

Vancomycin-resistant enterococci in New Zealand, 2024

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Prepared by/Author(s):

Sarah Bakker, Alexandra Eustace, Hilary Miller, Kristin Dyet, Julianna Lees and
Juliet Elvy

PREPARED FOR: Ministry of Health - Manatū Hauora

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REVIEWED BY: Andrea McNeill and Audrey Tiong

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LIST OF ABBREVIATIONS

- CC17 – Clonal complex 17 – a population level grouping for molecular characterisation of bacteria.
- cgMLST – Core genome multilocus sequence typing – a high-resolution molecular typing method; more discriminatory than MLST.
- CLSI – Clinical and Laboratory Standards Institute – used for interpreting antibiotic susceptibility data.
- EUCAST – European Committee on Antimicrobial Susceptibility Testing - used for interpreting antibiotic susceptibility data.
- MIC – Minimum inhibitory concentration.
- MLST – Multilocus sequence typing, a molecular typing method that characterises isolates; It is less discriminatory than cgMLST.
- PHF Science – Institute for Public Health and Forensic Science Limited.
- SKA – Split Kmer Analysis – reference free phylogenetic analysis, provides high resolution comparison of closely related genomes.
- SNP – Single nucleotide polymorphism - a single base-pair change in the DNA sequence.
- ST – Sequence type – a numerical designation that identifies a strain based on MLST data.
- VRE – Vancomycin-resistant enterococci - in this report it includes the following species: *Enterococcus faecium*, *Enterococcus faecalis*, *Enterococcus gallinarum* and *Enterococcus lactis*.
- VREfm – Vancomycin-resistant *E. faecium*.
- VREfs – Vancomycin-resistant *E. faecalis*.
- WGS – Whole genome sequencing - method used to determine the complete DNA sequence of an organism's genome.

EXECUTIVE SUMMARY

PHF Science conducts passive surveillance of vancomycin-resistant enterococci (VRE) in New Zealand, with voluntary participation by all diagnostic laboratories nationwide.

As part of routine passive surveillance, PHF Science performs antimicrobial susceptibility testing, verifies the presence of the *van* gene(s), and determines strain type through analysis of whole genome sequencing (WGS) data.

In 2024, 636 VRE from 631 patients were confirmed, the highest annual number of VRE isolates ever identified in New Zealand. The majority of VRE were from screening specimens, with only 36 (5.7%) VRE from clinical specimens referred to PHF Science in 2024.

Within the 636 VRE isolates, there were 625 vancomycin-resistant *Enterococcus faecium* (VREfm, 621) and vancomycin-resistant *Enterococcus faecalis* (VREfs, 4) from 623 patients. *E. faecium* remains the dominant vancomycin-resistant enterococcal species in New Zealand (621/625, 99.4%).

Among the VRE referred to PHF Science, VREfm with *vanB* predominated. Of the 625 VREfm and VREfs received, 14.2% were *vanA* (89/625), 85.3% were *vanB* (533/625) 0.2% were *vanD* (1/625), 0.2% were *vanE* (1/625) and 0.2% were *vanN* (1/625).

Waikato Hospital referred the highest number of VREfm and VREfs isolates (45.0%, 281/625). Of the remaining isolates, most (36.3%, 227/625) were referred from five other hospitals: Middlemore (54/625), Whangārei (50/625), North Shore (49/625), Tauranga (40/625) and Auckland City (34/625).

WGS was used to characterise a subset of VREfm (508/621, 81.8%) and all four VREfs. The majority of VREfm in New Zealand in 2024 belonged to the ST17 *vanB E. faecium* 2022 Waikato Hospital cluster (229/508, 45.1%), identified in New Zealand in 2022. The second largest cluster involved 105 isolates, identified as the ST2529 *vanB E. faecium* 2023 North Shore Hospital cluster.

The increase in VRE detections highlights the importance of well-resourced and supported infection prevention and control strategies to identify, contain and eliminate VRE from New Zealand healthcare facilities.

METHODS

ISOLATES AND PATIENT INFORMATION

Hospital and community diagnostic laboratories are requested to refer all VREfm and VREfs to PHF Science for the national surveillance.

Patient hospital admission information was supplied by the referring laboratory. The relevant Health New Zealand region was determined by the recorded patient domicile address. Where the domicile of the patient was overseas, the district of the referring laboratory was used. If the information was not supplied, the referring hospital was assumed to be the primary hospital in the area. The referring hospital may not reflect the hospital of acquisition.

