



# Integration of AMR into surveillance and outbreak investigation

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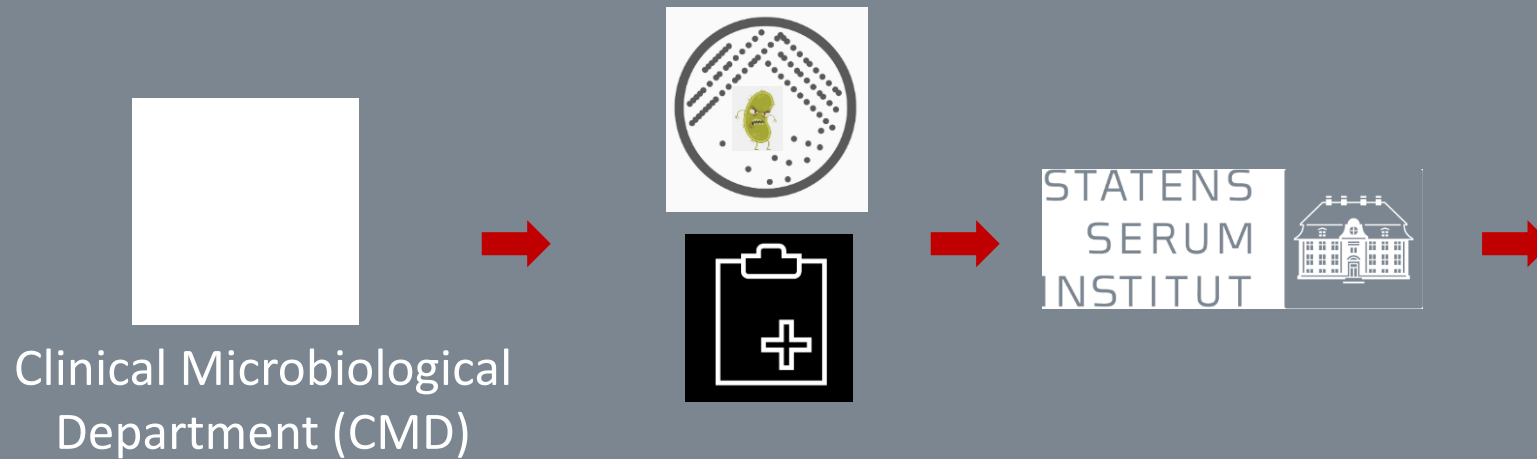
# Today's presentation



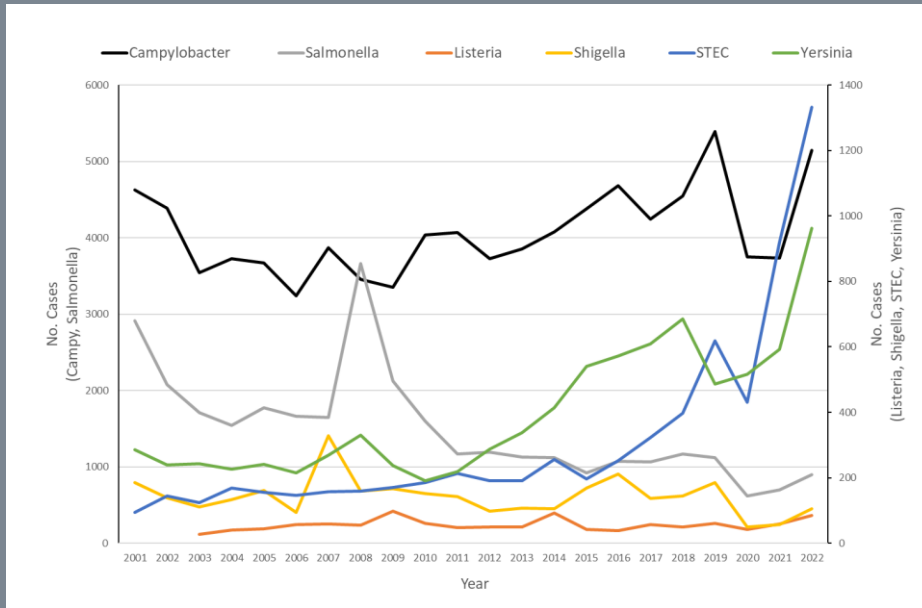
## Danish AMR surveillance of *Salmonella* and *Campylobacter* from human infection

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

# Surveillance of human *Salmonella* and *Campylobacter* infections



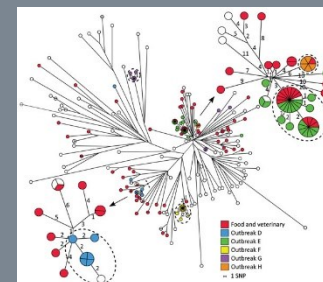
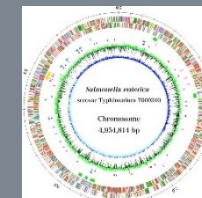
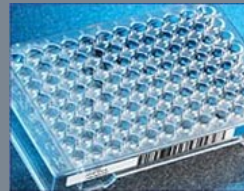
Case-based surveillance  
Isolate based surveillance



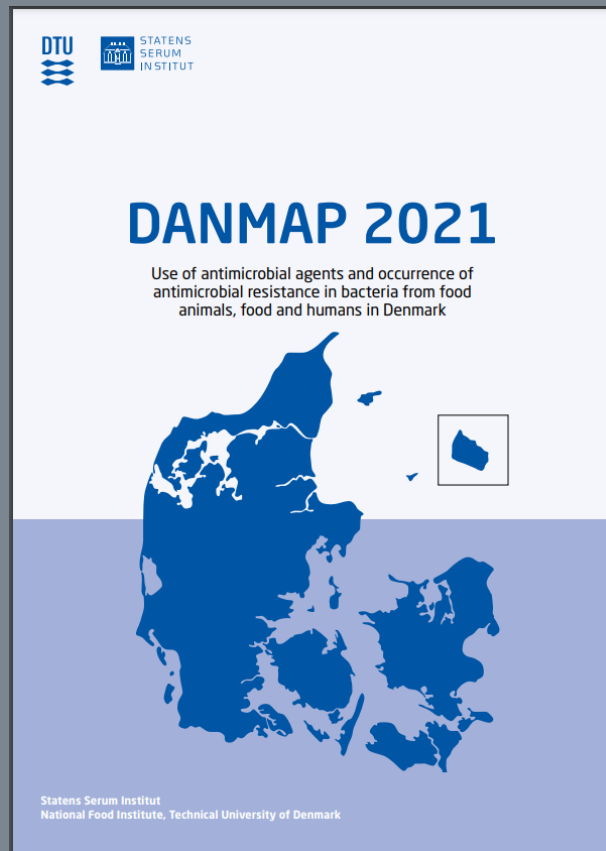
# Isolate based surveillance

- 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).

