

Carbapenemase-producing Enterobacterales and *Pseudomonas* spp. in New Zealand, 2024

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Prepared by/Authors:

Meghna Ramchandani, Kristin Dyet, Hilary Miller, Shamma Santa Agata, Julianna Lees, Juliet Elvy

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REVIEWED BY: Andrea McNeill and Michael Addidle

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EXECUTIVE SUMMARY

- Carbapenem-resistant Enterobacterales and *Pseudomonas* spp. are a major global health concern and remain World Health Organization (WHO) priority pathogens, due to limited available treatment options.
- Carbapenemase-producing organisms (CPO) are not notifiable in New Zealand. Surveillance relies on diagnostic microbiology laboratories voluntarily submitting all confirmed or suspected CPOs to PHF Science, along with patient metadata, susceptibility data and available travel history.
- The number of detections of carbapenemase-producing Enterobacterales (CPE) in New Zealand is increasing, with the majority of the isolates identified as carbapenemase-producing *Escherichia coli*, followed by *Klebsiella* species.
- Most CPE in New Zealand are identified through screening specimens. The proportion of CPE isolated from clinical specimens has remained stable, although the absolute number of clinical CPE isolates has increased as the total number of CPE detections has risen.
- The predominant carbapenemase genes in CPE in 2024 were subtypes of NDM and OXA-48-like β -lactamases.
- There was a modest increase in the number of CPE with more than one carbapenemase gene in 2024. The most common combination was isolates with both an NDM and OXA-48-like gene.
- There is epidemiological and genomic evidence of transmission of CPE within New Zealand in 2024. This highlights the importance of ongoing genomic surveillance of these pathogens.
- Only a small number of carbapenemase-producing *Pseudomonas* spp. (CPP) were identified in 2024, with the predominant carbapenemase being VIM.
- Genomic analyses indicate that whilst there is significant variation and diversity in the CPE and CPP identified in New Zealand, many of the globally recognised “high-risk clones” are present.
- Ongoing prospective surveillance is important for monitoring trends and for the prompt identification of transmission events. Enhancing the epidemiological data available would help to strengthen AMR surveillance.

BACKGROUND

Acquired carbapenem resistance in gram-negative pathogens is a major, on-going public health concern due to the high morbidity and mortality associated with these infections (World Health Organization, 2024). Carbapenemase genes confer resistance to carbapenems, antimicrobials reserved for treating severe bacterial infections with resistant organisms, and many other β -lactams antimicrobials. Carbapenemase genes are commonly found on plasmids, along with genes conferring resistance to multiple other classes of antimicrobials, leading to multidrug-resistance (Queenan AM & Bush K, 2007). Such plasmids can frequently transfer between bacteria and play a critical role in the spread of antimicrobial resistance.

The acquired or transferable carbapenemases found in gram negative bacteria belong to three of the four major classes of β -lactamases: classes A, B and D (Queenan AM & Bush K, 2007).

- Ambler class A includes IMI, KPC and GES enzymes.
- Ambler class B are metallo- β -lactamases (MBLs), which include NDM, VIM and IMP.
- Ambler class D includes the OXA-23, OXA-40, OXA-48 and OXA-51 groups of β -lactamases.

New Zealand diagnostic microbiology laboratories are requested to refer all confirmed or suspected carbapenemase-producing organisms (CPO) to PHF Science for confirmation and further investigation. This report summarises the characteristics of carbapenemase-producing Enterobacterales (CPE) and carbapenemase-producing *Pseudomonas* spp. (CPP) in 2024.

Previous CPE and CPP reports are available on the PHF Science website at <https://www.phfscience.nz/expertise/public-health/antimicrobial-resistance>.

METHODS

Diagnostic microbiology laboratories were asked to submit all confirmed or suspected CPOs to PHF Science, together with patient metadata, susceptibility data, and relevant travel history. Isolates from screening specimens and clinical infections were included.

Non-duplicate isolates, with a carbapenemase gene detected by the referring laboratory, underwent Illumina-based whole genome sequencing (WGS). Isolates that were carbapenemase PCR negative, or had not been tested by PCR by the referring laboratory, underwent phenotypic testing, including the modified carbapenem inactivation method (mCIM) (Clinical and Laboratory Standards Institute, 2024). All mCIM positive isolates were characterised by Illumina-based sequencing.

Selected isolates, including all with an IMI gene, were characterised using Nanopore-based long-read WGS to determine the location of the carbapenemase gene. Isolates with chromosomally located carbapenemase genes were excluded from this report.

For WGS analysis, genomic DNA was extracted using the Chemagic 360 (Perkin Elmer) or the Roche High Pure PCR template preparation. DNA libraries were created using the plexWell Library Preparation kit (SeqWell), purePlex Library Preparation kit (SeqWell) or the gDNA Rapid Barcoding kit (Oxford Nanopore Technologies), and sequencing was performed using Illumina or Nanopore technology. Illumina data were analysed using an in-house developed pipeline linking together open-source packages and in-house scripts, which enables the carbapenemase gene subtype, the acquired resistome and the multilocus sequence type to be determined. Open-source packages included mlst v2.19.0 (Seemann T), AMRfinderplus v4.0.3 (Feldgarden M et al., 2021) and Mob Suite v3.1.6 (Robertson J & Nash JHE, 2018). Nanopore sequencing data were assembled using Flye (Kolmogorov M et al., 2019). Hybrid Illumina and long-read assembly was performed using Pilon (Walker BJ et al., 2014). To investigate the genomic relatedness of isolates, core genome multilocus sequence typing (cgMLST) was performed using chewBBACA v.3.2.0 (Silva M, 2018) for *E. coli*, *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* using the schemas available at <https://www.cgmlst.org/ncs>. SNP typing using either core genome SNP analysis, Snippy v. 4.6 (Seemann T), or Split Kmer analysis, SKA v. 1.0 (Harris SR, 2018) was performed to provide further resolution of clusters where required.

LIMITATIONS

As CPOs are not a notifiable disease in New Zealand, referral of isolates to PHF Science is voluntary, and the true number of CPO detections is likely to be underestimated.

Interpretation of travel-associated CPO surveillance data is limited by incomplete or inconsistently collected travel histories. Collection of travel history relies on patients being asked about relevant travel and healthcare exposures, and on this information being accurately documented and communicated to PHF Science. Consequently, travel-associated acquisition may be underestimated or misclassified.

