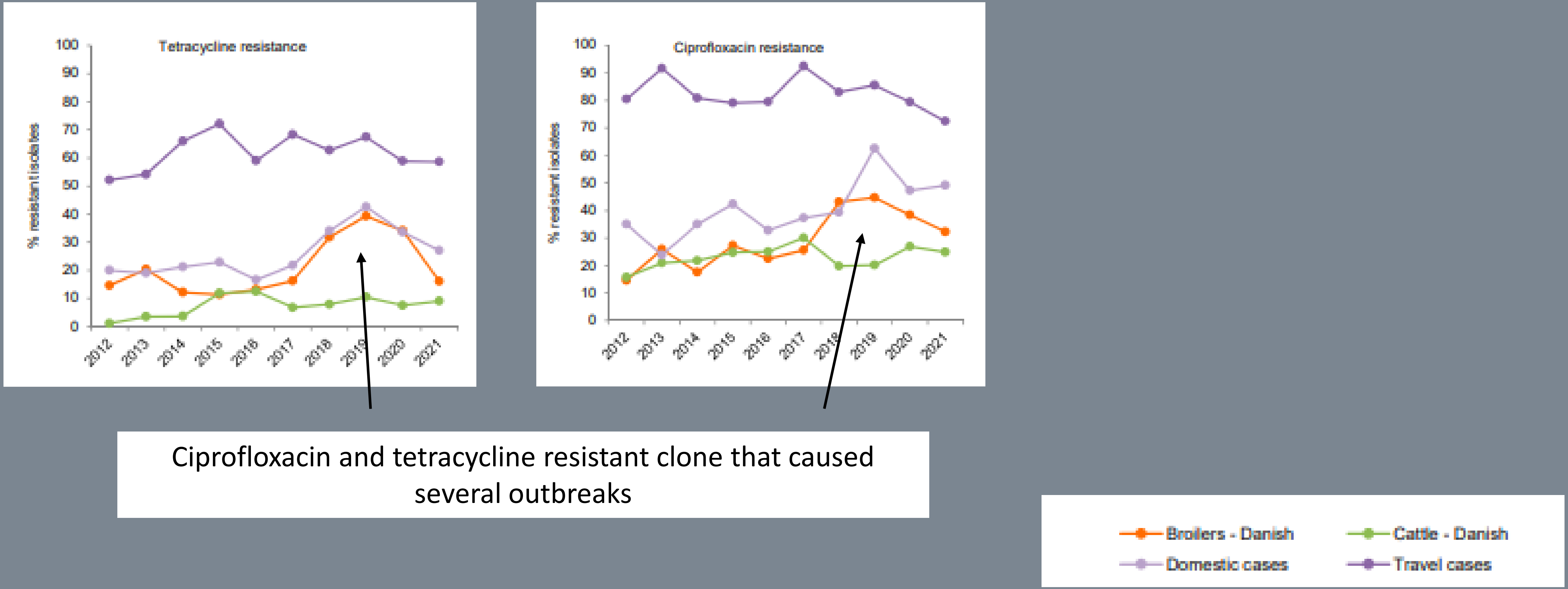


Figure 6.1 Distribution (%) of AMR profiles in *Campylobacter jejuni* from broilers, cattle and human cases, Denmark DANMAP 2021

DANMAP 2021 - Use of antimicrobial agents and occurrence of antimicrobial resistance in bacteria from food animals, food and humans in Denmark. ISSN 1600-203

Campylobacter

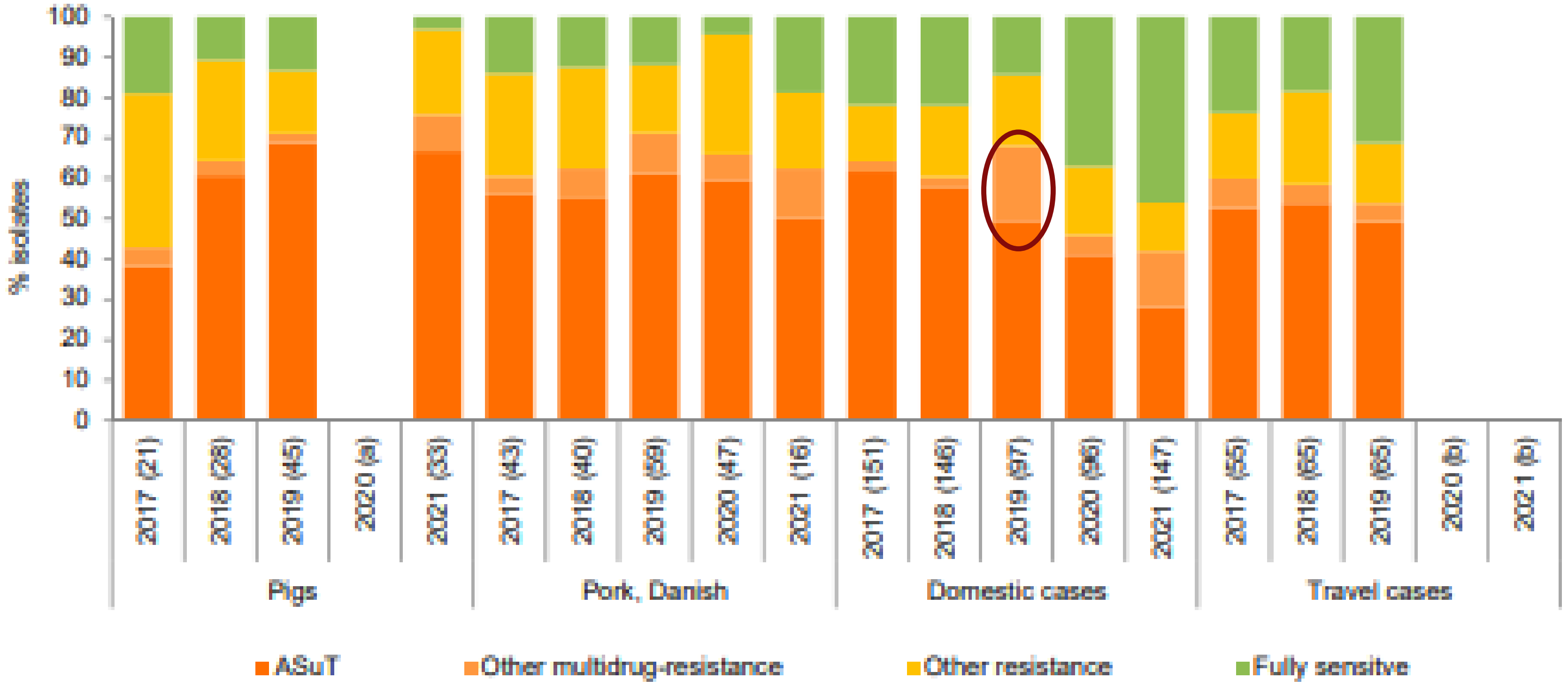


Ciprofloxacin and tetracycline resistant clone that caused several outbreaks

DANMAP 2021 - Use of antimicrobial agents and occurrence of antimicrobial resistance in bacteria from food animals, food and humans in Denmark. ISSN 1600-203

Salmonella Typhimurium/monophasic

Figure 6.3 Relative distribution (%) of multidrug-resistant, resistant and fully sensitive *S.* Typhimurium from pigs, domestic pork and human cases, Denmark
DANMAP 2021