Specimen	Plade	Amikac	Ampici	Azithr	Cefota	Ceftaz
SAL.SP	EUVSEC3	<= 4 S	= 4 S	= 4 S	<= 0,25 S	= 0,5 S
SAL.SP	EUVSEC3	<= 4 S	> 32 R	= 4 S	<= 0,25 S	= 0,5 S
SAL.SP	EUVSEC3	= 8 S	> 32 R	= 8 S	> 4 R	> 8 R
SAL.SP	EUVSEC3	<= 4 S	> 32 R	= 32 R	> 4 R	> 8 R
SAL.SP	EUVSEC3	<= 4 S	> 32 R	= 8 S	> 4 R	> 8 R



## The Danish Integrated Antimicrobial Resistance Monitoring and Research Programme



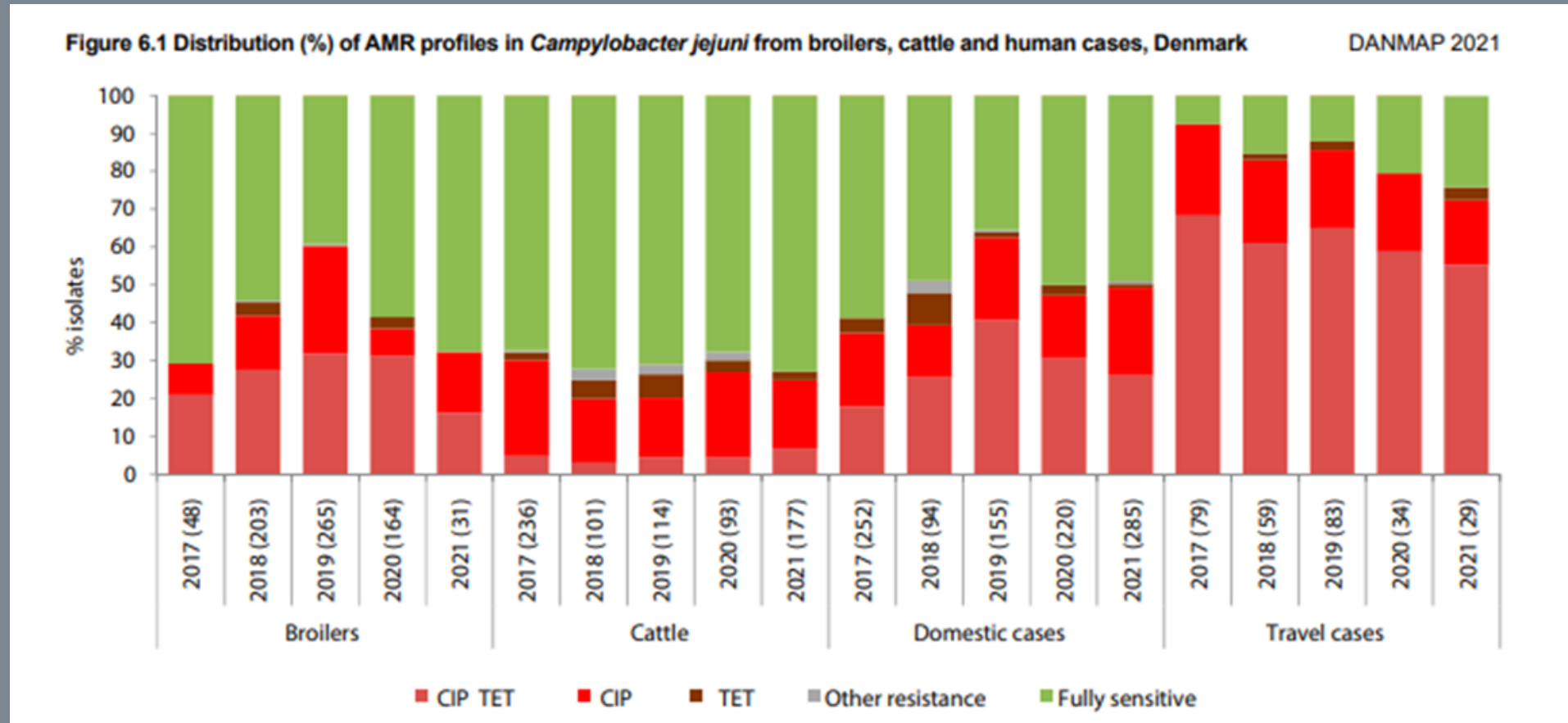
- Including AMR data on *Salmonella* Typhimurium/monophasic variant and a subset of *Campylobacter* from human infection
- Currently developed including more serotypes of *Salmonella* and WGS-derived AMR genes.

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

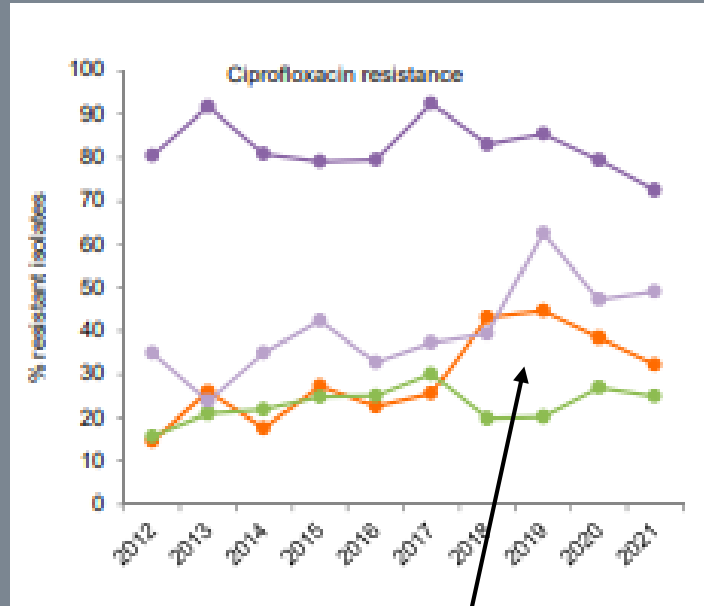
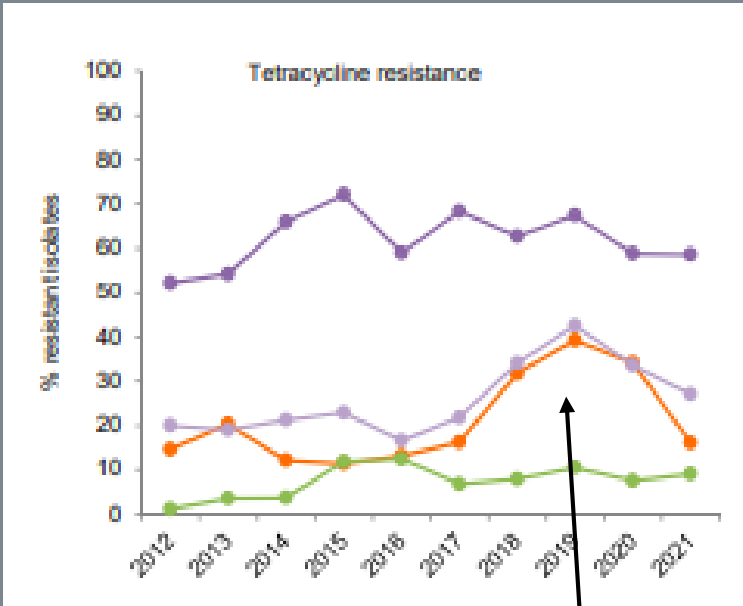
## Visionary national programme