PHF Science began requesting antimicrobial susceptibility data from diagnostic laboratories for CPOs in 2021. In 2025, the range of antimicrobials for which susceptibility data were collected was expanded to include amikacin, aztreonam-avibactam, cefepime, cefiderocol, ceftriaxone, ceftazidime, ceftazidime-avibactam, ceftolozane-tazobactam, colistin, and tobramycin. Susceptibility results for these additional antimicrobials will be reported for the first time in the 2025 report, but are not included in this 2024 report.

RESULTS

CARBAPENEMASE-PRODUCING ENTEROBACTEREALES

Numbers of carbapenemase-producing Enterobacterales

A total of 296 distinct CPE were isolated from 247 patients in 2024 (Figure 1 and Table 1). The number of CPE identified in New Zealand has increased in the last two years, with 46.2% of all CPE identified in New Zealand found in the two-year period from 2023 to 2024.

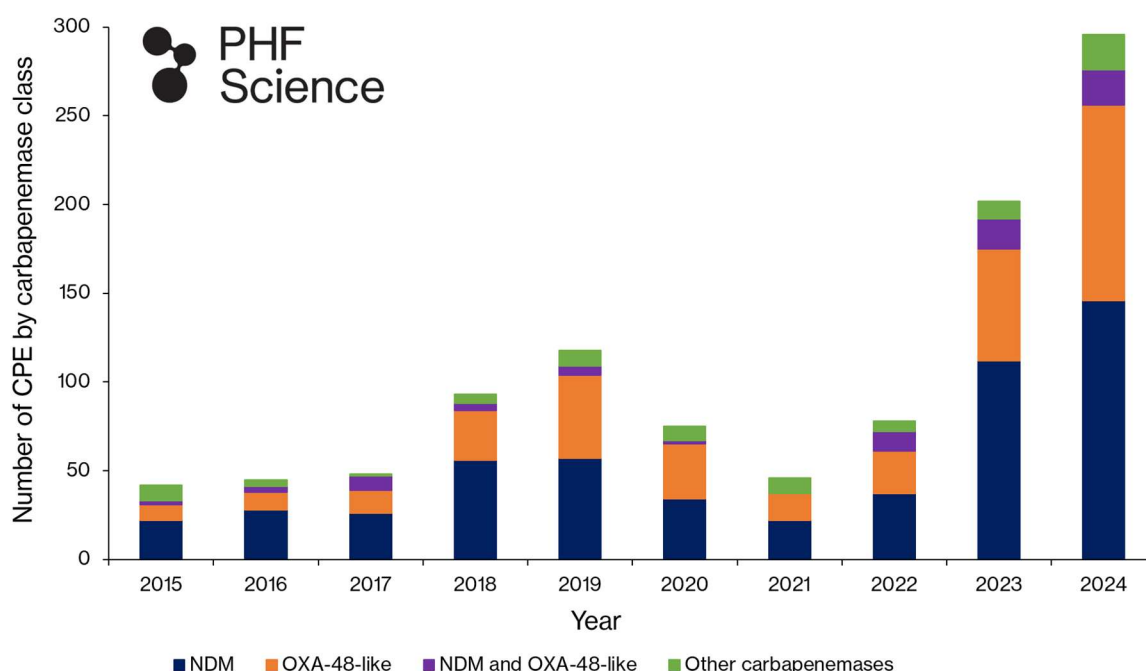


Figure 1: Number of carbapenemase-producing Enterobacterales isolates identified in New Zealand, by carbapenemase class, from 2015 to 2024

In 2024, the species of CPE were predominantly *Escherichia coli* (76.7%, 227/296), followed by *Klebsiella* spp. (15.5%, 46/296). Thirty-seven patients had more than one CPE identified: one patient had five distinct CPE, two patients had four CPE, four patients had three CPE, and 30 patients had two CPE (Appendix Table A1). Both the number of CPE and the number of patients from whom CPE were isolated from increased in 2024 compared to 2023. In 2023, a total of 202 distinct CPE were isolated from 176 patients, reflecting an increase of 94 isolates and 71 additional patients. The increase was largely due to a 40.1% increase in the number of carbapenemase-producing *E. coli*, from 162 isolates in 2023 to 227 isolates in 2024. A similar trend was observed in carbapenemase-producing *Klebsiella* species, which doubled, from 23 isolates in 2023 to 46 in 2024.

Table 1: Types of carbapenemase genes identified among carbapenemase-producing Enterobacterales by species, 2024

Carbapenemase type and subtype	Number of isolates per species					All species
	<i>Escherichia coli</i>	<i>Klebsiella</i> spp.	<i>Enterobacter cloacae</i> complex	<i>Citrobacter</i> spp.	<i>Proteus mirabilis</i>	
NDM	111	21	2	11	1	146
NDM-1	3	8 ¹	2	5 ⁶	1	19
NDM-4	0	2 ¹	0	0	0	2
NDM-5	102	8 ²	0	6 ⁷	0	116
NDM-7	4	2 ³	0	0	0	6
NDM-13	1	0	0	0	0	1
NDM-91	1	0	0	0	0	1
NDM-1 & NDM-5	0	1 ¹	0	0	0	1
OXA-48-like	99	10	0	0	1	110
OXA-48	20	0	0	0	0	20
OXA-181	30	4 ¹	0	0	1	35
OXA-232	0	3 ¹	0	0	0	3
OXA-244	9	0	0	0	0	9
OXA-484	13	0	0	0	0	13
OXA-1181	1	0	0	0	0	1
OXA-1205	16	3 ¹	0	0	0	19
OXA-1207	10	0	0	0	0	10
NDM & OXA-48-like	12	8	0	0	0	20
NDM-1 & OXA-48	0	1 ¹	0	0	0	1
NDM-1 & OXA-181	0	1 ¹	0	0	0	1
NDM-5 & OXA-181	6	5 ¹	0	0	0	11
NDM-5 & OXA-232	1	1 ¹	0	0	0	2
NDM-5 & OXA-484	1	0	0	0	0	1
NDM-5 & OXA-1205	2	0	0	0	0	2
NDM-5 & OXA-1207	2	0	0	0	0	2
Other carbapenemase genes	5	7	6	2	0	20
IMI-13	0	0	1	0	0	1
IMP-4	0	3 ⁴	5	2 ⁸	0	10
KPC-2	1	1 ¹	0	0	0	2
KPC-3	0	2 ¹	0	0	0	2
OXA-23	4	0	0	0	0	4
VIM-1	0	1 ⁵	0	0	0	1
Total	227	46	8	13	2	296⁹

