

CARBAPENEMASE-PRODUCING ORGANISMS (CPO)

Quarterly report
Quarter 2 (Q2) – (01 April to 30 June) 2026

Summary

This report summarises the characteristics of CPO isolates received by PHF Science between 01 April 2026 and 30 June 2026 (Q2-2026).

- Carbapenem resistance in gram-negative bacteria continues to be of concern in New Zealand.
- A total of 106 non-duplicate CPO were referred to PHF Science in Q2-2026 (01 April to 30 June 2026) from 93 patients. Similar numbers were referred in Q1-2026 (111 isolates from 96 patients).
- The predominant species of CPO was *E. coli* (69.8%, 74/106 isolates).
- NDM genes were predominant (58.5%) in this quarter, followed by OXA-48-like genes (30.2%). An additional three isolates contained both an NDM and OXA-48-like gene.
- The highest number of isolates were referred from the Auckland region (65.1%, 69/106), with Middlemore Hospital (22.6%, 24/106) referring the most isolates in Q2-2026 compared with all other healthcare facilities in New Zealand.
- Clinical infections due to CPO remain uncommon in this quarter. Of the total, 85.8% (91/106) of isolates were from screening samples.
- CPO continue to be associated primarily with people who have travelled internationally. Travel history was reported for 71/93 patients, of which 84.5% (60/71) reported overseas travel in the previous 12 months.
- Of the 60 patients with a known history of overseas travel, 26.7% (16/60) were reported to have received healthcare overseas.
- Where region of travel was known, the Indian subcontinent was the most frequent travel location (50.0%, 32/64).
- In 2026 Q2, three new clusters of genomically related CPO were identified, and additional isolates were found to cluster with two existing CPO clusters. All CPO clusters that increased in size during 2026 Q2 contained fewer than five isolates, except for an *Acinetobacter baumannii-calcoaceticus* complex cluster, which comprises 21 isolates.

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 -lactam 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.

Methods

Isolates with a carbapenemase gene detected by PCR at 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.

Genomic DNA was extracted, sequencing was performed using Illumina 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 06 August 2026 and filtered to include isolates received between 01 April 2026 and 30 June 2026. Analyses were conducted in RStudio, version 2025.09.2, Build 418.

Limitations

CPO are not notifiable 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 106 CPO referred to PHF Science from 01 April 2026 to 30 June 2026 (Q2) from 93 patients. In the previous quarter (Q1/2026 – 01 January to 31 March 2025), there were 111 CPO isolates referred from 93 patients.

In Q2 2026, the predominant CPO species detected was *Escherichia coli* (69.8%, 74/106 isolates), followed by *Klebsiella spp.* (15.1%, 16/106 isolates) (Table 1).

Table 1. Number (percent) of CPO species isolated, 01 April to 30 June 2026

Species	Isolates n (%)
<i>Escherichia coli</i>	74 (69.8)
<i>Klebsiella</i> species ^a	16 (15.1)
<i>Citrobacter</i> species ^b	6 (5.7)
<i>Acinetobacter baumannii-calcoaceticus</i> complex	4 (3.8)
<i>Enterobacter cloacae</i> complex	2 (1.9)
<i>Pseudomonas aeruginosa</i>	2 (1.9)
<i>Morganella morganii</i>	1 (0.9)
<i>Proteus mirabilis</i>	1 (0.9)
Total	106 (100.0)

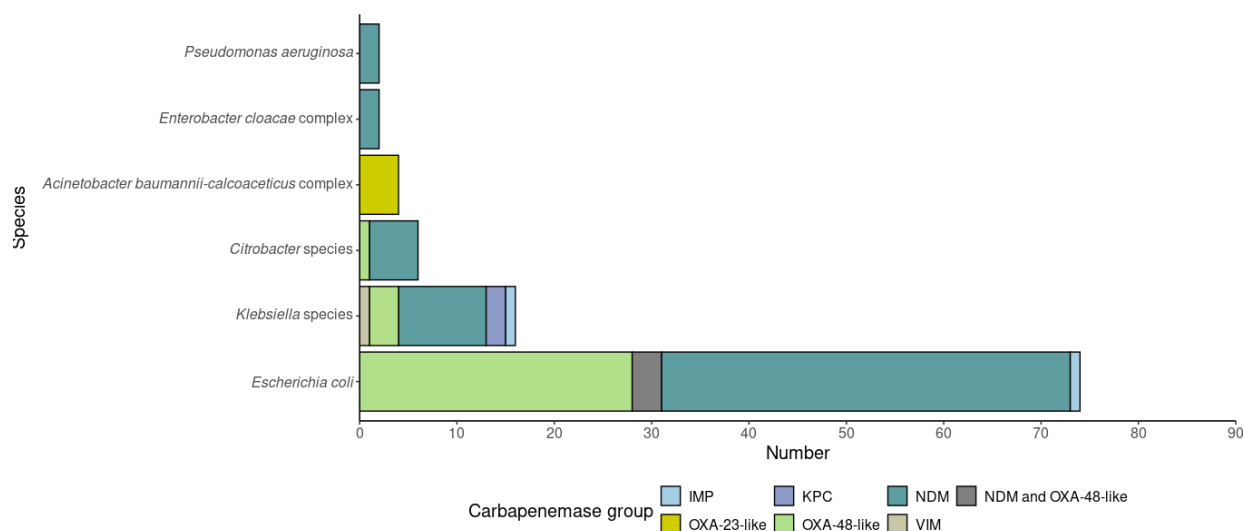
^a*Klebsiella* species includes *Klebsiella pneumoniae* (11), *Klebsiella michiganensis* (n=2), *Klebsiella quasipneumoniae* (n=1) and *Klebsiella oxytoca* (n=2).