- 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

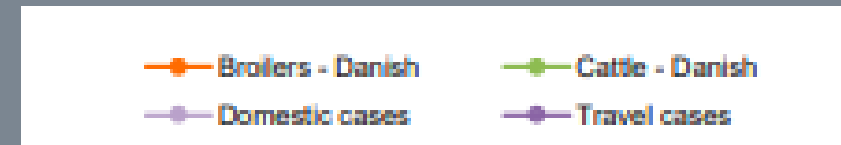
# Campylobacter



# Campylobacter



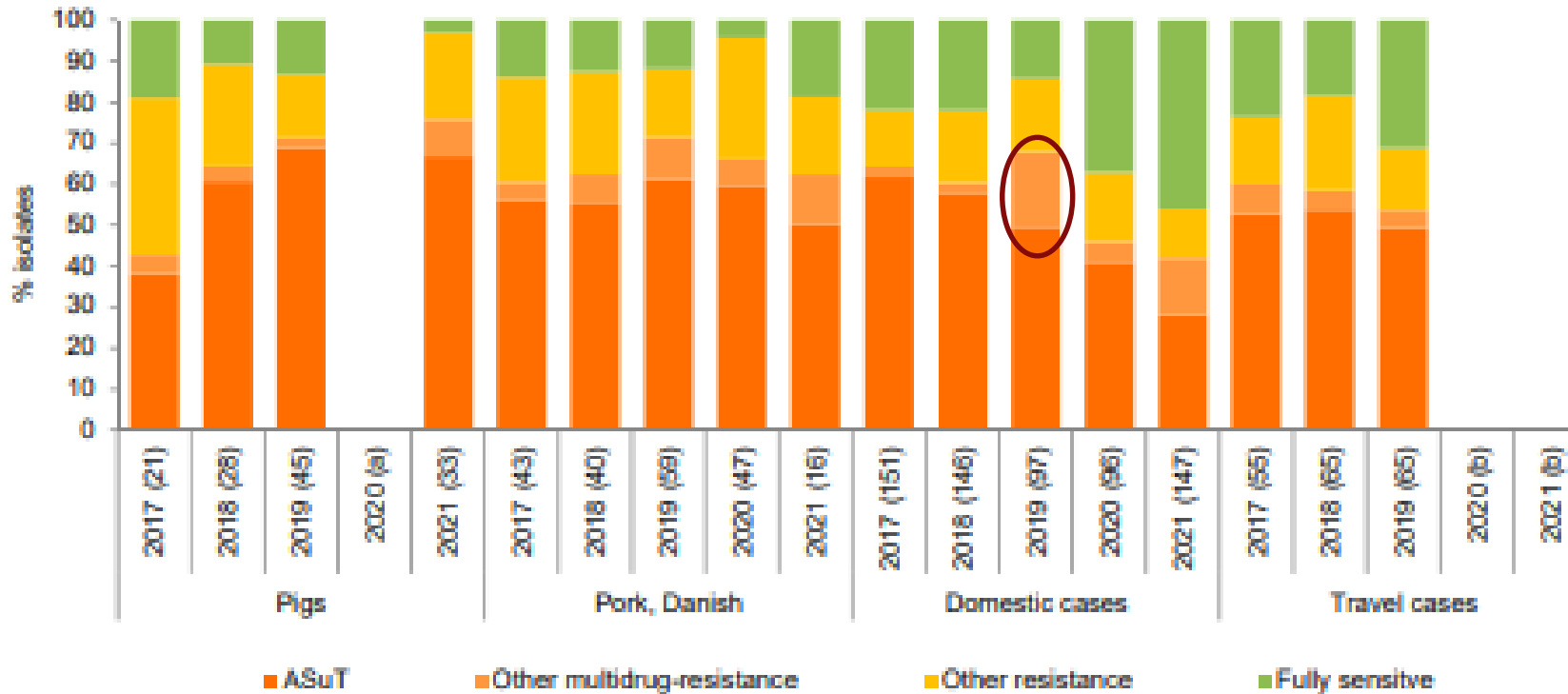
Ciprofloxacin and tetracycline resistant clone that caused several outbreaks





# Salmonella Typhimurium/monophasic

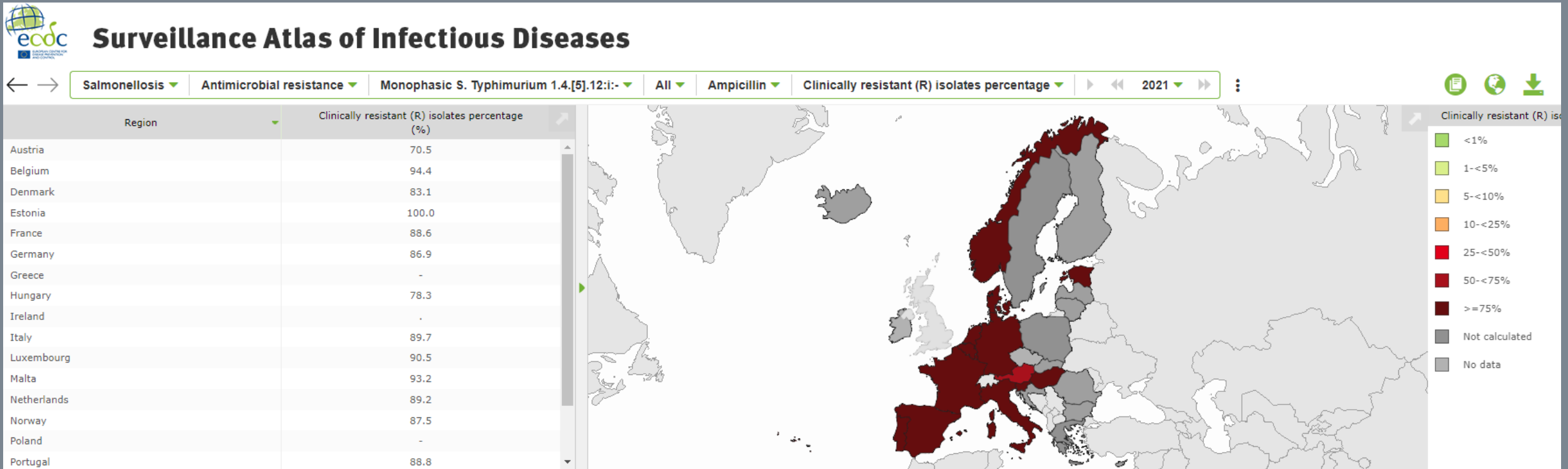
Figure 6.3 Relative distribution (%) of multidrug-resistant, resistant and fully sensitive *S. Typhimurium* from pigs, domestic pork and human cases, Denmark DANMAP 2021



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



# EU AMR surveillance

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

## SCIENTIFIC REPORT

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  $\beta$ -lactamases (ESBL)/AmpC  $\beta$ -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*<sub>OXA-48</sub>, *bla*<sub>OXA-181</sub>, and *bla*<sub>NDM-5</sub> 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.

