

GALWAY REFERENCE LABORATORY REPORT

Years 2019 - 2023

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Galway Reference Laboratory Report: Years 2019-2023

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:

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

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

<https://www.saolta.ie/sites/default/files/publications/microbiology/NSRLFM001%20Version%202.2.pdf>

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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.

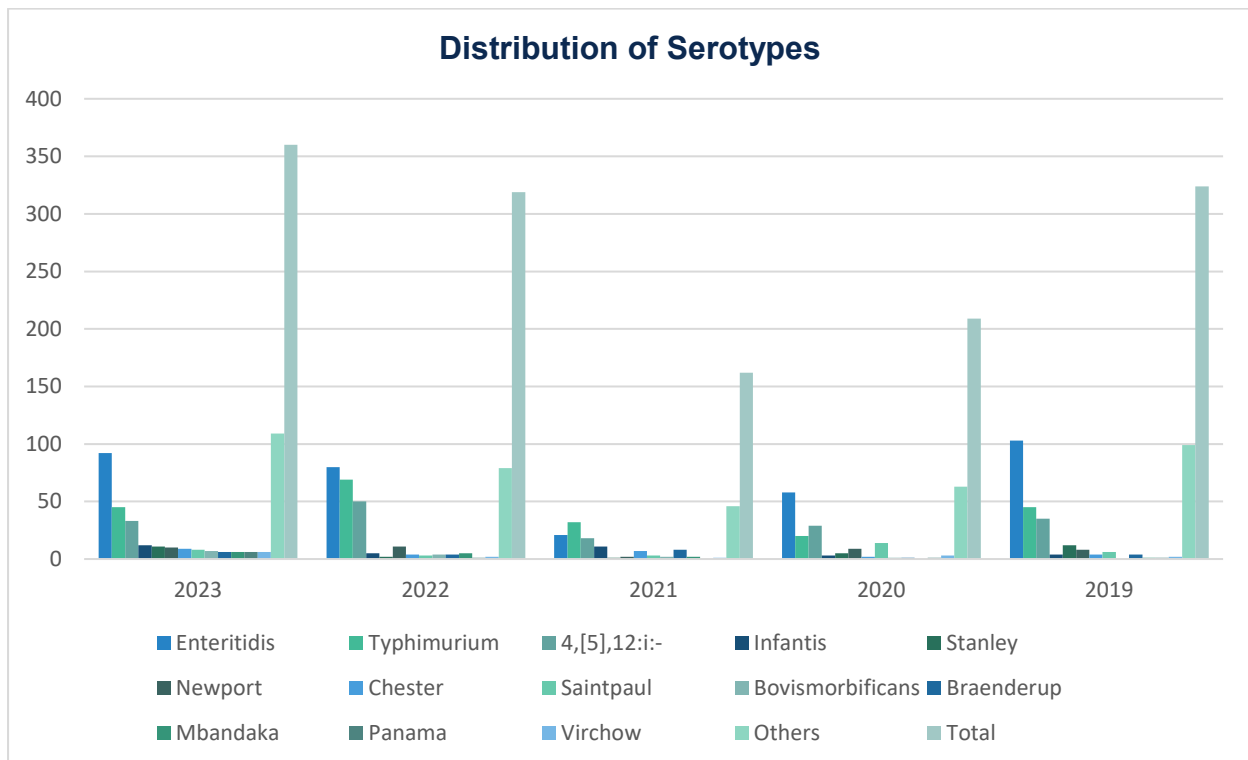
M Cormican, MCRN 011105

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

SECTION 1 *Salmonella* spp.

Table 1 and Figure 1. Top 10 serotypes of Non-Typhoid *Salmonella enterica* submitted in 2023 in descending order of the number of isolates received. For each serotype the number of isolates received in each of the previous 4 years 2019 to 2022 is also provided.