Footnotes Table 1

1. *Klebsiella pneumoniae*
2. Eight isolates of *K. pneumoniae*, and one isolate each of *Klebsiella aerogenes* and *Klebsiella oxytoca*
3. One isolate each of *K. pneumoniae* and *K. oxytoca*
4. Two isolates of *K. oxytoca* and one isolate of *K. pneumoniae*
5. *Klebsiella variicola*
6. One isolate each of *Citrobacter freundii*, *Citrobacter braakii* and *Citrobacter* spp., and two *Citrobacter youngae*
7. Three isolates of *C. freundii*, two isolates of *Citrobacter farmeri*. and one isolate of *C. braakii*
8. *C. freundii* complex
9. The 296 isolates include multiple distinct CPE from 37 patients (see Appendix Table A1)

Patient demographics for carbapenemase-producing Enterobacterales

The majority of confirmed CPE were referred from patients in the Auckland region (202/296, 68.2%): specifically Counties Manukau (88/202, 29.7%), Auckland (62/202, 22.0%), and Waitematā (20/202, 6.8%), with 32 (10.8%) from patients not defined further than the Auckland region. The only other Health New Zealand districts with ten or more CPE were Canterbury (34, 11.5%) and Capital, Coast and Hutt (17, 5.7%).

41.2% of CPE were from patients ≥ 65 years of age, 26.7% of cases among people aged 45-64 years, 24.7% of cases among people aged 15-44 year, and 7.4% under 15 years.

Of the 296 CPE confirmed in 2024, the sample site was available for 294 isolates (Table 2). Among the 65 CPE from clinical specimens, 75.4% (49/65) were from urinary sources, 16.9% (11/65) were from sterile sites, 4.6% (3/65) were from respiratory specimens and 3.1% (2/65) were from skin and soft tissue infections (Table 2).

Table 2: Sample sources for carbapenemase-producing Enterobacterales in 2024

Specimen Site	Number of isolates	Percent
Screen ¹	229	77.4
Urine	49	16.6
Sterile site ²	11	3.7
Respiratory tract	3	1.0
Skin and Soft Tissue Infections	2	0.7
Unspecified	2	0.7
Total	296	100

1 Include isolates from rectum, groin, axilla, and faeces.

2 Include isolates from blood, tissue and sterile fluid.

In 2024, 77.9% (229/294) of CPE were isolated from screening specimens (Figure 2). The percentage of CPE isolated from screening specimens has fluctuated over the last ten years, from a high of 78.6% in 2015 to a low of 54.2% in 2017. However, since 2022, there has been a large increase in the number of CPE isolates identified, this has been accompanied by a small increase in the percentage of isolates identified from screening specimens.

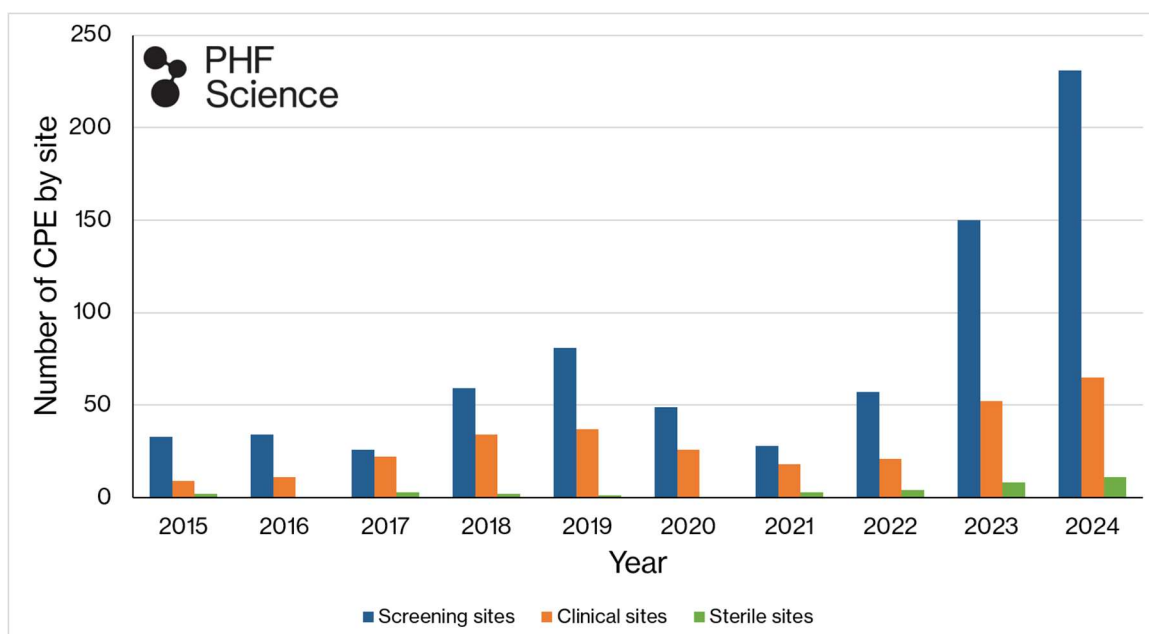


Figure 2: Number of carbapenemase-producing Enterobacterales isolated from screening, clinical and sterile sites, 2015 to 2024

Types of carbapenemase genes identified in carbapenemase-producing Enterobacterales

As observed in previous years, the most frequently identified carbapenemase genes were MBL, with various subtypes of NDM found in 56.1% (166/296) of all CPE with carbapenemase genes in 2024 (Figure 1 and Table 1) and 58.5% (631/1078) of all CPE in New Zealand to date. There were ten isolates with an IMP carbapenemase gene found in 2024 (3.4%, 10/296), and one isolate with VIM gene 0.3% (1/296). Together IMP and VIM MBLs have accounted for 3.2% (35/1078) of all CPE identified in New Zealand to date.

OXA-48-like genes were the second most common carbapenemase gene identified in New Zealand CPE in 2024. They were found in 43.9% (130/296) of all CPE in 2024 (Table 1) and 40.2% (433/1078) of all CPE in New Zealand to date.

