GALWAY REFERENCE LABORATORY ANNUAL REPORT

2025

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Galway Reference Laboratory Report 2025

This summary report is presented as a series of self-explanatory tables. In each case duplicate isolates of the same species from the same person have been removed.

Background

The Galway Reference Laboratory service is based primarily on sequencing of isolates (short read, massively parallel sequencing). Raw data are analysed using proprietary software. Supplementary long-read sequencing may be used for some isolates. Maldi-TOF is used to confirm identification of isolates before sequencing. Where a poor ID is generated by Maldi-TOF identification is supported by ribosomal MLST or Mash identification. Certain other phenotypic methods are used in further evaluation of unexpected results. The Reference Laboratory also provides a limited service for phenotypic susceptibility testing. Individual isolate reports are provided to the sending laboratory

The user manual and isolate request forms are available at:

NSSLRL CPERL User Guide: https://www.saolta.ie/documents/galway-reference-laboratory-service-incorporating-national-salmonella-shigella-listeria

CPE Request Form: https://www.saolta.ie/documents/cpe-request-form-issue-21

NSSLRL request form: https://www.saolta.ie/documents/nsslrl-request-form

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Acknowledgement

I would like to thank all users of the Reference Laboratory for your continuing support. I appreciate that preparing and dispatching isolates is an additional burden on services that are already very busy. I would also like to acknowledge HSE AMRIC for supporting upgrading of equipment in recent years. I also acknowledge the skill and commitment of the Medical Scientists who make the service work and the support we have from Galway University Hospital Information and Communications Technology Team. If you have questions or suggestions for improvement of future reports please email martin.cormican@hse.ie.

M Cormican, MCRN 011105
Medical Director of the Galway Reference Laboratory Service. May 2026.

Some noteworthy points

There was a marked increase in the number of cases of *Salmonella* Paratyphi in 2026 compared to previous years.

There is a change in antimicrobial resistance determinants in *S.* Typhi in 2025 compared to 2024. In 2024 72.4% of isolates had a determinant of resistance to amoxicillin and 20.7% has a determinant of resistance to ceftriaxone.

The number of cases of *Shigella flexneri* showed a further marked increase compared to 2025. This continues a trend established over the previous 3 years.

Antimicrobial resistance is very common in *S. flexneri* and *S. sonnei* with a high proportion of isolates carrying resistance determinants for amoxicillin, azithromycin and ciprofloxacin. Resistance determinants to ceftriaxone (blaCTX-M mediated) is also very common in *S. sonnei* though less frequent in *S. flexneri*. One isolate of S. flexneri with blaOXA-181 encoding a carbapenemase was received in 2025.

The increase in number of isolates of *L. monocytogenes* serotype 4b in 2025 was linked to a specific outbreak.

As of January 2025, quarterly quotas have been implemented for the number of isolates detected from testing for rectal colonisation (screening) that can be sent to GRLS for whole genome sequencing. These quotas only apply to Model 4 hospitals. The reduction in number of isolates from rectal colonisation is an artefact of this change in laboratory policy and should not be understood to suggest improved control of transmission. The number of CPE isolates from diagnostic samples should not be impacted by this change and is therefore a more appropriate as a gauge to compare 2025 with previous years. The number of isolates from diagnostic sites increased by 32% from 189 in 2024 to 249 in 2025. There were 19 invasive isolates in 2025 compared with 14 in 2024. The data reflect an progressive year on year loss of control of dissemination of CPE.

There is a notable increase in diagnostic isolates carrying blaNDM-1 and blaNDM-5 in 2025 compared to 2024. Also of note the change in laboratory policy has resulted in lower numbers of isolates with most types of carbapenemase but the total number of isolates carrying blaNDM has increased even in the context of that change.

As per table 14 and figure 14 the commonly used antigen detection and nucleic acid amplification tests are expected to detect most carbapenemases circulating. In the first 4 months of 2026 we have detected an outbreak of *E. cloacae* carrying blaIMI in one hospital. Laboratories using molecular testing for the common 5 CPE genes as their primary test for colonisation are not likely to detect IMI carbapenemase.

SECTION 1 *Salmonella* spp.

Table 1 and Figure 1. Top 10 serotypes of Non-Typhoid *Salmonella enterica* submitted in 2025 and 2024 in descending order of the number of isolates received.

2025			2024		
Ranking	Serotype	Number of isolates	Ranking	Serotype	Number of isolates
1	Enteritidis	76	1	Enteritidis	73
2	Typhimurium	70	2	Typhimurium	50
3	4,[5],12:i:- (note)	27	3	4,[5],12:i:-	40
4	Infantis	14	4	Newport	14
	Newport		5	Java	12
5	Saintpaul	10	6	Infantis	9
6	Mikawasima	9	7	Bareilly	8
	Strathcona			Panama	
	Virchow		8	Adjame	7
7	Stanley	8		Chester	
8	Branderup	7		Hessarek	
	Java			Mikawasima	
9	Panama	6		Stanley	
	Agona		9	London	6
	Bovismorbificans		10	Bovismorbificans	5
	Chester			Coeln	
10	Bredeney	5		Muenster	
	Bareilly			Napoli	
	Others	101		Others	137
	Total	395		Total	412

Note. 4,[5],12:i:- is often referred to as monophasic *Salmonella* Typhimurium

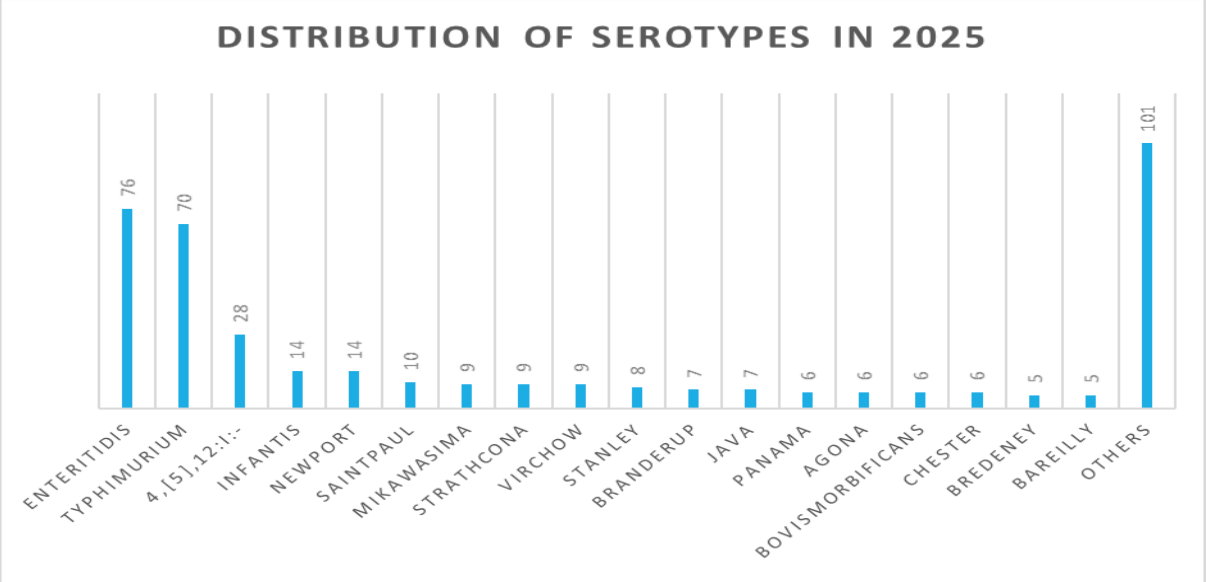

Fig.1 *Note: vertical axis shows number of non-duplicate isolates.*

Table 2 and Figure 2a and 2b. *Salmonella* Typhi and Paratyphi submitted in 2025. The number of isolates received in each of the previous 5 years 2020 to 2024 is also provided.

Serotype	Number of isolates					
	2025	**2024**	**2023**	**2022**	**2021**	**2020**
S. Typhi	17	29	20	30	7	2
S. Paratyphi A	18	6	9	6	0	1
S. Paratyphi B	1	4	3	0	0	1
S. Paratyphi C	0	0	0	0	0	0
Others	0	0	0	0	0	0
Total	36	39	32	36	7	4

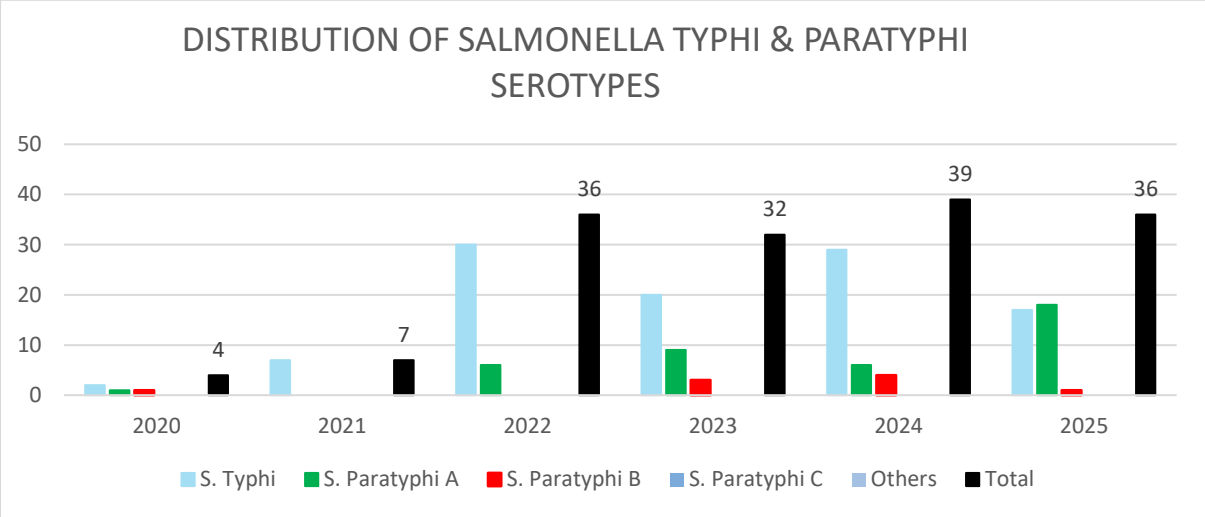

Fig.2.a *Note: vertical axis shows number of non-duplicate isolates.*

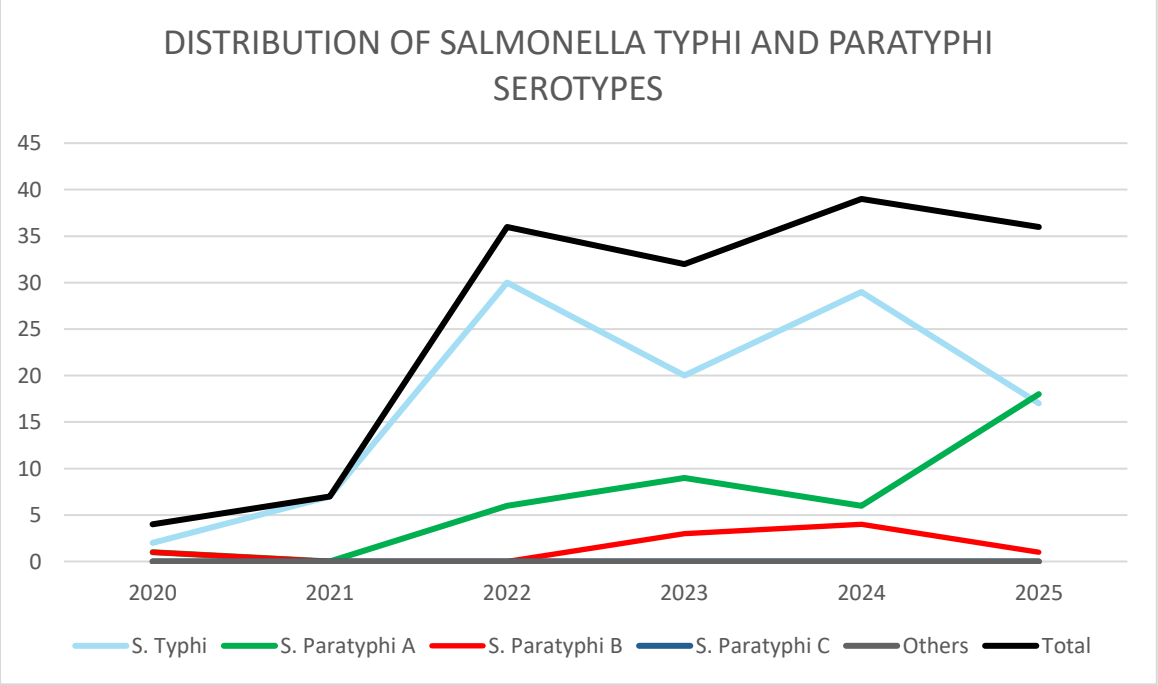

Fig.2.b *Note: vertical axis shows number of non-duplicate isolates.*

Table 3. Predicted antimicrobial resistance (based on sequence) in key *Salmonella enterica* serotypes (Typhoid and non-Typhoid) in 2025. Resistance is predicted based on genetic markers of resistance.