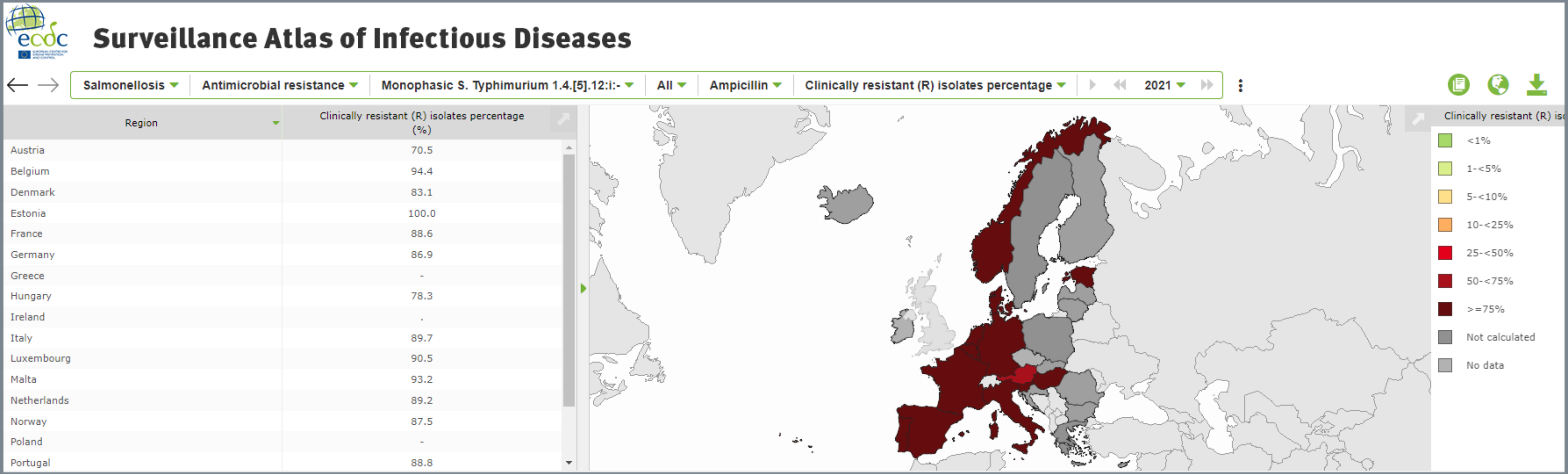
DANMAP 2021 - Use of antimicrobial agents and occurrence of antimicrobial resistance in bacteria from food animals, food and humans in Denmark. ISSN 1600-203

ECDC

Responsible for EU-level AMR surveillance from human infection including the zoonotic bacteria *Salmonella* and *Campylobacter*

- All Danish phenotypic AMR test results uploaded annually to TESSy
- Also providing genotypic data, especially regarding critical resistance

ECDC AMR surveillance



Surveillance Atlas of Infectious Diseases

Salmonellosis | Antimicrobial resistance | Monophasic S. Typhimurium 1.4.[5].12:i:- | All | Ampicillin | Clinically resistant (R) isolates percentage | 2021

Region	Clinically resistant (R) isolates percentage (%)
Austria	70.5
Belgium	94.4
Denmark	83.1
Estonia	100.0
France	88.6
Germany	86.9
Greece	-
Hungary	78.3
Ireland	.
Italy	89.7
Luxembourg	90.5
Malta	93.2
Netherlands	89.2
Norway	87.5
Poland	-
Portugal	88.8

EU AMR surveillance

- Data combined with AMR data on zoonotic bacteria from animal and food
- EU-level EFSA and ECDC

SCIENTIFIC REPORT

efsa JOURNAL

APPROVED: 31 January 2023

doi: 10.2903/j.efsa.2023.7867

The European Union Summary Report on Antimicrobial Resistance in zoonotic and indicator bacteria from humans, animals and food in 2020/2021

European Food Safety Authority (EFSA) and
European Centre for Disease Prevention and Control (ECDC)

Abstract

Antimicrobial resistance (AMR) data on zoonotic and indicator bacteria from humans, animals and food are collected annually by the EU Member States (MSs) and reporting countries, jointly analysed by EFSA and ECDC and presented in a yearly EU Summary Report. This report provides an overview of the main findings of the 2020–2021 harmonised AMR monitoring in *Salmonella* spp., *Campylobacter jejuni* and *C. coli* in humans and food-producing animals (broilers, laying hens and turkeys, fattening pigs and bovines under 1 year of age) and relevant meat thereof. For animals and meat thereof, indicator *E. coli* data on the occurrence of AMR and presumptive Extended spectrum β-lactamases (ESBL)-/AmpC β-lactamases (AmpC)-/carbapenemases (CP)-producers, as well as the occurrence of methicillin-resistant *Staphylococcus aureus* are also analysed. In 2021, MSs submitted for the first time AMR data on *E. coli* isolates from meat sampled at border control posts. Where available, monitoring data from humans, food-producing animals and meat thereof were combined and compared at the EU level, with emphasis on multidrug resistance, complete susceptibility and combined resistance patterns to selected and critically important antimicrobials, as well as *Salmonella* and *E. coli* isolates exhibiting ESBL-/AmpC-/carbapenemase phenotypes. Resistance was frequently found to commonly used antimicrobials in *Salmonella* spp. and *Campylobacter* isolates from humans and animals. Combined resistance to critically important antimicrobials was mainly observed at low levels except in some *Salmonella* serotypes and in *C. coli* in some countries. The reporting of a number of CP-producing *E. coli* isolates (harbouring *bla*$_{\text{OXA-48}}$, *bla*$_{\text{OXA-181}}$, and *bla*$_{\text{NDM-5}}$ genes) in pigs, bovines and meat thereof by a limited number of MSs (4) in 2021, requests a thorough follow-up. The temporal trend analyses in both key outcome indicators (rate of complete susceptibility and prevalence of ESBL-/AmpC-producers) showed that encouraging progress have been registered in reducing AMR in food-producing animals in several EU MSs over the last years.

Keywords: antimicrobial resistance, zoonotic bacteria, indicator bacteria, ESBL, MRSA

Requestor: European Commission

Question number: EFSA-Q-2021-00768

Correspondence: zoonoses@efsa.europa.eu (EFSA); FWD@ecdc.europa.eu (ECDC)