^b*Citrobacter* species includes *Citrobacter freundii* (n=5) and *Citrobacter amalonaticus* (n=1).

In Q2, the most common genes detected were NDM (58.5% 62/106), followed by OXA-48-like genes (30.2%, 32/106). There were also 3 isolates with both NDM + OXA-48-like genes identified (3/106, 2.8%).

Figure 1 shows the number and proportion of carbapenemase gene types within species. For the most predominant species (*E. coli*), the most common carbapenemase genes identified were NDM (56.8%, 42/74 isolates) and OXA-48-like (37.8%, 28/74 isolates). All isolates with OXA-23-like genes in this quarter (4) were identified in isolates belonging to the *A. baumannii-calcoaceticus* complex.

Figure 1. CPO species grouped by carbapenemase gene type, 01 April 2026 to 30 June 2026



Note: The figure shows species detected at least twice in quarter 2 (n = 104). Other species identified in Q2: *P. mirabilis* (1) and *M. morganii* (1).

Sequence types

All isolates were characterised using WGS and 7-gene multilocus sequence typing (MLST) data was available for 97.2% (103/106) of isolates). MLST provides information on isolate relatedness, although its discriminatory power is limited compared with other whole genome sequencing-based typing methods.

For isolates with MLST data, 49 different sequence types (STs) were identified. Eleven sequence types were found in at least three isolates (Table 2). Within *E. coli*, the most common STs were ST131 and ST405, detected in 9 isolates each (12.3%) of 73 *E. coli* with MLST data.

Table 2. Number (percent) of CPO isolates by species and MLST, 01 April to 30 June 2026

Species/Sequence type	Isolates n (%) ^a
<i>E. coli</i> ^b	
ST131	9 (12.3)
ST405	9 (12.3)
ST167	8 (11.0)
ST648	7 (9.6)
ST410	6 (8.2)
ST224	4 (5.5)
ST38	3 (4.1)
ST44	3 (4.1)
<i>Klebsiella</i> species	
ST11	4 (25.0)
ST437	3 (18.8)
<i>A. baumannii-calcoaceticus</i> complex	
ST2	4 (100.0)

^a % of total isolates by species, calculated for those isolates with sequence type available (n = 103).

^b Isolates with no ST available were found in: *E. coli* (1), *M. morganii* (1) and *P. mirabilis* (1).

Note: Table showing data for ST found in three or more isolates. There were 39 other ST identified once or twice in 43 isolates: *Citrobacter* spp. (6 ST in 6 isolates); *E. cloacae* complex (2 ST in 2 isolates); *E. coli* (additional 20 ST in 24 isolates); *Klebsiella* spp. (additional 9 ST in 9 isolates); *P. aeruginosa* (2 ST in 2 isolates).

Genomic clusters

Genome-wide analyses were used to identify clusters of closely related isolates. In 2026 Q2, there were three new genomic clusters identified (Table 3). There were also two isolates identified that belonged to an existing *K. pneumoniae* cluster and two isolates that belonged to an existing cluster of *A. baumannii-calcoaceticus* complex isolates.

The first new cluster involved two ST18455 *E. coli* isolates with the OXA-1205 gene. Both isolates were identified in 2026 Q2 and both patients reported a travel history to India.

The second new cluster identified in 2026 Q2 involved two ST410 *E. coli* isolates. Both isolates carried the NDM-5 gene and one also carried the OXA-1207 gene. The cluster involves patients in the Auckland and Waitematā regions. One patient had no history of international travel, and travel history was not available for the other patient.

The third new cluster involved two ST131 *E. coli* isolates that carried the OXA-244 gene. The first isolate was from 2025 Q3 from a patient from the Waitematā region with recent travel to Europe. The second isolate, identified in the current quarter, was from a patient in Canterbury with no history of international travel.

In Q2 2026, two ST11 *K. pneumoniae* isolates with the NDM-4 gene were found to cluster with a previously identified genomic cluster, which contained two isolates (1 each) from 2025 Q1 and 2026 Q1. The new isolates were from patients in the Waitematā region, with neither reporting recent travel history.