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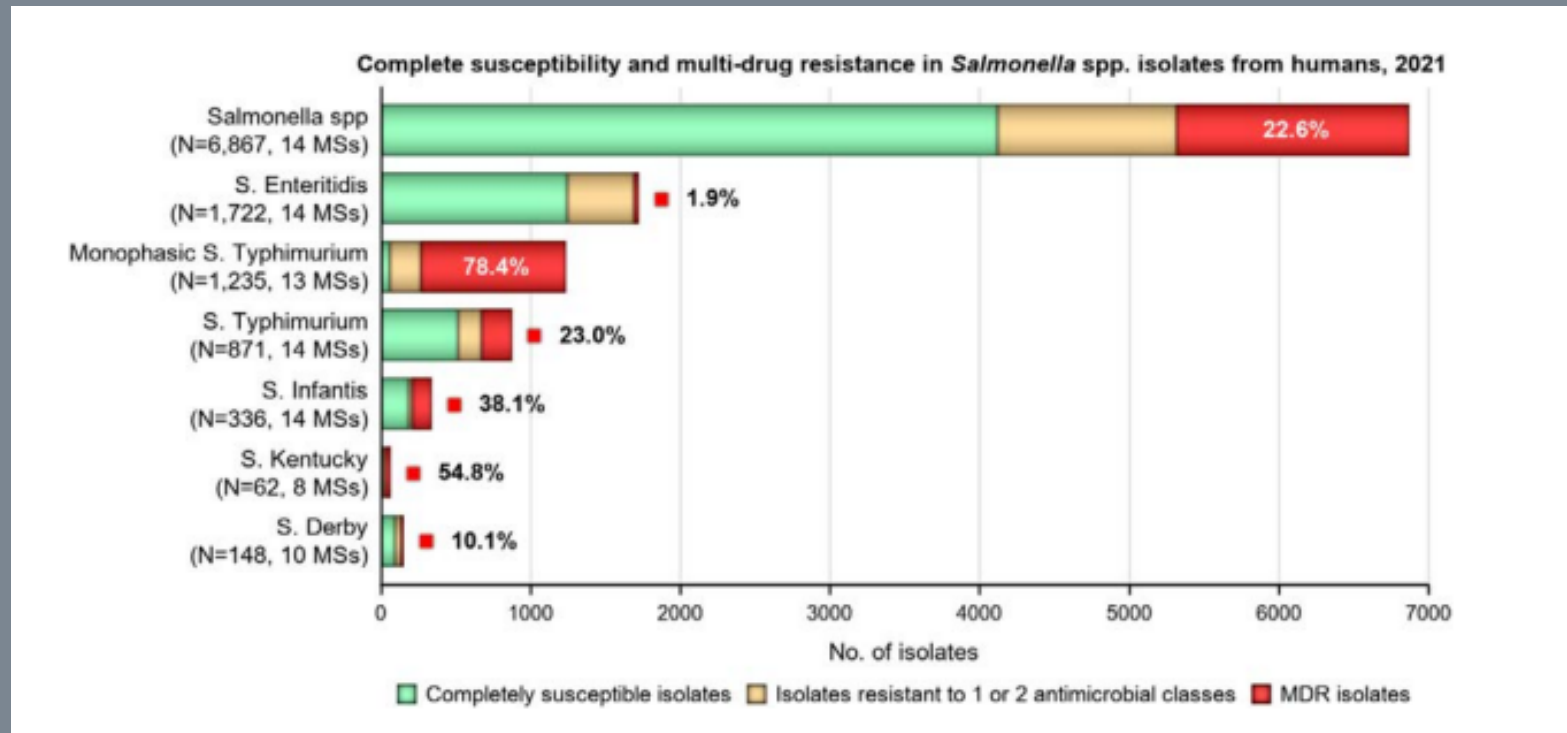
**Keywords:** antimicrobial resistance, zoonotic bacteria, indicator bacteria, ESBL, MRSA

**Requestor:** European Commission

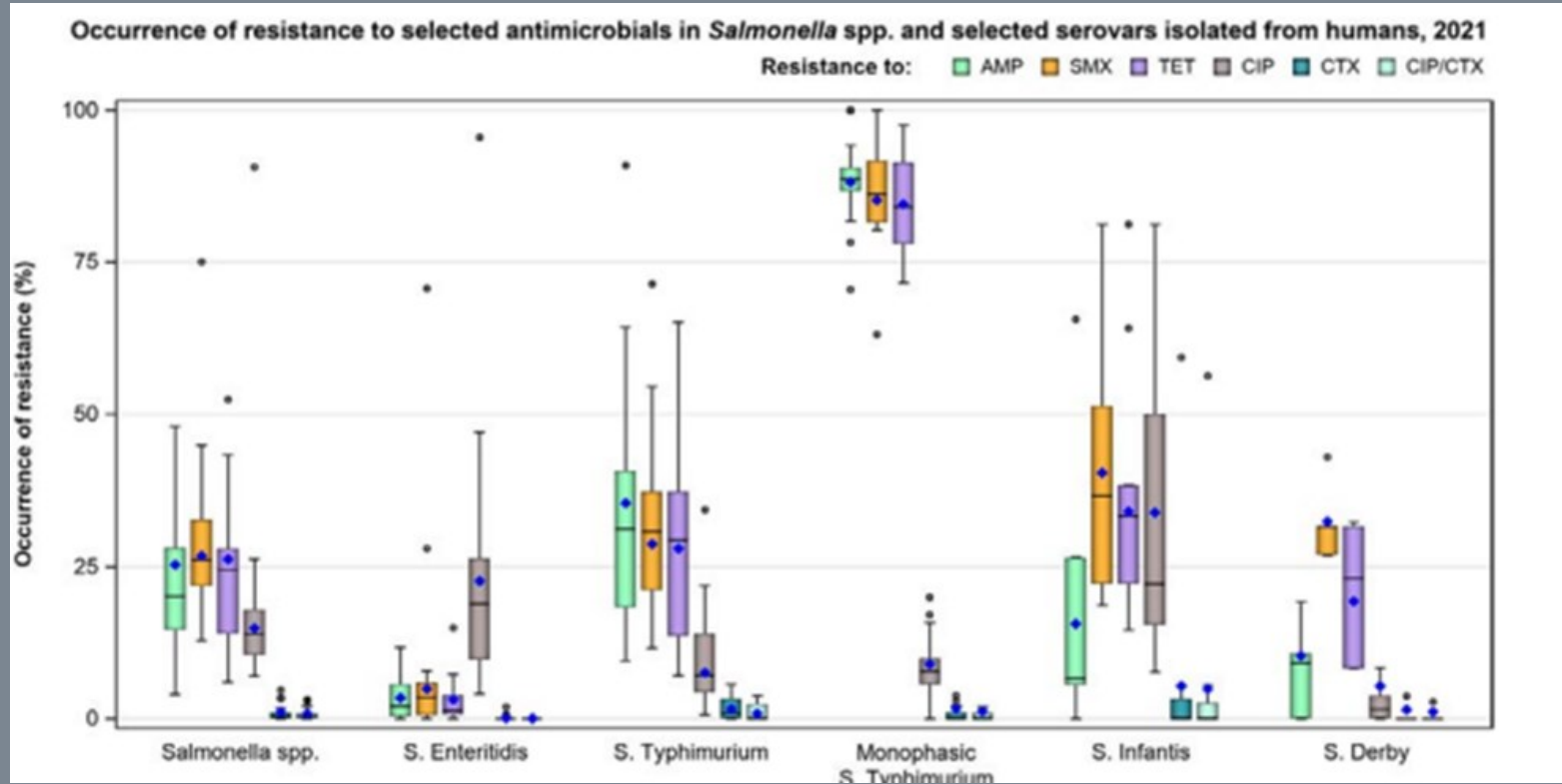
**Question number:** EFSA-Q-2021-00768

**Correspondence:** [zoonoses@efsa.europa.eu](mailto:zoonoses@efsa.europa.eu) (EFSA); [FWD@ecdc.europa.eu](mailto:FWD@ecdc.europa.eu) (ECDC)

# Salmonella isolates from humans in 2021



# Resistance to selected and critically important antimicrobials



# 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 <i>Salmonella</i> 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
<b>Total (25 MSs)</b>	<b>12,157</b>	<b>1.9</b>	<b>55.9</b>	<b>42.2</b>
Iceland	55	12.7	54.5	32.7
Norway	222	9.9	65.3	24.8

