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GALWAY REFERENCE LABORATORY REPORT 2024

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Galway Reference Laboratory Report 2024

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: <u>https://www.saolta.ie/documents/galway-reference-laboratory-service-incorporating-national-salmonella-shigella-listeria</u>

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

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

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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 <u>martin.cormican@hse.ie.</u>

M Cormican, MCRN 011105

Medical Director of the Galway Reference Laboratory Service. March 2025.

SECTION 1 Salmonella spp.

 Table 1 and Figure 1. Top 10 serotypes of Non-Typhoid Salmonella enterica submitted in 2024 and 2023 in descending order of the number of isolates received.

2024			2023			
Ranking	Serotype	Number of isolates	Ranking	Serotype	Number of isolates	
1	Enteritidis	73	1	Enteritidis	92	
2	Typhimurium	50	2	Typhimurium	45	
3	4,[5],12:i:-	40	3	4,[5],12:i:-	33	
4	Newport	14	4	Infantis	12	
5	Java	12	5	Stanley	11	
6	Infantis	9	6	Newport	10	
7	Bareilly	8	7	Chester	9	
	Panama		8	Saintpaul	8	
8	Adjame	7	9	Bovismorbificans	7	
	Chester		10	Braenderup	6	
	Hessarek			Mbandaka	6	
	Mikawasima			Panama	6	
	Stanley			Virchow	6	
9	London	6				
10	Bovismorbificans	5				
	Coeln					
	Muenster					
	Napoli					
	Others	137		Others	109	
	Total	412		Total	360	





Table 2 and Figure 2a and 2b.Salmonella Typhi and Paratyphi submitted in 2024. Thenumber of isolates received in each of the previous 4 years 2020 to 2023 is also provided.

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



Fig.2.a

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





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 2024. Resistance is predicted based on genetic markers of resistance.

Serotype	% Resistance							
	Amoxicillin	Azithromycin	Ceftriaxone	Ciprofloxacin	Meropenem			
S. Enteritidis	6/73	0/73	0/73	19/73	0/73			
	8.2%	0%	0%	26%	0%			
S. Typhimurium	11/50	0/50	0/50	3/50	0/50			
	22%	0%	0%	6%	0%			
<i>S.</i> Typhi	21/29	0/29	6/29	26/29	0/29			
	72.4%	0%	20.7%	89.7%	0%			
All Salmonella	93/412	2/412	12/412	217/412	0/412			
	22.6%	0.49%	2.9%	52.7%	0%			

Clusters of similar isolates

In 2024 the Reference Laboratory identified 48 new clusters of *Salmonella enterica* isolates with a range of 2 to 7 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 S24-003 is the third cluster of *Salmonella enterica* identified in 2024.

SECTION 2 Shigella spp.

Table 4 and Figures 4a and 4b. Shigella species submitted in 2024 in alphabetical order.For each species the number of isolates received in each of the previous 4 years 2020 to 2023is also provided.

Serotype	Number of isolates							
	2024	2023	2022	2021	2020			
S. boydii	1	1	2	0	1			
S. dysenteriae	1	2	1	1	0			
S. flexneri	77	65	50	24	37			
S. sonnei	50	79	28	22	10			
S. flexneri 6	1	0	2	1	0			
Other	0	0	0	0	0			
Total	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.

Serotype	% Resistance (or number when total isolates is less than 10)							
	Amoxicillin	Azithromycin	Ceftriaxone	Ciprofloxacin	Meropenem			
<u> </u>	0/1	0/1	0/1	1/1	0/1			
S.DOyali	0%	0%	0%	100%	0%			
S.dysenteriae	0/1	0/1	0/1	1/1	0/1			
	0%	0%	0%	100%	0%			
C flownori	74/77	46/77	6/77	58/77	0/77			
S.JIexneri	96.1%	59.7%	7.8%	75.3%	0%			
C. compoi	35/50	31/50	32/50	44/50	0/50			
S.sonnei	70%	62%	64%	88*%	0%			
All Shigella	109/130	77/130	38/130	104/130	0/130			
	83.8%	59.2%	29.2%	80%	0%			

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

Clusters of similar isolates

In 2024 the Reference Laboratory identified 1 new *Shigella* cluster with 2 isolates in the cluster. 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. For example SH24-001 is the first cluster of *Shigella* identified in 2024.