ANTIMICROBIAL SUSCEPTIBILITY TESTING

Vancomycin and teicoplanin minimum inhibitory concentrations (MICs) were determined by gradient strip on Mueller-Hinton agar. Susceptibility to ampicillin, ciprofloxacin, high-level gentamicin, linezolid, nitrofurantoin (*E. faecalis* only), high-level streptomycin and tetracycline were determined by disc testing. Susceptibility to daptomycin was determined by broth microdilution using ISO 20776-1 (2019) (International Organization for Standardization, 2019). Susceptibility testing results were interpreted according to European Committee on Antimicrobial Susceptibility Testing (EUCAST) breakpoints (European Committee on Antimicrobial Susceptibility Testing, 2022), except for tetracycline and daptomycin, which were interpreted using Clinical and Laboratory Standards Institute breakpoints (Clinical and Laboratory Standards Institute, 2024). Information on the antimicrobials tested, and the classes they belong to, is outlined in Table C1.

WHOLE GENOME SEQUENCING

The *van* genes present were determined from WGS data. Results were compared to *van* gene data supplied by diagnostic laboratories.

Isolates were typed using WGS-based methods. DNA libraries were created using the plexWell Library Preparation kit (SeqWell), and sequencing was performed using Illumina technology. Data were analysed using either an in-house pipeline using open-source software, or MBioSEQ Ridom typer software (Bruker)– formerly known as Ridom SeqSphere+ (SS) software. Resistance genes were identified using AMRFinderPlus

v4.0.3 with database version 2024-10-22.1 (Feldgarden M et al., 2021). The in-house pipeline links together open-source packages and in-house scripts, which enables the resistome and the genetic relatedness of isolates to be determined. Open-source packages used included SKESA (Souvorov, 2018), 7-gene MLST (Seemann T), AMRFinderPlus (Feldgarden M et al., 2021), and core genome MLST (cgMLST) using Chewbacca (Silva M et al., 2018). The Bruker software uses similar tools to those in the inhouse pipeline, but is run in its own user interface, rather than on the PHF Science high performance computer cluster. MLST clonal complexes were assigned using the PubMLST website (Jolley et al., 2018).

A cgMLST pairwise allelic difference threshold of ≤ 20 was used to identify possible clusters. These were investigated further by core-genome single nucleotide polymorphism (SNP) analysis using Snippy v. 4.6.0 (Seemann T) with recombination correction using Gubbins v. 3.3.5 (Croucher et al., 2015) for large clusters, with kmer based Split Kmer Analysis (SKA) (Connor CH et al., 2025) used for smaller clusters. Clusters likely to reflect recent transmission were identified using a threshold of six core-genome SNPs (Gouliouris et al., 2021) or 7 SKA SNPs (Higgs C et al.).

RESULTS

VRE DATASET

E. faecium continue to be the dominant VRE species in New Zealand. A total of 636 viable, non-duplicate enterococci were referred to PHF Science in 2024 as potential VRE: 621 *E. faecium*, four *E. faecalis*, nine *Enterococcus gallinarum* and two *Enterococcus lactis*. All nine *E. gallinarum* contained *vanC*, with two isolates also containing *vanB*. Both *E. lactis* contained *vanN*. Isolates of *E. gallinarum* and *E. lactis* were excluded from further analysis due to their low prevalence among referred VRE isolates and the intrinsic vancomycin resistance of *E. gallinarum*.

The number of VREfm and VREfs confirmed each year over the last 10 years is shown in Figure 1. Prior to 2024 the highest annual number of VREfm and VREfs in New Zealand was 391 isolates in 2023. Of the 625 VREfm and VREfs, 85.3% contained *vanB* (533), 13.9% contained *vanA* (87), 0.2% contained *vanD* (1), 0.2% contained *vanE* (1) and 0.2% contained *vanN* (1). Two of the *E. faecalis* isolates contained *vanA*, one contained *vanB* and the other contained *vanE*.