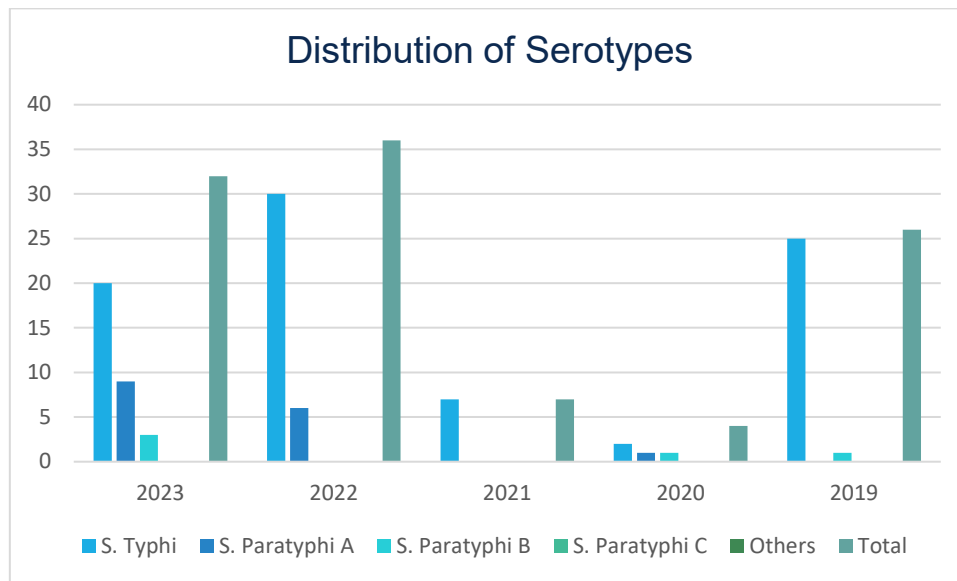
	Serotype	Number of isolates				
		2023	2022	2021	2020	2019
1	Enteritidis	92	80	21	58	103
2	Typhimurium	45	69	32	20	45
3	4,[5],12:i:-	33	50	18	29	35
4	Infantis	12	5	11	3	4
5	Stanley	11	2	1	5	12
6	Newport	10	11	2	9	8
7	Chester	9	4	7	2	4
8	Saintpaul	8	3	3	14	6
9	Bovismorbificans	7	4	2	1	0
10	Braenderup	6	4	8	1	4
	Mbandaka	6	5	2	0	1
	Panama	6	1	0	1	1
	Virchow	6	2	1	3	2
	Others	109	79	53	63	99
	Total	360	319	161	209	324



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

Table 2 and Figure 2a and 2b. *Salmonella* Typhi and Paratyphi submitted in 2023. The number of isolates received in each of the previous 4 years 2019 to 2022 is also provided.

Serotype	Number of isolates				
	2023	2022	2021	2020	2019
<i>S. Typhi</i>	20	30	7	2	25
<i>S. Paratyphi A</i>	9	6	0	1	0
<i>S. Paratyphi B</i>	3	0	0	1	1
<i>S. Paratyphi C</i>	0	0	0	0	0
Others	0	0	0	0	0
Total	32	36	7	4	26



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 2023. Resistance is predicted based on genetic markers of resistance.

Serotype	% Resistance				
	Amoxicillin	Azithromycin	Ceftriaxone	Ciprofloxacin	Meropenem
<i>S. Enteritidis</i>	5/92	0	0	37/92	0
	5%	0%	0%	40%	0%
<i>S. Typhimurium</i>	8/45	0	1/45	1/45	0
	18%	0%	2%	2%	0%
<i>S. Typhi</i>	8/20	1/20	4/20	20/20	0
	40%	5%	20%	100%	0%
All <i>Salmonella</i>	75/392	4/392	7/392	220/392	0
	19%	1%	2%	56%	0%