SECTION 3 Listeria monocytogenes

Table 6. and Figure 6 *L. monocytogenes* predicted serotypes submitted in 2024. For each serotype the number of isolates receive in each of the previous 4 years 2020 to 2023 is also provided.

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



Fig6.

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

Clusters of similar isolates

In 2024 the Reference Laboratory identified 3 new clusters of *Listeria monocytogenes* with a range of 2 to 4 isolates per 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. L24-001 is the first cluster of *Listeria monocytogenes* species identified in 2024.

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

Table 7. and Figure 7. Species/Genus of CPO submitted in 2024 in alphabetical order. For each species the number of isolates received in each of the previous 4 years 2020 to 2023 is also provided.

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

Footnote 1. Total other CPO refers to CPO other than CPE



Fig.7

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

Species	Number of each carbapenemase type							
	КРС	IMP	OXA-48	NDM	VIM	Other		
			family					
Acinetobacter spp.	0	1	0	9	0	7		
Citrobacter spp.	91	3	184	9	13	0		
Enterobacter spp.	36	14	278	21	52	4		
Escherichia spp.	22	2	643	105	6	0		
K. oxytoca	13	5	103	3	6	0		
K. pneumoniae	89	1	308	41	1	0		
Pseudomonas spp.	0	1	0	5	3	1		
Others	17	2	56	16	3	0		
Total	268	29	1,572	209	84	12		

Table 8. and Figure 8. Type of carbapenemase detected in each major group of organisms in 2024.





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

Table 9, Figures 9a and 9b. Number of each type of carbapenemase in Enterobacterales (in alphabetical order) in 2024 with the corresponding number for each year from 2020 to 2023 for comparison

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

Table 9. Number of each type of carbapenemase enzyme detected in human samples.



Fig 9a. Number of each type of carbapenemase enzyme detected. *Note: vertical axis shows number of non-duplicate isolates.*





Fig 9b. Number of each type of carbapenemase enzyme detected *Note: vertical axis shows number of non-duplicate isolates.*

Carbapenemase	Number of isolates							
Enzyme in Enterobacterales	2024	Rectal/faeces Screening	Diagnostic (including invasive)	Diagnostic Invasive	Unknown			
IMI	3	3	0	0	0			
IMP	27	27	0	0	0			
КРС	268	248	19	2	1			
NDM	195	168	27	0	0			
OXA-48	1179	1077	101	9	1			
OXA-181	95	83	12	1	0			
OXA-244	265	238	27	2	0			
Other OXA-48 Like	33	31	2	0	0			
VIM	81	76	5	0	0			
Others	1	1	0	0	0			
Total	2,094	1,903	189	14	2			
Isolates With >1 CPE enzyme found	53	49	4	0	0			

Table 10. and Figure 10. Number of each type of carbapenemase enzyme detected, broken down by specimen type.

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.





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

Carbapenemase Gene Variants Detected in Enterobacterales in 2024								
OXA-48 Variants	OXA-48	OXA-181	OXA-244	OXA-232	OXA-484	OXA-48 like		
Total	1179	95	265	3	12	18		
IMI Variants	IMI-4	IMI-6						
Total	1	2						
IMP Variants	IMP-13	IMP-22	IMP-4					
Total	1*	1*	25*					
KPC Variants	KPC-2	KPC-3						
Total	198*	70*						
NDM Variants	NDM-1	NDM-4	NDM-5	NDM-7	NDM-13			
Total	68*	1	123*	2*	1			
VIM Variants	VIM-1	VIM-5						
Total	80*	1						

Table 11. and Figure 11. Number of each type of carbapenemase enzyme detected broken down by variant identified.

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



Fig11.