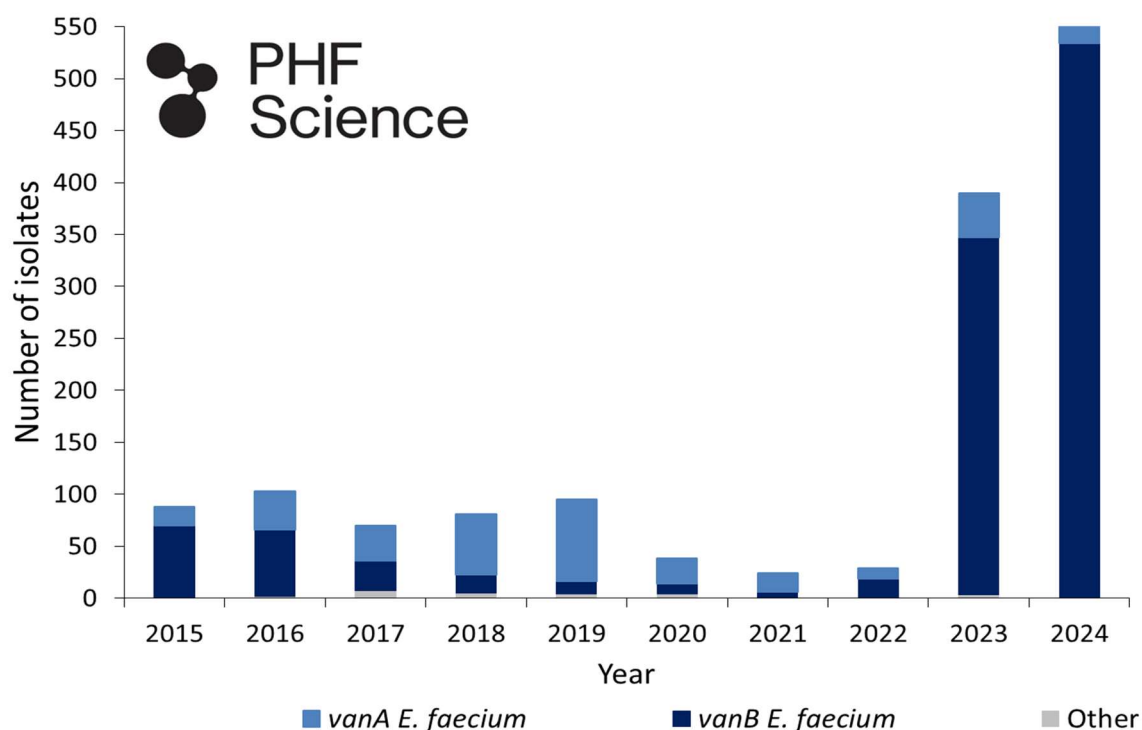


Figure 1: Species and *van* genotype of VREfm and VREfs in New Zealand, 2015-2024

Note: The 'Other' category includes all VREfs as well as VREfm carrying non-*vanA/vanB* genes.

In 2024 New Zealand had a similar percentage of *vanB* VREfm to 2023. Historical surveillance data displayed in Figure 1 demonstrates the changes in the predominant VREfm genotype in New Zealand. From 2015 and 2016 *vanB* VREfm predominated. However, from 2017 to 2019 the proportion of *vanB* VREfm declined substantially, reaching a low of 13.7% in 2019, and *vanA* VREfm isolates were the dominant lineage between 2018 and 2021. Since 2022, *vanB* VREfm has again predominated, accounting for 85.7% (532/621) of VREfm isolates in 2024.

The site of isolation was reported for 623 of the 625 VREfm and VREfs isolates. The majority (589/623, 94.5%) were isolated from screening specimens (i.e. rectal swabs and faecal specimens). The remaining specimens were from urine (20/623, 3.2%), blood (6/623, 1.0%) or other clinical specimens (8/623, 1.3%).

HEALTHCARE FACILITIES REFERRING VRE ISOLATES

In 2024, the largest share of VREfm and VREfs isolates were referred by Waikato Hospital (281/625, 45.0%). Other major contributors, which collectively referred 36.2% of isolates, were Middlemore (54, 8.6%), Whangārei (50, 8.0%), North Shore (49, 7.8%), Tauranga (40, 6.4%) and Auckland City (34, 5.4%) Hospitals. All other healthcare facilities referred between one and 16 isolates each, together totalling less than 20% of the total number of VREfm and VREfs referred.

The majority of submissions were from the Waikato district (296, 47.4%) followed by Northland (60, 9.6%), Counties Manukau (52, 8.3%) and Bay of Plenty (58, 9.3%) districts.