www.efsa.europa.eu/efsajournal EFSA Journal 2023;21(3):7867

Salmonella isolates from humans in 2021

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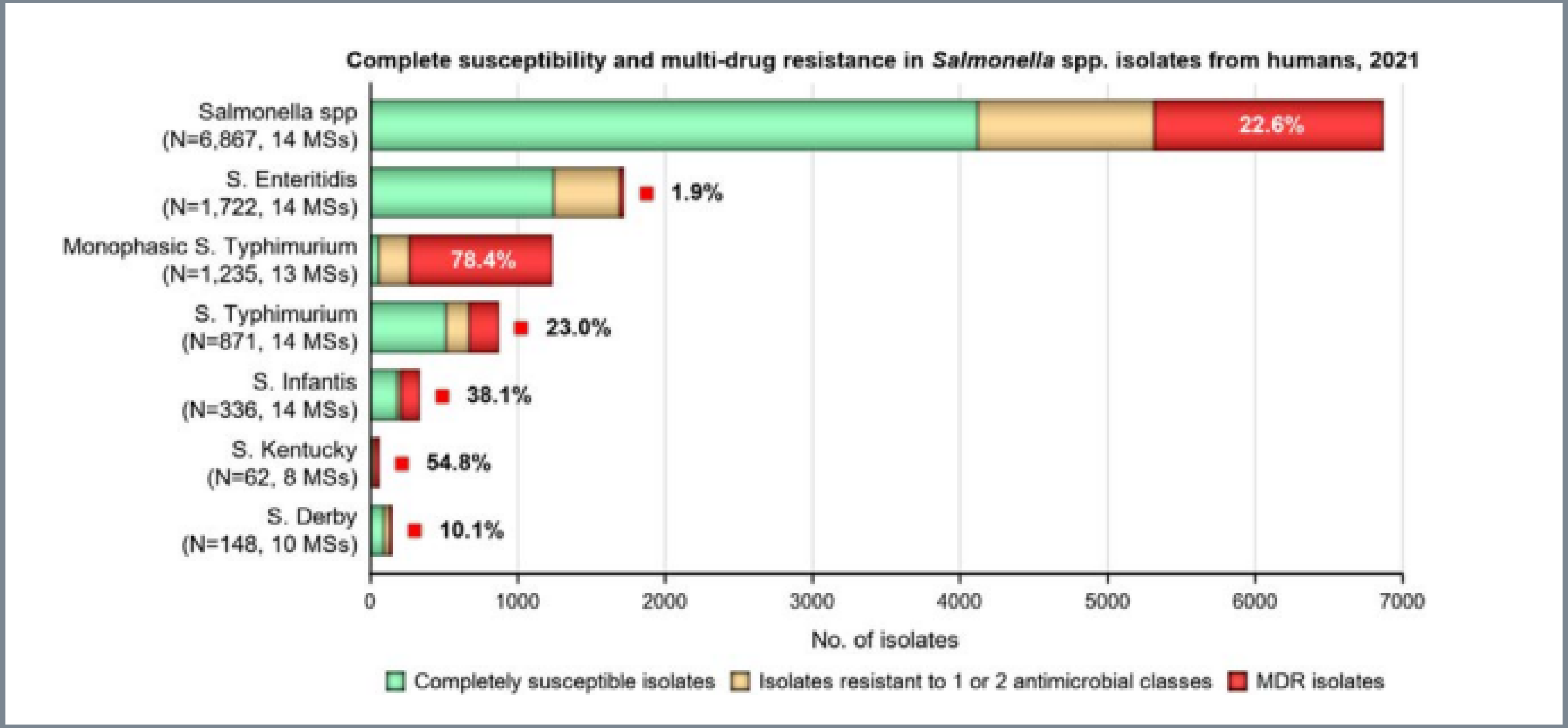
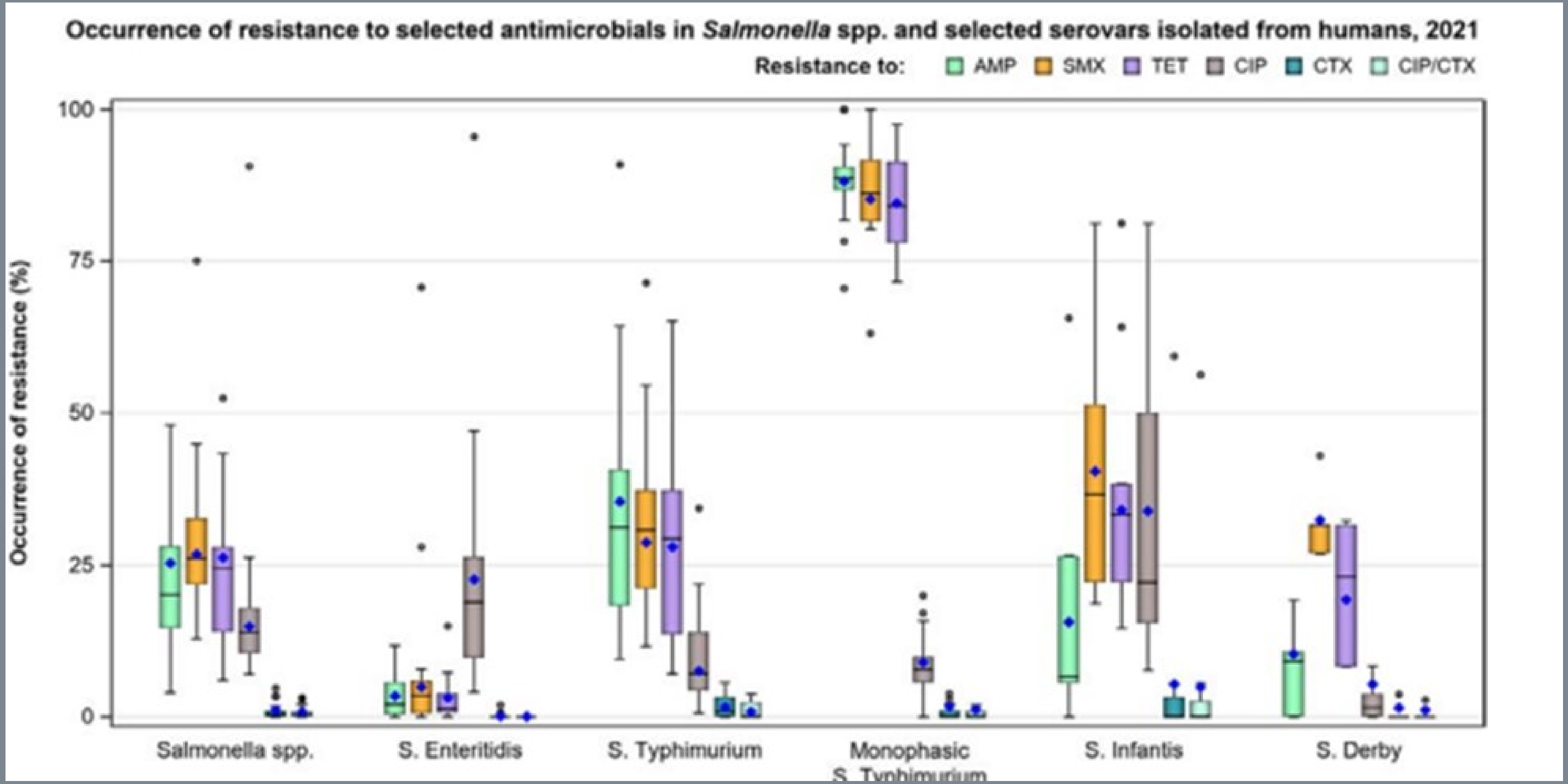


EUSR on AMR in zoonotic and indicator bacteria from humans, animals and food 2020/2021

ecdc efsa JOURNAL

Resistance to selected and critically important antimicrobials



EUSR on AMR in zoonotic and indicator bacteria from humans, animals and food 2020/2021

Isolates tested and travel information by country

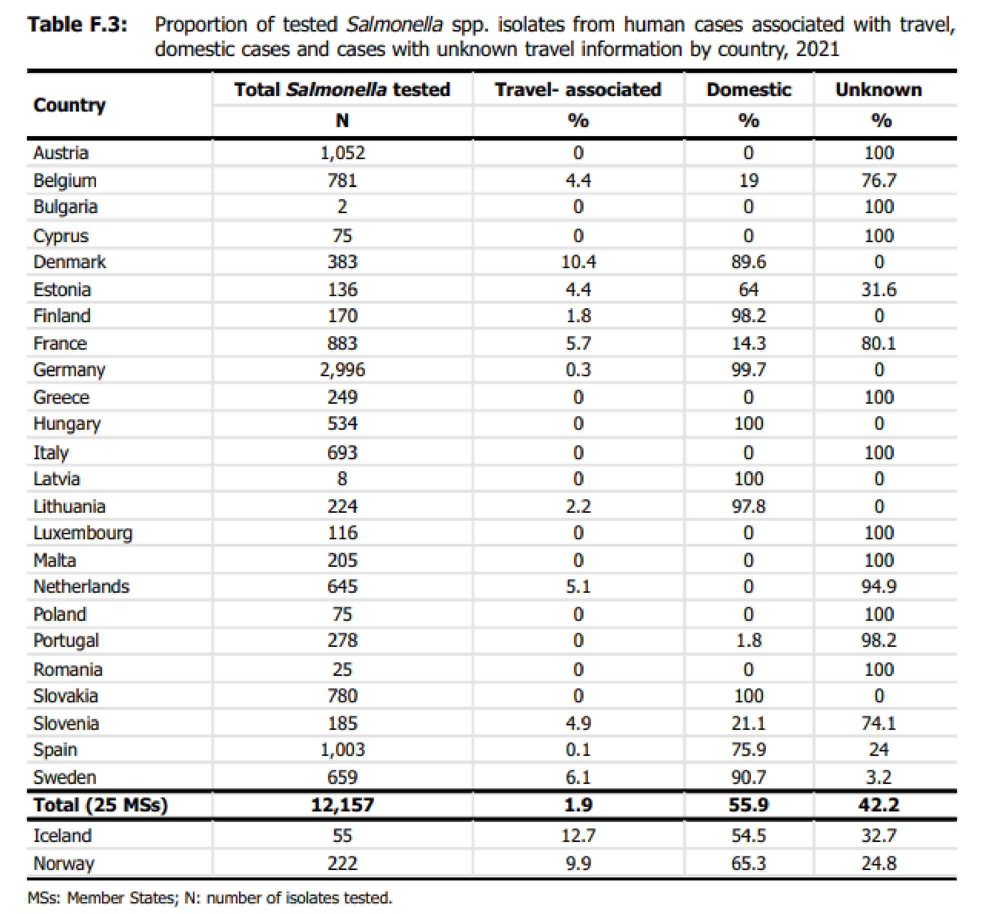


Table F.3: Proportion of tested *Salmonella* spp. isolates from human cases associated with travel, domestic cases and cases with unknown travel information by country, 2021

Country	Total *Salmonella* tested	Travel- associated	Domestic	Unknown
	N	%	%	%
Austria	1,052	0	0	100
Belgium	781	4.4	19	76.7
Bulgaria	2	0	0	100
Cyprus	75	0	0	100
Denmark	383	10.4	89.6	0
Estonia	136	4.4	64	31.6
Finland	170	1.8	98.2	0
France	883	5.7	14.3	80.1
Germany	2,996	0.3	99.7	0
Greece	249	0	0	100
Hungary	534	0	100	0
Italy	693	0	0	100
Latvia	8	0	100	0
Lithuania	224	2.2	97.8	0
Luxembourg	116	0	0	100
Malta	205	0	0	100
Netherlands	645	5.1	0	94.9
Poland	75	0	0	100
Portugal	278	0	1.8	98.2
Romania	25	0	0	100
Slovakia	780	0	100	0
Slovenia	185	4.9	21.1	74.1
Spain	1,003	0.1	75.9	24
Sweden	659	6.1	90.7	3.2
Total (25 MSs)	**12,157**	**1.9**	**55.9**	**42.2**
Iceland	55	12.7	54.5	32.7
Norway	222	9.9	65.3	24.8

MSs: Member States; N: number of isolates tested.