	Nu	mber of is	olates		
Carbapenemase Enzyme	2024	2023	2022	2021	2020
IMI	0	0	0	0	0
IMP	2	3	1	3	0
КРС	0	0	0	0	0
NDM	14*	8	3	3	3
OXA-48 Family	0	0	0	0	0
OXA-23	7	15	5	3	7
OXA-24	0	1	0	0	0
OXA-58	1*	0	0	1	0
OXA-72	0	0	0	1	0
VIM	3	3	6	4	5
Others	0	0	3	0	0
Isolates With >1 Carbapenemase enzyme found	1	0	1	1	0

Table 12. and Figure 12. Carbapenemase Genes Detected in *Acinetobacter* spp. and *Pseudomonas* spp. in 2024.

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

* indicates there are dual carbapenemase producers in this data.



Fig.12

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

Table 13.Carbapenemase Gene Variants Detected in Acinetobacter spp. and
Pseudomonas spp. in 2024.

Carbapenemase Gene Variants Detected in <i>Acinetobacter</i> spp. and <i>Pseudomonas</i> spp. in 2024					
IMP Variant	IMP-1				
Total	2				
NDM Variant	NDM-1	NDM-5			
Total	13*	1			
VIM Variant	VIM-2				
Total	3				

* indicates there are dual carbapenemase producers in this data.

Table	14.	Тор	sequence	types	detected	in	K .	pneumonia,	Κ.	variicola	and	Κ.
quasip	oneum	onaie	e in 2024 an	d 2023	(only ST's	; wit	:h >	4 isolates inc	lude	ed. This ta	ble al	SO
includ	es noi	n-CPE	E isolates a	s they a	are includ	ed i	n th	e hvKp figure	es).			

	202	4		2023	
Ranking	ST	Number	Ranking	ST	Number
1	ST 478	47	1	ST 307	14
2	ST 307	22	2	ST 23	13
3	ST 23	20*	3	ST 111	9
4	ST 405	15	4	ST 449	7
5	ST 13	14		ST 14	7
6	ST 104	13	5	ST 45	6
	ST 147		6	ST 35	5
7	ST 268	12		ST 478	
	ST 35			ST 37	
8	ST 37	10	7	ST 147	4
9	ST 490	9		ST 1083	
10	ST 14	8		ST 268	
				ST 323	
				ST 36	
	Others	244		Others	113
	Total	439		Total	233

* 17 of the 20 ST23 isolates were hvKp

Table 15.	Number o	of K. pneumoniae id	dentified as	hypervirulent (I	vKp) and nor	n-hvKp
(this table	includes b	ooth CPE's and nor	n CPE K. pn	eumoniae isolat	e)	

	Number of isolates						
	2024	2023	2022	2021	2020		
hvKp	39*	20	38	14	22		
non-hvKp	366	184	199	153	140		
Total	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. Of the 39 hvKp 17 were ST23

	2024			2023	
Ranking	ST	Number of Isolates	Ranking	ST	Number of Isolates
1	ST 648	70	1	ST 38	46
2	ST 10	68	2	ST 69	37
3	ST 69	61	3	ST 10	35
4	ST 131	54	4	ST 648	32
5	ST 38	39	5	ST 131	16
6	ST 167	26	6	ST 58	14
7	ST 410	21	7	ST 410	12
8	ST 58	17	8	ST 405	11
9	ST 12	14	9	ST 399	9
10	ST 405	10	10	ST 3541	8
	Others	383		Others	296
	Total	763		Total	516

Table 16. Top 10 sequence types detected in *E.coli* in 2024 and 2023

Table 17. Subtypes of OXA detected in *E. coli*

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

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

	2024			2023	
Ranking	ST	Number of Isolates	Ranking	ST	Number of Isolates
1	ST 176	9	1	ST 36	10
	ST 50		2	ST 416	9
2	ST 223	8	3	ST 176	8
	ST 53		4	ST 223	7
3	ST 232	7	5	ST 2	6
4	ST 199	4	6	ST 186	4
	ST 258			ST 226	
	ST 616			ST 52	
	Others	71		Others	53
	Total	124		Total	105

Table 18. Top sequence types detected in *K. oxytoca* in 2024 and 2023 (only ST's with >4 isolates included)

Table 19. Top 10 sequence types detected in *Enterobacter cloacae* in 2024 and 2023.