During 2024, an average of 50 VREfm and VREfs were submitted per month (Figure 2). Submissions peaked in March and April 2024 (Figure 2), with the lowest number of submissions in the last two months of the year.

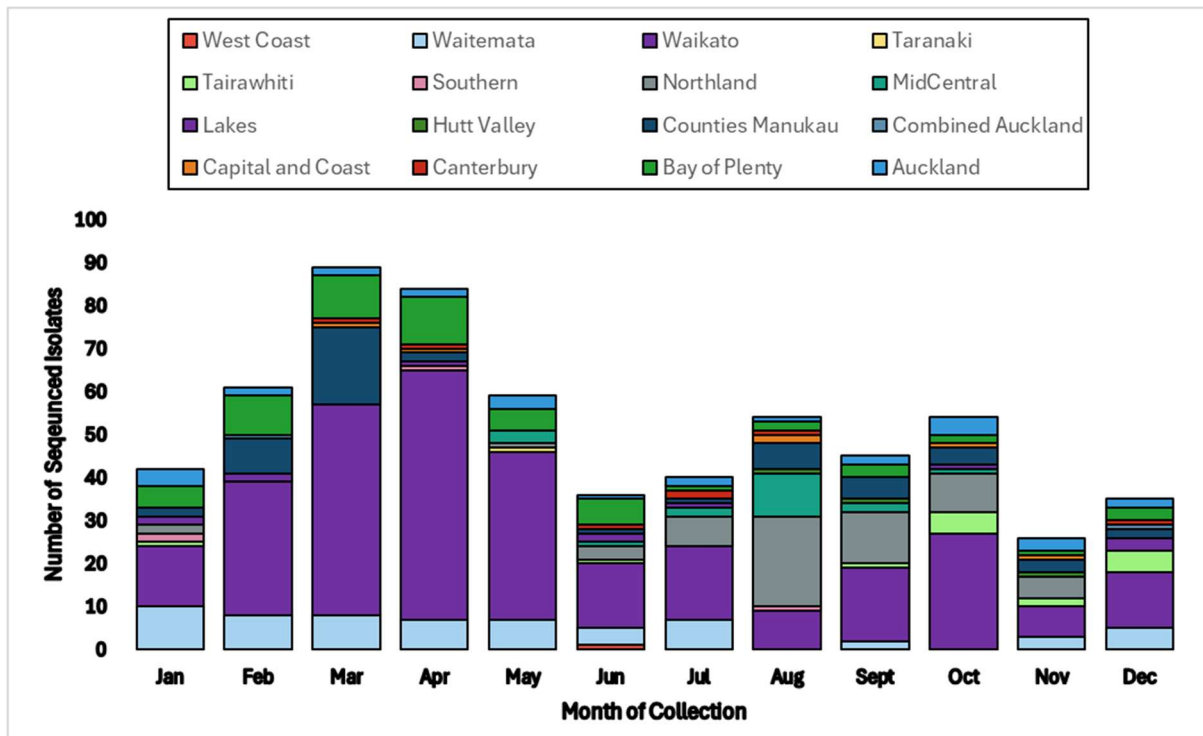


Figure 2: Epidemic curve by Health New Zealand district for VREfm and VREfs in New Zealand 2024

MOLECULAR TYPING

A total of 512 VREfm and VREfs referred to PHF Science in 2024, from 510 patients, were characterised using WGS. There were 113 VREfm referred by Waikato Hospital that were not sequenced as they did not meet the criteria, (see Appendix B) these were assumed to be genetically related to the ST17 Waikato Hospital outbreak strain.

The 7-gene multilocus sequence types for VREfm with either *vanA* or *vanB* in 2024 are shown in Table 1 and Table 2 respectively. The majority (499/508, 98.2%) of sequence types identified belonged to clonal complex 17 (CC17), a hospital-adapted *E. faecium* lineage (Tables 1 and 2).

Twelve different sequence types were identified within *vanA* VREfm in 2024 (Table 1). The two most common sequence types were: ST80 (37/87, 42.5%) and ST1424 (36/87, 41.4%). Other sequence types in *vanA* VREfm in 2024 were uncommon, being found in no more than three isolates (3.4%) each. The *vanA* VREfm isolates were more commonly referred from facilities in the Northern Health New Zealand region, specifically Middlemore and Auckland City Hospitals. (see Appendix A, Table A1).