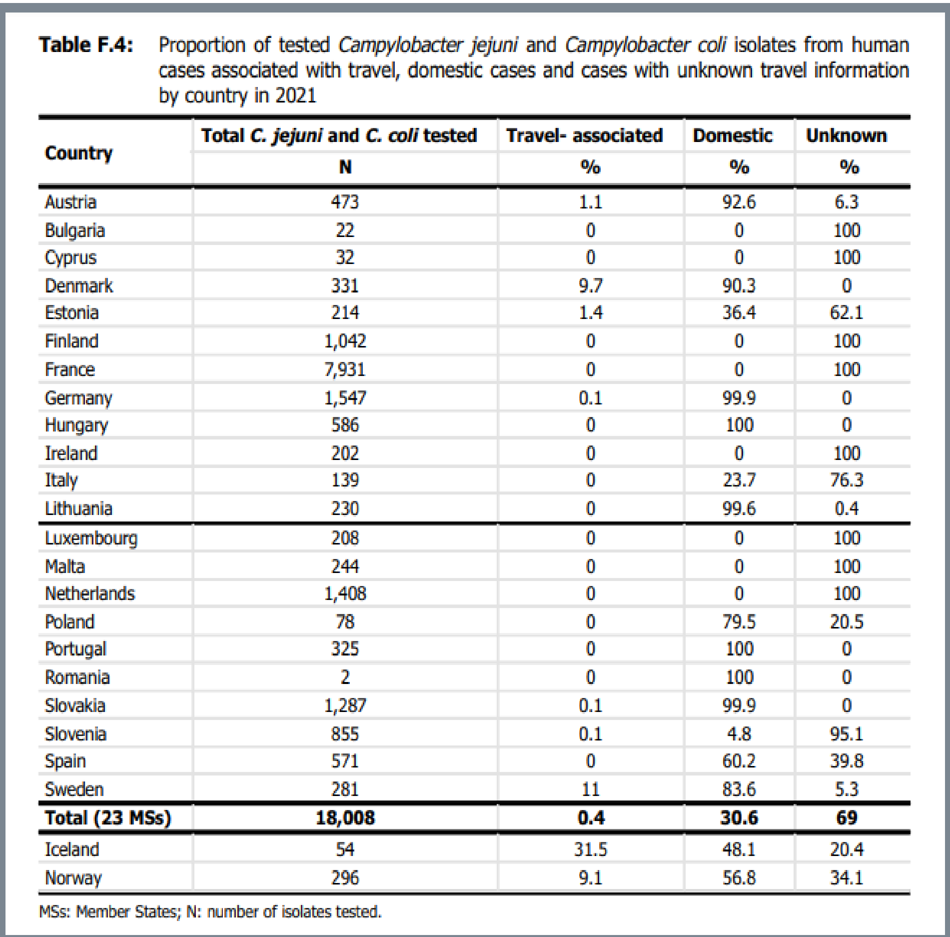
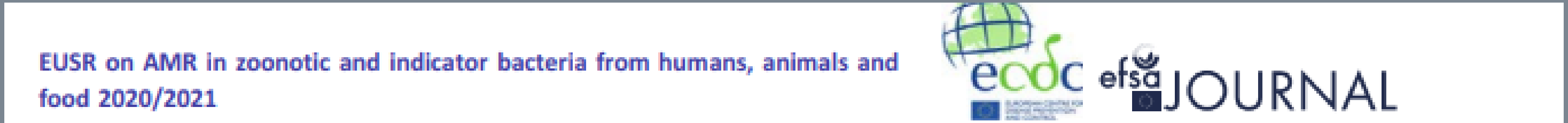


Table F.4: Proportion of tested *Campylobacter jejuni* and *Campylobacter coli* isolates from human cases associated with travel, domestic cases and cases with unknown travel information by country in 2021

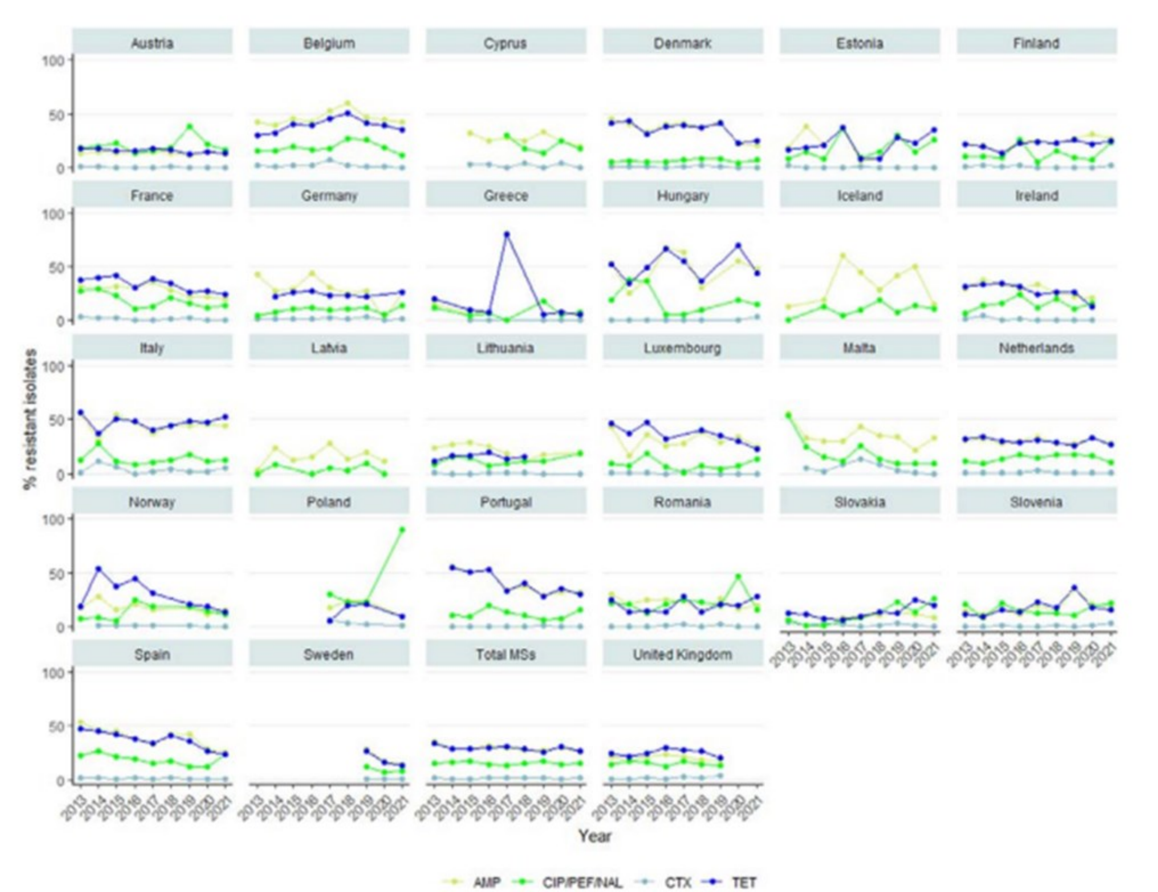
Country	Total *C. jejuni* and *C. coli* tested	Travel- associated	Domestic	Unknown
	N	%	%	%
Austria	473	1.1	92.6	6.3
Bulgaria	22	0	0	100
Cyprus	32	0	0	100
Denmark	331	9.7	90.3	0
Estonia	214	1.4	36.4	62.1
Finland	1,042	0	0	100
France	7,931	0	0	100
Germany	1,547	0.1	99.9	0
Hungary	586	0	100	0
Ireland	202	0	0	100
Italy	139	0	23.7	76.3
Lithuania	230	0	99.6	0.4
Luxembourg	208	0	0	100
Malta	244	0	0	100
Netherlands	1,408	0	0	100
Poland	78	0	79.5	20.5
Portugal	325	0	100	0
Romania	2	0	100	0
Slovakia	1,287	0.1	99.9	0
Slovenia	855	0.1	4.8	95.1
Spain	571	0	60.2	39.8
Sweden	281	11	83.6	5.3
Total (23 MSs)	**18,008**	**0.4**	**30.6**	**69**
Iceland	54	31.5	48.1	20.4
Norway	296	9.1	56.8	34.1