Three other acquired carbapenemase genes were found in New Zealand CPE in 2024. Four *E. coli* isolates contained OXA-23, a gene more commonly found in isolates belonging to the *Acinetobacter calcoaceticus-baumannii* complex. To date, there have been 19 isolates with an OXA-23 carbapenemase gene identified in New Zealand. Four further isolates contained KPC, which have been found in 2.4% (26/1078) of all CPE in New Zealand to date, of which 22 were in *K. pneumoniae*, two in *E. coli* and one was in each of

an isolate belonging to the *Enterobacter cloacae* complex and a *Klebsiella oxytoca*. In 2024, there was one *E. cloacae* complex isolate with an acquired IMI gene.

In 2024, 21 isolates were identified that contained more than one carbapenemase gene (Table 1). Of these, 20 isolates contained an NDM and an OXA-48-like carbapenemase gene and one contained two NDM genes. Isolates with more than one carbapenemase gene are becoming more common. To date 72 CPE with an NDM and an OXA-48-like gene have been found, with 27.8% (20/72) of these found in 2024.

Probable place of acquisition of carbapenemase–producing Enterobacterales

The probable place of acquisition of all identified CPE is shown in Table 3. The probable place of acquisition is determined by the reported travel history; patients without any recent overseas travel history are assumed to have acquired CPE in New Zealand.

Of the 296 CPE isolates, 232 were from patients with known travel history, while 64 were from patients with unknown travel history (Table 3). Of the CPE from patients with known travel history, most (182/232, 78.9%) were likely to have been acquired overseas, specifically in the Indian subcontinent (43.1%, 100/232), other parts of Asia (10.3%, 24/232), the Western Pacific (8.6%, 20/232) or other known country/overseas 16.8% (38/232).

The 296 CPE in 2024 were cultured from 247 patients, of which 76.9% (190/247) had known travel history, 76.8% (146/190) had recently travelled overseas and 25.3% (48/190) received healthcare while overseas. Of patients that had travelled overseas, 51.7% (76/147) were likely to have acquired their carbapenemase genes in the Indian subcontinent, 14.3% (21/147) in other parts of Asia, 10.9% (16/147) in the Western Pacific, and 22.4% (33/147) in other parts of the world. Patients with CPE that had been overseas but had not been hospitalised, had travelled to a wide range of regions, with the most common being the Indian subcontinent (56.1%, 55/98) and other parts of Asia (14.3%, 14/98).

Table 3: Probable place of acquisition of carbapenemase-producing Enterobacterales, 2024

Carbapenemase type and subtype	Number of isolates from each probable region of acquisition ¹							Total
	Indian subcontinent	New Zealand ²	Other parts of Asia ³	Other known country ⁴	Western Pacific	Overseas ⁵	Not known ⁶	
NDM	44	24	17	4	14	9	34	146
NDM-1	3	3	1	2	4	1	5	19
NDM-4	1	0	0	0	1	0	0	2
NDM-5	37	21	15	2	4	8	29	117
NDM-7	1	0	0	0	5	0	0	6
NDM-13	0	0	1	0	0	0	0	1
NDM-91	1	0	0	0	0	0	0	1
NDM-1 & NDM-5	1	0	0	0	0	0	0	1
OXA-48-like	44	17	7	10	2	7	23	110
OXA-48	0	7	5	1	0	3	4	20
OXA-181	10	8	1	6	0	1	10	35
OXA-232	2	0	0	1	0	0	0	3
OXA-244	2	1	0	2	0	1	3	9
OXA-484	8	0	0	1	1	1	2	13
OXA-1181	1	0	0	0	0	0	0	1
OXA-1205	15	1	0	0	1	1	1	19
OXA-1207	6	0	1	0	0	0	3	10
NDM & OXA-48-like	12	1	0	2	0	0	5	20
NDM-1 & OXA-48	0	0	0	1	0	0	0	1
NDM-1 & OXA-181	0	0	0	1	0	0	0	1
NDM-5 & OXA-181	5	1	0	0	0	0	5	11
NDM-5 & OXA-232	2	0	0	0	0	0	0	2
NDM-5 & OXA-484	1	0	0	0	0	0	0	1
NDM-5 & OXA-1205	2	0	0	0	0	0	0	2
NDM-5 & OXA-1207	2	0	0	0	0	0	0	2
Other carbapenemase genes	0	8	0	6	4	0	2	20
IMI-13	0	0	0	0	1	0	0	1
IMP-4	0	7	0	0	2	0	1	10
KPC-2	0	0	0	2	0	0	0	2
KPC-3	0	0	0	2	0	0	0	2
OXA-23	0	1	0	1	1	0	1	4
VIM-1	0	0	0	1	0	0	0	1
Total	100	50	24	22	20	16	64	296¹

Footnotes Table 3

- 1 Includes multiple isolates from 37 patients who had multiple distinct CPE (see Appendix Table A1). Other part of Asia = all Asia other than the Indian subcontinent. New Zealand = no recent travel history. Other known country = travel to multiple known countries or regions such as the Americas, Africa and Europe. Overseas = travel to an unspecified country. Not known = no travel history available.
- 2 Includes 50 isolates from patients with no recent travel history indicating their CPE was most likely acquired in New Zealand, or they contained a CPE that was genomically related to a known cluster in New Zealand. The likely source of transmission was determined for nine of the isolates, but not for the other 41 CPE.
- 3 All Asia other than the Indian subcontinent.
- 4 Nine isolates from eight patients who travelled to Europe.
Seven isolates from four patients who travelled to Africa.
Two isolates from two patients who travelled to the Americas.
Two isolates from two patients who travelled to the Eastern Mediterranean.
Two isolates from two patients who travelled to multiple international countries.
- 5 Sixteen isolates from fifteen patients who had recent travel to an unspecified country.
- 6 Isolates from 64 patients where the travel history was not reported.

Carbapenemase-producing Enterobacterales phenotypic antimicrobial susceptibility testing results

Referring laboratories were asked to provide PHF Science with their susceptibility results (Table 4). No data were supplied for 101 isolates (34.1%), with data on 3-10 antimicrobials supplied for most isolates (60.5%). Multidrug-resistance, defined as resistance to three or more antimicrobial classes (Magiorakos AP, 2012), was common. There were exceptions, as nine isolates with an OXA carbapenemase were not multidrug-resistant, as they only were resistant to two antimicrobials despite susceptibility data being available for at least four antimicrobials.