Serotype	% Resistance				
	Amoxicillin	**Azithromycin**	**Ceftriaxone**	**Ciprofloxacin**	**Meropenem**
***S.* Enteritidis**	6/77	0/77	0/77	41/77	0/77
	7.8%	0%	0%	53.2%	0%
***S.* Typhimurium**	13/70	1/70	0/70	5/70	0/70
	18.6%	1.4%	0%	7.1%	0%
***S.* Typhi**	0/17	0/17	0/17	15/17	0/17
	0%	0%	0%	88.2%	0%
All *Salmonella*	70/431	11/431	5/431	137/431	0/431
	16.2%	2.6%	1.2%	31.8%	0%

Note that there is a change in antimicrobial resistance determinants in *S.* Typhi in 2025 compared to 2024. In 2024 72.4% of isolates had a determinant of resistance to amoxicillin and 20.7% has a determinant of resistance to ceftriaxone.

Clusters of similar isolates

In 2025 the Reference Laboratory identified 35 new clusters of *Salmonella enterica* isolates with a range of 2 to 8 isolates per cluster. When an isolate is part of an identified cluster this is indicated on the report returned to the sender of that isolate. Clusters are designated by an alpha-numeric string in which the first one or two characters are letters related to the species, the first two numerals indicate the year and the final three numerals indicate the order of identification of clusters in that years. For example S25-003 is the third cluster of *Salmonella enterica* identified in 2025.

Criteria for cluster designation are presented on pages 36 and 37.

SECTION 2 *Shigella* spp.

Table 4 and Figures 4a and 4b. *Shigella* species submitted in 2025 in alphabetical order. For each species the number of isolates received in each of the previous 5 years 2020 to 2024 is also provided.

Serotype	Number of isolates					
	2025	**2024**	**2023**	**2022**	**2021**	**2020**
S. boydii	4	1	1	2	0	1
S. dysenteriae	1	1	2	1	1	0
S. flexneri	118	77	65	50	24	37
S. sonnei	45	50	79	28	22	10
***S. flexneri* 6**	0	1	0	2	1	0
Other	0	0	0	0	0	0
Total	168	130	147	83	48	48

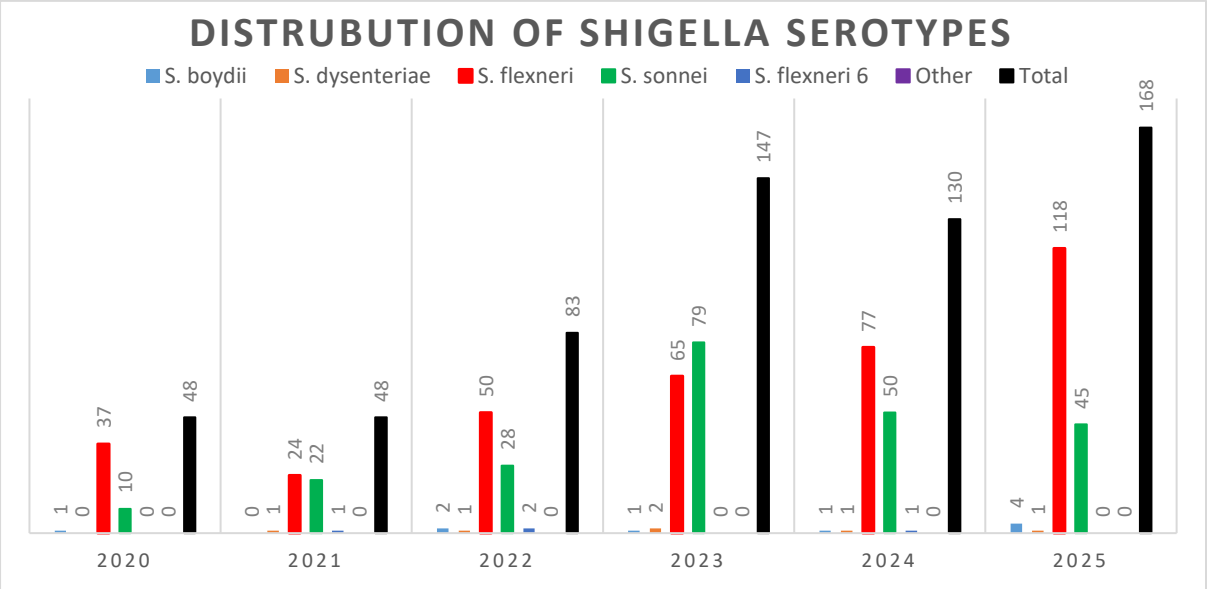

Fig.4a

Note: vertical axis shows number of non-duplicate isolates.

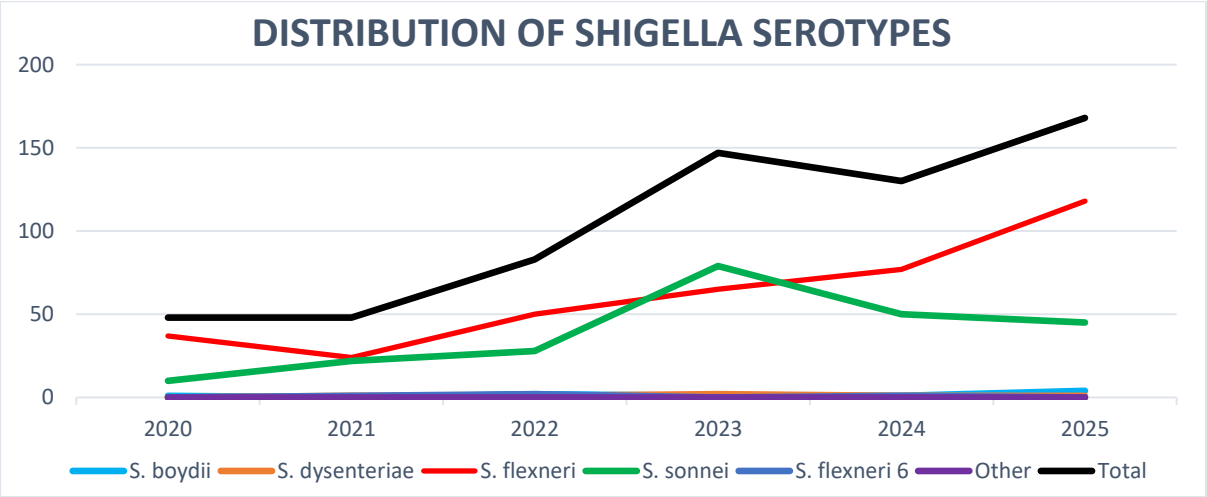

Fig.4b

Note: vertical axis shows number of non-duplicate isolates.

Table 5. Predicted antimicrobial resistance (based on sequence) in *Shigella* spp. Resistance is predicted based on genetic markers of resistance.

Serotype	% Resistance (or number when total isolates is less than 10)				
	Amoxicillin	**Azithromycin**	**Ceftriaxone**	**Ciprofloxacin**	**Meropenem***
S.boydii	1/4	0/4	0/4	2/4	0/4
	25%	0%	0%	50%	0%
S.dysenteriae	1/1	0/1	0/1	1/1	0/1
	100%	0%	0%	100%	0%
S.flexneri	116/118	72/118	17/118	69/18	1/118
	98%	61%	14.4%	58%	<1%
S.sonnei	35/45	22/45	30/45	35/45	0/45
	78%	49%	67%	78%	0%
All Shigella	155/168	94/168	140/168	107/168	1/168
	92%	56%	83%	64%	<1%

* 1 *S.flexneri* was received to the laboratory that harboured blaOXA-181 which was susceptible to meropenem on phenotypic testing.

Clusters of similar isolates*

In 2025 the Reference Laboratory identified 7 new *Shigella* clusters. There are many ongoing clusters of shigella at present. Some ongoing clusters were identified as far back as 2016. When an isolate is part of an identified cluster this is indicated on the report returned on the isolate. Clusters are designated by an alpha-numeric string in which the first one or two characters are letters related to the species, the first two numerals indicate the year and the final three numerals indicate the order of identification of clusters in that year. Thus for example SH25-001 is the first cluster of *Shigella* identified in 2025.

Criteria for cluster designation are presented on pages 36 and 37.

SECTION 3 *Listeria monocytogenes*

Table 6. and Figure 6 *L. monocytogenes* predicted serotypes submitted in 2025. For each serotype the number of isolates receive in each of the previous 5 years 2020 to 2024 is also provided.

Serotype	Number of isolates					
	2025	2024	2023	2022	2021	2020
Serotype 4b	9	5	5	6	5	2
Serotype 2a	0	0	0	0	0	0
Serotype 1/2a	10	9	5	2	3	2
Serotype 1/2b	0	4	1	1	0	1
Serotype 1/2c	0	3	0	0	0	0
Total	19	21	11	9	8	5

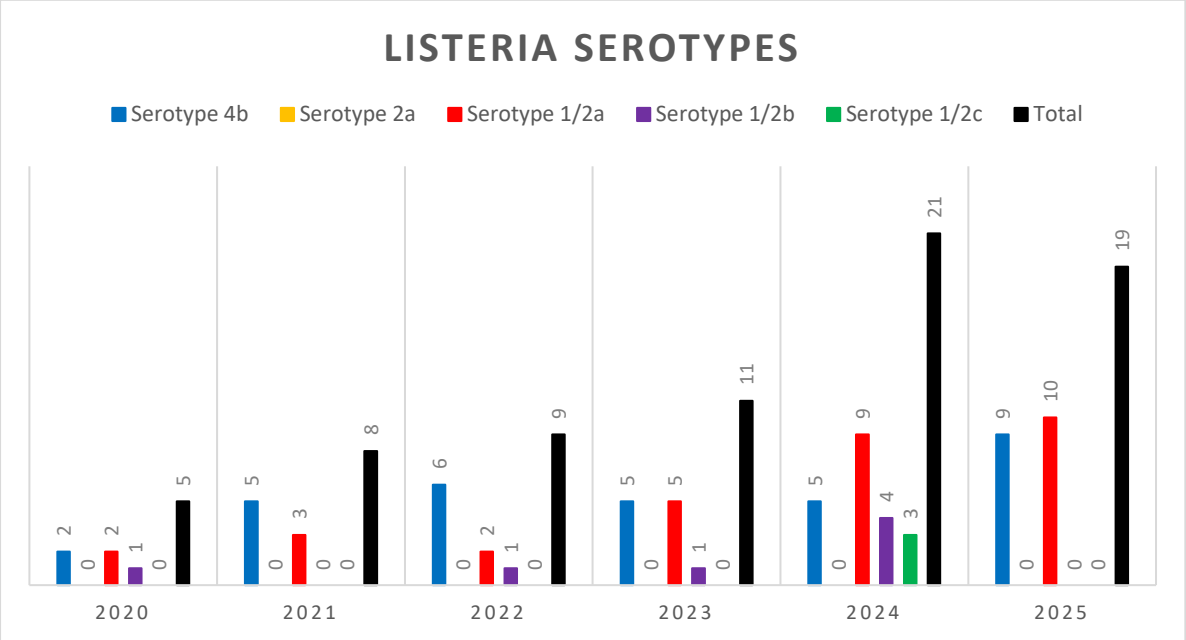

Fig6.

Note: vertical axis shows number of non-duplicate isolates.

Clusters of similar isolates

In 2025 the Reference Laboratory did not identify any new clusters of *Listeria monocytogenes*. However, there were five isolates added to an existing 2024 cluster. In total, there were nine isolates part of this cluster. When an isolate is part of an identified cluster this is indicated on the isolate report. Clusters are designated by an alpha-numeric string in which the first one to two characters are letters related to the species, the first two numerals indicate the year and the final three numerals indicate the order of identification of clusters in that years. L25-001 is the first cluster of *Listeria monocytogenes* species identified in 2025.

Criteria for cluster designation are presented on pages 36 and 37.

Section 4 Carbapenemase producing organisms (CPO) including Carbapenemase producing Enterobacterales (CPE)

As of January 2025, quarterly quotas have been implemented for the number of isolates detected from testing for rectal colonisation (screening) that can be sent to GRLS for whole genome sequencing. These quotas only apply to Model 4 hospitals. This has lowered the total number of cases identified from the rectal colonisation in this annual report. The reduction is an artefact of a change in laboratory policy and should not be understood to suggest improved control of transmission.

The number of cases from diagnostic samples should not be impacted by this change and is therefore a more appropriate as a gauge to compare 2025 with previous years.

Also to note that there are exceptions to the quarterly quotas during a CPE hospital outbreak.

New CPE's are still being detected and reported to the HSE Business Information Unit (BIU) and reports generated monthly by AMRIC. Reports on these are available from HSPC website at:

https://www.hpsc.ie/a-z/microbiologyantimicrobialresistance/carbapenemresistantenterobacteriaceaecre/surveillanceofcpeinireland/cpemonthlysurveillancereports/

Table 7. Number of each type of carbapenemase enzyme detected, broken down by specimen type in 2024 & 2025. This includes Enterobacterales, *Pseudomonas species* and *Acinetobacter species*.