Clusters of similar isolates

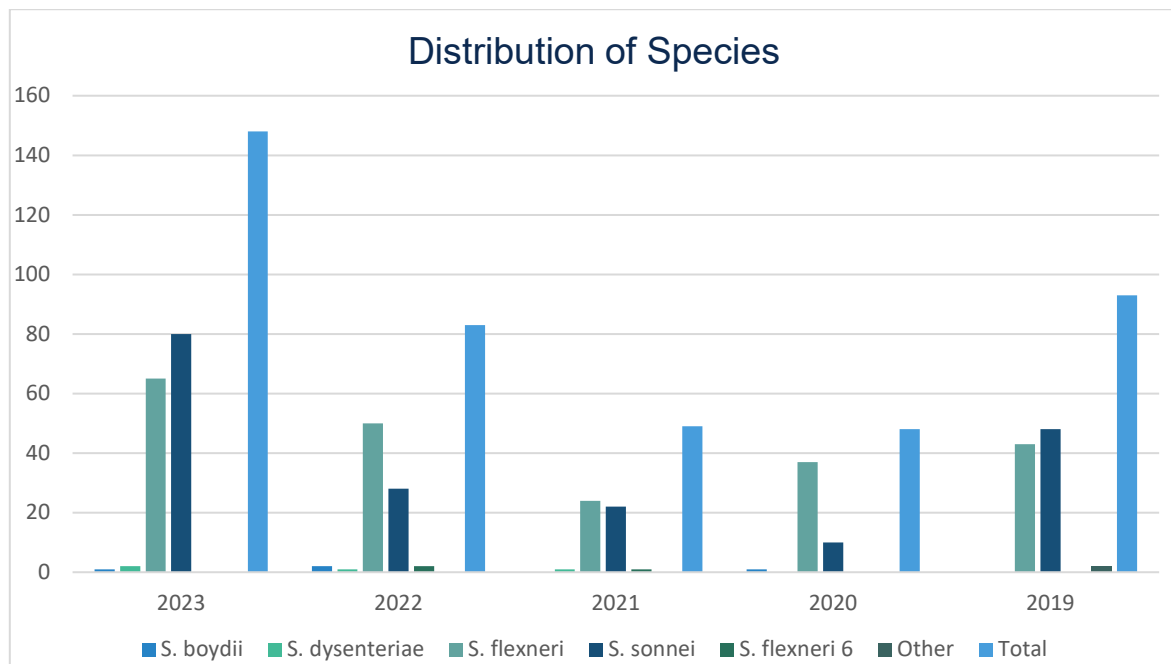
In 2023 the Reference Laboratory identified 34 new clusters of *Salmonella enterica* isolates with a range of 2 to 7 isolates per cluster. When an isolate is part of an identified cluster this is indicated on the report returned to the sender of that isolate. Clusters are designated by an alpha-numeric 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 S23-003 is the third cluster of *Salmonella enterica* identified in 2023.

SECTION 2 *Shigella* spp.

Table 4 and Figures 4a and 4b. *Shigella* species submitted in 2023 in alphabetical order. For each species the number of isolates received in each of the previous 4 years 2019 to 2022 is also provided.

Serotype	Number of isolates				
	2023	2022	2021	2020	2019
<i>S. boydii</i>	1	2	0	1	*
<i>S. dysenteriae</i>	2	1	1	0	0
<i>S. flexneri</i>	65	50	24	37	43
<i>S. sonnei</i>	79	28	22	10	48
<i>S. flexneri</i> 6	0	2	1	0	*
Other	0	0	0	0	2*
Total	147	83	48	48	93

* These isolates were ST145 and can be *S.flexneri* or *S.boydii*, further differentiation was not possible in these 2 cases.



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
<i>S.boydii</i>	1/1	0	0	1/1	0
	100%	0%	0%	100%	0%
<i>S.dysenteriae</i>	1/2	0	0	2/2	0
	50%	0%	0%	100%	0%
<i>S.flexneri</i>	62/65	27/65	11/65	21/65	0
	95%	42%	17%	32%	0%
<i>S.sonnei</i>	46/80	33/80	39/80	74/80	0
	58%	41%	49%	93%	0%
Total:	110/148	60/148	50/148	98/148	0
	74%	41%	34%	66%	0%

Clusters of similar isolates

In 2023 the Reference Laboratory identified 7 new *Shigella* clusters with a range of 2 to 16 isolates per cluster. 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 SH23-003 is the third cluster of *Shigella* identified in 2023. There are a number of clusters of *Shigella* identified some years ago that continue to circulate.

SECTION 3 *Listeria monocytogenes*

Table 6. *L. monocytogenes* predicted serotypes submitted in 2023. For each serotype the number of isolates received in each of the previous 4 years 2019 to 2022 is also provided.

Serotype	Number of isolates				
	2023	2022	2021	2020	2019
Serotype 4b	5	6	5	2	9
Serotype 2a	0	0	0	0	0
Serotype 1/2a	5	2	3	2	4
Serotype 1/2b	1	1	0	1	3
Others	0	0	0	0	0
	11	9	8	5	16

Clusters of similar isolates

From 2019 to 2022 the Reference Laboratory identified 5 new clusters of *Listeria monocytogenes* with a range of 2 to 5 isolates per cluster. There were no new clusters on 2023. When an isolate is part of an identified cluster this is indicated on the isolated 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 year. L22-001 is the first cluster of *Listeria monocytogenes* species identified in 2022.