MSs: Member States; N: number of isolates tested.



EUSR on AMR in zoonotic and indicator bacteria from humans, animals and food 2020/2021

Selected antimicrobials by country



EUSR on AMR in zoonotic and indicator bacteria from humans, animals and food 2020/2021

Five years of *Salmonella* 2017 – 2021 - Denmark

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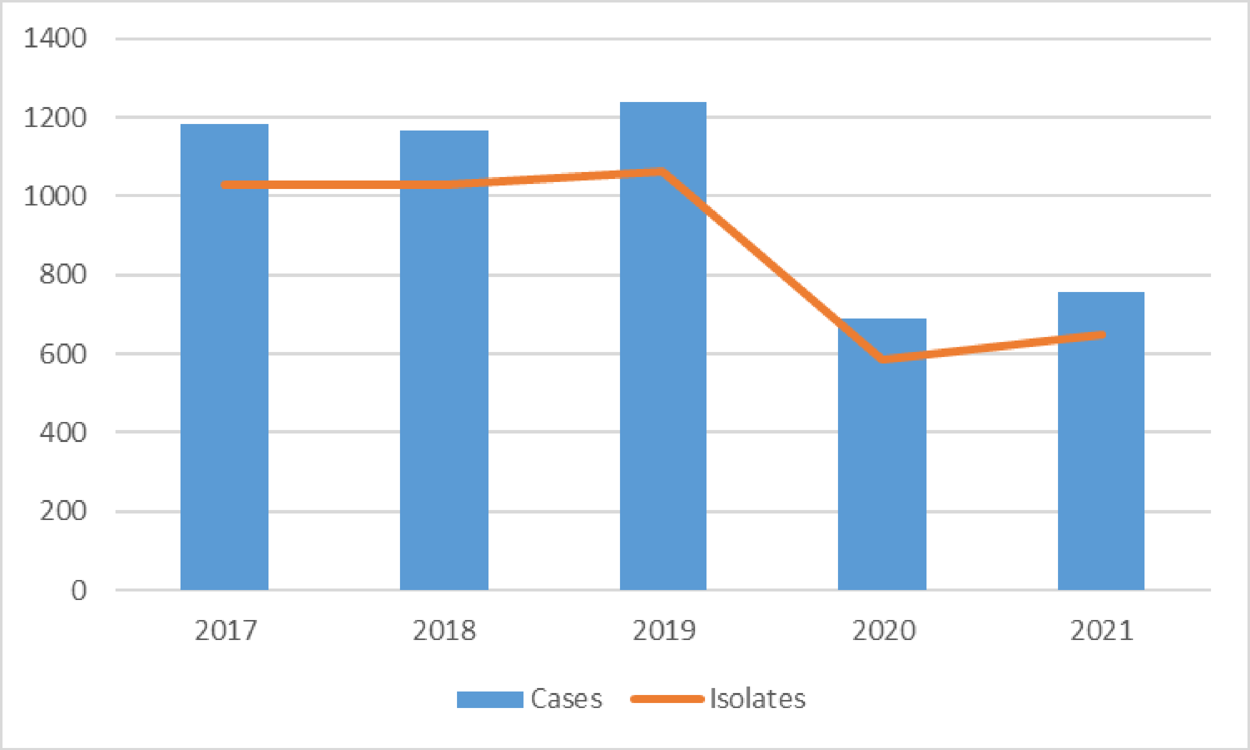
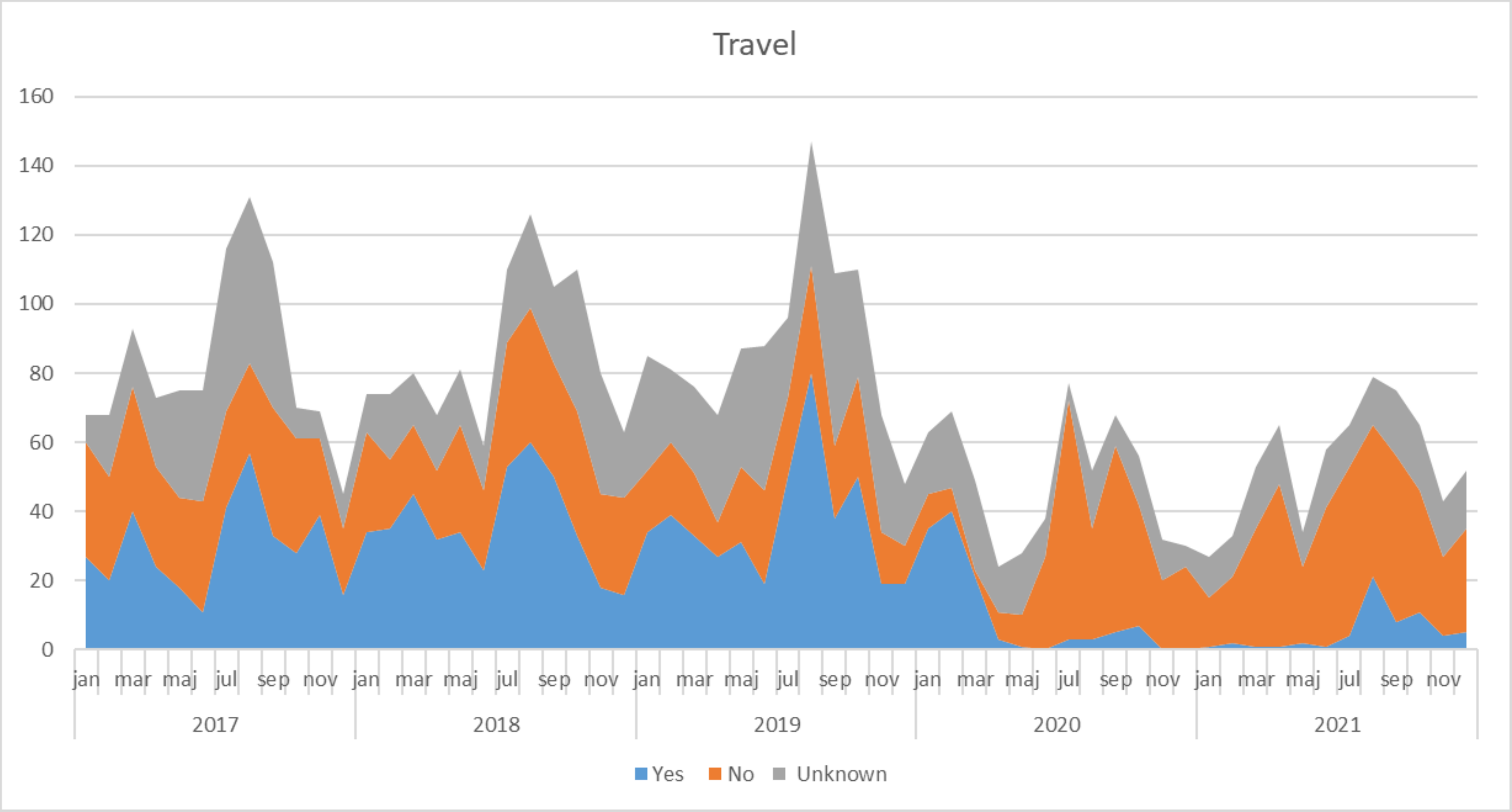
- Total number of cases (5036) and isolates (4358)