Table 1. Distribution of *vanA* VREfm by Health New Zealand region and multilocus sequence type, 2024

Health NZ Region	Clonal complex/sequence types												Total
	CC17											Unassigned CC	
	ST80	ST1424	ST1299	ST761	ST17	ST736	ST1421	ST787	ST2675	ST18	ST117	ST2701	
Northern	29	31		2	1		1	1	1	1	1		68
South Island	4		1		1	1						1	8
Central	2	2	2										6
Midland	2	3											5
Total	37	36	3	2	2	1	1	1	1	1	1	1	87

Table 2. Distribution of *vanB* VREfm by Health New Zealand region and multilocus sequence type, 2024

Health NZ Regions	Clonal complex/sequence types																			Total
	CC17												CC94		Unassigned CC					
	ST17	ST2529	ST80	ST78	ST2584	ST26	ST2217	ST375	ST18	ST2667	ST2582	ST2588	ST1052	ST2142	ST623	ST874	ST2293	ST2686	ST2687	
Midland	221 ¹	1	25	1	2	1		1	1	1	1	1	1	1	1	1	1	1	1	263
Northern	13	112		5																130
Central	19		2	1																22
South Island	3						1													4
Total	256	113	27	7	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	419

1. Includes one isolate that has an incomplete *atpA* allele, likely due to low depth sequence data, but clustered with other ST17 isolates.

Within *vanB* VREfm there were 19 sequence types identified (Table 2). There were two predominant types: ST17 (256/419, 61.1%) followed by ST2529 (113/419, 27.0%). Of the remaining sequence types in *vanB* VREfm, there were 27 ST80 (6.4%), seven ST78 (1.7%), two ST2584 (0.5%) and 14 sequence types of one isolate each (Table 2).

E. faecium with *vanB* were identified more frequently in Midland Health New Zealand districts, predominantly from Waikato (164/419, 39.1%) and Tauranga Hospitals (39/419, 9.3%), followed by facilities in the Northern Health New Zealand region, predominantly from Whangārei (47/419, 11.2%) and North Shore (40/419, 9.5%) Hospitals (see Appendix A, Table A2).

Two of the four *E. faecalis* isolates were ST179 with one containing *vanA* and the other *vanB*. The *vanE* VREfs isolate was ST32 and the other *vanA* VREfs was ST1926.

The population structure of VREfm isolates in New Zealand were analysed using core genome MLST (cgMLST). A minimum spanning tree (MST) shows the genomic relationships visually with the presence of multiple closely related clusters, each centred in single geographic region (Figure 3).

In 2024, eight VREfm genomic clusters with three or more isolates were identified (Table 3). These eight clusters involved 389 of the 512 WGS-characterised isolates. The largest, the ST17 Waikato Hospital *vanB* *E. faecium* outbreak strain, included 229 sequenced isolates plus 113 epidemiologically linked VREfm, totalling 342 isolates in 2024 and 530 since it was first identified in 2022. The ST17 Waikato Hospital *vanB* *E. faecium* outbreak strain was initially detected in Waikato Hospital in 2022 and has subsequently spread across the Midland region. However, it is still predominantly associated with three hospitals: Waikato, Tauranga and Gisborne. In 2024, the second largest cluster, with 105 isolates, was also a *vanB* *E. faecium* cluster. This cluster consists of isolates belonging to sequence types ST2529 and ST2800 (a single locus variant of ST2529), identified in the Northern region and is shown in the MST tree (Figure 3) as grey and light blue circles in the bottom right.