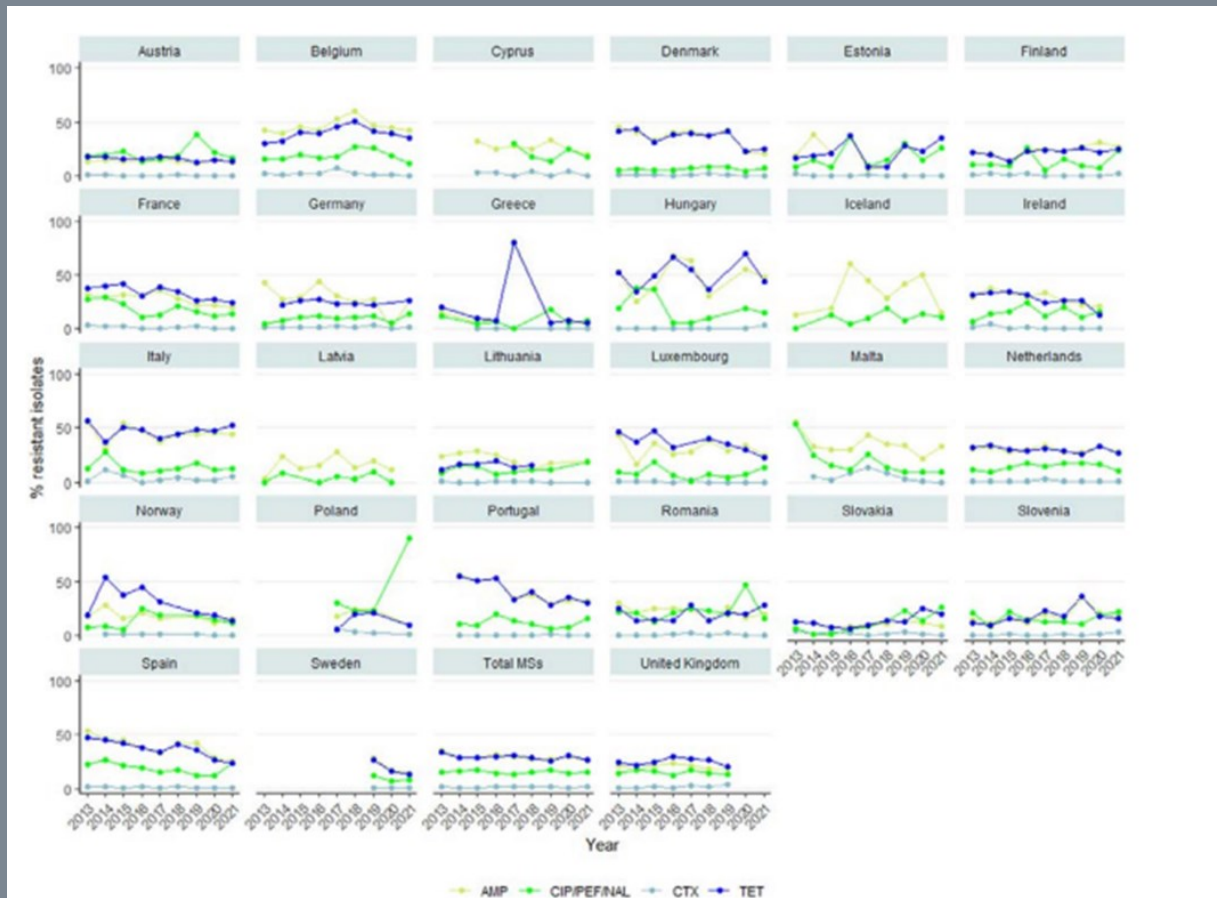
MSs: Member States; N: number of isolates tested.

**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 <i>C. jejuni</i> and <i>C. coli</i> 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
<b>Total (23 MSs)</b>	<b>18,008</b>	<b>0.4</b>	<b>30.6</b>	<b>69</b>
Iceland	54	31.5	48.1	20.4
Norway	296	9.1	56.8	34.1

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

# Selected antimicrobials by country





# Five years of *Salmonella* 2017 – 2021 - Denmark

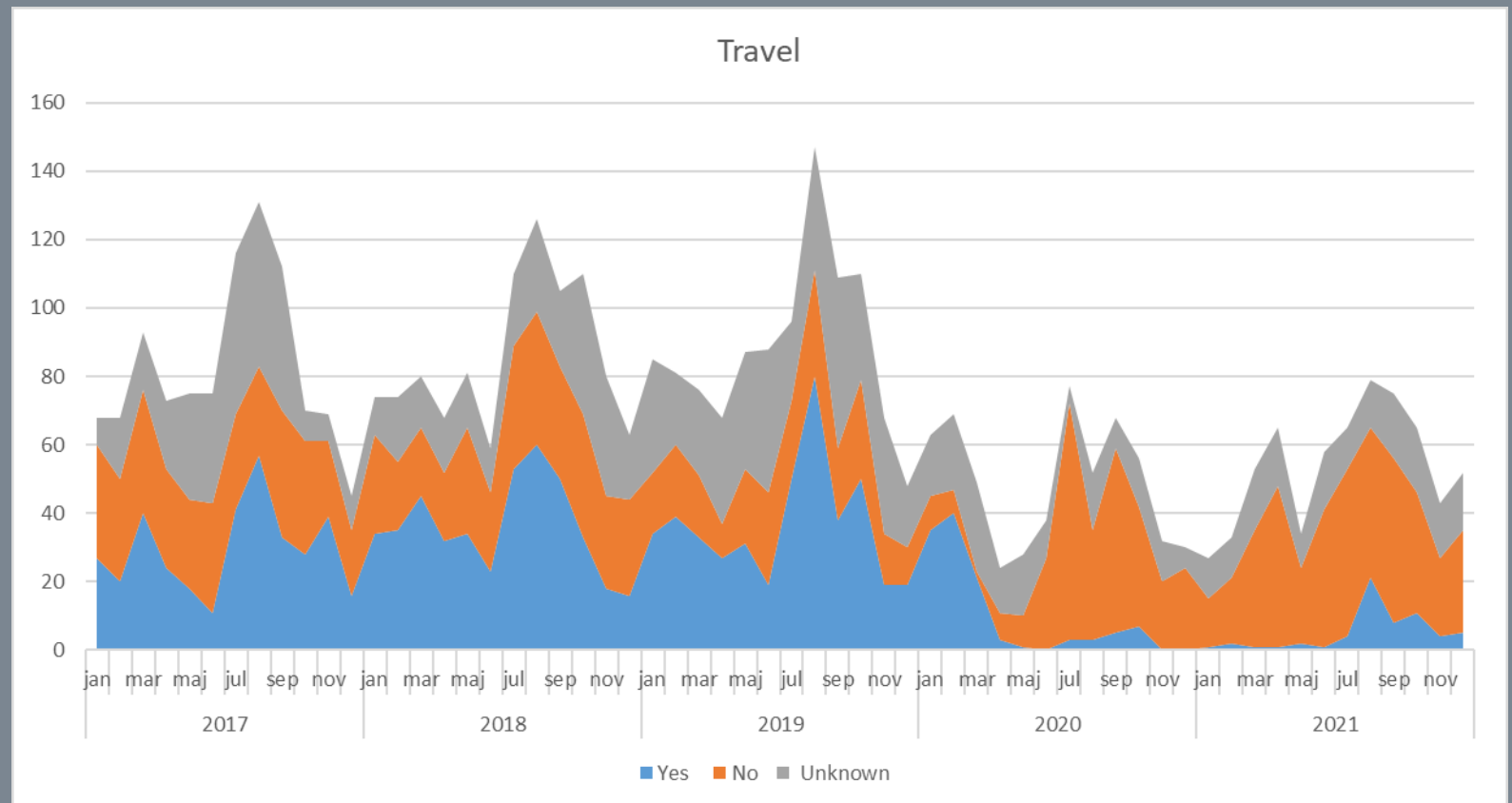
- Total number of cases (5036) and isolates (4358)



