PHF Science

New Zealand Institute
for Public Health and
Forensic Science

CARBAPENEMASE-PRODUCING ORGANISMS (CPO)

Quarterly report

Quarter 1 (Q1) – (01 January to 31 March) 2026

Summary

- Carbapenem resistance in gram-negative bacteria continues to be of concern in New Zealand.
- A total of 111 CPO were referred to PHF Science in Q1-2026 (01 January to 31 March 2026) from 96 patients. This is an increase from Q4-2025 (93 isolates from 82 patients).
- The predominant species of CPO was *E. coli* (72.1%, 80 isolates).
- NDM genes were predominantly detected (51.4%) in this quarter, followed by OXA-48-like genes (35.1%).
- The highest number of isolates were referred from the Auckland region (56.7%), with Middlemore Hospital (27.9%, 31/111) referring the most isolates in Q1-2026 compared with other health facilities.
- Clinical infections due to CPO remain uncommon. Of the total, 84.7% (94/111) of isolates were from screening samples.
- CPO continue to be associated primarily with people who have travelled internationally. Travel history was reported for 50/96 patients, of which 96.0% (48/50) reported overseas travel in the previous 12 months.
- Of the 48 patients with a known history of overseas travel, 33.3% (16/48) received healthcare overseas.
- Where region or travel was known, the Indian subcontinent was the most frequent place of likely acquisition (61.9%, 26/42).
- Epidemiological and genomic evidence support local acquisition of CPO in some patients, although no new genomic clusters were identified in the quarter ending 31 March 2026.

Background

Carbapenemase-producing organisms (CPOs) are a significant, ongoing public health concern due to the high morbidity and mortality associated with these infections [1]. Resistance is primarily mediated by acquired carbapenemase genes, which confer resistance to carbapenems, that are often reserved for treating severe bacterial infections, and many other β-lactams antibiotics. Detection in hospitals is critical to prevent transmission between patients.

Carbapenemase genes are commonly found on plasmids, along with genes conferring resistance to multiple other classes of antimicrobials, leading to multidrug-resistance [2]. The presence of multiple resistance genes on the same plasmid, coupled with the plasmid's ability to transfer between bacteria, plays a critical role in the rapid spread of both carbapenem resistance and multidrug resistance.

Carbapenemases are classified into three Ambler classes: class A serine carbapenemases (e.g. KPC); class B metallo-β-lactamases (e.g. NDM); and class D oxacillinases (e.g. OXA-48-like enzymes) [2].

In New Zealand, based on national guidance and local epidemiology, all patients at high risk of CPO carriage should be screened on admission to healthcare facilities [3, 4]. Diagnostic microbiology laboratories are requested to refer all suspected CPO isolates to PHF Science for confirmation and further investigation. Laboratories are asked to provide susceptibility testing results and information on risk factors, such as recent travel history.

This report summarises the characteristics of CPO isolates received by PHF Science between 1 January 2026 and 31 March 2026 (Q1-2026).

Methods

Isolates with a carbapenemase gene detected by PCR by the referring laboratory underwent Illumina-based whole genome sequencing (WGS). Isolates that were PCR negative, or not tested by the referring laboratory, underwent inhibitor-based phenotypic tests, including the modified carbapenemase inactivation method (mCIM). Isolates that were positive in any of these tests also underwent WGS. Selected isolates, including all with an IMI carbapenemase, were further characterised using Nanopore-based long-read sequencing.

Genomic DNA was extracted, sequencing was performed using Illumina or Nanopore technology, and data were analysed using an in-house developed pipeline as described elsewhere [5].

Data was extracted from the PHF Science laboratory information management system on 28 April 2026 and filtered to include isolates received between 01 January 2026 and 31 March 2026. Analyses were conducted in RStudio, version 2025.09.2, Build 418.

Limitations

CPO are not a notifiable disease in New Zealand, and due to voluntary referral of isolates there is likely some degree of under ascertainment of the true number of CPO detections in New Zealand. There are also limitations to the epidemiological information available for analysis.