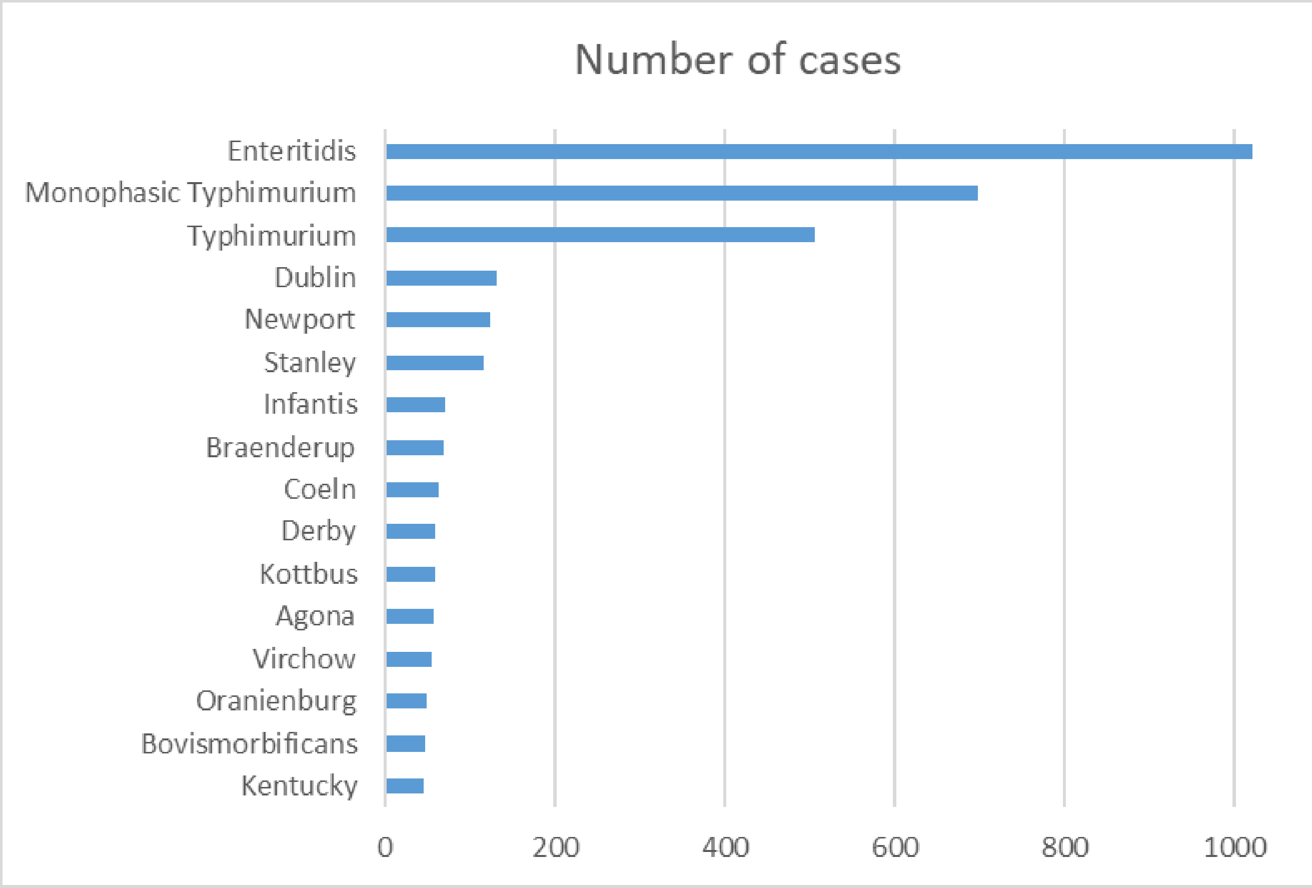


Case travel status

Travel status (%)		
Yes	No	Unknown
32,2	37,7	30,1



Predicted serotypes

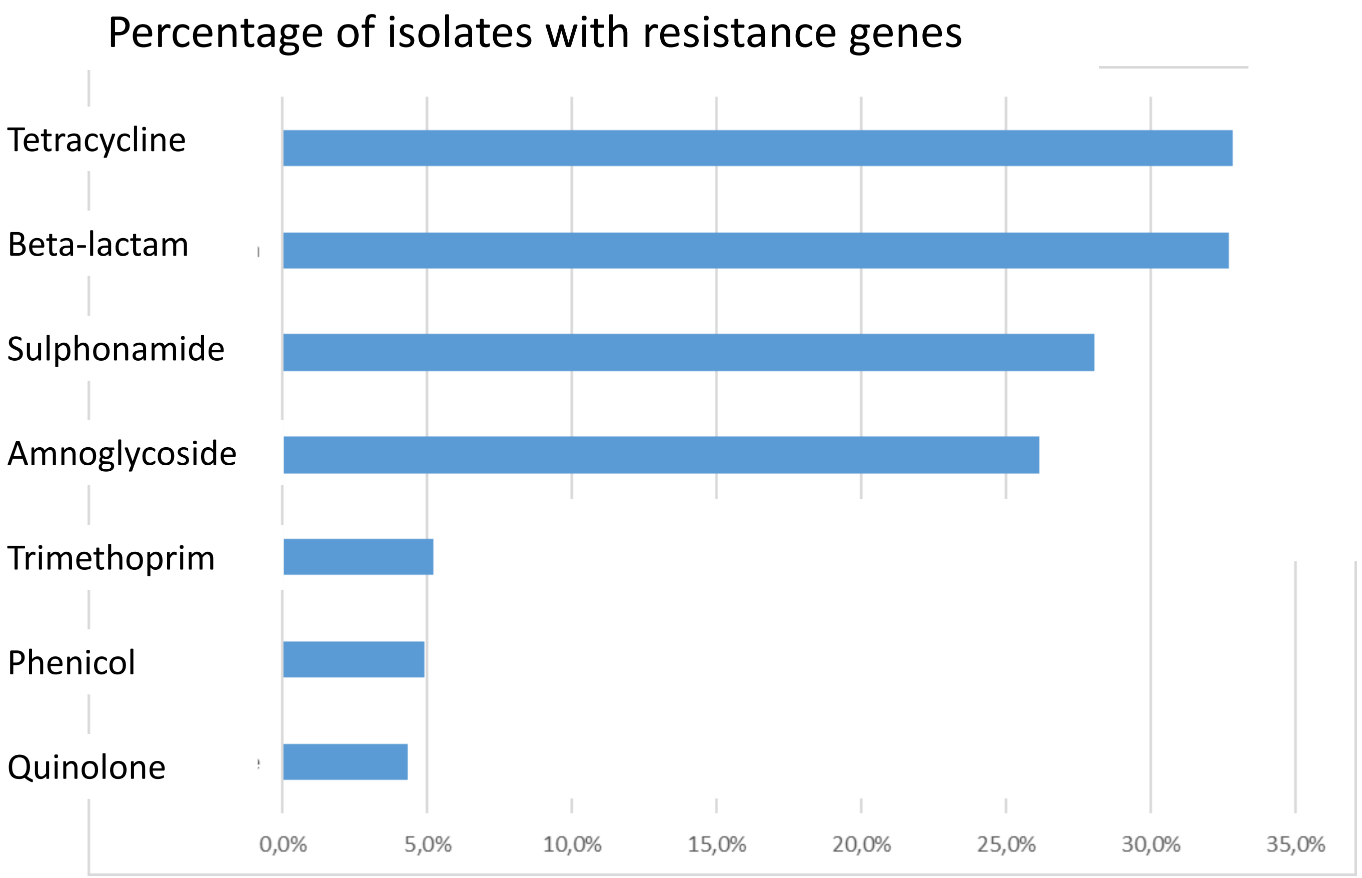