A proportion (21.6%, 64/296) of CPE remained susceptible to meropenem, particularly isolates with OXA-48-like carbapenemases: OXA-181 (19 isolates), OXA-48 (10 isolates), OXA-1205 (10 isolates), OXA-484 (7 isolates), OXA-1207 (5 isolates), OXA-244 (4 isolates), IMP-4 (4 isolates), OXA-23 (3 isolates), OXA-1181 (1 isolate) or NDM-1 (1 isolate).

Resistance genes found in carbapenemase-producing Enterobacterales

WGS data were available for all CPE in 2024. Most CPE contained multiple resistance genes, including genes conferring resistance to fluoroquinolones (270, 91.2%), cephalosporins (224, 75.7%), sulphonamides (218, 73.6%), macrolides (217, 73.3%), trimethoprim (215, 72.6%), aminoglycosides (111, 37.5%), and tetracycline (154, 52.0%).

Extended-spectrum β -lactamase (ESBL) genes were identified in 129 CPE. All carried a CTX-M gene, with the most common subtype being CTX-M-15, found in 104 isolates.

A total of 103 (34.8%) isolates contained a mutation in the *ftsI* gene likely to confer resistance to cefiderocol. Of these 76 contained an NDM gene, 20 contained an OXA-48-like gene and seven contained both an NDM and an OXA-48-like gene. Isolates with a mutation in the *ftsI* gene were isolated from 89 patients, 71 of whom had known travel history. The most common region of travel was the Indian subcontinent (46/71, 64.8%).

Thirty-six isolates from 31 patients contained a 16S ribosomal methyl transferase gene, likely to confer high-level resistance to all clinically relevant aminoglycosides. Travel history was known for 28 of the 31 patients, with 21 (75.0%) reporting recent international travel. The most common region of travel was the Indian subcontinent (61.9%, 13/21).

Fifteen isolates from 15 different patients contained the mobile colistin resistance genes. Thirteen isolates had *mcr9* gene, while two isolates had the *mcr1* gene. In addition to this, 18 isolates contained the *pmrB*_R256G mutation associated with colistin resistance.

Table 4: Susceptibility results for CPE in 2024, generated by diagnostic laboratories interpreted by EUCAST 2024 breakpoints

Antimicrobial ¹	Percentage of isolates for each carbapenemase group											
	Total CPE (n=296)			MBL ² (n=157)			NDM and OXA (n=20)			OXA-48-like (n = 110)		
	S ³	R ³	No. tested	S ³	R ³	No. tested	S ³	R ³	No. tested	S ³	R ³	No. tested
Amoxicillin-clavulanate	0.0	100.0	182	0.0	100.0	97	0.0	100.0	10	0.0	100.0	70
Cefoxitin	20.4	77.3	172	1.1	97.8	90	0.0	100.0	8	49.3	46.4	69
Ciprofloxacin	16.5	81.4	188	24.5	73.5	102	0.0	100.0	11	8.6	88.6	70
Co-trimoxazole	35.0	64.5	183	22.2	77.8	99	25.0	75.0	8	54.2	44.4	72
Ertapenem	7.4	91.4	81	4.6	95.5	44	0.0	100.0	7	15.4	80.8	26
Fosfomycin	92.9	7.1	56	96.4	3.6	28	66.7	33.3	3	100.0	0.0	21
Gentamicin	63.5	35.9	192	54.4	44.7	103	9.1	90.9	11	86.3	13.7	73
Imipenem	41.1	57.1	56	6.7	90.0	30	0.0	100.0	2	100.0	0.0	21
Meropenem ⁴	35.6	55.0	180	5.1	83.8	99	0.0	81.8	11	89.2	6.2	65
Nitrofurantoin	79.2	20.0	120	76.1	22.4	67	71.4	28.6	7	88.4	11.6	43
Norfloxacin	16.2	81.9	105	23.1	75.4	65	0.0	100.0	5	6.1	90.9	33
Piperacillin-tazobactam	1.3	98.7	150	2.3	97.7	86	0.0	100.0	8	0.0	100.0	52
Trimethoprim	27.1	72.9	129	15.1	84.9	73	12.5	87.5	8	50.0	50.0	44

¹ Data on 13 antimicrobials were collected. Additional antimicrobials will be included in the 2025 report (see the limitations section for details).

² Includes all isolates with an MBL gene only.

³ S = susceptible, R = resistant ≥ 90% Susceptible 70 – 89% Susceptible < 70% Susceptible

⁴ The 64 meropenem-susceptible isolates contained either OXA-181 (19), OXA-1205 (10), OXA-48 (10), OXA-484 (7), OXA-1207 (5), OXA-244 (4), IMP-4 (4), OXA-23 (3), OXA-1181 (1) or NDM-1 (1).

Multilocus sequence types identified in carbapenemase-producing Enterobacterales

The 7-gene multilocus sequence type (MLST) was available for 96.9% of *E. coli* isolates (220/227) with acquired carbapenemase genes. There were 72 distinct *E. coli* sequence types found, with only 12 sequence types found in five or more isolates (Table 5).

Table 5: Sequence types found in carbapenemase-producing Enterobacterales in 2024

Species/ sequence type	No. of isolates	Carbapenemase genes present (No. of isolates)
<i>Escherichia coli</i>¹	227	
ST167	22	NDM-5 (13), OXA-1207 (2), NDM-91 (1), OXA-48 (1), OXA-181 (1), OXA-244 (1), OXA-484 (1), OXA-1205 (1), NDM-5 & OXA-1207 (1)
ST410	21	NDM-5 (5), NDM-484 (5), NDM-7 (2), OXA-1207 (2), OXA-181 (2), NDM-1 (1), OXA-48 (1), NDM-5 & OXA-181 (1), NDM-5 & OXA-1205 (1), NDM-5 & OXA-484 (1)
ST405	16	NDM-5 (13), OXA-181 (2), NDM-5 & OXA-181 (1)
ST648	15	NDM-5 (13), OXA-1207 (1) and OXA-181 (1)
ST131	13	OXA-48 (8) ² , OXA-1205 (2), NDM-5 (1), NDM-13 (1), OXA-181 (1),
ST617	11	NDM-5 (6), OXA-181 (3), OXA-1205 (1), NDM-5 & OXA-1207 (1)
ST69	9	OXA-244 (4), NDM-5 (2), NDM-5 and OXA-181 (2), OXA-48 (1)
ST361	7	NDM-5 (7)
ST372	6	OXA-181 (5) ³ , OXA-1205 (1)
ST38	6	OXA-244 (2), OXA-181 (2), OXA-48 (1), NDM-5 (1)
ST10	6	NDM-5 (3), OXA-23 (1), OXA-484 (1), OXA-48 (1)
ST443	5	OXA-181 (2), OXA-1205 (1), OXA-244 (1), NDM-5 (1)
Other ST	83	
Unknown ST	7	NDM-5 (3), NDM-1 (1), OXA-1207 (1), OXA-484 (1), OXA-23 (1)
<i>Klebsiella pneumoniae</i>	40	
ST147	8	NDM-5 & OXA-181 (3), NDM-5 (2), NDM-1 (2), OXA-181 (1)
ST11	2	NDM-1 (1), NDM-4 (1)
ST14	2	NDM-5 (1), OXA-181 (1)
ST15	2	NDM-4 (1), NDM-1 & OXA-48 (1)
ST16	2	NDM-5 & OXA- 181 (2)
ST437	2	OXA-232 (1), NDM-5 & OXA-232 (1)
Other ST	21	
Unknown ST	1	NDM-5 (1)