Information presented is based on provisional data.

Results

Species identified

There were 111 CPO referred to PHF Science from 01 January 2026 to 31 March 2026 (Q1) from 96 patients. In the previous quarter (Q4/2025 - 01 October to 31 December 2025), there were 93 CPO isolates referred from 82 patients.

In Q1 2026, the predominant CPO species detected was *Escherichia coli* (72.1%, 80/111 isolates), followed by *Klebsiella spp.* (16.2%, 18/111 isolates) (Table 1).

Table 1. Number (percent) of CPO species isolated, 01 January to 31 March 2026

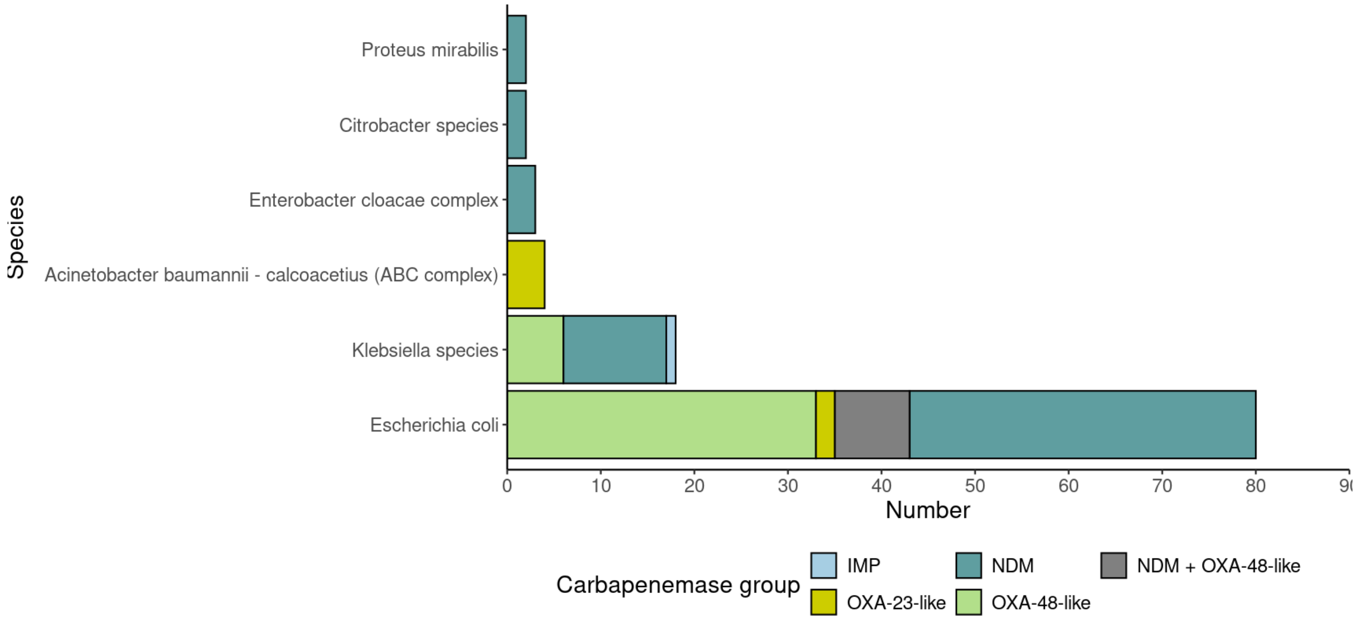
Species	**Isolates n (%)**
Escherichia coli	80 (72.1)
Klebsiella species[a]	18 (16.2)
Acinetobacter baumannii-calcoacetius complex	4 (3.6)
Enterobacter cloacae complex	3 (2.7)
Citrobacter species[b]	2 (1.8)
Proteus mirabilis	2 (1.8)
Atlantibacter subterraneus	1 (0.9)
Pseudomonas aeruginosa	1 (0.9)
Total	**111 (100.0)**

[a] *Klebsiella* spp includes *Klebsiella pneumoniae* (15), *Klebsiella michiganensis* (n=1), *Klebsiella quasipneumoniae* (n=1) and *Klebsiella variicola* (n=1).
[b] *Citrobacter spp* includes *Citrobacter freundii* (n=1) and *Citrobacter pasteurii* (n=1).