Carbapenemase Enzyme in Enterobacterales	Number of isolates					
	Diagnostic (including invasive) 2025	Diagnostic (including invasive) 2024	Diagnostic Invasive 2025	Diagnostic Invasive 2024	Rectal/ faeces Screening 2025	Rectal/ faeces Screening 2024
IMI	0	0	0	0	4	3
IMP	4	0	0	0	19	27
KPC	12	19	0	2	117	248
NDM	53	27	2	0	198	168
OXA-48	117	101	8	9	586	1077
OXA-181	11	12	1	1	62	83
OXA-244	46	27	6	2	202	238
Other OXA-48 Like	11	2	1	0	32	31
VIM	4	5	1	0	43	76
Others	0	0	0	0	1	1
Total	249	189	19	14	1,229	1,903
Isolates With >1 CPE enzyme found	9	4	0	0	35	49

Table 8. Breakdown of Genus/Species, harbouring a carbapenemase gene, received to the reference laboratory in 2024 and 2025, from human isolates. This includes Enterobacterales, *Pseudomonas species* and *Acinetobacter species*.

Species	Number of isolates					
	Diagnostic (including invasive) 2025	Diagnostic (including invasive) 2024	Diagnostic Invasive 2025	Diagnostic Invasive 2024	Rectal/ faeces Screening 2025	Rectal/ faeces Screening 2024
***Acinetobacter* spp.**	6	6	0	0	13	11
***Citrobacter* spp.**	10	9	0	0	174	275
***Enterobacter* spp.**	49	29	3	3	195	360
E. coli	92	59	11	5	526	704
K. oxytoca complex	9	15	1	1	87	109
K. pneumoniae complex	75	60	4	3	206	373
***Pseudomonas* spp.**	6	1	1	0	3	8
Others	14	17	0	2	42	81
Total CPE	249	189	19	14	1,229	1,902
Total CPO other than CPE[1]	12	7	1	0	17	19
Total	261	196	20	14	1,246	1,921

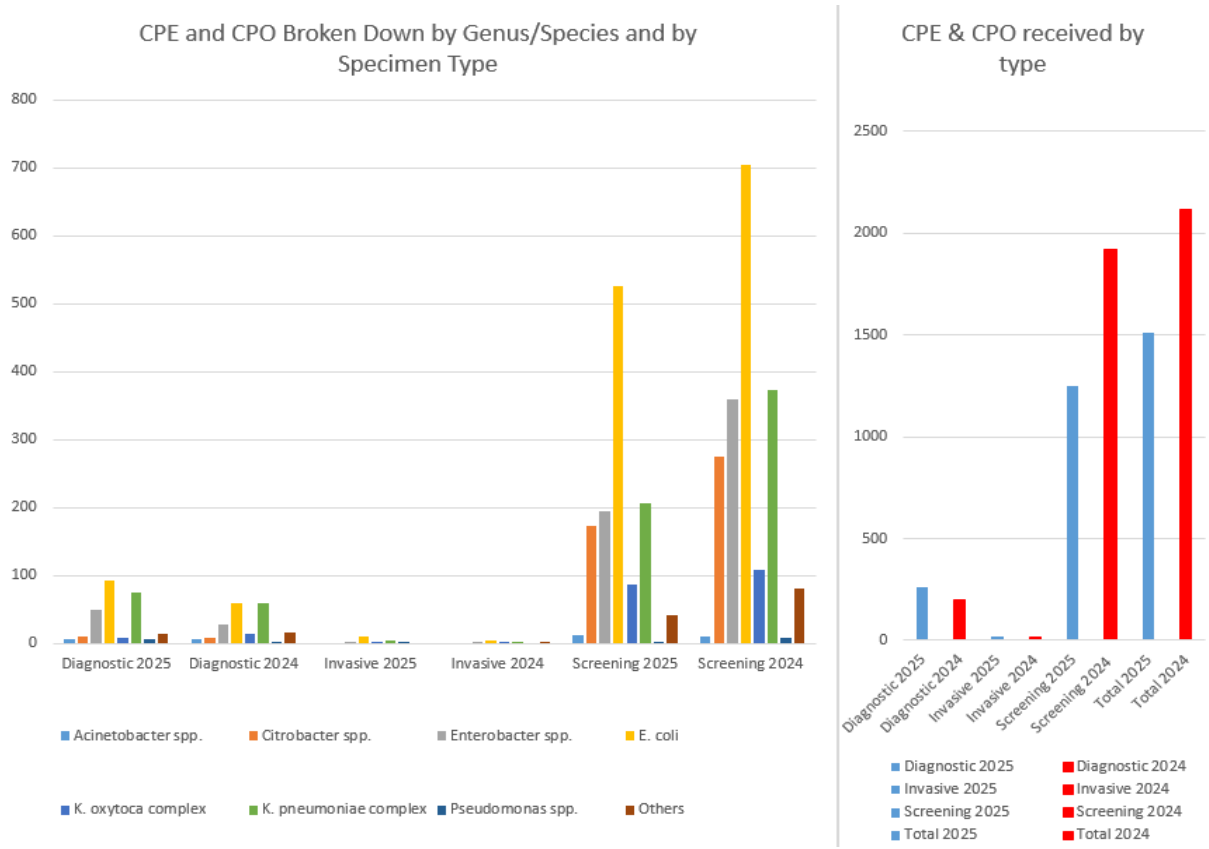

Fig.8

Note: vertical axis shows number of non-duplicate isolates.

Table 9. Number of each type of carbapenemase enzyme detected broken down by variant identified for 2024 & 2025, from human isolates. This includes Enterobacterales, *Pseudomonas species* and *Acinetobacter species*.

D= Diagnostic isolate

R= Rectal/screening isolate

Carbapenemase Gene Variants Detected in Enterobacterales in 2025														
OXA-48 Variants	**OXA-48**		**OXA-181**		**OXA-244**		**OXA-48 like other**							
	D	**R**	**D**	**R**	**D**	**R**	**D**	**R**						
2025	117	586	11	62	46	202	11	32						
2024	101	1077	12	83	27	238	2	31						
IMI Variants	**IMI-2**		**IMI-3**		**IMI-4**		**IMI-6**							
	D	**R**	**D**	**R**	**D**	**R**	**D**	**R**						
2025	0	3	0	1	0	0	0	0						
2024	0	0	0	0	0	1	0	2						
IMP Variants	**IMP-1**		**IMP-4**		**IMP-13**		**IMP-22**		**IMP-like**					
	D	**R**	**D**	**R**	**D**	**R**	**D**	**R**	**D**	**R**				
2025	1	0	4	17	0	1	0	1	0	1				
2024	0	2	0	25	0	1	0	1	0	0				
KPC Variants	**KPC-2**		**KPC-3**											
	D	**R**	**D**	**R**										
2025	9	105	3	12										
2024	10	187	9	61										
NDM Variants	**NDM-1**		**NDM-4**		**NDM-5**		**NDM-6**		**NDM-7**		**NDM-13**		**NDM-14**	
	D	**R**	**D**	**R**	**D**	**R**	**D**	**R**	**D**	**R**	**D**	**R**	**D**	**R**
2025	27	109	1	1	28	94	1	0	0	0	0	0	0	2
2024	13	68	0	1	16	108	0	0	0	2	0	1	0	0
VIM Variants	**VIM-1**		**VIM-2**		**VIM-5**		**VIM-like**							
	D	**R**	**D**	**R**	**D**	**R**	**D**	**R**						
2025	**5**	43	0	1	0	0	0	1						
2024	4	76	0	3	1	0	0	0						
Others	**OXA-23**		**OXA-58**		**GES-11**		**GES-24**		**FRI-8**					
	D	**R**	**D**	**R**	**D**	**R**	**D**	**R**	**D**	**R**				
2025	6	6	0	2	0	1	0	1	0	0				
2024	5	2	0	1	0	0	0	0	0	1				

Table 10. and Figure 10. Species/Genus of CPO submitted in 2025 in alphabetical order. For each species the number of isolates received in each of the previous 5 years 2020 to 2024 is also provided. **Note reduction in total number of isolates of a species in 2025 compared to 2024 is generally an artefact of a change in laboratory policy.**

Species	Number of isolates					
	2025	2024	2023	2022	2021	2020
Acinetobacter spp.	19	17	18	8	8	9
Citrobacter spp.	184	284	180	168	131	137
Enterobacter spp.	244	390	323	252	215	227
E. coli	622	763	516	367	297	250
K. oxytoca complex	96	124	105	87	78	97
K. pneumoniae complex	282	433	204	228	162	158
Pseudomonas spp.	9	9	12	9	6	6
Others	56	99	95	65	50	46
Total CPE	1,483	2,093	1,423	1,167	933	915
Total CPO other than CPE[1]	29	26	30	17	14	15
Total	**1,512***	**2,119**	**1,453**	**1,184**	**947**	**930**

*Footnote 1. Total other CPO refers to CPO other than CPE Note:*Quotas introduced in 2025*

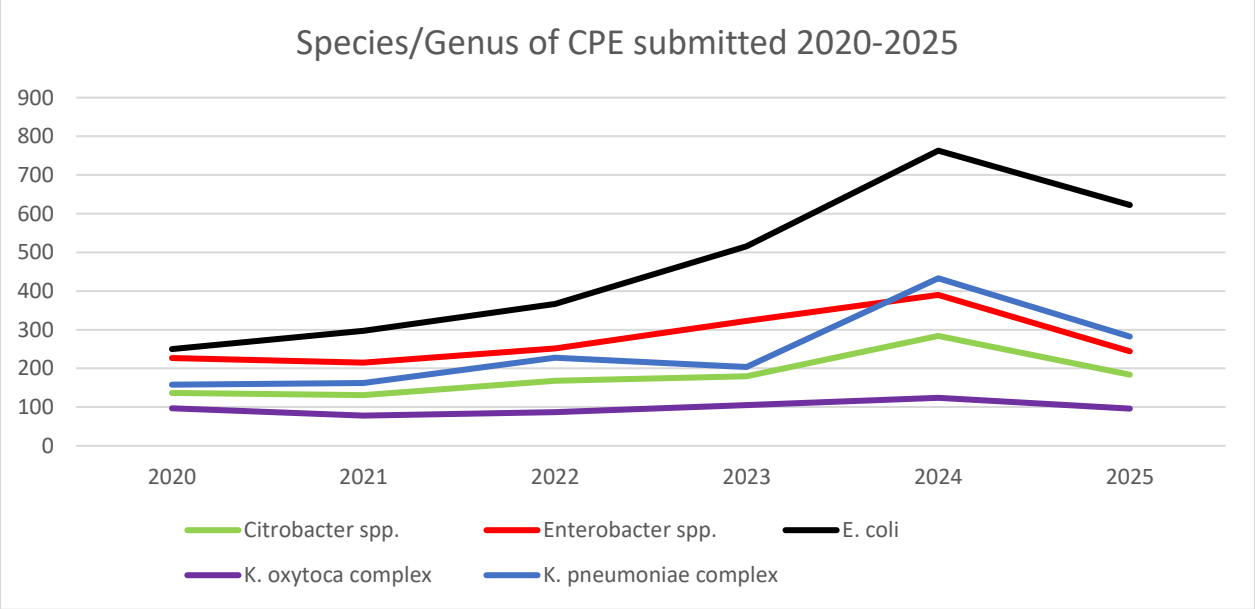

Fig.10

Note: vertical axis shows number of non-duplicate isolates.

Table 11. and Figure 11. Type of carbapenemase detected in each major group of organisms in 2025 (not inclusive of environmental isolates).

Species	Number of each carbapenemase type								
	KPC	IMP	OXA-48 family	NDM	VIM	OXA-23	OXA-58	GES	IMI
Acinetobacter spp.	0	0	0	6	0	12	2	1	0
Citrobacter spp.	45	3	127	12	4	0	0	1	0
Enterobacter spp.	11	16	147	44	26	0	0	0	4
Escherichia spp.	18	1	509	100	2	0	0	0	0
K.oxytoca complex	15	1	77	2	11	0	0	0	0
K.pneumoniae complex	32	2	182	79	1	0	0	0	0
Pseudomonas spp.	0	2	0	5	3	0	0	0	0
Others	8	0	29	15	3	0	0	0	0
Total	**129**	**25**	**1,071**	**263**	**50**	**12**	**2**	**2**	**4**

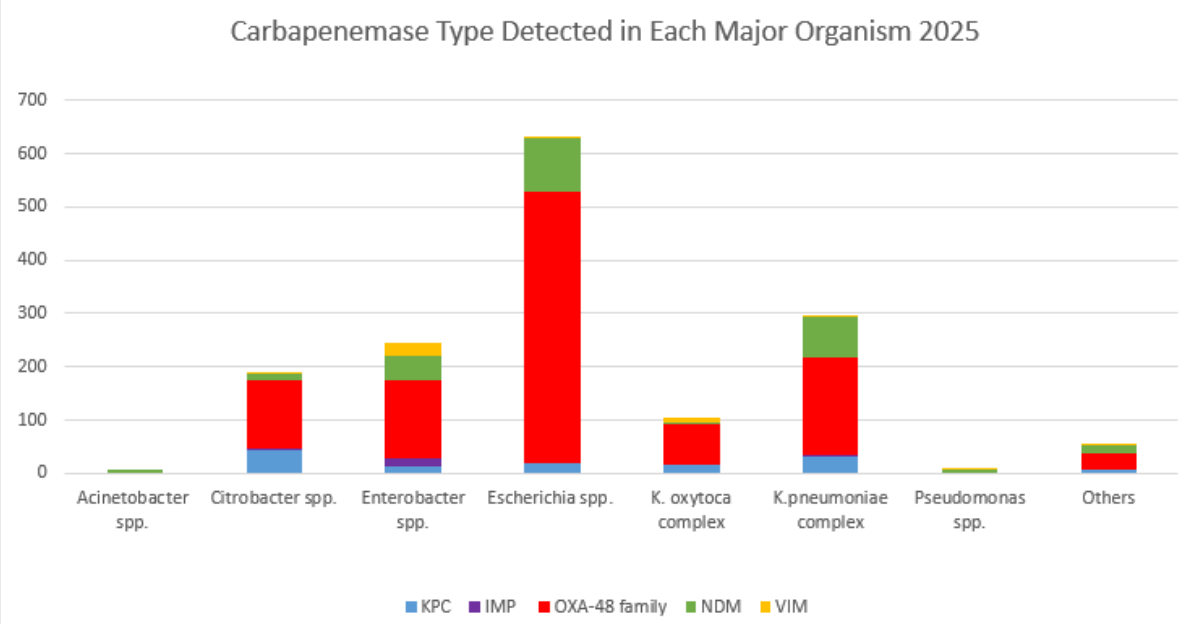

Fig.11

Note: vertical axis shows number of non-duplicate isolates.