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

Table 7. Species/Genus of CPO submitted in 2023 in alphabetical order. For each species the number of isolates received in each of the previous 4 years 2019 to 2022 is also provided.

Species	Number of isolates				
	2023	2022	2021	2020	2019
<i>Acinetobacter</i> spp.	18	8	8	9	12
<i>Citrobacter</i> spp.	180	168	131	137	121
<i>Enterobacter</i> spp.	323	252	215	227	205
<i>E. coli</i>	516	367	297	250	304
<i>K. oxytoca</i>	105	87	78	97	95
<i>K. pneumoniae</i>	204	228	162	158	192
<i>Pseudomonas</i> spp.	12	9	6	6	2
Others	95	65	50	46	46
Total CPE	1,423	1,167	933	915	963
Total other CPO¹	30	17	14	15	14
Total	1,453	1,184	947	930	977

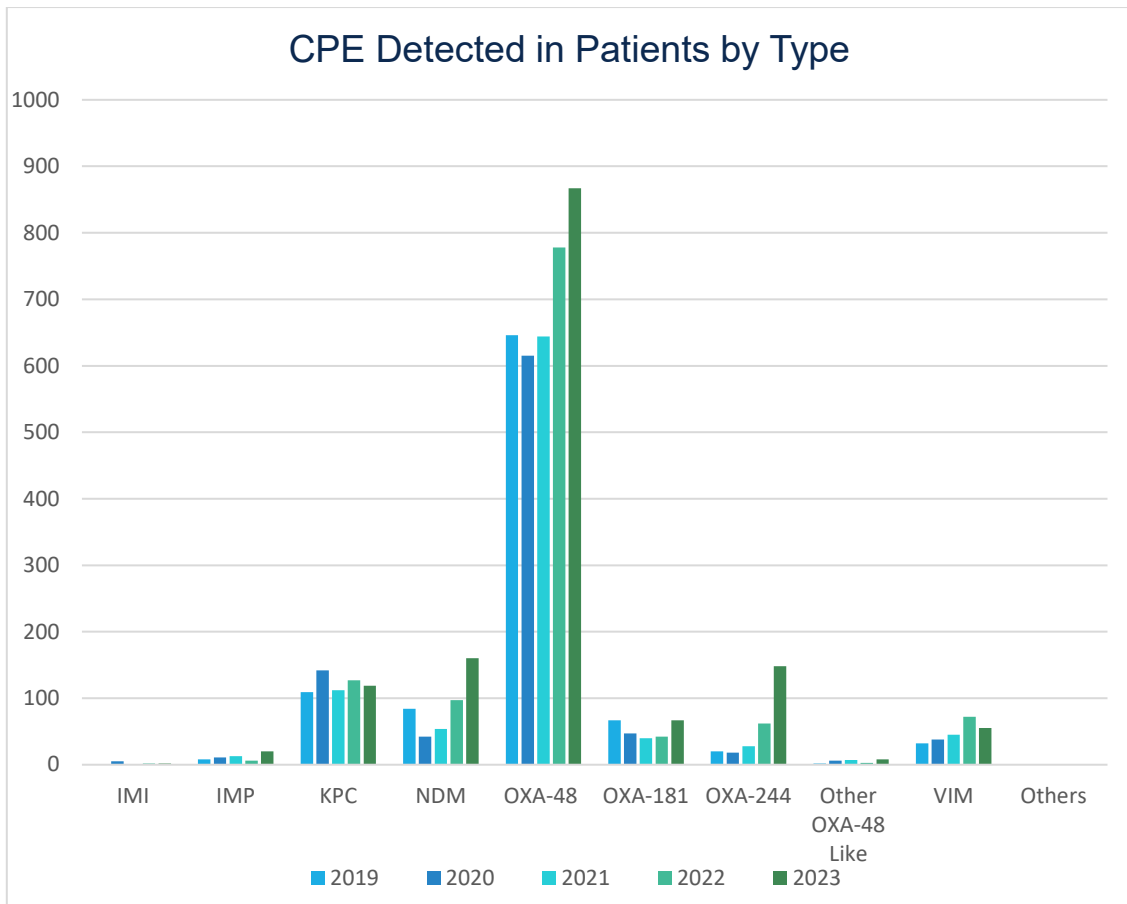
Footnote 1. Total other CPO refers to CPO other than CPE