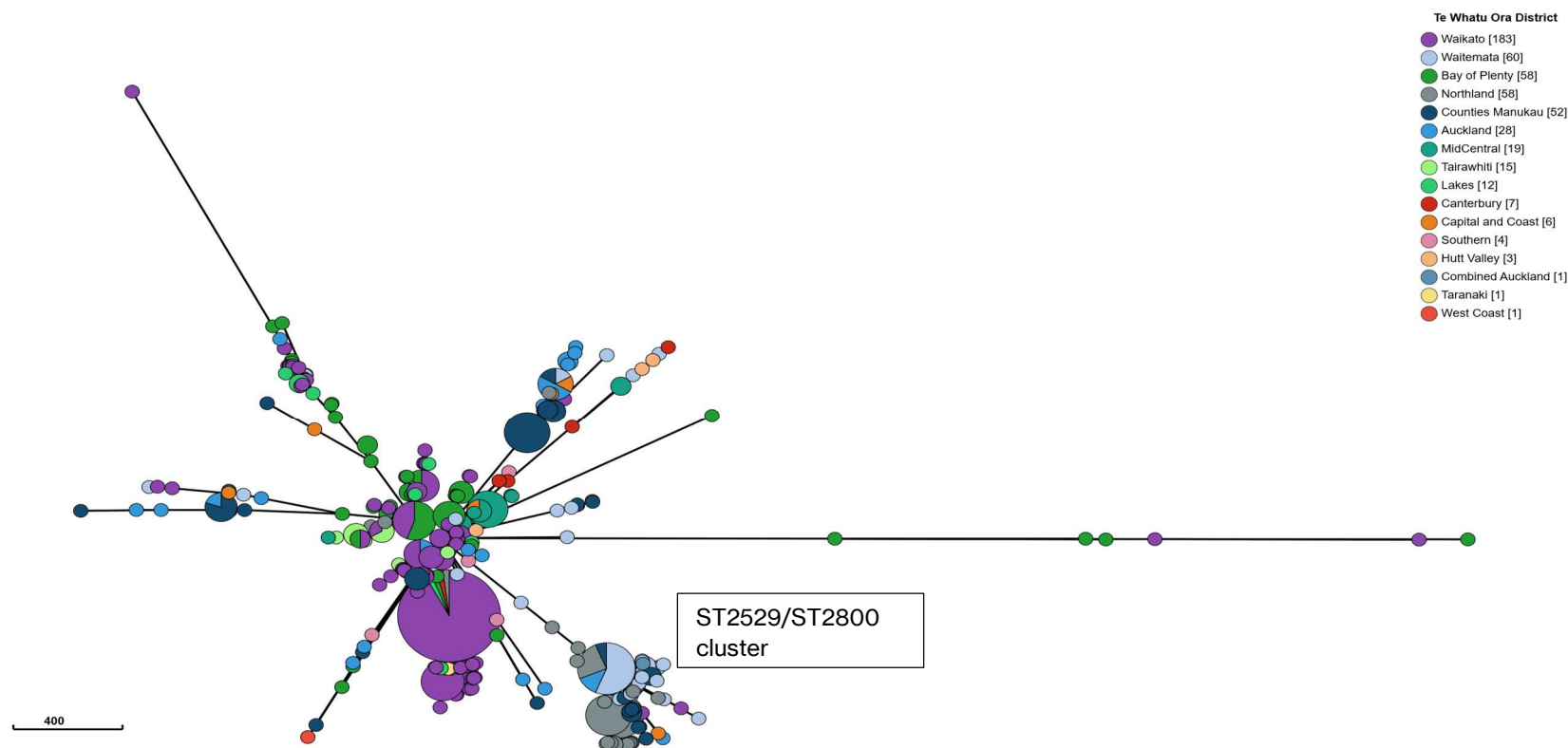


Figure 3: Minimum spanning tree containing all 2024 VREfm. Each node represents one unique cgMLST type, with size scaled according to the number of genomes with that type. Nodes coloured by Health New Zealand district.

Table 3: Clusters of VREfm found in New Zealand 2024

Cluster Name	ST ¹	Number in cluster in 2024	Total number in cluster 2022-2024	Health NZ Region referred from (No.)	Healthcare Facilities with highest submissions. (No.)
vanB <i>E. faecium</i> 2022 Waikato Hospital	17	342 ²	530	Midland (331) Northern (9) South Island (2)	Waikato Hospital (257) Tauranga Hospital (26) Gisborne Hospital (15)
vanB <i>E. faecium</i> 2023 North Shore Hospital	2529/2800	105	109	Northern (105)	Whangarei Hospital (40) North Shore Hospital (34) Middlemore Hospital (11)
vanA <i>E. faecium</i> 2024 Middlemore Hospital	ST1424	18	18	Northern (18)	Middlemore Hospital (18)
vanA <i>E. faecium</i> 2024 Samoa	ST1424	12	12	Central (1) Northern (12)	Auckland City Hospital (8)
vanB <i>E. faecium</i> 2022 Palmerston North Hospital	ST17	12	12	Central (12)	Palmerston North Hospital (11)
vanB <i>E. faecium</i> 2023 Waikato Hospital Cluster 1	ST80	7	16	Midland (7)	Waikato Hospital (4) Rotorua Hospital (3)
vanA <i>E. faecium</i> 2023 Fiji	ST80	3	4	Northern (2) South Island (1)	Christchurch Hospital (1) Middlemore Hospital (1) Mercy Hospital (1)
vanA <i>E. faecium</i> 2023 Waikato Hospital	ST1424	3	11	Midland (3)	Waikato Hospital (3)

¹ Includes closely related sequence types

² ST17 Waikato Hospital *vanB* outbreak strain. Number comprised of 229 isolates sequenced in 2024 and an additional 113 isolates referred by Waikato Hospital that were not sequenced but epidemiologically linked and assumed to be genetically related to the outbreak strain.