Table 12. Number of each type of carbapenemase enzyme detected in human samples.

Carbapenemase Enzyme	Number of isolates					
	2025	2024	2023	2022	2021	2020
IMI	4	3	2	2	1	5
IMP	23	27	20	6	13	11
KPC	129	268	119	127	112	142
NDM	251	195	160	97	54	42
OXA-48	704	1179	867	778	644	615
OXA-181	75	95	67	42	40	47
OXA-244	250	265	148	62	28	18
Other OXA-48 Like	43	33	8	3	7	6
VIM	47	81	55	72	45	38
Others	1	1	0	1	1	1
Isolates With >1 CPE enzyme found	44	53	26	23	12	10

Figures 12a and 12b. Number of each type of carbapenemase in Enterobacterales (in alphabetical order) in 2025 with the corresponding number for each year from 2020 to 2024 for comparison

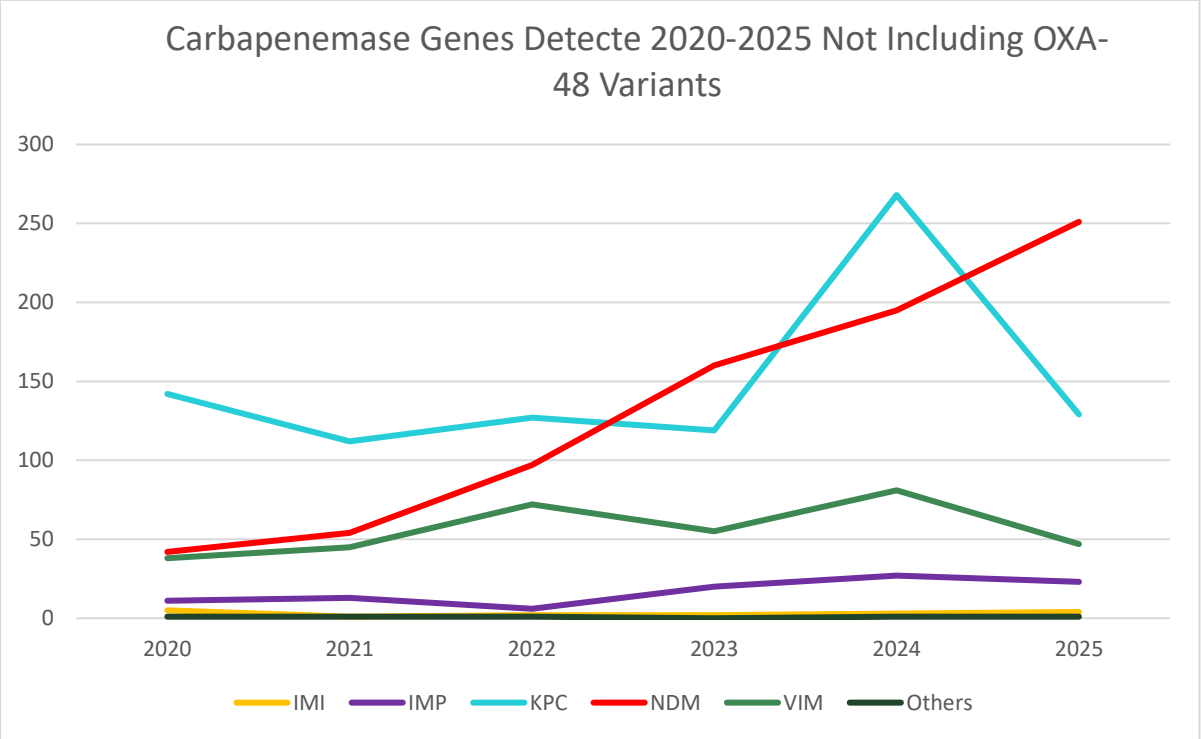

Fig 12a. Number of each type of carbapenemase enzyme detected.
Note: vertical axis shows number of non-duplicate isolates.

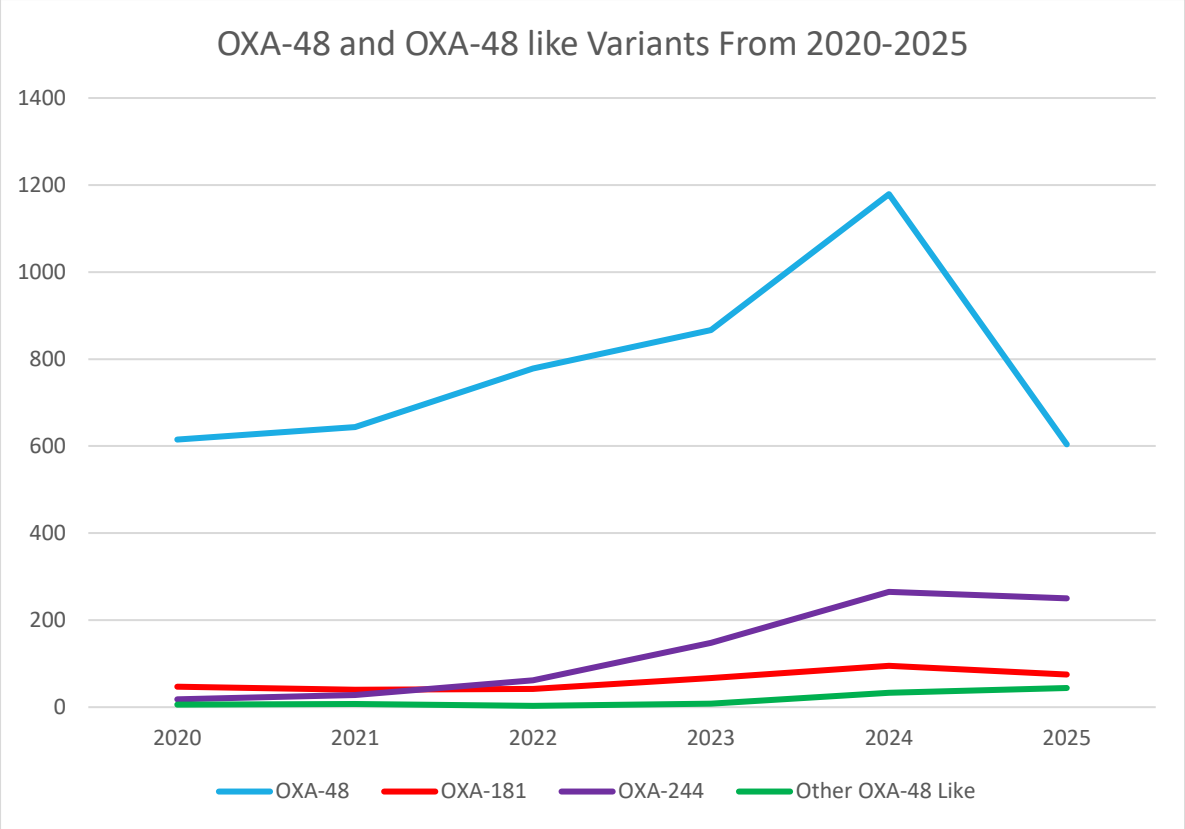

Fig 12b. Number of each type of carbapenemase enzyme detected
Note: vertical axis shows number of non-duplicate isolates.

Table 13. and Figure 13. Number of each type of carbapenemase enzyme detected from Enterobacterales, broken down by specimen type.

Carbapenemase Enzyme in Enterobacterales	Number of isolates				
	2025	Rectal/faeces Screening	Diagnostic (including invasive)	Diagnostic Invasive	Unknown
IMI	4	4	0	0	0
IMP	23	19	4	0	0
KPC	129	117	12	0	0
NDM	251	198	53	2	1
OXA-48	704	586	117	8	1
OXA-181	75	62	11	1	2
OXA-244	250	202	46	6	2
Other OXA-48 Like	43	32	11	1	0
VIM	47	43	4	1	0
Others	1	1	0	0	0
Total	1,483	1,229	249	19	5
Isolates With >1 CPE enzyme found	44	35	9	0	0

Diagnostic includes isolates from specimens such as wounds, urine, sputum and blood. The laboratory does not receive information that permits differentiation between infection and colonisation in most cases. Diagnostic invasive are isolates from normally sterile body sites, in almost all cases blood.

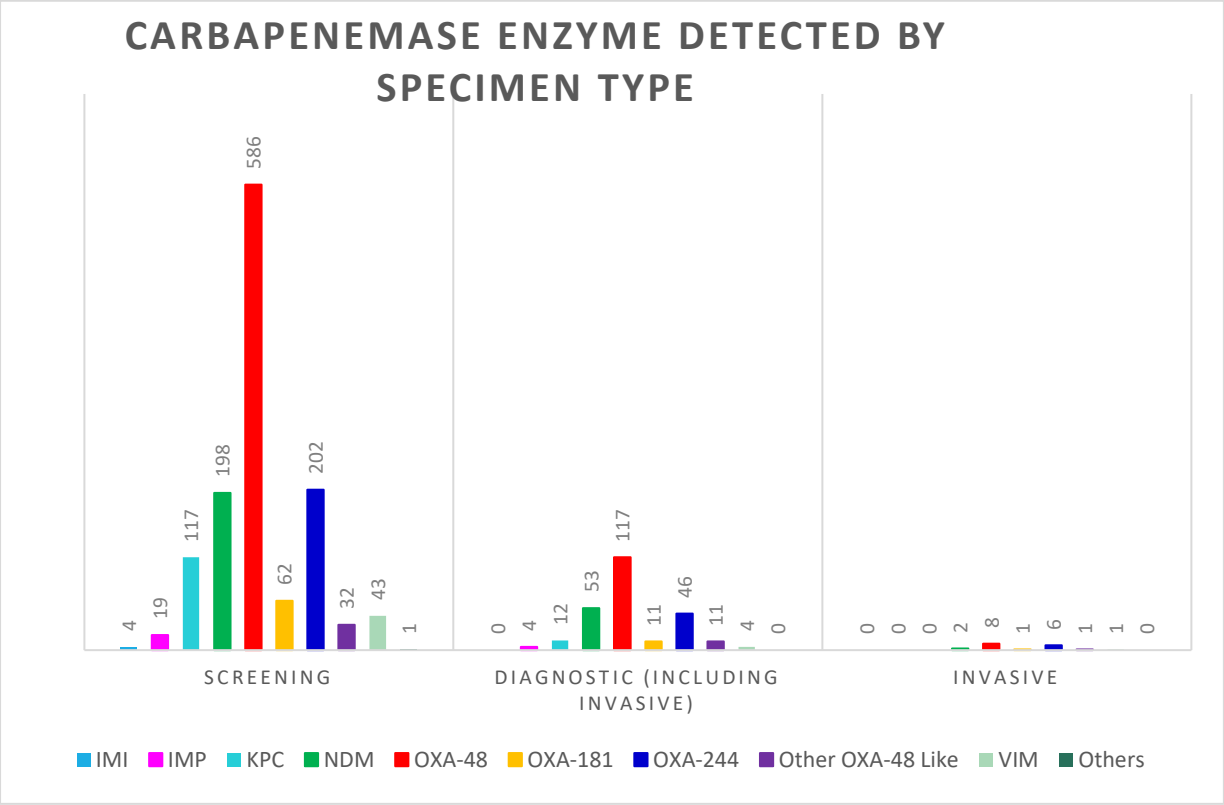

Fig.13 *Note: vertical axis shows number of non-duplicate isolates.*

Table 14. and Figure 14. Number of each type of carbapenemase enzyme detected in Enterobacterales broken down by variant identified.

Carbapenemase Gene Variants Detected in Enterobacterales in 2025						
OXA-48 Variants	**OXA-48**	**OXA-181**	**OXA-244**	**OXA-232**	**OXA-484**	**OXA-48 like**
Total	704*	75*	250*	3*	8	32*
IMI Variants	**IMI-2**	**IMI-3**				
Total	3	1				
IMP Variants	**IMP-4**	**IMP-13**	**IMP-22**			
Total	21*	1*	1			
KPC Variants	**KPC-2**	**KPC-3**				
Total	114	15				
NDM Variants	**NDM-1**	**NDM-4**	**NDM-5**	**NDM-6**	**NDM-14**	
Total	125*	2	121*	1	2	
VIM Variants	**VIM-1**	**VIM-like**				
Total	46*	1				

* indicates there are dual/triple carbapenemase producers in this data.