In Q2 2026, two *A. baumannii-calcoaceticus* complex isolates were found to be part of an existing cluster. The first isolate in this cluster was identified in 2020, with a total of 21 isolates found to the end of June 2026. All isolates were ST2 and contained an OXA-23 gene. Many were isolated from patients reporting a travel history to Samoa. Both isolates identified 2026 Q2 were from patients who reported recent hospitalisation in Samoa.

Table 3. Clusters of genomically related CPO isolates, 01 April to 30 June 2026

Species	Year ^a	Carbapenemase gene	ST	Travel history ^b	Isolates (n) in quarter	Total isolates (n) ^c
New clusters						
<i>E. coli</i>	2026	OXA-1205	ST18455	India	2	2
<i>E. coli</i>	2026	NDM-5	ST410	-	2	2
<i>E. coli</i>	2025	OXA-244	ST131	-	1	2
Existing clusters						
<i>K. pneumoniae</i>	2025	NDM-4	ST11	-	2	4
<i>A. baumannii-calcoaceticus</i> complex	2020	OXA-23-like	ST2	Samoa ^d	2	21

^a Year index isolate in cluster identified.

^b Refers to most common travel history in isolates within the cluster, when travel information was available. A blank cell indicates no common travel history or no overseas travel associated or reported for the cluster.

^c Total isolates in the cluster to 30 June 2026.

^d A total of 18 of 21 isolates in the cluster reported travel to Samoa.

Indication for testing

From 01 April to 30 June 2026, 14.2% (15/106 isolates) of CPO were from clinical specimens and 85.8% (91/106 isolates) were from screening specimens (Table 3). This is similar to the percentage observed in Q1 2026 (15.3% of isolates were from clinical specimens).

Referring laboratories

Over half of the CPO isolates were referred from laboratories in the Auckland region (65.1%, 69/106 isolates). The laboratories referring the highest number of isolates were Middlemore Hospital (22.6%, 24/106 isolates), LabPLUS, Auckland (19.8%, 21/106 isolates), Canterbury Health Laboratories (16.0%, 17/106 isolates) and Awanui Labs, Auckland (13.2%, 14/106 isolates) (Table 4).

Table 4. Number (percent) of clinical and screening CPO isolates by referring laboratories, 01 April to 30 June 2026

Referring laboratory	Clinical isolates n (%) ¹	Screening isolates n (%) ^{1,2}	Total isolates n (%)
Middlemore Hospital	1 (6.7)	23 (25.3)	24 (22.6)
LabPLUS, Auckland	6 (40.0)	15 (16.5)	21 (19.8)
Canterbury Health Laboratories	1 (6.7)	16 (17.6)	17 (16.0)
Awanui Labs, Auckland	3 (20.0)	11 (12.1)	14 (13.2)
North Shore Hospital	0 (0.0)	10 (11.0)	10 (9.4)
Awanui Labs, Wellington	1 (6.7)	7 (7.7)	8 (7.5)
Awanui Labs, Dunedin	0 (0.0)	5 (5.5)	5 (4.7)
Pathlab, Bay of Plenty	1 (6.7)	3 (3.3)	4 (3.8)
Awanui Labs, Canterbury	2 (13.3)	0 (0.0)	2 (1.9)
Hawke's Bay Hospital	0 (0.0)	1 (1.1)	1 (0.9)
Total³	15 (14.2)	91 (85.8)	106 (100.0)

¹ Percentage calculated as referring laboratory within source of isolates.

² Includes isolates from axilla, rectum, groin, nose, faeces and rectum.

³ Total percentage calculated within specimen type (clinical and screening isolates).

Travel history

From 01 April to 30 June 2026, travel history was available for 76.3% (71/93) of patients, of which 84.5% (60/71) indicated overseas travel in the 12 months prior to sample collection. The percentage of patients with no history of international travel has increased in this quarter (15.5%), compared to Q1 2026 (4.0%). Of patients where region of travel was known (64/71), the Indian subcontinent (50.0%, 32/64) was the most frequently reported travel location (Table 5).

Of the patients who reported overseas travel, 26.7% (16/60) received healthcare while overseas.

Table 5. Travel history locations reported by patients with CPO, 01 April to 30 June 2026

Region ¹	Isolates ² n (%) ³	Received healthcare overseas n (%) ⁴
Indian subcontinent	32 (50.0)	4 (25.0)
New Zealand	11 (17.2)	-
Other parts of Asia ⁵	13 (20.3)	5 (31.3)
Pacific Islands/Australia	5 (7.8)	3 (18.8)
Other known countries	3 (4.7)	2 (12.5)
Overseas - no region specified	7	2 (12.5)
Total	71	16
Travel history unknown	22	-

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 = 64), excludes "Overseas – no region specified" (7) and "Travel history unknown" (22).

⁴ Percent of patients with known overseas travel (n = 60), excludes New Zealand (11).

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.