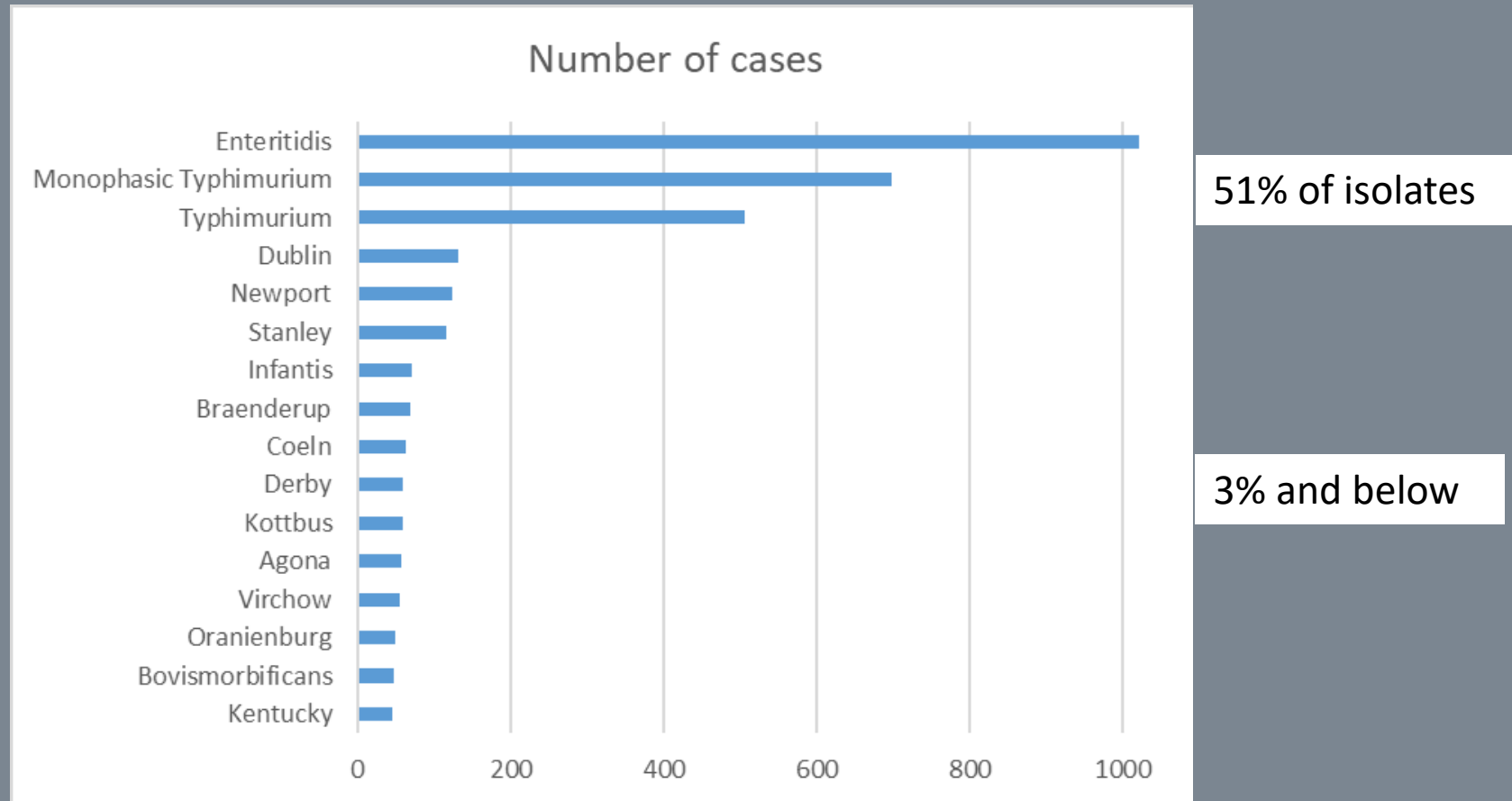
# Case travel status



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



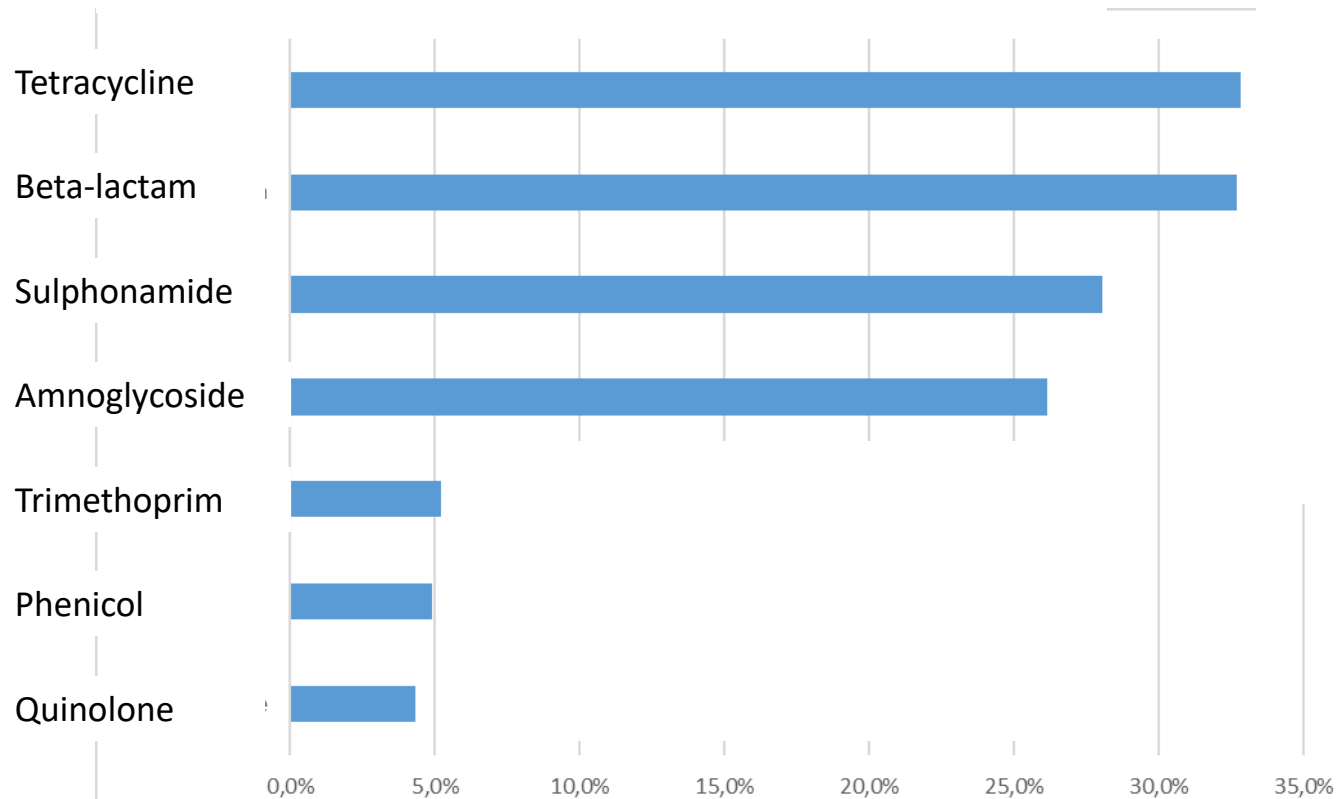
# Predicted serotypes



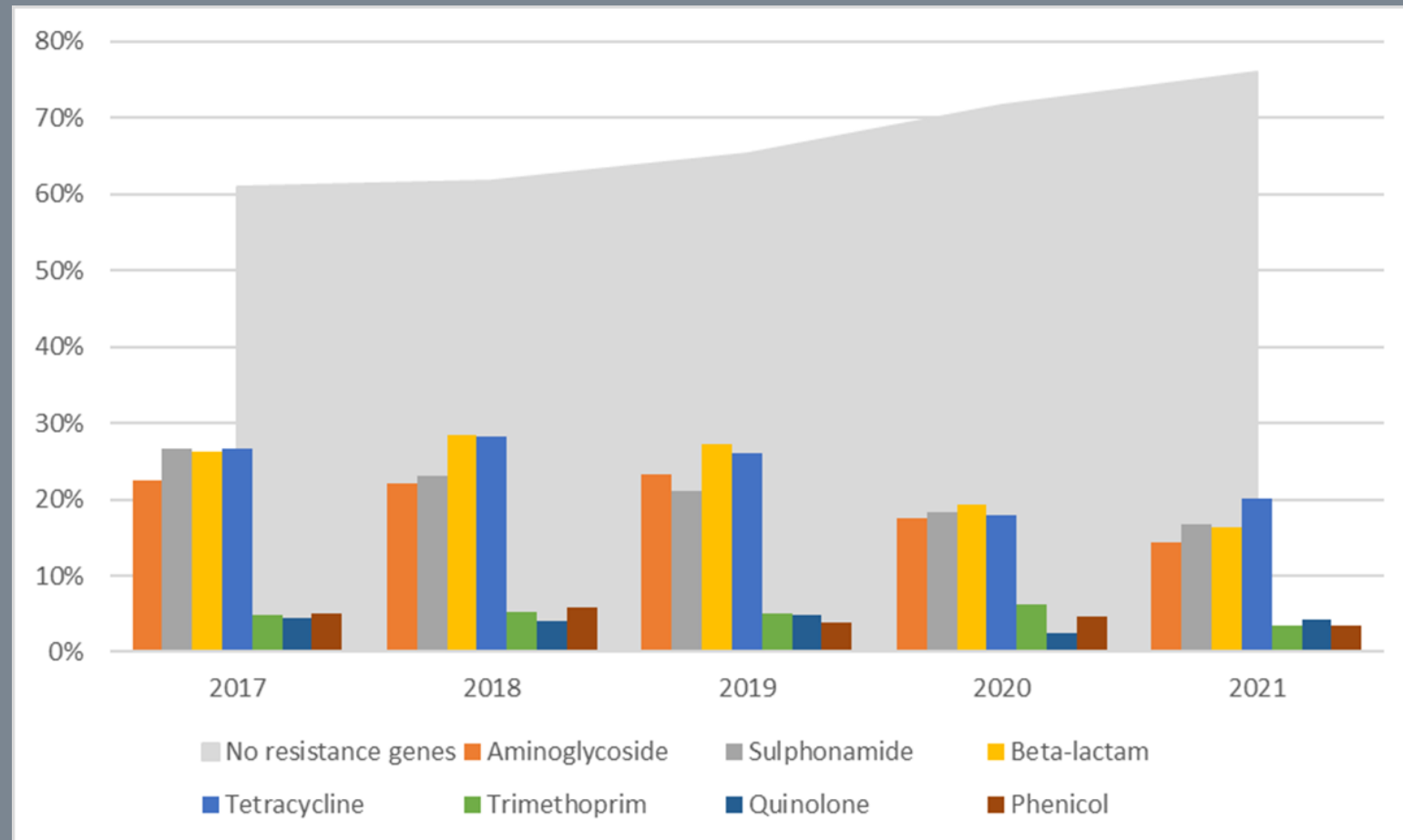