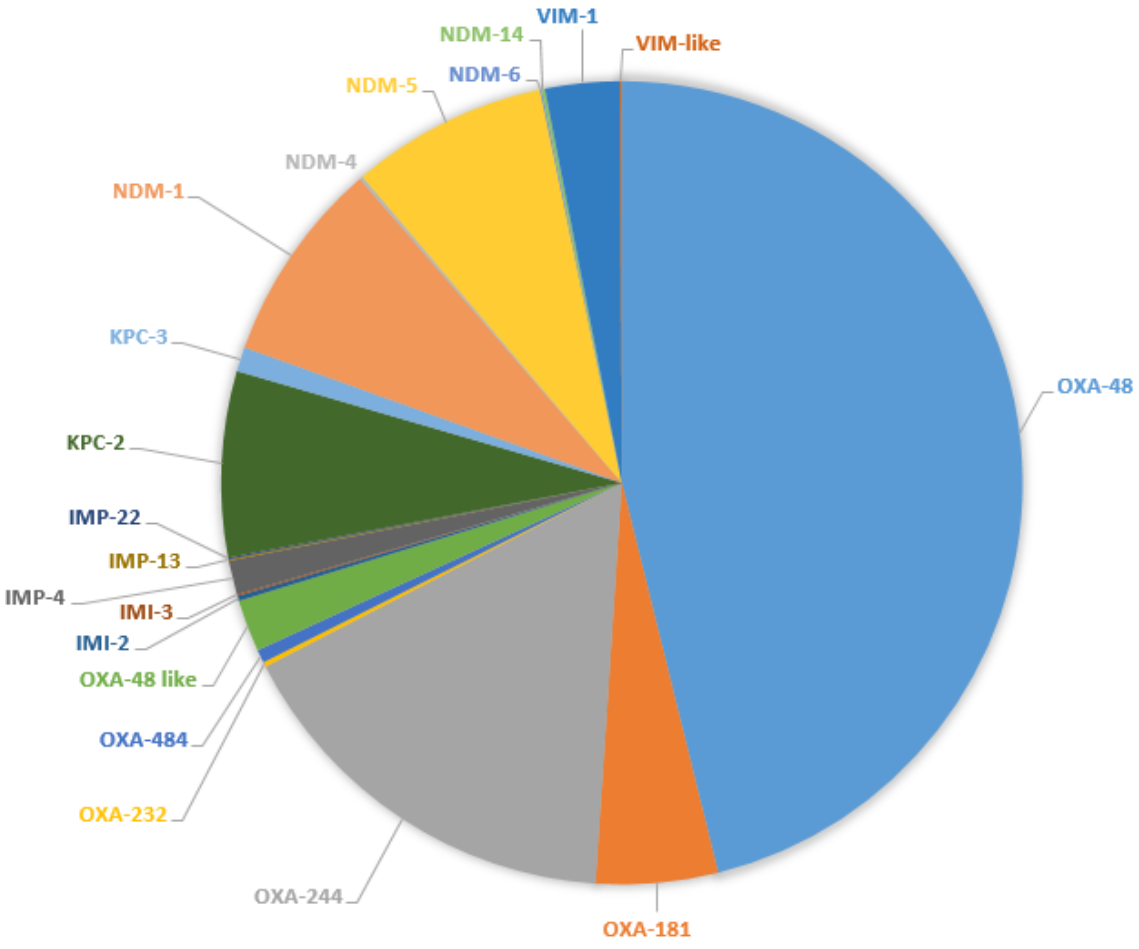

Fig14.

Table 15. and Figure 15. Carbapenemase Genes Detected in *Acinetobacter* spp. and *Pseudomonas* spp. in 2025 and previous years.

Carbapenemase Enzyme	Number of isolates					
	2025	2024	2023	2022	2021	2020
IMI	0	0	0	0	0	0
IMP	2*	2	3	1	3	0
KPC	0	0	0	0	0	0
NDM	12*	14*	8	3	3	3
OXA-48 Family	0	0	0	0	0	0
OXA-23	12*	7	15	5	3	7
OXA-24	0	0	1	0	0	0
OXA-58	2*	1*	0	0	1	0
OXA-72	0	0	0	0	1	0
VIM	3*	3	3	6	4	5
Others	1*	0	0	3	0	0
Isolates With >1 Carbapenemase enzyme found	3	1	0	1	1	0

Note: a trend towards increased numbers of NDM *Pseudomonas aeruginosa*.

* indicates there are dual carbapenemase producers in this data.

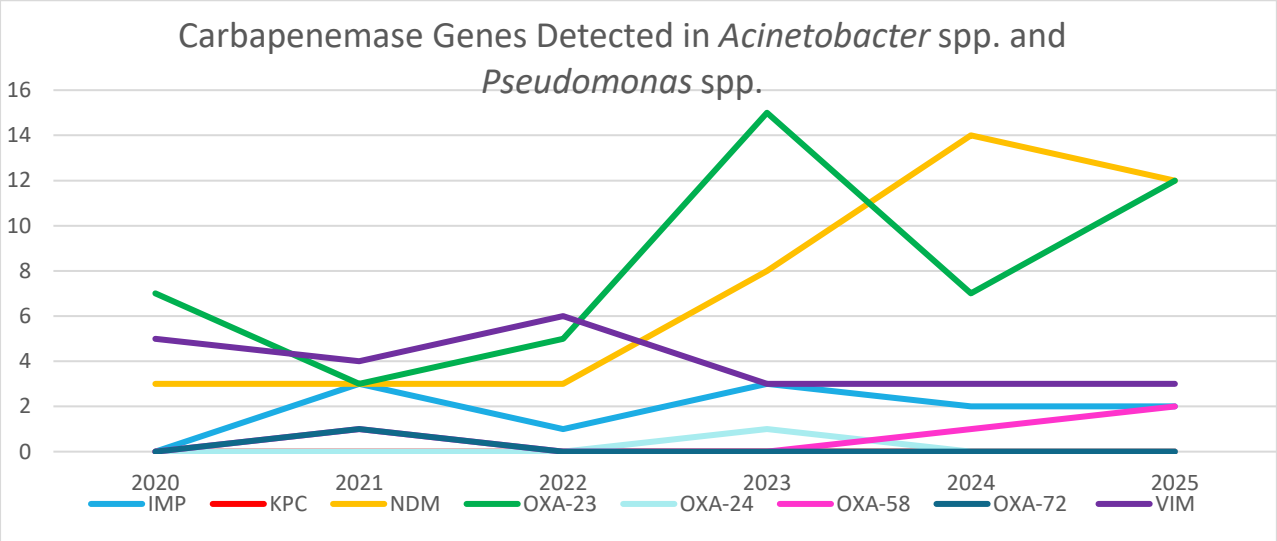

Fig.15

Note: vertical axis shows number of non-duplicate isolates.

Table 16. Carbapenemase Gene Variants Detected in *Acinetobacter* spp. and *Pseudomonas* spp. in 2025.

Carbapenemase Gene Variants Detected in *Acinetobacter* spp. and *Pseudomonas* spp. in 2025		
IMP Variant	IMP-1	IMP-like
Total	1	1*
NDM Variant	NDM-1	NDM-5
Total	11*	1
VIM Variant	VIM-1	VIM-2
Total	2*	1

* indicates there are dual carbapenemase producers in this data.

Table 17. Top sequence types detected in *K. pneumoniae* complex (*K. pneumoniae, K.variicola, K.quasivariicola* and *K.quasipneumoniae)* in 2025 and 2024 (only ST's with >4 isolates included. This table also includes non-CPE isolates as they are included in the hvKp figures). Reduction in numbers of isolates in 2025 compared with 2024 is likely to be an artefact of change in laboratory policy.

2025			2024		
Ranking	**ST**	**Number**	**Ranking**	**ST**	**Number**
1	ST 307	27	**1**	ST 478	47
2	ST 22	24	**2**	ST 307	22
3	ST 147	20	**3**	ST 23	20
4	ST 23	13	**4**	ST 405	15
5	ST 39	12	**5**	ST 13	14
6	ST 111	9	**6**	ST 104	13
				ST 147	
7	ST 13	8	**7**	ST 268	12
	ST 54			ST 35	
8	ST 17	7	**8**	ST 37	10
9	ST 27	6	**9**	ST 490	9
10	ST 299	5	**10**	ST 14	8
	ST 478				
	Others	149		Others	244
	Total	293		Total	439

Table 18. Number of *K. pneumoniae* identified as hypervirulent (hvKp) and non-hvKp (this table includes both CPE's and non CPE *K. pneumoniae* isolate, not including environmental isolates) Reduction in numbers of isolates in 2025 compared with 2024 is likely to be an artefact of change in laboratory policy.

	Number of isolates					
	2025	**2024**	**2023**	**2022**	**2021**	**2020**
hvKp	32	39	20	38	14	22
non-hvKp	234	366	184	199	153	140
Total	266	405	204	237	167	162

Classification as hypervirulent is based on the widely used Kleborate score although the pattern of markers *iucA*, *iroB*, *rmpA*, *rmpA2* and *peg-344* may correlate more closely with the virulence phenotype in the mouse model. Hypervirulence is strongly though not exclusively associated with ST23.

Table 19. Top 10 sequence types detected in *E.coli* in 2025 and 2024, from Humans. Reduction in numbers of isolates in 2025 compared with 2024 is likely to be an artefact of change in laboratory policy.

2025			2024		
Ranking	**ST**	**Number of Isolates**	**Ranking**	**ST**	**Number of Isolates**
1	ST 131	85	**1**	ST 648	70
2	ST 69	60	**2**	ST 10	68
3	ST 38	52	**3**	ST 69	61
4	ST 10	46	**4**	ST 131	54
5	ST 648	28	**5**	ST 38	39
6	ST 167	23	**6**	ST 167	26
7	ST 410	22	**7**	ST 410	21
8	ST 361	14	**8**	ST 58	17
9	ST 127 ST 405	11	**9**	ST 12	14
10	ST 1722	10	**10**	ST 405	10
	Others	260		Others	383
	Total	622		Total	763
	blaOXA-244	250 *1 DP		blaOXA-244	265 *1 DP

Table 20. Subtypes of OXA detected in *E. coli.* Reduction in numbers of isolates in 2025 compared with 2024 is likely to be an artefact of change in laboratory policy.

Gene	Number of isolates					
	2025	**2024**	**2023**	**2022**	**2021**	**2020**
blaOXA48	202	312	249	230 *	206 *	178
blaOXA181	27	37	31 *	13 *	20 *	21*
blaOXA244	250*	265*	147 *	61 *	28	18
Others	28 *	25	5	1	2	4
Total	507	639	432	305	256	221

* indicates there are dual/triple carbapenemase producers in this data.

Table 21. Top sequence types detected in *K. oxytoca* complex (*K. oxytoca, K.grimontii, K.pasteurii, K.michaginensis* in 2025 and 2024 (only ST's with ≥4 isolates included). Reduction in numbers of isolates in 2025 compared with 2024 is likely to be an artefact of change in laboratory policy.

2025			2024		
Ranking	**ST**	**Number of Isolates**	**Ranking**	**ST**	**Number of Isolates**
1	ST 223	18	**1**	ST 176	9
2	ST 186	8		ST 50	
3	ST 53	7	**2**	ST 223	8
				ST 53	
			3	ST 232	7
			4	ST 199	4
				ST 258	
				ST 616	
	Others	63		Others	71
	Total	96		Total	124

Table 22. Top 10 sequence types detected in *Enterobacter cloacae* complex in 2025 and 2024. Reduction in numbers of isolates in 2025 compared with 2024 is likely to be an artefact of change in laboratory policy.

2025			2024		
Ranking	**ST**	**Number of Isolates**	**Ranking**	**ST**	**Number of Isolates**
1	ST 78	41	**1**	ST 527	78
2	ST 66	20	**2**	ST 66	36
3	ST 527	17	**3**	ST 78	24
4	ST 134	11	**4**	ST 796	21
5	ST 141	9	**5**	ST 133	17
	ST 88		**6**	ST 90	15
				ST 113	15
6	ST 133 ST 45	8	**7**	ST 45	11
7	ST 97	7	**8**	ST 32	10
8	ST 113 ST 1373	6	**9**	ST 88	9
9	ST 90	5	**10**	ST 97	8
				ST 120	
				ST 1348	
10	ST 93 ST 104 ST 118	4			
	Others	85		Others	130
	Total	244		Total	390

Table 23. Top sequence types detected in *Citrobacter freundii* complex in 2025 and 2024 (only ST's with ≥4 isolates included). Reduction in numbers of isolates in 2025 compared with 2024 is likely to be an artefact of change in laboratory policy.