51% of isolates

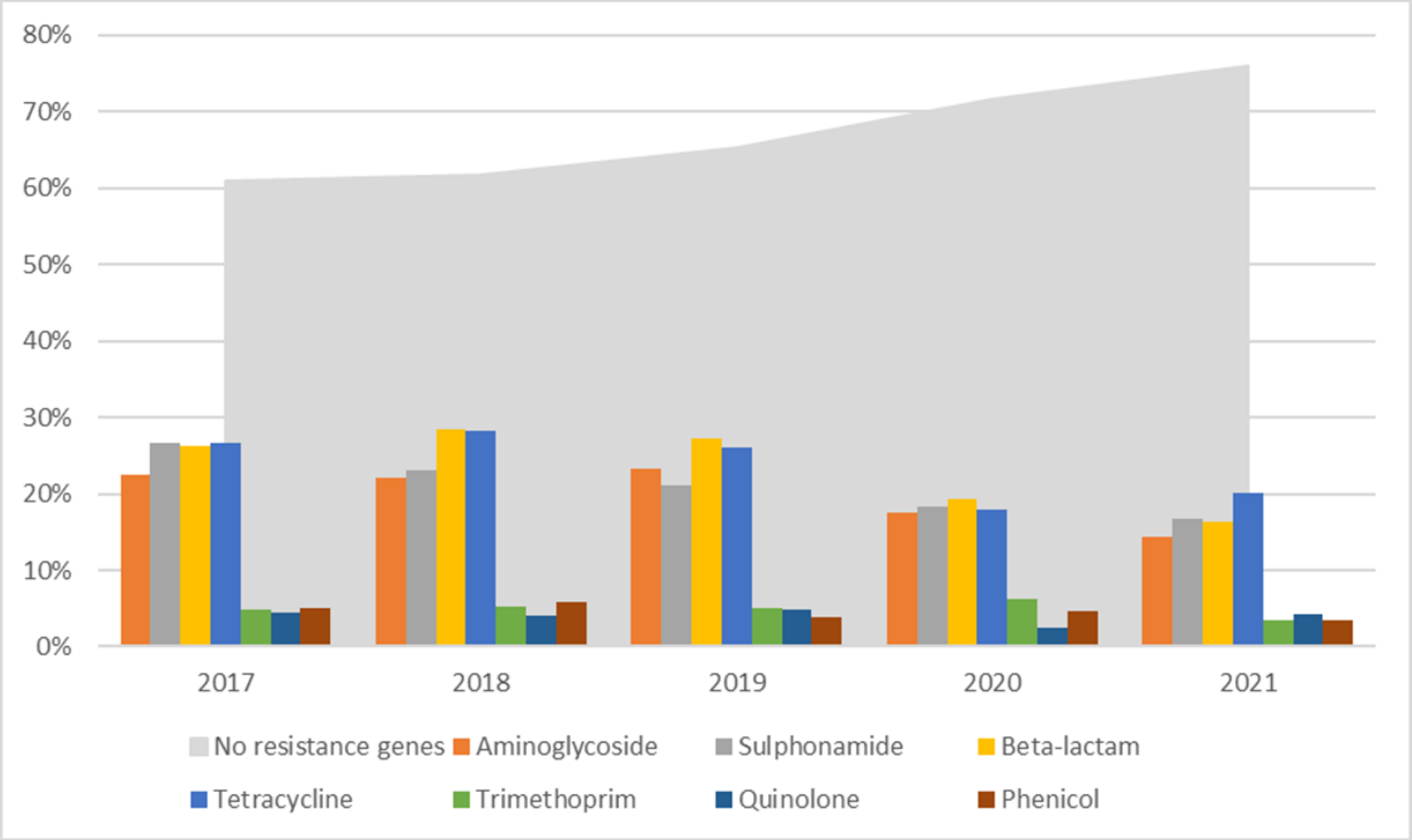
3% and below

Resistance detected

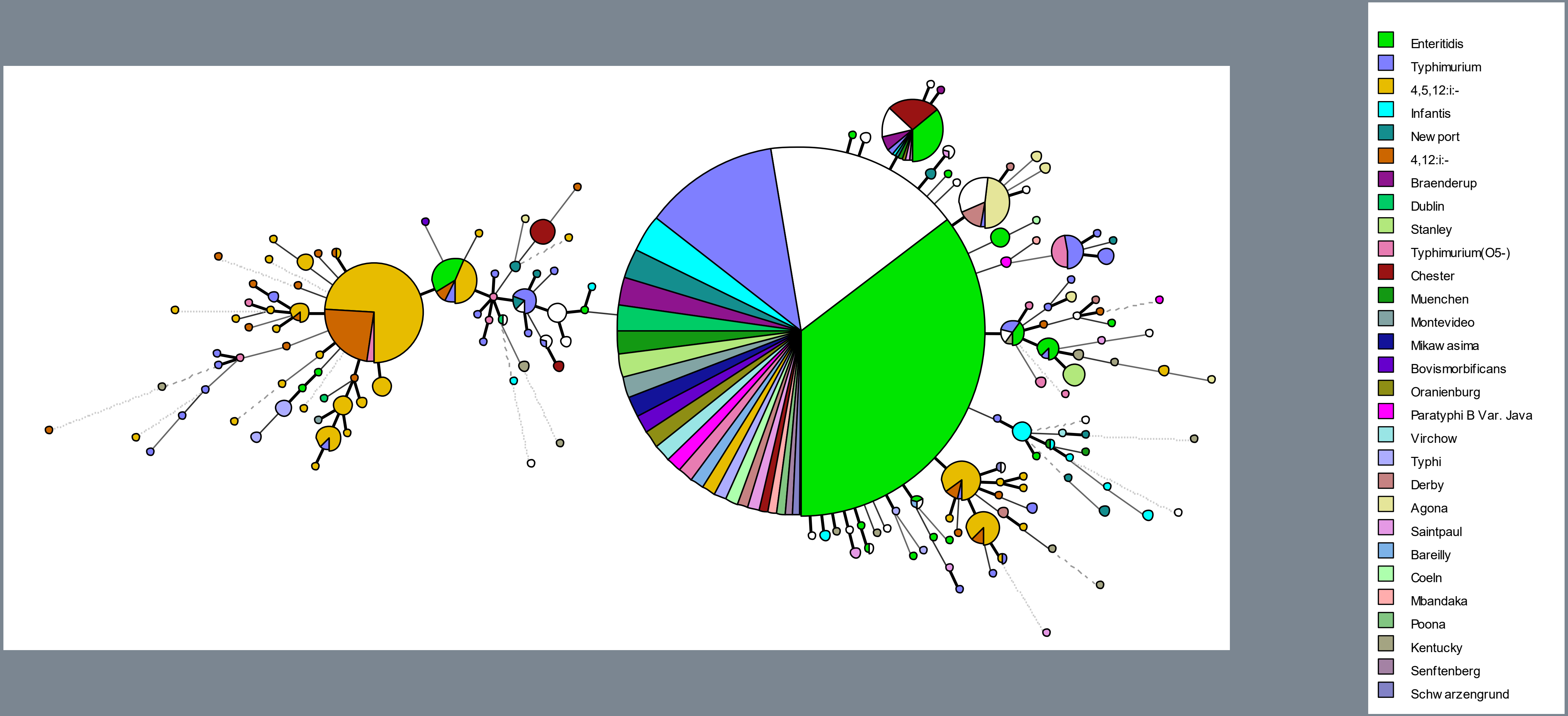
- **2869 (66%) - NO resistance genes detected**