Table 8. Type of carbapenemase detected in each major group of organisms in 2023, note *DP = Dual Producer

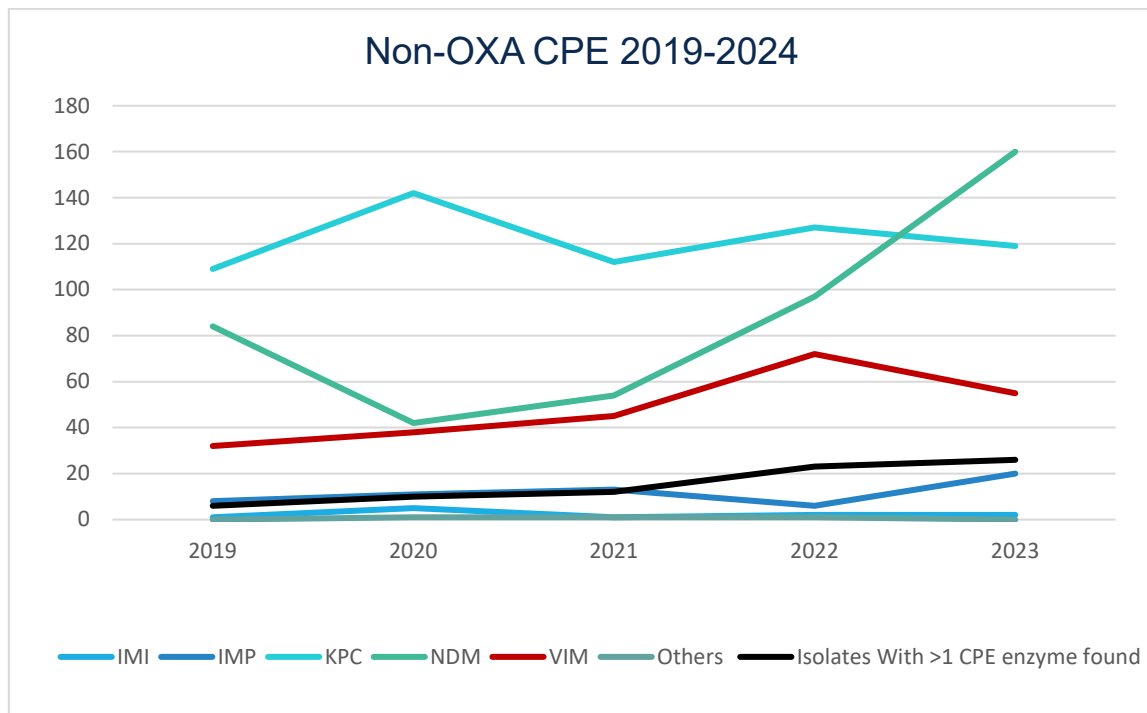
Species	Number of each carbapenemase type					
	KPC	IMP	OXA	NDM	VIM	Other
<i>Acinetobacter</i> spp.	0	0	16 15 OXA-23 1 OXA-24	2	0	0
<i>Citrobacter</i> spp.	46 *1 DP	4 *1 DP	122 *3 DP	10 *1 DP	1	0
<i>Enterobacter</i> spp.	17 3* DP	12 *1 DP	224 *12 DP	44 *7 DP	38 *6 DP	2
<i>E. coli</i>	12	3	432 *3 DP	66 *3 DP	6	0
<i>K. oxytoca</i>	14	1	84 *1 DP	5 *1 DP	2	0
<i>K. pneumoniae</i>	22	0	152 *4 DP	28 *4 DP	6	0
<i>Pseudomonas</i> spp.	0	3	0	6	3	0
Others	8	0	77	8	2	1
Total	119	20	1090	160	55	2

Table 9 and Figure 9a, 9b and 9c. Number of each type of carbapenemase (in alphabetical order) in 2023 with the corresponding number for each year from 2019 to 2022 for comparison