2025			2024		
Ranking	**ST**	**Number of Isolates**	**Ranking**	**ST**	**Number of Isolates**
1	ST 22	29	**1**	ST 22	48
2	ST 98	13	**2**	ST 420	22
3	ST 116	10	**3**	ST 98	12
4	ST 62	6	**4**	ST 62	11
5	ST 111 ST 396 ST 420	5	**5**	ST 111	10
			6	ST 64	7
				ST 116	
6	ST 169 ST 252	4	**7**	ST 150	5
				ST 95	
			8	ST 114	4
	Other	87		Other	123
	Total	168		Total	254

Table 24. and Figure 24. Species/Genus of CPO from the healthcare environment submitted in 2025 in alphabetical order. For each species the number of isolates received in each of the previous 5 years 2020 to 2024 is also provided. **Reduction in the number of isolates in 2025 is likely to be an artefact of change in laboratory policy.**

Species	Number of isolates					
	2025	**2024**	**2023**	**2022**	**2021**	**2020**
***Acinetobacter* spp.**	7	0	2	0	2	0
***Citrobacter* spp.**	23	35	58	31	24	25
***Enterobacter* spp.**	55	61	45	32	45	36
E. coli	2	2	2	1	0	0
E.hermannii	2	5	6	1	0	3
***K. oxytoca* complex**	8	15	14	6	3	6
***K. pneumonia* complex**	7	11	6	4	3	8
***Pseudomonas* spp.**	0	1	3	0	1	1
Others	5	11	13	6	11	3
Total CPE	102	140	144	81	86	81
Total CPO[1]	7	1	5	0	3	1
Total	**109**	**141**	**149**	**81**	**89**	**82**

[1]*Excluding Enterobacterales*

Footnote. The healthcare environment in this context is overwhelmingly the acute hospital setting. Sampling is conducted by the hospital to assist them in understanding sources of transmission. Hospitals generally use the national recommended method for sampling the environment. The large majority of isolates are from areas from which water is drained such as sinks, showers and toilets facilities. Laboratories submit a selection of the CPO isolated to the reference laboratory for characterisation.

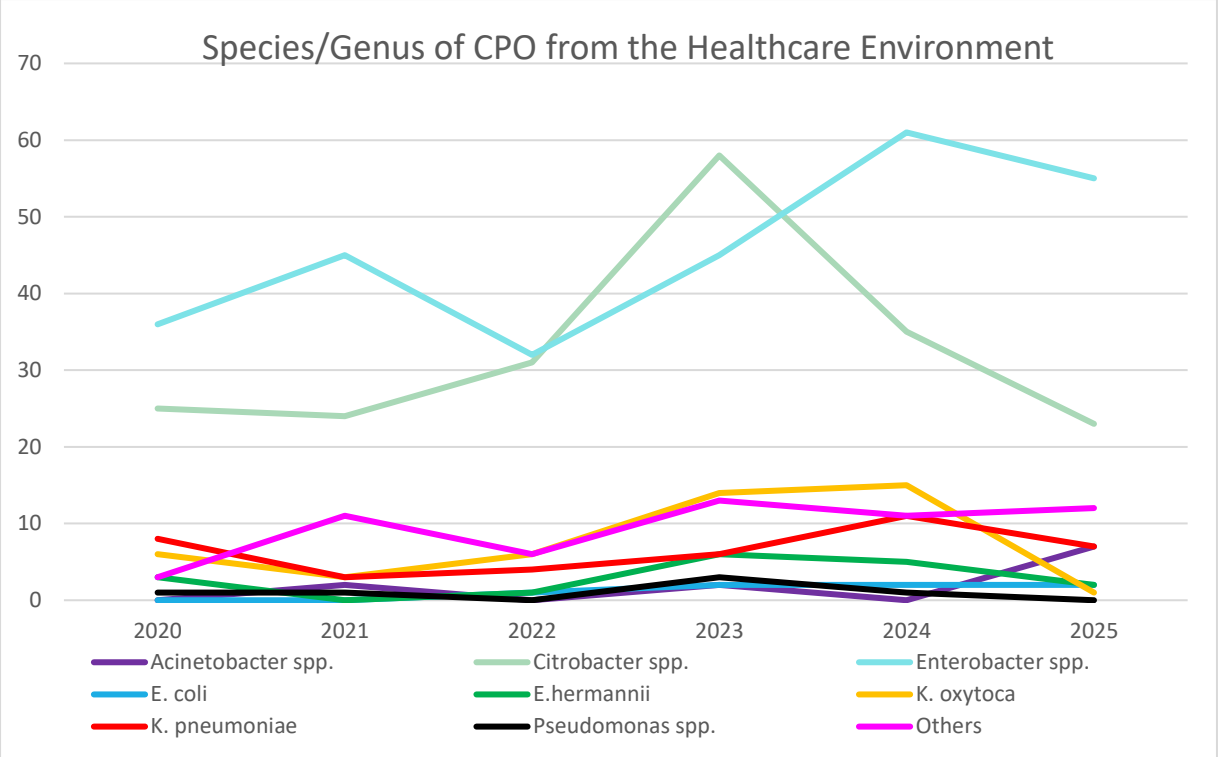

Fig 24.

Table 25. and Fig.25 Species/Genus of CPO with breakdown of CPE Enzyme detected from the healthcare environment submitted in 2025

Species	Number of each carbapenemase type for 2025					
	KPC	IMP	OXA-48 family	NDM	VIM	OXA-23
Acinetobacter spp.	0	0	0	5	0	2
Citrobacter spp.	4*	2*	15*	3	2*	0
Enterobacter spp.	1	3*	30*	16*	9*	0
Escherichia spp.	2	0	1	0	1	0
K. oxytoca complex	3	0	5	0	0	0
K. pneumoniae complex	3	0	2	2	0	0
Pseudomonas spp.	0	0	0	0	0	0
Others	1	0	1	3	0	0
Total	**14**	**5**	**54**	**29**	**12**	**2**

* indicates there are dual carbapenemase producers in this data

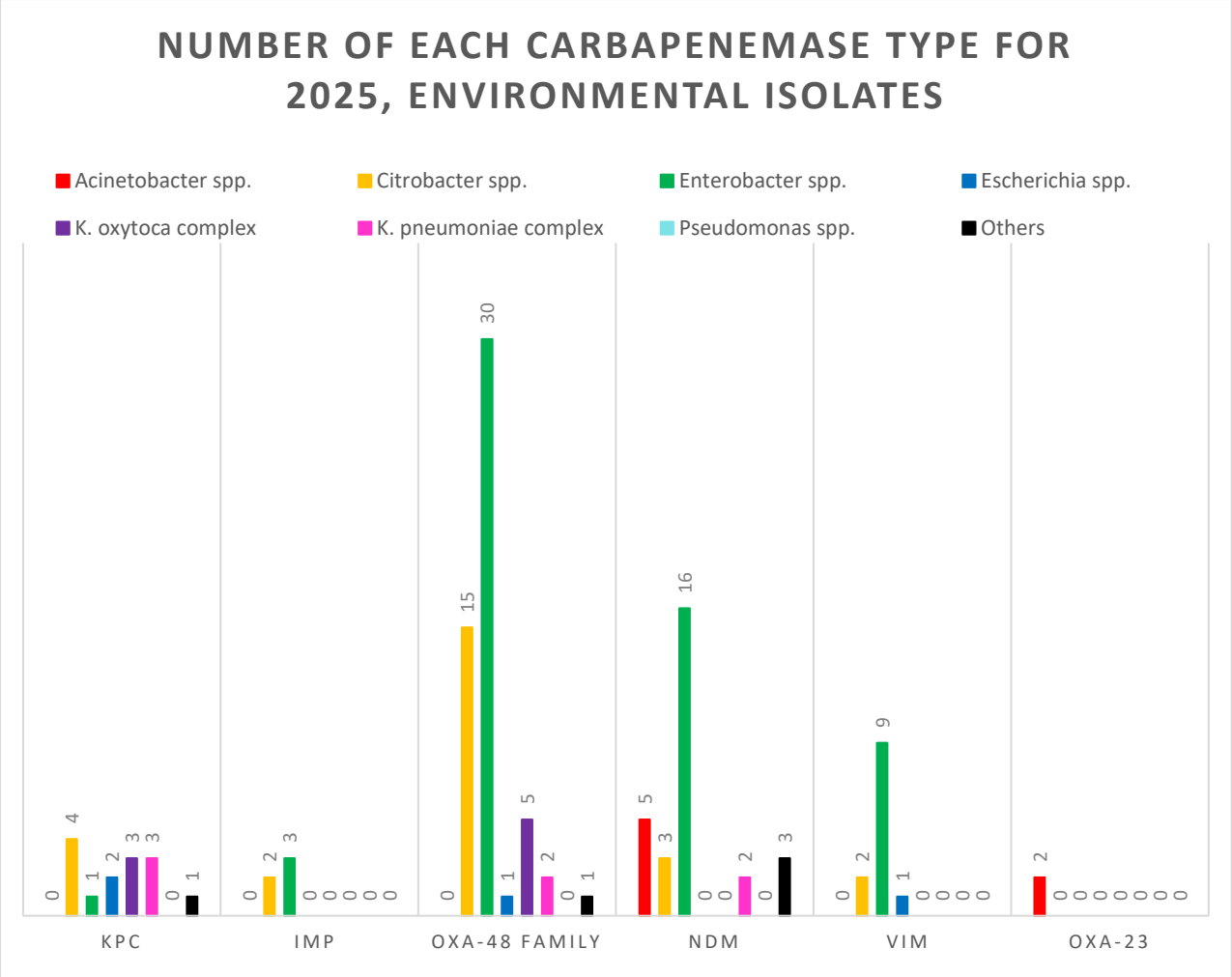

Fig.25

Clusters of similar isolates

Multiple clusters of similar isolates were detected in each year. In a number of cases related isolates (clusters) have been detected over a period of years within a given hospital and in some cases in multiple hospitals. Some clusters include both human and hospital environment isolates, mainly from sinks, showers, drain and other moist areas. A detailed analysis of clusters is beyond the scope of this report. When an isolate is part of an identified cluster this is indicated on the isolate report. Clusters are designated by an alpha-numeric string in which the first two characters are letters related to the species, the first two numerals indicate the year and the final three numerals indicate the order of identification of clusters in that years. EC25-003 is the third cluster of *E. coli* identified in 2025. There are a number of clusters of carbapenemase producing organisms identified some years ago that continue to circulate.

Criteria for cluster designation are presented on pages 36 and 3.

Appendix to Galway Reference Laboratory Annual Report 2025.

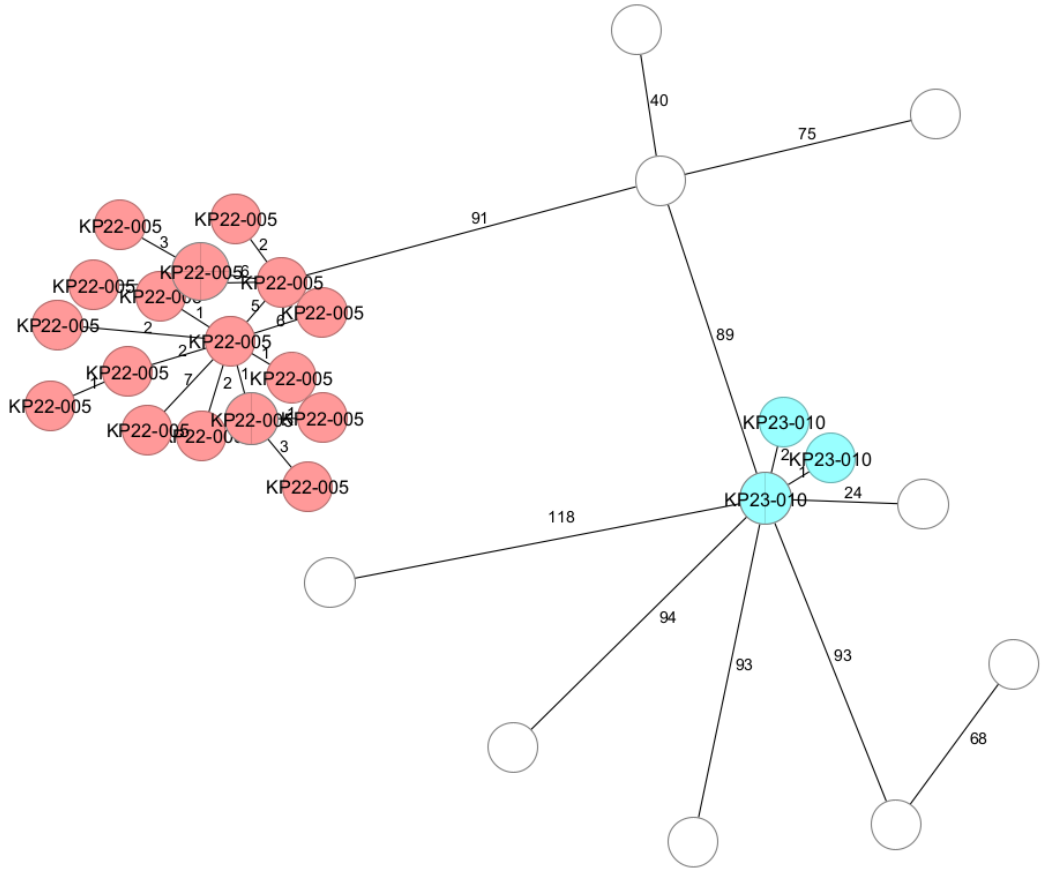

Figure 1. This figure represents all *K. pneumoniae* ST307 isolates received in 2025. The numbers illustrate the number of allelic differences between nodes. A larger partitioned node represents a number of isolates that are indistinguishable at cgMLST level. The number of partitions reflects the number of isolates.