Resistance trends 2017-2021



AMR-gene-variants tree – with colour coded serotypes



140 Enteritidis (14%) – cgMLST dendrogram

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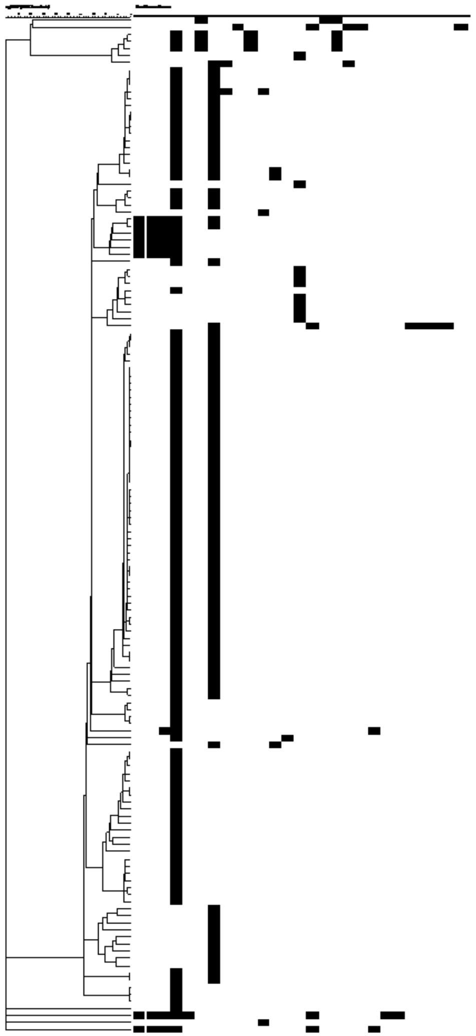
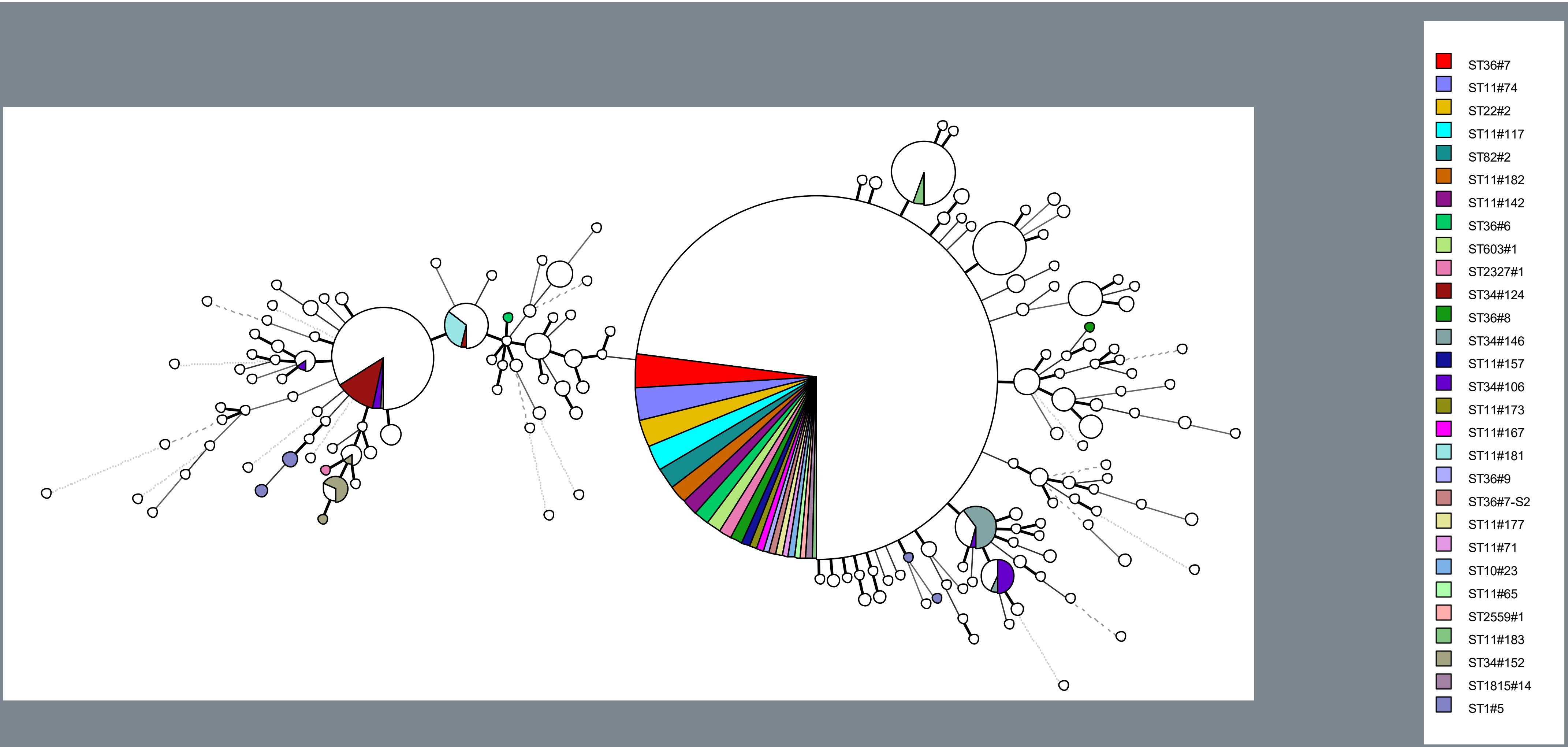


Surveillance data summarised

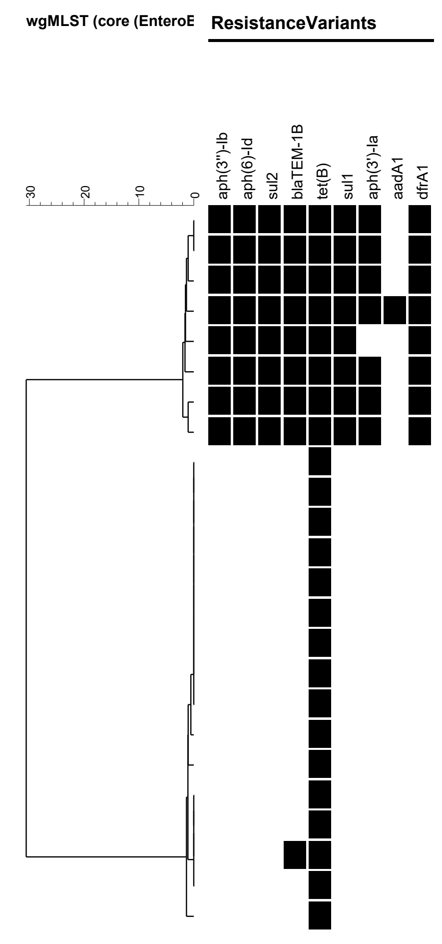
- Number of assigned serotypes, STs, clusters and outbreaks investigated

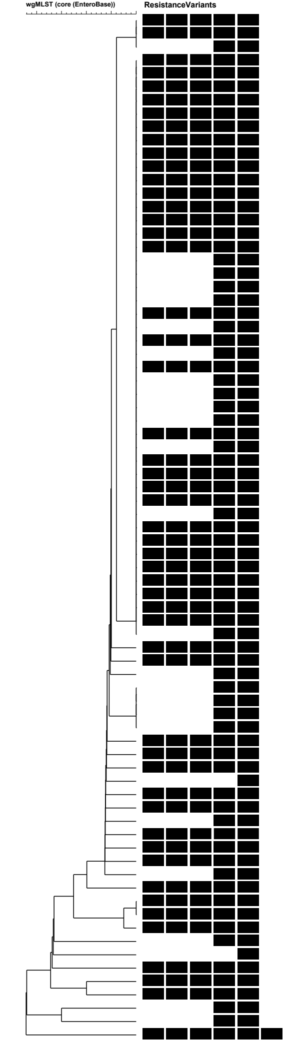
Year	Number of serotypes	Number of STs	Number of Clusters	% of cases included in clusters	Number of national outbreaks	% of cases included in national outbreaks investigated
2017	102	180	176	44,8%	17	17,3%
2018	100	163	194	48,1%	10	14,5%
2019	112	181	154	43,2%	9	13,8%
2020	81	124	107	51,5%	10	18,9%
2021	82	123	98	54,2%	12	29,1%
Total	**208**	**374**	**486**	**48,4%**	**58**	**18,7%**

Clusters mapped on the AMR-gene-tree



cgMLST dendrogram and resistance gene variants





Concluding remarks

- Phenotypic and/or genotypic AMR testing is an important part of surveillance of *Salmonella* and *Campylobacter*

- When doing AMR surveillance and trend analysis it is important to include knowledge on clusters and outbreaks

- No approach can stand alone when doing surveillance
  - Include patient metadata (travel history)

- Remember the international aspect/context
  - Use validated/international tools available for deriving AMR genes from WGS-data
  - Use the EU protocol for harmonized monitoring of AMR
  - Use the data that are already there: reports, sequences, EpiPulse, articles etc.

Thank you