In Q1, the most common genes detected were NDM (51.4% 57/111), followed by OXA-48-like genes (35.1%, 39/111), and OXA-23 genes (5.4%, 6/111). There were also 8 isolates with both NDM + OXA-48-like genes identified (8/111, 7.2%).

Figure 1 shows the number and proportion of carbapenemase gene types within species. For the most predominant species *(E. coli*), the most common gene identified was NDM (46.2%, 37/80 isolates) and OXA-48-like (41.2%, 33/80 isolates).

Figure 1. CPO species grouped by carbapenemase gene type, 01 January to 31 March 2026



Note: Only shows species detected least twice in quarter (n = 109). Other species identified in Q1: *Atlantibacter subterraneus* (1) and *Pseudomonas aeruginosa* (1).

Sequence types

The 7-gene MLST data was available for 92.8% (103/111) of isolates). MLST provides information on isolate relatedness, although its discriminatory power is limited compared with other whole genome sequencing analysis methods.

For isolates with MLST data, 54 different sequence types were identified. There were eight sequence types found in least three isolates (Table 2). The most common ST detected among *E. coli* isolates was ST168 (16.5%, 13/79 isolates with ST identified).

Table 2. Number (percent) of CPO specimens by species and MLST, 01 January to 31 March 2026

Species/Sequence type	Isolates n (%)[1]
Escherichia coli	
ST648	13 (16.5)
ST167	11 (13.9)
ST405	7 (8.9)
ST361	6 (7.6)
ST940	3 (3.8)
ST38	3 (3.8)
ST131	3 (3.8)
Acinetobacter baumannii-calcoacetius complex	
ST2	4 (100.0)

[1] % of total isolates by species, calculated for those isolates with sequence type available (n = 103).
Note: showing data for ST found in three or more isolates. There were 46 other ST identified once or twice in 53 isolates: *Citrobacter* spp. (1 ST in 1 isolate); *Enterobacter cloacae* complex (3 ST in 3 isolates); *Escherichia coli* (additional 28 ST in 33 isolates); *Klebsiella* spp. (14 ST in 16 isolates).

Genomic clusters

Genome-wide analyses were used to identify clusters of related isolates. In Q1 2026, there were no new genomic clusters identified.

There were two new isolates found to be part of an existing cluster of isolates belonging to the *A. baumannii-calcoacetius* complex (ST-2 and the OXA-23 gene). The cluster now involves 24 isolates, with the first isolate identified in 2020. The isolates identified in this quarter were from patients that reported travel to Samoa, with one patient hospitalised in Samoa.

Indication for testing

From 01 January to 31 March 2026, 15.3% (17/111 isolates) of CPO were from clinical specimens and 84.7% (94/111 isolates) were from screening specimens (Table 3).

Table 3. Number (percent) of clinical and screening CPO specimens by referring laboratories, 01 January to 31 March 2026