1 Limited to ST with 5 or more isolates

2 Linked to a community cluster in the Wellington region

3 Linked to a cluster of cases in the Auckland region

Multilocus sequence types were available for 39 *K. pneumoniae* isolates. Twenty-seven distinct sequence types were found, with the most common sequence type, ST147, found in eight isolates (Table 5).

Transmission of carbapenemase–producing Enterobacterales in New Zealand

Genome-wide analyses were undertaken to investigate the genetic relatedness of CPE in 2024, which were compared to other CPE in the PHF Science database. These analyses provide greater resolution than 7-gene MLST and were undertaken in near-real time to detect any genomic clusters of CPE isolates in New Zealand. Data were combined with epidemiological information provided by referring laboratories. No new clusters were identified in 2024, although new isolates belonging to two previously identified clusters were detected.

Forty-three patients, with a total of 49 CPE, had no history of recent overseas travel. For 41 of these 49 isolates there was no epidemiological or genomic evidence that would support transmission in New Zealand. However, for the remaining eight isolates transmission in New Zealand may have occurred. For one patient who reported recent international travel history, genomic data indicated that their CPE was likely acquired in New Zealand. This patient had travelled to the Americas, but the isolate was genomically related to a New Zealand cluster of CPE with ST372.

The first probable transmission events involved ST372 *E. coli* with OXA-181. The first case in this cluster was reported in March 2023. Eighteen genomically related patient isolates belonging to this cluster had been detected by the end of 2024. Five new cases were identified in 2024, the last in May 2024. An investigation into this outbreak was undertaken, led by Health New Zealand Te Toka Tumai Auckland. No epidemiological links between patients were identified.

The second probable transmission event involved *E. coli* containing OXA-48 linked to a community cluster in the Wellington region that was first identified in August 2018 (related to a food outlet) (Thornley CN et al., 2025). To the end of 2024, a total of 35 genomically related isolates belonging to this cluster have been isolated. Four new isolates in this cluster were identified in 2024, the last in May 2024.

CARBAPENEMASE-PRODUCING *PSEUDOMONAS* SPP.

A total of 4 distinct CPP were isolated from four patients in 2024 (Figure 3), which is fewer than the number of CPP isolated in 2023 when seven CPP were found. All four CPP were *P. aeruginosa* and all four were derived from screening samples. Three patients with CPP were in the Auckland region (one each from Auckland, Counties Manukau and Waitematā districts), and one was from the Canterbury district. The carbapenemase genes found were VIM-2 (2 isolates), VIM-4 (1 isolate) and NDM-1 (1 isolate). Three patients had known international travel with hospitalisation overseas. Susceptibility data was supplied for three of the CPP, with all three resistant to carbapenems (3/3), piperacillin-tazobactam (3/3), fluoroquinolones (3/3) and gentamicin (3/3). Resistome data showed all isolates contained *aac(6')-II* likely to confer resistance to amikacin and tobramycin although no mutations were detected in the *ftsI* gene likely to confer resistance to cefiderocol. The 7-gene MLST was available for all four isolates, which were ST308 (2), ST233 (1), and ST235 (1).