# Resistance detected

- 2869 (66%) - NO resistance genes detected

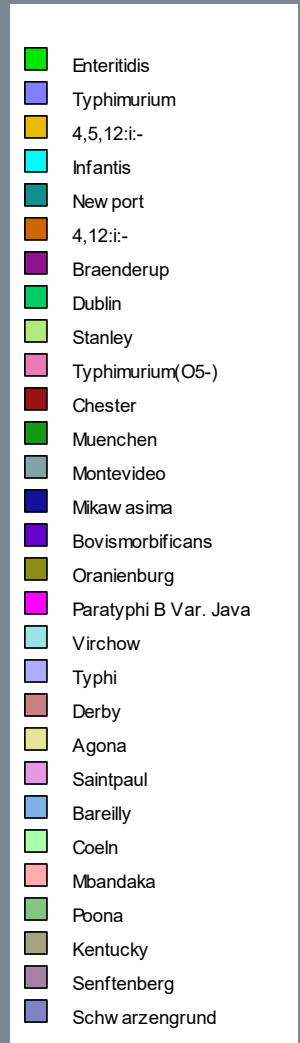
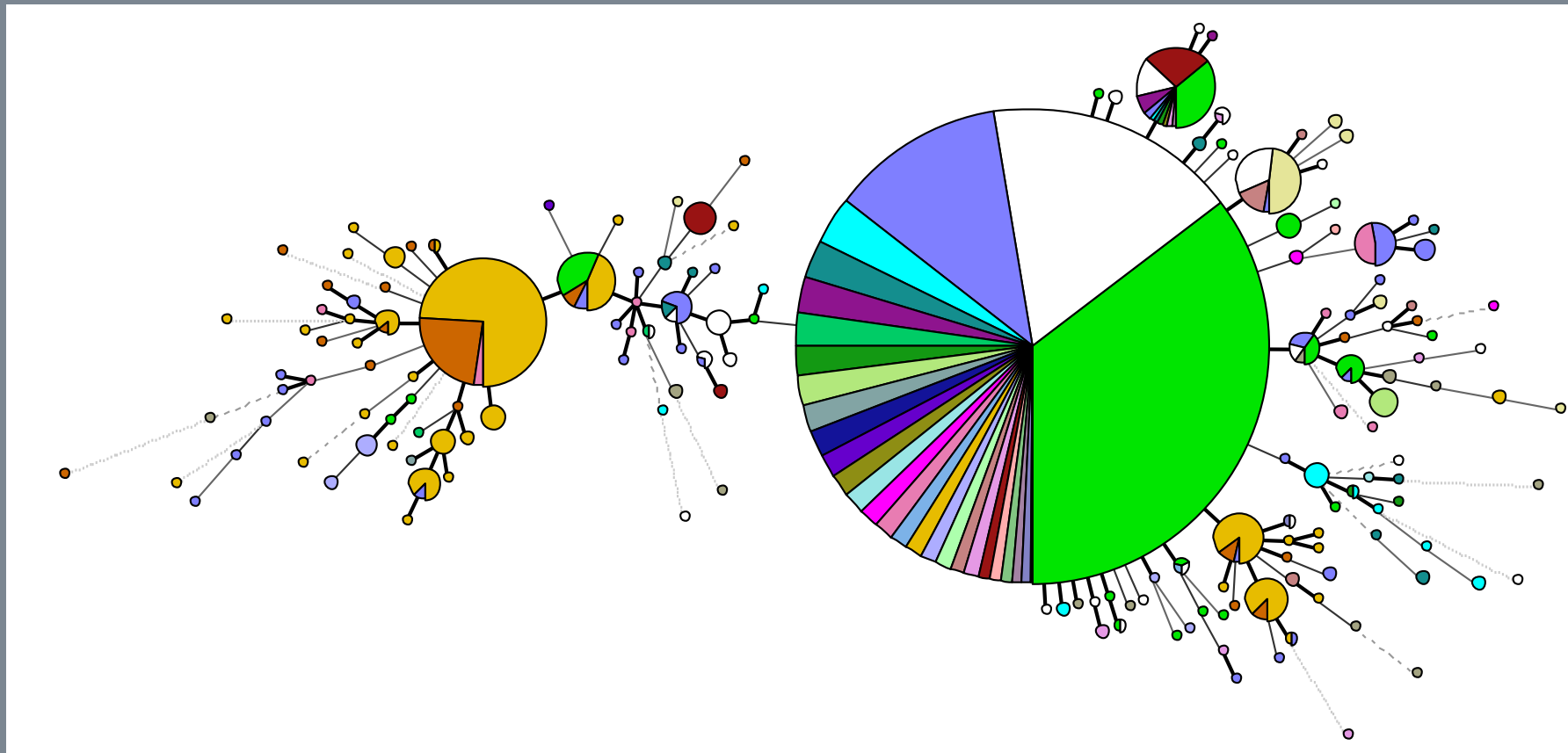
Percentage of isolates with resistance genes