ST23 *K.pneumoniae*

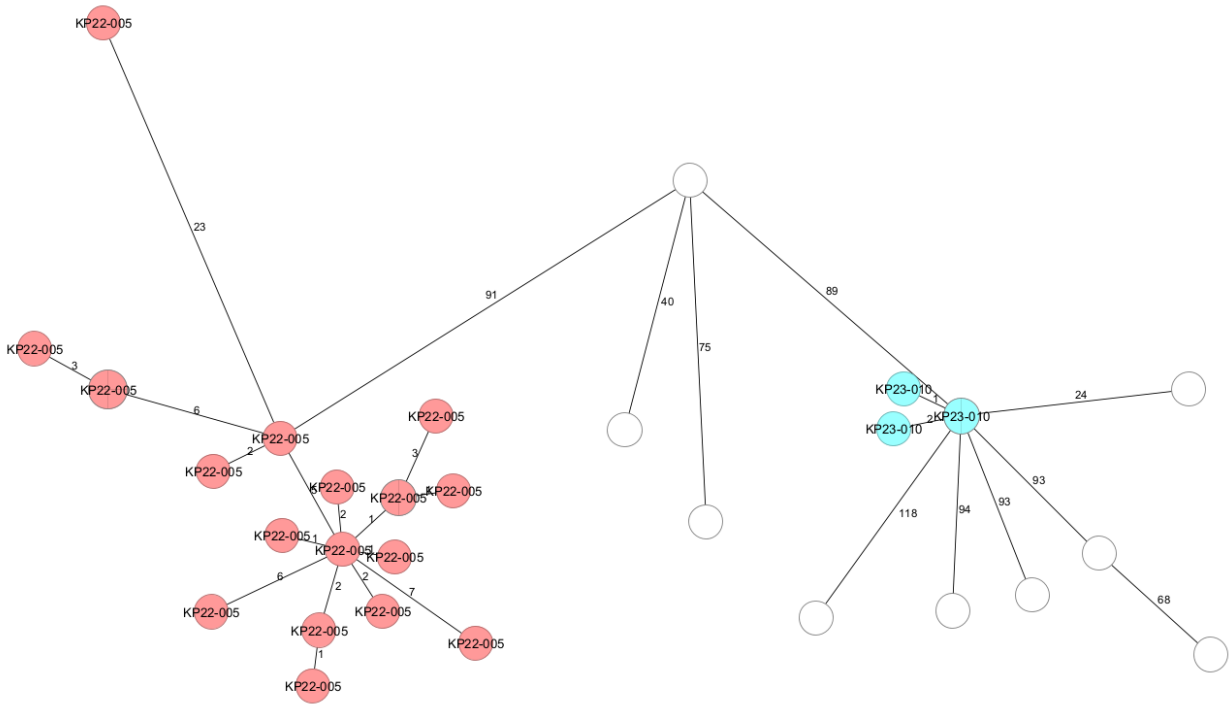

Figure 2. This figure represents all *K. pneumoniae* ST23 isolates received in 2025. The numbers illustrate the number of allelic differences between nodes. A larger partitioned node represents a number of isolates that are indistinguishable at cgMLST level. The number of partitions reflects the number of isolates.

ST78 *E. cloacae* complex

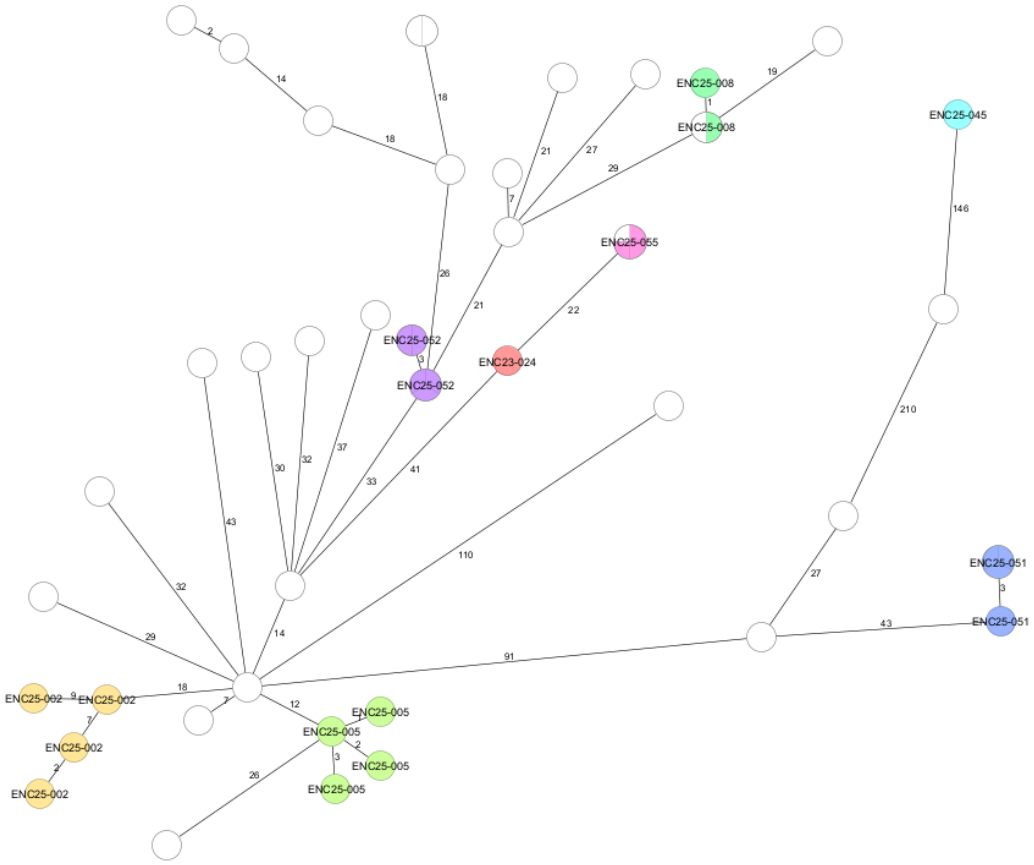

Figure 3. This figure represents all *E. cloacae* ST78 isolates in our database, from 2025. The pgMLST method used was developed by RIVM. A larger partitioned node represents a number of isolates that are indistinguishable at pgMLST level. The number of partitions reflects the number of isolates. The colours represent assignation to a specific cluster by the reference laboratory. Nodes in white were not assigned to a cluster.

ST131 *E. coli*

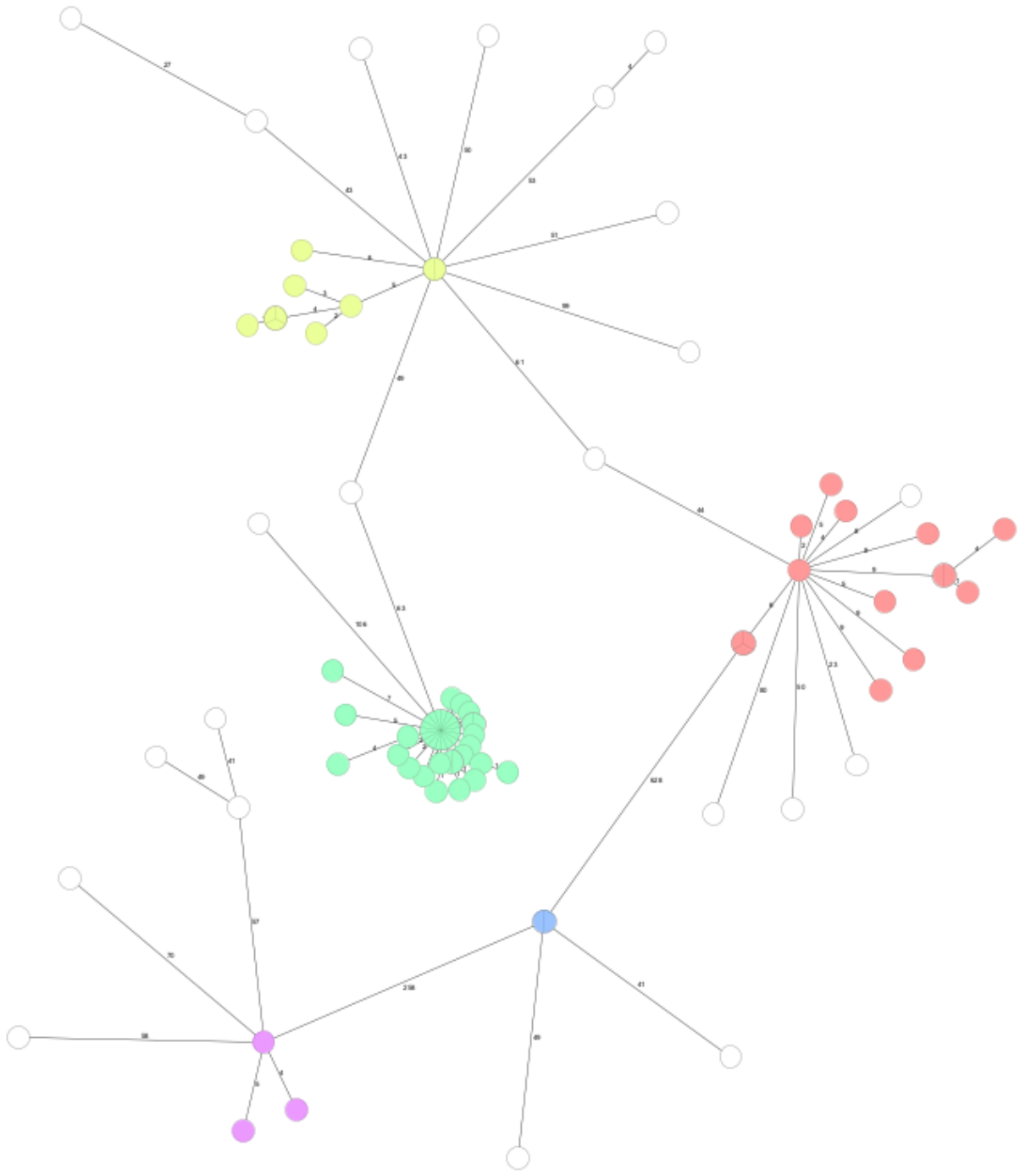

Figure 4. This figure represents all *E. coli* ST131 in our database, from 2025. A larger partitioned node represents a number of isolates that are indistinguishable at cgMLST level. The number of partitions reflects the number of isolates. The colours represent assignation to a specific cluster by the reference laboratory. Nodes in white were not assigned to a cluster.

ST69 *E. coli*

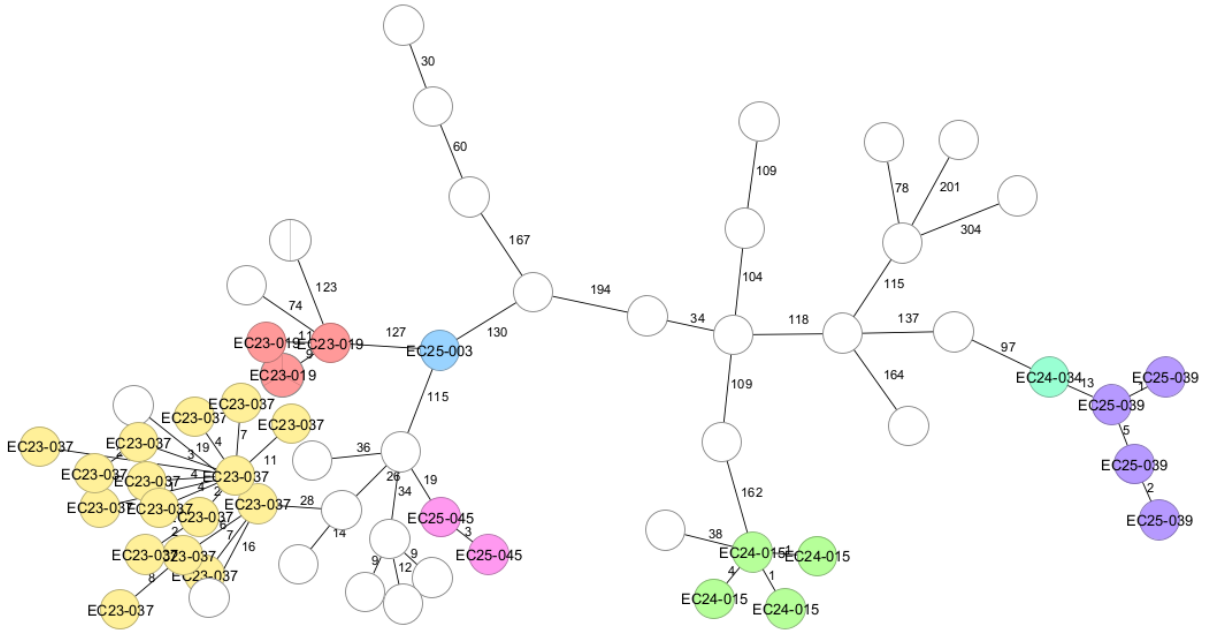

Figure 5. This figure represents all *E. coli* ST69 isolates in our database from 2025. A larger partitioned node represents a number of isolates that are indistinguishable at cgMLST level. The number of partitions reflects the number of isolates. The colours represent assignation to a specific cluster by the reference laboratory. Nodes in white were not assigned to a cluster.