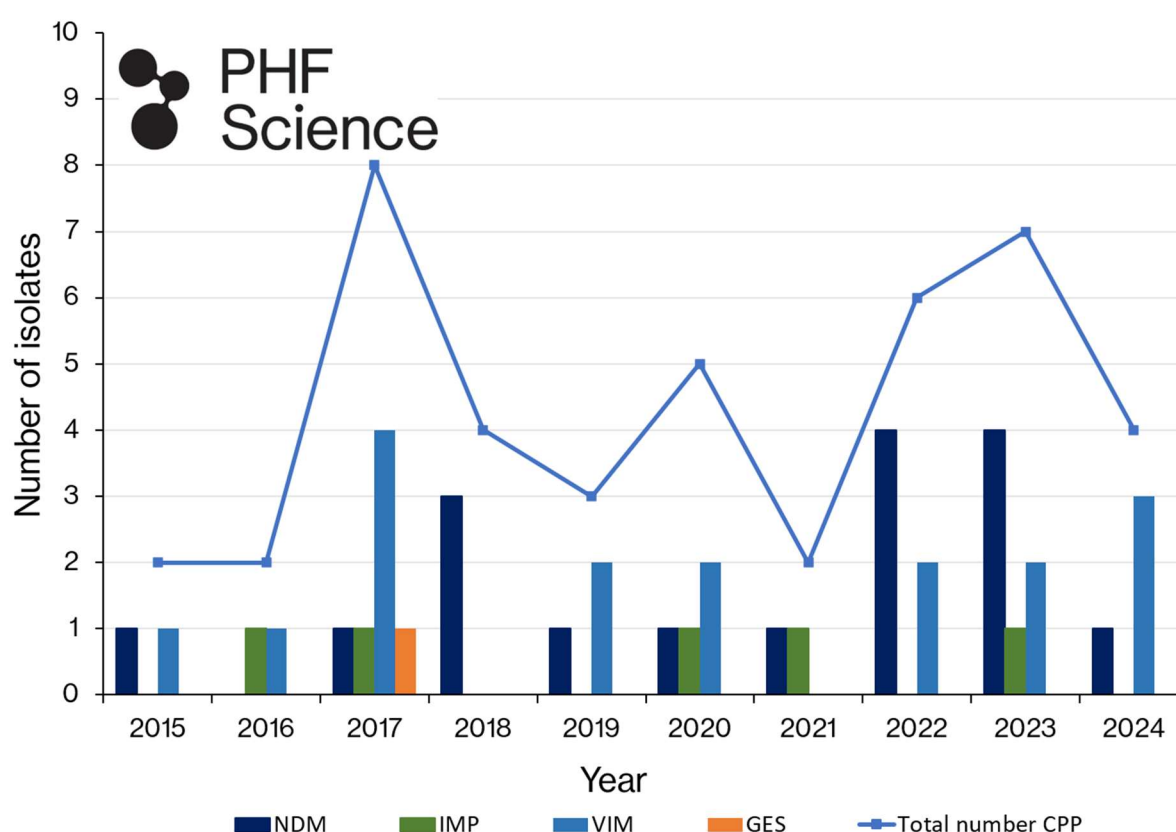


Figure 3: Number of carbapenemase-producing *Pseudomonas* spp. identified in New Zealand, by carbapenemase class, from 2015 to 2024

CONCLUSION

Carbapenem resistance continues to be of concern in New Zealand, with the number of CPE increasing by 46.5%, from 202 in 2023 to 296 in 2024. The increase was largely attributable to the increase in *E. coli* and *K. pneumoniae* with acquired carbapenemase genes. By contrast the number of *Pseudomonas* spp. with acquired carbapenemase genes decreased, although there were only 11 isolates over the two-year period. In patients with known travel history, most CPO were isolated from patients who had recently travelled overseas. This supports the theory that most CPO identified in New Zealand are acquired overseas.

In New Zealand, clinical infections due to CPE continue to be uncommon, relative to the number of CPE identified from screening. However, the number of CPE isolated from clinical sites, as well as sterile sites, has increased. This was most notable in 2023 and 2024, and is of concern, as it suggests an increasing burden of clinically significant and invasive CPE infections.

The proportion of CPO likely to have been acquired in New Zealand remains low, but the numbers are increasing. In 2023, 38 CPE were from patients with no recent travel history, but this increased to 49 isolates in 2024. It will be important to continue to monitor the number of locally acquired cases in the future. The increase in patients with CPE that have no reported recent travel history may be partially due to the limitations in the available epidemiological data. As CPO are not notifiable in New Zealand, robust epidemiological data are not available. Enhancing the epidemiological data available for surveillance would help to strengthen CPO surveillance.

NDM and OXA-48-like genes remain the dominant carbapenemase genes in CPO in New Zealand, although VIM genes were common in CPP. Numbers of CPE with multiple carbapenemase genes remain high, with the most common combination being isolates with an NDM and an OXA-48-like gene. As expected, CPO described in this report are highly multidrug resistant, with limited treatment options available.

Epidemiological and genomic evidence support some limited local acquisition of CPO in 2024. This highlights the importance of ongoing, continuous surveillance to monitor the burden and epidemiology of CPO in New Zealand and ensure clusters of genomically related isolates are detected early to support infection prevention and control activities.

REFERENCES

- Clinical and Laboratory Standards Institute. (2024). Performance Standards for Antimicrobial Susceptibility Testing M100 - 34th edition. In.
- Feldgarden M, Brover V, Gonzalez-Escalona N, Frye JG, Haendiges J, Haft DH, Hoffmann M, Pettengill JB, Prasad AB, Tillman GE, Tyson GH, & W., K. (2021). AMRFinderPlus and the Reference Gene Catalog facilitate examination of the genomic links among antimicrobial resistance, stress response, and virulence. Available at <https://github.com/ncbi/amr>. *Sci Rep.*, 11(1), 12728.
- Harris SR. (2018). SKA: split kmer analysis toolkit for bacterial genomic epidemiology. *bioRxiv* <https://doi.org/10.1101/453142>
- Kolmogorov M, Yuan J, Lin Y, & PA., P. (2019). Assembly of long, error-prone reads using repeat graphs. *Nat Biotechnol*, 37(5), 540-546. Available at <https://github.com/mikolmogorov/Flye>.
- Magiorakos AP, S. A., Carey RB, Carmeli Y, Falagas ME, Giske CG, Harbarth S, Hindler JF, Kahlmeter G, Olsson-Liljequist B, Paterson DL, Rice LB, Stelling J, Struelens MJ, Vatopoulos A, Weber JT, Monnet DL. (2012). Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. *Clin Microbiol Infect*. <https://doi.org/10.1111/j.1469-0691.2011.03570.x>.
- Queenan AM, & Bush K. (2007). Carbapenemases: the versatile β -lactamases. *Clin Microbiol Rev*, 20, 440-458.
- Robertson J, & Nash JHE. (2018). MOB-suite: software tools for clustering, reconstruction and typing of plasmids from draft assemblies. *Microb Genom.*, 4(8), e000206. Available at: <https://github.com/phac-nml/mob-suite>.
- Seemann T. mlst Available at <https://github.com/tseemann/mlst>.
- Seemann T. snippy. Available at <https://github.com/tseemann/snippy>.
- Silva M, M. M., Silva DN, Rossi M, Moran-Gilad J, Santos S, Ramirez M, Carriço JA. 2018.. doi:10.1099/mgen.0.000166. (2018). chewBBACA: A complete suite for gene-by-gene schema creation and strain identification. *Microb Genom* 4:000166. Available at <https://github.com/B-UMMI/chewBBACA>.
- Thornley CN, Kelly M, Bloomfield M, Mangalasseril L, Nesdale A, Underwood C, Dyet K, Elvy J, Szeto J, Perez H, Ren X, Woodhouse R, & RT., W. (2025). Community outbreak of OXA-48-producing *Escherichia coli* linked to food premises, New Zealand, 2018-2022. *Emerg Infect Dis*, 31(7), 1300-1308.
- Walker BJ, Abeel T, Shea T, Priest M, Abouelliel A, Sakthikumar S, Cuomo CA, Zeng Q, Wortman J, Young SK, & AM., E. (2014). Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement. *PLoS One*, 9(11), e112963. Available at <https://github.com/broadinstitute/pilon>.
- World Health Organization. (2024). *WHO Bacterial Priority Pathogens List, 2024: bacterial pathogens of public health importance to guide research, development and strategies to prevent and control antimicrobial resistance*.