	2024			2023	
Ranking	ST	Number of Isolates	Ranking	ST	Number of Isolates
1	ST 527	78	1	ST 78	38
2	ST 66	36	2	ST 527	28
3	ST 78	24	3	ST 66	27
4	ST 796	21	4	ST 88	23
5	ST 133	17	5	ST 269	21
6	ST 90	15	6	ST 141	18
	ST 113	15	7	ST 97	11
7	ST 45	11		ST 45	
8	ST 32	10		ST 145	
9	ST 88	9	8	ST 133	9
10	ST 97	8		ST 796	
	ST 120				
	ST 1348				
	Others	130		Others	117
	Total	390		Total	323

2024			2023		
Ranking	ST	Number of	Ranking	ST	Number of
		Isolates			Isolates
1	ST 22	48	1	ST 22	34
2	ST 420	22	2	ST 420	15
3	ST 98	12	3	ST 111	8
4	ST 62	11	4	ST 98	6
5	ST 111	10		ST 116	
6	ST 64	7		ST 62	5
	ST 116		5	ST 415	
7	ST 150	5		ST 261	
	ST 95			ST 95	
8	ST 114	4		ST 114	
				ST 942	4
			6	ST 1027	
	Others	123		Others	62
	Total	254		Total	161

Table 20. Top sequence types detected in *Citrobacter freundii* complex in 2024 and 2023 (only ST's with >4 isolates included).

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. EC23-003 is the third cluster of *E. coli* identified in 2023. There are a number of clusters of carbapenemase producing organisms identified some years ago that continue to circulate.

 Table 21. and Figure 21. Species/Genus of CPO from the healthcare environment

 submitted in 2024 in alphabetical order. For each species the number of isolates received in

 each of the previous 4 years 2020 to 2023 is also provided.

Species	Number of isolates						
Species	2024	2023	2022	2021	2020		
Acinetobacter spp.	0	2	0	2	0		
Citrobacter spp.	35	58	31	24	25		
Enterobacter spp.	61	45	32	45	36		
E. coli	2	2	1	0	0		
E.hermanii	5	6	1	0	3		
K. oxytoca	15	14	6	3	6		
K. pneumoniae	11	6	4	3	8		
Pseudomonas spp.	1	3	0	1	1		
Others	11	13	6	11	3		
Total CPE	140	144	81	86	81		
Total CPO ¹	1	5	0	3	1		
Total	141	149	81	89	82		

¹Excluding 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 21.

Number of each carbapenemase type for 2024								
Species	КРС	IMP	OXA-48 family	NDM	VIM	Other		
Acinetobacter spp.	0	0	0	0	0	0		
Citrobacter spp.	12*	0	20*	1	3	0		
Enterobacter spp.	6	5	32*	13	6*	0		
Escherichia spp.	0	0	2	1	4	0		
K. oxytoca	5	0	10	0	0	0		
K. pneumoniae	2	0	8*	1*	1	0		
Pseudomonas spp.	0	0	0	0	1	0		
Others	2	2	4*	2*	2	0		
Total	27	7	76	18	17	0		

Table 22. Species/Genus of CPO with breakdown of CPE Enzyme detected from thehealthcare environment submitted in 2024

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

Appendix to Galway Reference Laboratory Annual Report 2024.

This appendix presents illustrations of diversity in some key sequence types. The final figure is to illustrate how widely disseminated one specific plasmid subtype is within genera of Enterobacterales.

Figure 1. This figure represents all *K. pneumoniae* ST478 isolates received in 2024. 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.



Figure 2. This figure represents all *K. pneumoniae* ST23 isolates received in 2024. 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.



Figure 3. This figure represents all *E. cloacae* ST527 isolates in our database. The pgMLST method used was developed by RIVM. 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 4. This figure represents all *E. coli* ST648 isolates in our database. 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 5. This figure represents all *E. coli* ST131 isolates in our database. 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 6. This figure represents all *E. coli* ST10 isolates in our database. 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 2024. 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 = 415)



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