ST38 *E. coli*

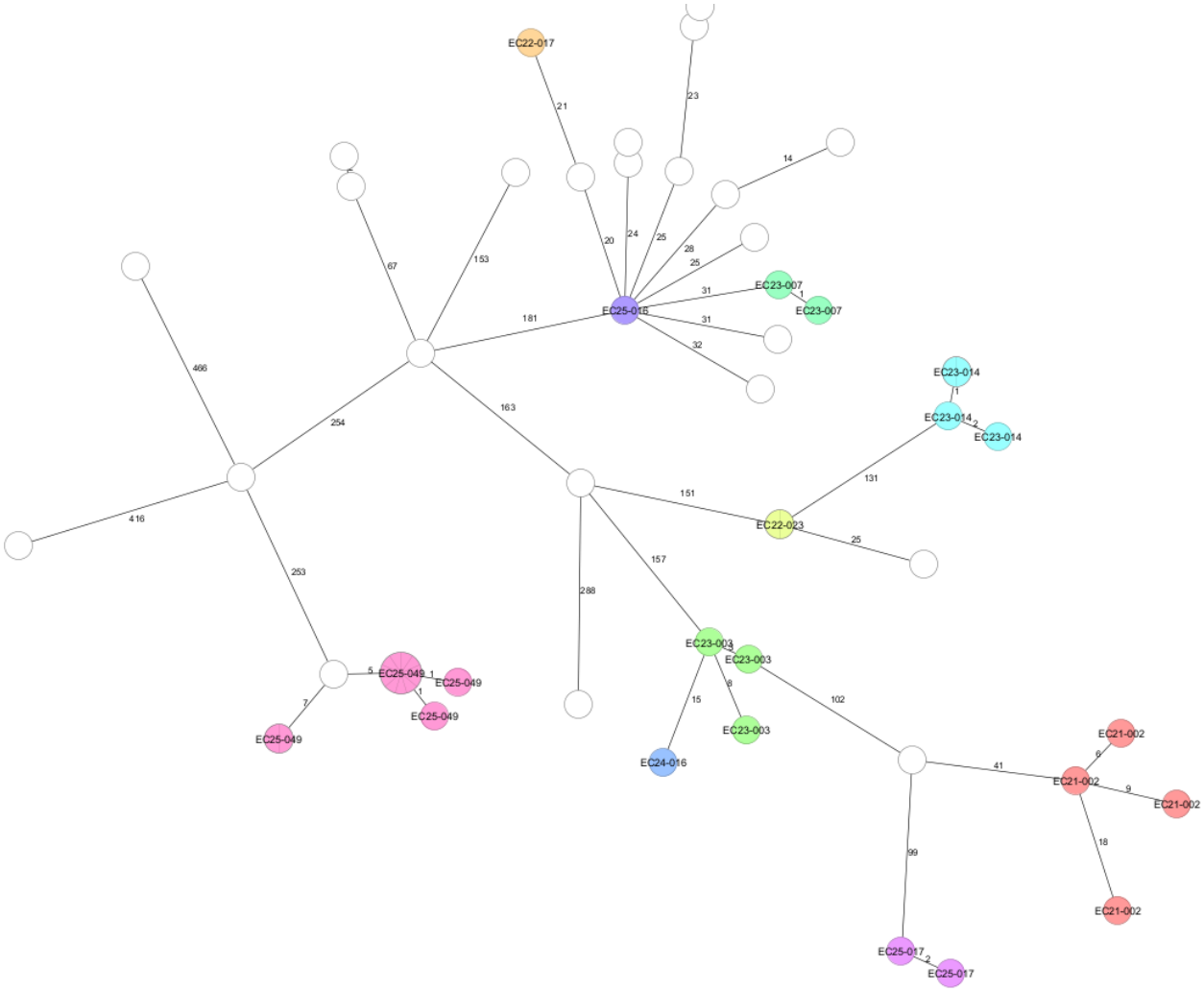

Figure 6. This figure represents all *E. coli* ST38 isolates in our database, from 2025. A larger partitioned node represents a number of isolates that are indistinguishable at cgMLST level. The number of partitions reflects the number of isolates. The colours represent assignation to a specific cluster by the reference laboratory. Nodes in white were not assigned to a cluster.

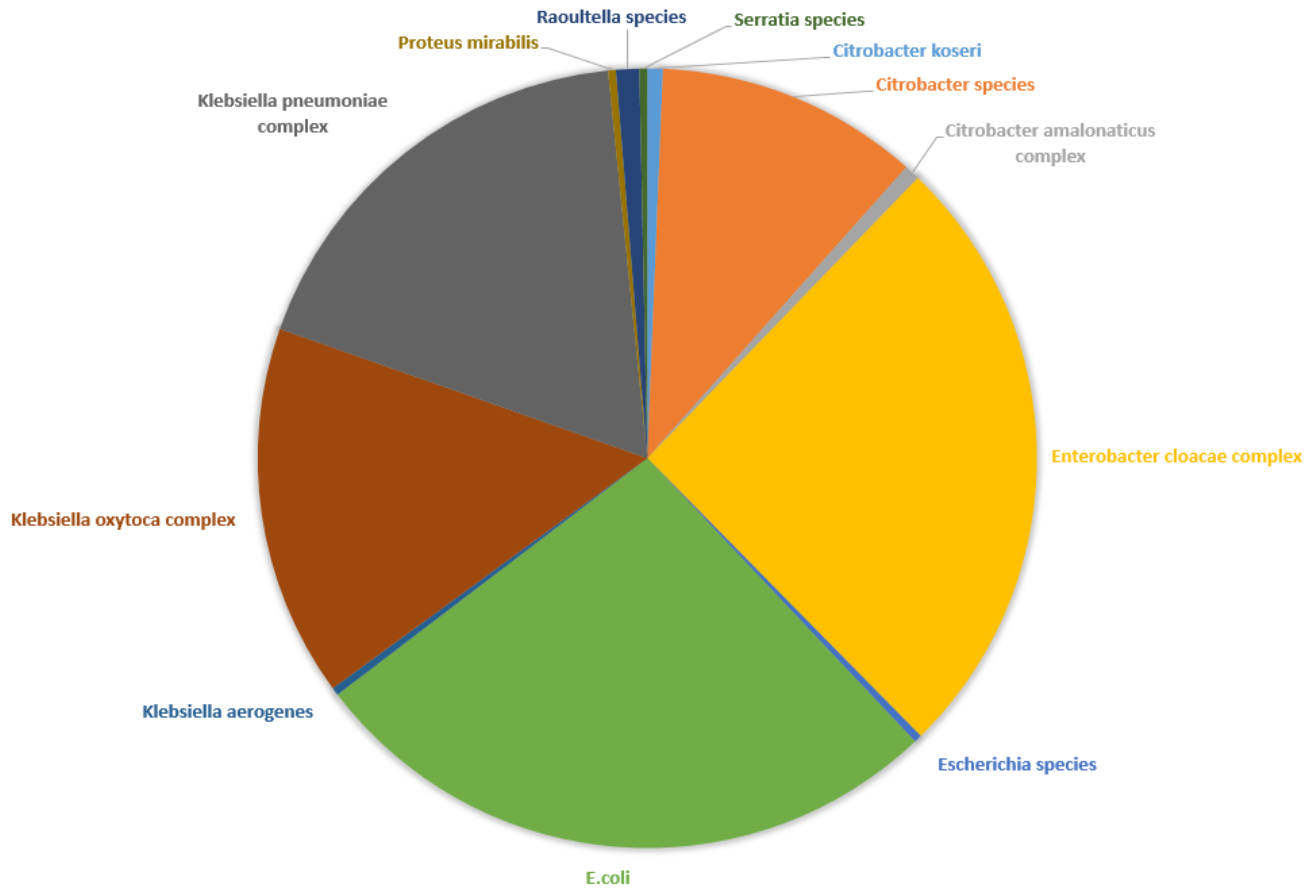

Figure 7. The blaOXA-48 carbapenemase is generally carried on an IncL/M plasmid. The Reference Laboratory uses an in-house method based on differences in the plasmid alleles (similar to MLST) to sub-classify the IncL/M plasmid in two major groups (A and B) and into sub-groups designated A, A1, A2 etc. This figure illustrates the wide distribution of a single plasmid sub-type (A) in multiple genera of Enterobacterales in isolates received in 2025. Horizontal plasmid transfer appear to contribute to chains of transmission that may be overlooked if the focus is only on a single species or single ST type (total of sub-type A plasmids represented =311)

Note on calling clusters

This sets out the approach to be applied in general to calling clusters based on cgMLST. Any such rule set includes cut-offs that are somewhat arbitrary. Identification of a cluster by these criteria is a signal of potential significance. It does not establish that transmission of infection of clinical or public health significance is occurring. Absence of a signal based on these criteria does not exclude transmission of infection of clinical or public health significance. Specifically these criteria do not consider horizontal transmission between individuals of mobile genetic elements (such as plasmids and transposons encoding antimicrobial resistance) carried in different bacterial species or different strains of a particular bacterial species. It remains essential be vigilant to rare or new phenomena and to emerging patterns not captured by these criteria. Users of the Reference Laboratory are always welcome to make contact regarding concerns or for advice on interpretation.

In addition to the following 2 or more isolates of any species matching to an ECDC alert/EPIS inquiry should be designated as a cluster.

Notes:

1. Our experience with S. Enteritidis suggests that there is limited genetic diversity compared to many other salmonella serotypes. Applying the general criteria for *S. enterica* would be likely to generate many signals that were not relevant for clinical or public health purposes therefore more stringent criteria are applied.
2. The criteria applied here to cluster calling for shigella are more stringent than those used in some publications. This is with a view to limiting signals that are not likely to be relevant for clinical or public health purposes.

Listeria monocytogenes

2 or more isolates with 0 to 7 AD is designated a cluster. Subsequent isolates are added to the cluster if they are 0 to 7 AD from any isolate previously designated as belonging to the cluster. No time limits are applied to initial definition of *L. monocytogenes* clusters as there is significant potential for low numbers of cases dispersed in time to be epidemiologically linked.

Salmonella enterica

2 or more isolates with 0 to 7 AD within 100 days or 5 or more isolates with 0 to 7 AD within 2 years is designated a cluster. Subsequent isolates are added to the cluster if they are no more than 7 AD from any isolate previously designated as belonging to the cluster.

***Salmonella enterica* serovar Enteritidis**

2 or more isolates with 0 to 3 AD within 100 days is designated a cluster. Subsequent isolates are added to the cluster if they are no more than 3 AD from any isolate previously designated as belonging to the cluster.

Shigella species

2 or more isolates with 0 to 5 AD within a 100 days is designated a cluster. Subsequent isolates are added to the cluster if they are no more than 5 AD from any isolate previously designated as belonging to the cluster

CPE, CPO, ESBL and other Enterobacterales

3 or more isolates from one institution **or** 5 or more isolates from 2 or more institutions with 0 to 10 AD within 100 days is designated a cluster.

10 or more isolates with 0 to 10 AD within 2 years is designated a cluster.

Subsequent isolates are added to the cluster if they are no more than 10 AD from any isolate previously designated as belonging to the cluster

For CPE and CPO 2 isolates from one institution with 0 to 10 AD is not designated a cluster but the report on the second isolate will include the comment "This isolate is indistinguishable from/closely related to isolate [Insert number] from your laboratory]".

Cluster naming.

Clusters are named with reference to the year the cluster was identified, the species (or serotype in the case of salmonella) and the temporal order in which clusters are designated in a given year. For example

EC-25-001 is the first *E. coli* cluster identified in 2025. This may include 1 or more isolates from previous years that are now recognised as part of the cluster but which were received before the cluster was identified. It will also include isolates that belong to this cluster received in years after 2025.

Duration of cluster

Clusters designation is not time limited. The data base reflects that cluster designation for each included isolate. An isolate that meets the criteria for inclusion in the cluster is assigned the cluster designation even if detected after an interval of some years when no members of the cluster were detected.

Cluster diversity

Clusters differ with respect to the degree of diversity within the cluster. In a classical point source outbreak where a number of people present with infection in a short time window we expect to find very little diversity with the cluster. In these cases, typically the isolates are indistinguishable by cgMLST or differ only by 1 to 2 AD. In other cases people presenting with infection are dispersed in space and time, possible exposed to a persistent source or there may be two or more sources that are linked in some way. As genetic diversity tends to increase with passage of time from "the common ancestor" these clusters tend to include greater diversity from the outset and to become progressively more diverse with years passed from the initial cluster designation. Understanding the diversity within a cluster can be useful in understanding the clinical and public health significance of a cluster. This can be represented diagrammatically as a minimum spanning tree (MST). Additional definition is sometime possible and useful, for example by considering similarity at the whole genome (core and accessory genes) level.

ENDS