ANTIMICROBIAL SUSCEPTIBILITY

Antimicrobial susceptibility among the 2024 VREfm and VREfs isolates is shown in Table 4. Resistance to ampicillin and ciprofloxacin is characteristic of the CC17 lineage, which was observed in 94.9% (282/297) of New Zealand isolates in 2024 (Table 4). The most common resistance profile found, excluding glycopeptides (see Appendix C), was resistance to ampicillin, aminoglycosides, ciprofloxacin and tetracycline, which was observed in 58.9% (175/297) of isolates with susceptibility data. In general, the presence of *vanA* conferred high-level teicoplanin resistance whereas isolates with *vanB* were teicoplanin-susceptible.

Table 4: Phenotypic resistance among VREfm and VREfs in New Zealand, 2024

Antimicrobial	Percent resistance (%) in <i>E. faecium</i>			
	<i>vanA</i> n = 87	All <i>vanB</i> n = 204	ST2529 <i>vanB</i> 2023 North Shore Hospital outbreak strain n = 105	Percent resistance (%) in all VRE ^{1,2} n = 297
Ampicillin	100.0	98.0	100	97.0
Ciprofloxacin	98.9	96.6	100	96.0
Daptomycin ³	3.5	0.0 ³	0.0 ³	1.0 ³
High-level gentamicin	28.7	56.4	95.2	47.5
Linezolid	2.3	0.5	0.0	1.0
Nitrofurantoin ⁴	-	-	-	0.0 ⁴
High-level streptomycin	32.2	34.3	1.0	33.3
Teicoplanin	97.7	0.5	1.0	30.0
Tetracycline	87.4	79.4	97.1	81.5
Vancomycin	97.7	99.5	100	98.7
Multiresistant ⁵	93.1	96.1	100	93.6

1 Includes all 2024 VREfm and VREfs with susceptibility data. Data were available for 297 isolates, which were all VREfm and VREfs except for those belonging to, or assumed to belong to, the Waikato Hospital ST17 outbreak strain where only 14 of 229 were tested.

2 Includes all isolates with susceptibility data, including VREfm with *vanA* (87), *vanB* (204), *vanD* (1) and *vanN* (1), and VREfs with *vanA* (2), *vanB* (1) and *vanE* (1).

3 One *vanB E. faecium* was unable to have its daptomycin MIC determined due to poor growth.

4 Four *E. faecalis* only, as the EUCAST nitrofurantoin breakpoints are specifically for *E. faecalis*.

5 Resistant to three classes of antimicrobials, as defined by (Magiorakos AP, 2012), in addition to glycopeptides

Of the 297 isolates tested for susceptibility to vancomycin, all were vancomycin-resistant, with the exception of four *E. faecium*. Of these three had a vancomycin MIC of 4 mg/L (*vanB* ST80, *vanA* ST3675 and *vanN* ST2426) and the fourth had a vancomycin MIC of 0.5 mg/L (*vanA* ST80). The three vancomycin-susceptible isolates with a vancomycin MIC of 4 mg/L contained all their *van* regulatory genes. However, the *E. faecium* ST80 *vanA* isolate that had a vancomycin MIC of 0.5 mg/L did not have the *vanY* or *vanZ* regulatory genes. These four isolates are characterized as vancomycin-variable enterococci, (genotypically resistant, phenotypically susceptible), and none are linked to a VREfm cluster in the PHF Science surveillance dataset.