# Resistance trends 2017-2021



# AMR-gene-variants tree – with colour coded serotypes



# 140 Enteritidis (14%) – cgMLST dendrogram



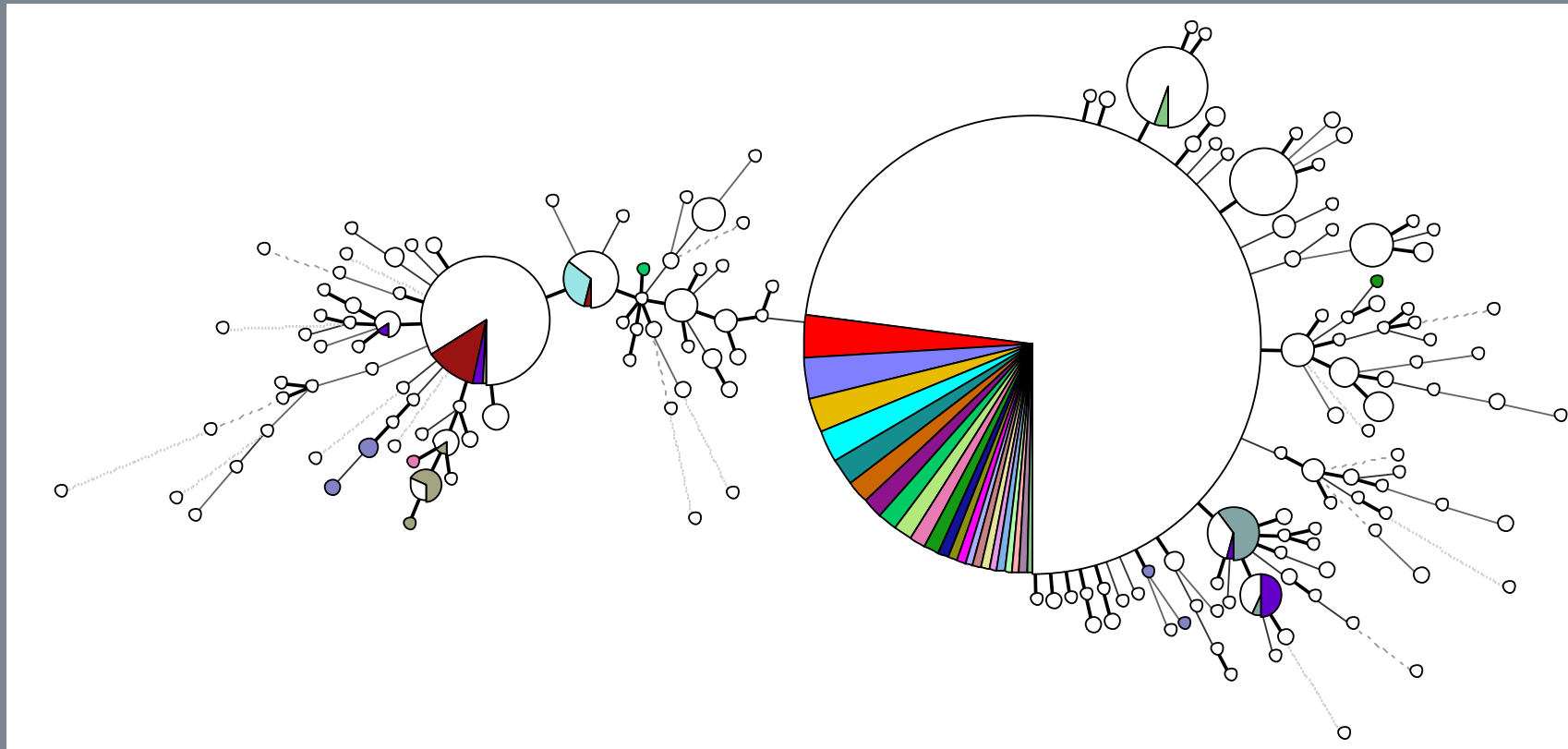
# Surveillance data summarised





























- 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%
<b>Total</b>	<b>208</b>	<b>374</b>	<b>486</b>	<b>48,4%</b>	<b>58</b>	<b>18,7%</b>

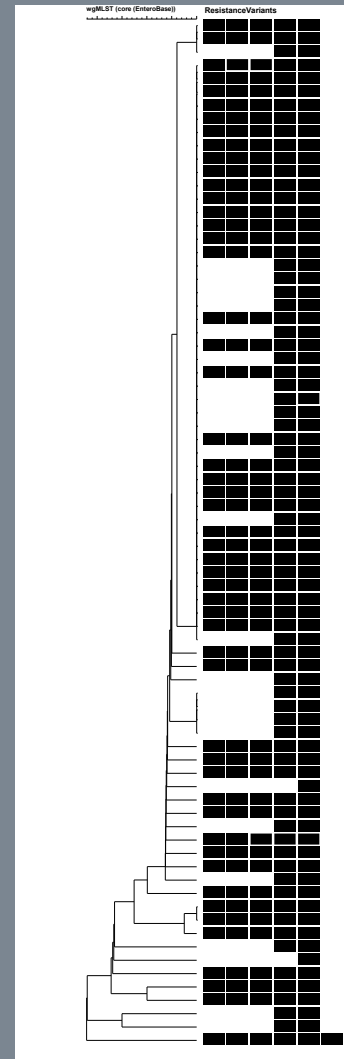
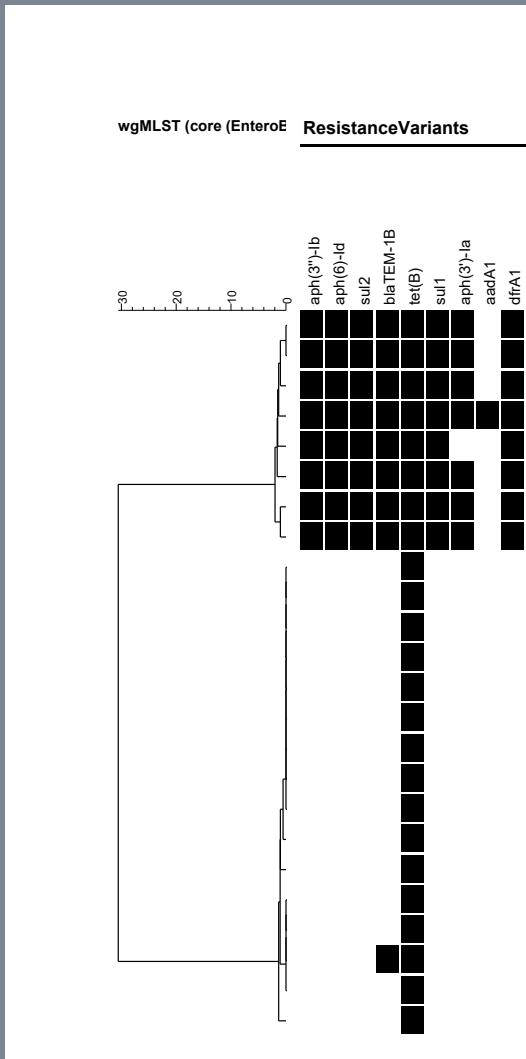


# Clusters mapped on the AMR-gene-tree



-  ST36#7
-  ST11#74
-  ST22#2
-  ST11#117
-  ST82#2
-  ST11#182
-  ST11#142
-  ST36#6
-  ST603#1
-  ST2327#1
-  ST34#124
-  ST36#8
-  ST34#146
-  ST11#157
-  ST34#106
-  ST11#173
-  ST11#167
-  ST11#181
-  ST36#9
-  ST36#7-S2
-  ST11#177
-  ST11#71
-  ST10#23
-  ST11#65
-  ST2559#1
-  ST11#183
-  ST34#152
-  ST1815#14
-  ST1#5

# 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