Referring laboratory	Clinical isolates n (%)[1]	Screening isolates n (%)[1, 2]	Total isolates n (%)
Middlemore Hospital	3 (17.6)	28 (29.8)	31 (27.9)
Canterbury Health Laboratories	4 (23.5)	12 (12.8)	16 (14.4)
Awanui Labs, Wellington	2 (11.8)	11 (11.7)	13 (11.7)
LabPLUS, Auckland	0 (0.0)	13 (13.8)	13 (11.7)
North Shore Hospital	1 (5.9)	9 (9.6)	10 (9.0)
Awanui Labs, Auckland	0 (0.0)	9 (9.6)	9 (8.1)
PathLab Bay of Plenty	2 (11.8)	5 (5.3)	7 (6.3)
Awanui Labs, Dunedin	1 (5.9)	4 (4.3)	5 (4.5)
Waikato Hospital	2 (11.8)	2 (2.1)	4 (3.6)
Awanui Labs, Canterbury	1 (5.9)	0 (0.0)	1 (0.9)
Awanui Labs, Nelson	1 (5.9)	0 (0.0)	1 (0.9)
Whangārei Hospital	0 (0.0)	1 (1.1)	1 (0.9)
Total[2]	**17 (15.3)**	**94 (84.7)**	**111 (100.0)**

[1] Percentage calculated as referring laboratory within source of isolates.
[2] Includes isolates from axilla, rectum, groin, nose, faeces and rectum.

Referring laboratories

Over half of the CPO isolates were referred from laboratories in the Auckland region (56.7%). The laboratories referring the highest number of isolates were Middlemore Hospital (27.9%, 31/111 isolates), Canterbury Health Laboratories (14.4%, 16/111 isolates) and Awanui Labs, Wellington, and LabPLUS, Auckland (each with 11.7%, 13/111 isolates) (Table 3).

Travel history

From 01 January to 31 March 2026, travel history was available for 52.1% (50/96) of patients, of which 96.0% (48/50) indicated overseas travel in the 12 months prior to sample collection. Of patients where region of travel was known (42/50), the Indian subcontinent (61.9%, 26/42) was the most frequently reported probable region of acquisition (Table 4).

Of the patients who reported overseas travel, 33.3% (16/48) received healthcare while overseas.

Table 4. Specimens by probable region of acquisition, 01 January to 31 March 2026

Region[1]	**Isolates**[2] **n (%)**[3]	**Received healthcare overseas n (%)**[4]
Indian subcontinent	26 (61.9)	4 (25.0)
New Zealand	2 (4.8)	-
Other parts of Asia[5]	7 (16.7)	3 (18.8)
Pacific Islands	2 (4.8)	2 (12.5)
Americas	1 (2.4)	1 (6.3)
Europe	3 (7.1)	3 (18.8)
Africa	1 (2.4)	-
Overseas - no region specified	8	3 (6.3)
Total	50	16
Travel history unknown	46	-

[1] Patients with recent travel to a South and/or South-East Asian country will be more likely to be screened for a multidrug-resistant organism, such as a CPO, as recommended in the Health New Zealand screening guidance document [4].
[2] Only includes first specimen per patient-id.
[3] Percent of patients with known history and region of travel (n = 42), excludes “Overseas – no region specified” and “Travel history unknown”
[4] % of patients with overseas travel (n = 48, excludes New Zealand).
[5] All Asia other than the Indian subcontinent.

References

1. World Health Organization, *WHO Bacterial Priority Pathogens List, 2024: bacterial pathogens of public health importance to guide research, development and strategies to prevent and control antimicrobial resistance*. 2024, World Health Organization: Geneva.
2. Queenan AM and Bush K, *Carbapenemases: the versatile β-lactamases*. Clin Microbiol Rev, 2007. **20**: p. 440-58.
3. Clark M, et al., *Infection Prevention and Control and Management of Carbapenemase-producing Enterobacteriaceae. Guidelines for health care providers in New Zealand acute and residential care facilities*. 2018.
4. Health New Zealand Te Whatu Ora, *Interim minimal guidance for MDRO admission screening and placement in a NZ hospital. Available at: http://static.info.content.health.nz/docs/health-pros/topics/infection-prevention-control/Interim-minimal-guidance-for-MDRO.pdf*. June 2024.
5. Dyet K, et al., *Carbapenemase-producing organisms in New Zealand, 2023. Report number FW25038 prepared for the Ministry of Health. Available at: www.phfscience.nz*. 2025.