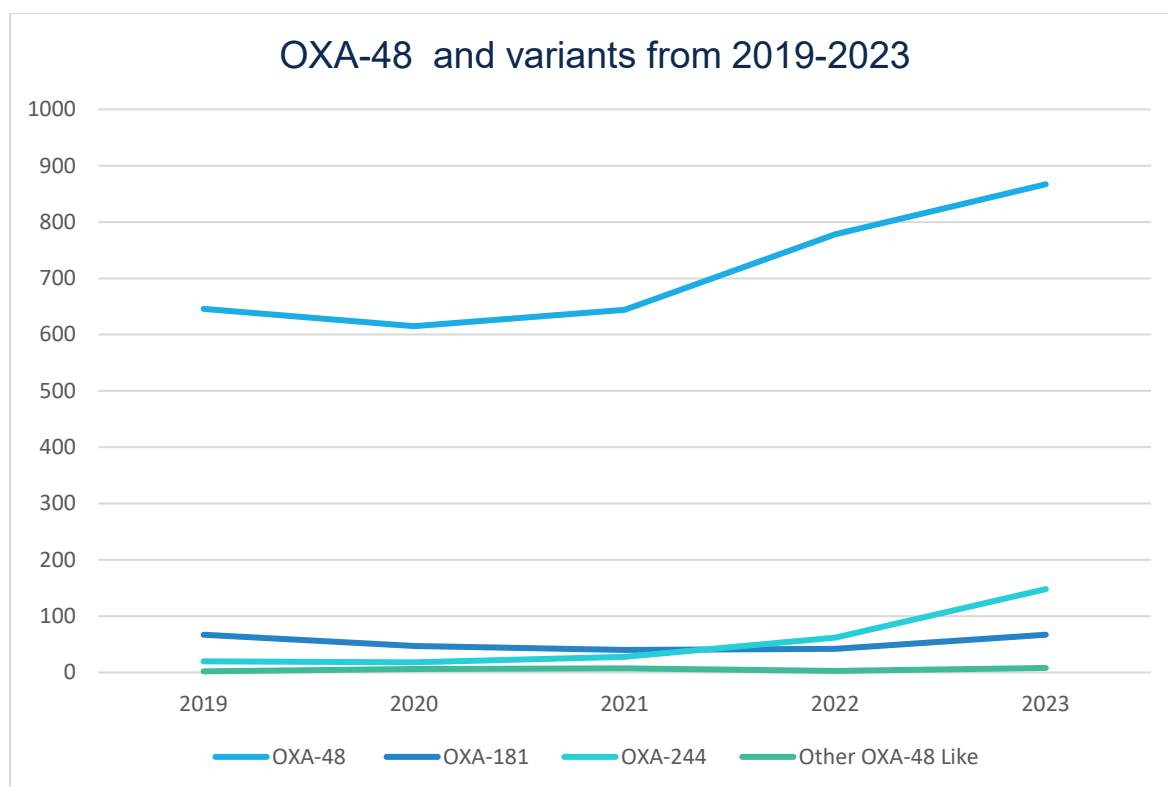
Carbapenemase Enzyme	Number of isolates				
	2023	2022	2021	2020	2019
IMI	2	2	1	5	1
IMP	20	6	13	11	8
KPC	119	127	112	142	109
NDM	160	97	54	42	84
OXA-48	867	778	644	615	646
OXA-181	67	42	40	47	67
OXA-244	148	62	28	18	20
Other OXA-48 Like	8	3	7	6	2
VIM	55	72	45	38	32
Others	0	1	1	1	0
Isolates With >1 CPE enzyme found	26	23	12	10	6



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



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



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

Table 10. *Acinetobacter* spp. and *Pseudomonas* spp.

Carbapenemase Enzyme	Number of isolates				
	2023	2022	2021	2020	2019
IMI	0	0	0	0	0
IMP	3	1	3	0	0
KPC	0	0	0	0	0
NDM	8	3	3	3	1
OXA-48 like	0	0	0	0	0
OXA-23	15	5	3	7	7
OXA-24	1	0	0	0	0
OXA-58	0	0	1	0	2
OXA-72	0	0	1	0	2
VIM	3	6	4	5	1
Others	0	3	0	0	1
Isolates With >1 Carbapenemase enzyme found	0	1	1	0	0

Table 11. Top 10 sequence types detected in *K. pneumoniae* in 2023 with the number of isolates of the ST in each of the previous 4 years