APPENDIX

Table A1: Patients with multiple distinct carbapenemase-producing Enterobacterales in 2024

Patient No.	No. of CPE	Bacterial species and carbapenemase gene(s)	Travel history ¹	Healthcare received overseas?
1	5	<i>E. coli</i> NDM-5 & OXA-181, <i>E. coli</i> NDM-5 & OXA-484, <i>E. coli</i> OXA-181, <i>K. pneumoniae</i> NDM-5 & OXA-181, <i>K. pneumoniae</i> OXA-232	Indian SC	Yes
2	4	<i>C. farmeri</i> NDM-5, <i>E. coli</i> NDM-5 (ST648 and ST877), <i>K. pneumoniae</i> NDM-5	Other part of Asia	Yes
3	4	<i>E. coli</i> OXA-181, <i>K. pneumoniae</i> NDM-1 & OXA-181, <i>K. pneumoniae</i> OXA-181, <i>P. mirabilis</i> OXA-181	Africa	Yes
4	3	<i>E. cloacae</i> complex NDM-1, <i>E. coli</i> NDM-1, <i>K. pneumoniae</i> NDM-1	Not known	No
5	3	<i>E. coli</i> NDM-5, <i>E. coli</i> NDM-5 & OXA-1205, <i>K. pneumoniae</i> NDM-5 & OXA-181	Indian SC	Yes
6	3	<i>E. coli</i> NDM- (ST617 and ST648), <i>E. coli</i> OXA-484	Indian SC	No
7	3	<i>C. farmeri</i> NDM-5, <i>E. coli</i> NDM-5 (ST156 and ST648)	Indian SC	Yes
8	2	<i>C. freundii</i> NDM-5, <i>K. pneumoniae</i> NDM-5 & OXA-181	Not known	No
9	2	<i>E. coli</i> NDM-7, <i>K. pneumoniae</i> NDM-7	Western Pacific	Yes
10	2	<i>C. braakii</i> NDM-5, <i>E. coli</i> NDM-5	New Zealand	No
11	2	<i>E. coli</i> NDM-7, <i>K. oxytoca</i> NDM-7	Western Pacific	No
12	2	<i>E. coli</i> NDM-5, <i>K. aerogenes</i> NDM-5	New Zealand	No
13	2	<i>C. freundii</i> NDM-5, <i>E. coli</i> NDM-5	New Zealand	No
14	2	<i>E. coli</i> KPC-2, <i>K. pneumoniae</i> KPC-2	Europe	No
15	2	<i>E. coli</i> NDM-5, <i>E. coli</i> NDM-5 & OXA-232	Indian SC	Yes
16	2	<i>E. coli</i> NDM-5, <i>K. pneumoniae</i> NDM-5	Not known	No
17	2	<i>C. freundii</i> NDM-5, <i>E. coli</i> NDM-5	New Zealand	No
18	2	<i>Citrobacter</i> spp. NDM-1, <i>E. coli</i> NDM-1	New Zealand	No
19	2	<i>E. coli</i> NDM-5, <i>K. pneumoniae</i> NDM-5	New Zealand	No

Table A1 continued.

Patient No.	No. of CPE	Bacterial species and carbapenemase gene(s)	Travel history¹	Healthcare received overseas?
20	2	<i>E. coli</i> NDM-5, <i>E. coli</i> OXA-1207	Indian SC	No
21	2	<i>E. coli</i> NDM-5 (ST405 and ST5552)	Not known	No
22	2	<i>E. coli</i> NDM-5, <i>E. coli</i> OXA-1207	Indian SC	No
23	2	<i>E. coli</i> NDM-5 & OXA-1207, <i>K. pneumoniae</i> NDM-5 & OXA-181	Indian SC	Yes
24	2	<i>E. coli</i> OXA-1205 (ST443 and ST8025)	Indian SC	No
25	2	<i>E. coli</i> NDM-5, <i>E. coli</i> OXA-1207	Indian SC	No
26	2	<i>E. coli</i> NDM-5 (ST46 and ST1284)	Overseas	No
27	2	<i>E. coli</i> NDM-5 & OXA-181, <i>K. pneumoniae</i> NDM-5 & OXA-181	Not known	No
28	2	<i>E. coli</i> OXA-484, <i>K. pneumoniae</i> NDM-1	Indian SC	Yes
29	2	<i>E. coli</i> NDM-5, <i>K. pneumoniae</i> NDM-4	Indian SC	Yes
30	2	<i>E. coli</i> NDM-5, <i>K. pneumoniae</i> NDM-1	Indian SC	No
31	2	<i>E. coli</i> OXA-1205, <i>K. pneumoniae</i> OXA-1205	Indian SC	No
32	2	<i>E. coli</i> NDM-5 & OXA-1207, <i>E. coli</i> OXA-181	Indian SC	No
33	2	<i>E. coli</i> NDM-7, <i>K. pneumoniae</i> NDM-4	Western Pacific	Yes
34	2	<i>E. coli</i> NDM-5 & OXA-1205, <i>E. coli</i> OXA-1181	Indian SC	No
35	2	<i>E. coli</i> OXA-1205, <i>K. pneumoniae</i> OXA-1205	Indian SC	No
36	2	<i>C. freundii</i> NDM-1, <i>K. pneumoniae</i> IMP-4	Western Pacific	Yes
37	2	<i>E. coli</i> OXA-1205, <i>K. pneumoniae</i> OXA-1205	Indian SC	No

1 Travel regions as specified in Table 3. Indian SC = Indian subcontinent. Other part of Asia = all Asia other than the Indian subcontinent. New Zealand = no recent travel history. Overseas = travel to an unspecified country or multiple known countries. Not known = no travel history available.



**NEW ZEALAND INSTITUTE
FOR PUBLIC HEALTH AND
FORENSIC SCIENCE LIMITED**

- **Kenepuru Science Centre**
34 Kenepuru Drive, Kenepuru, Porirua 5022
PO Box 50348, Porirua 5240
New Zealand
T: +64 4 914 0700
- **Mt Albert Science Centre**
120 Mt Albert Road, Sandringham, Auckland 1025
Private Bag 92021, Auckland 1142
New Zealand
T: +64 9 815 3670
- **Wallaceville Science Centre**
66 Ward Street, Wallaceville, Upper Hutt 5018
PO Box 40158, Upper Hutt 5140
New Zealand
T: +64 4 529 0600
- **Christchurch Science Centre**
27 Creyke Road, Ilam, Christchurch 8041
PO Box 29181, Christchurch 8540
New Zealand
T: +64 3 351 6019

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