Sequence type	Number of isolates				
	2023	2022	2021	2020	2019
ST 307	14	18	8	9	8
ST 23	13	18	7	14	18
ST 111	9	2	1	0	0
ST 449	7	0	0	1	0
ST 14	7	7	2	3	1
ST 45	6	5	4	3	7
ST 35	5	4	0	1	0
ST 478	5	0	1	0	0
ST 37	5	6	5	15	2
ST 147	4	14	1	1	6
ST 1083	4	1	1	1	0
ST 268	4	1	2	0	0
ST 323	4	11	1	2	0
ST 36	4	0	0	0	1
Others	113	141	129	108	149
Total	204	228	162	158	192
blaOXA244	1	1	0	0	0

Table 12. Number of *K. pneumoniae* identified as hypervirulent (hvKp) and non-hvKp

	Number of isolates				
	2023	2022	2021	2020	2019
hvKp	29	199	153	140	170
non-hvKp	184	38	14	22	22
Total	213	237	167	162	192

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 13. Top 10 sequence types detected in *E.coli* in 2023 with the number of isolates of the ST in each of the previous 4 years

Sequence type	Number of isolates				
	2023	2022	2021	2020	2019
ST 38	46	39	20	19	20
ST 69	37	21	19	16	17
ST 10	35	31	21	8	15
ST 648	32	2	8	2	9
ST 131	16	39	17	16	12
ST 58	14	6	3	3	6
ST 410	12	10	7	13	23
ST 405	11	11	4	4	10
ST 399	9	3	4	2	1
ST 3541	8	0	1	0	0
Others	296	205	193	167	191
Total	516	367	297	250	304
blaOXA244	147 *1 DP	61	28	18	20

Table 14. Subtypes of OXA detected in *E. coli*

Gene	Number of isolates				
	2023	2022	2021	2020	2019
blaOXA48	249	230 *1 DP	206 *1 DP	178	200 *1 DP
blaOXA181	31 *2 DP	13 *1 DP	20 *1 DP	21 *1 DP	29 *2 DP
blaOXA244	147 *1 DP	61 *1 DP	28	18	20
Others	5	1	2	4	2
Total	432	305	256	221	251

Table 15. Top (9 as only 9 ST>2 isolates) sequence types detected in *K. oxytoca* in 2023 with the number of isolates of the ST in each of the previous 4 years

Sequence type	Number of isolates				
	2023	2022	2021	2020	2019
ST 36	10	1	0	3	3
ST 416	9	3	2	7	6
ST 176	8	7	7	4	8
ST 223	7	15	10	4	7
ST 2	6	2	0	2	6
ST 186	4	1	0	0	2
ST 226	4	1	0	0	0
ST 52	4	1	0	0	0
ST 53	3	6	0	3	0
Others	50	50	59	74	63
Total	105	87	78	97	95
blaOXA244	0	0	0	0	0

Table 16. Top 10 sequence types detected in *Enterobacter cloacae* in 2023 with the number of isolates of the ST in each of the previous 4 years

Sequence type	Number of isolates				
	2023	2022	2021	2020	2019
ST78	38	22	23	61	51
ST527	28	1	9	1	1
ST66	27	31	26	30	30
ST88	23	5	5	3	7
ST269	21	46	35	2	4
ST141	18	0	0	6	0
ST97	11	3	4	7	3
ST45	11	8	1	2	3
ST145	11	10	6	11	8
ST133	9	7	6	3	1
ST796	9	19	4	0	1
Others	117	100	96	101	96
Total	323	252	215	227	205
blaOXA244	0	0	0	0	0

Table 17. Top 10 sequence types detected in *Citrobacter freundii* complex in 2023 with the number of isolates of the ST in each of the previous 4 years

Sequence type	Number of isolates				
	2023	2022	2021	2020	2019
ST22	34	35	13	21	14
ST420	15	21	16	36	26
ST111	8	5	4	0	1
ST98	6	5	9	2	2
ST116	6	10	6	7	3
ST62	5	7	4	8	4
ST415	5	5	3	3	2
ST261	4	2	1	3	0
ST95	4	2	1	2	0
ST96	3	2	0	2	1
ST114	3	0	2	2	2
ST942	3	0	0	0	0
ST1027	3	0	0	0	0
Others	62	63	63	36	55
Total	161	157	122	122	110
blaOXA244	0	0	0	0	0

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.

ENDS