Table 5. Correlation between phenotypic and genotypic susceptibility results for VREfm in 2024

Antimicrobial	Resistant gene(s)/ genes with mutation(s) ¹	Resistance determinant	Interpreted phenotypic susceptibility result ⁴			Concordance ²
			S ¹	I ¹	R ¹	
Ampicillin	<i>pbp5</i>	Present	0	- ³	285	99.0%
		Absent	5	- ³	3	
Ciprofloxacin	<i>gyrA, parC</i>	Present	1	- ³	282	99.0%
		Absent	8	- ³	2	
Daptomycin	<i>lia, dltC, rpoB, rpoC</i>	Present	199	- ³	2	68.5%
		Absent	90	- ³	1	
High-level gentamicin	<i>aac(6')-Ie, aph(2'')-Ia</i>	Present	0	- ³	121	93.2%
		Absent	152	- ³	20	
Linezolid	<i>cfr(D), poxtA</i>	Present	4	- ³	2	98.3%
		Absent	286	- ³	1	
High-level streptomycin	<i>aadE, ant(6)-IA</i>	Present	1	- ³	96	99.0%
		Absent	194	- ³	2	
Tetracycline	<i>tet</i>	Present	1	2	85	53.6%
		Absent	51	0	156	

- 1 Mutations detected based on information in the Bruker MBioSEQ Ridom Typer database, referencing the AMRFinder database v4.0.15 (Feldgarden M et al., 2019).
- 2 Concordance, represents the percentage of isolates in which genotype results agree with phenotypic susceptibility interpretations.
- 3 No 'I' for this antimicrobial.
- 4 Interpreted using clinical breakpoints as described in the Methods section; value is count of the number of isolates.

Genotypic and phenotypic concordance of 98.0% or over was found for several antimicrobials (Table 5): specifically, ampicillin, ciprofloxacin, high-level streptomycin, and linezolid. Reasonable concordance was also found for high-level gentamicin (93.2%). Concordance was poor for daptomycin and tetracycline with 68.5% and 53.6% respectively (Table 5). For daptomycin there were a high number of daptomycin-susceptible isolates with *lia*FSR mutations. There was also poor correlation for tetracycline, as there were a high number of tetracycline-resistant isolates that did not contain a *tet* resistance gene. Although the correlation was high for linezolid, there was one linezolid-resistant isolate that did not contain a mutation likely to confer linezolid resistance and four linezolid-susceptible isolates with mutations that are correlated with linezolid resistance (*cfr(D)* (2 isolates), *poxA* (1 isolate) and *cfr(D)+poxA* (1 isolate)).

DISCUSSION

The number of VRE identified in New Zealand in 2024 increased by more than 60% from that recorded in 2023, despite the large increase in VRE observed in 2023. The increase observed in 2024 is solely due to the increase in the number of VRE_{fm} cases and may be linked to expanded screening across New Zealand healthcare facilities. This has likely led to higher detection rates of VRE, along with increased identification of transmission events within and between healthcare facilities.

Current surveillance of VRE in New Zealand indicates that clinical infections are still uncommon, with the majority of VRE detected from screening specimens. However, without sustained efforts to prevent and control VRE contamination and colonisation, clinical infections are likely to increase (Qiu, 2026).

In 2024, the burden of VRE New Zealand primarily occurred in the Midland and Northern regions caused by two strains of VRE_{fm}: ST17 with *vanB* and ST2529 with *vanB*. The ST17 *vanB* outbreak strain was initially detected in Waikato Hospital in 2022, but high numbers of this strain continue to be found, particularly in the Midland region. The ST2529 strain was first detected at North Shore Hospital in 2023, where four isolates were identified. In 2024, the strain was identified at Auckland City Hospital and Whangārei Hospital, with an additional 105 isolates linked to the cluster.

Although two *vanB* VRE_{fm} strains were responsible for the majority of cases in New Zealand, *vanA* VRE_{fm} also increased substantially in 2024. The proportion of *vanA* VRE_{fm} strains increased by nearly 50%, from 11.6 % (43/371) in 2023 to 17.1% (87/508) in 2024. This substantial increase was attributable to *vanA* VRE_{fm} sequence type ST1424, which rose from 20.9% (9/43) in 2023 to 41.4% (36/87) in 2024. The increase in number of *vanA* VRE_{fm} ST1424 is primarily due to two distinct epidemiologically significant clusters in 2024; one linked to Middlemore Hospital and another involving patients with epidemiological connections to Samoa.

We continued to use WGS-based methods to type VRE in 2024. The higher level of discrimination offered by WGS-based methods has enabled the genetic relatedness of isolates, as well as transmission events to be investigated more thoroughly. Both the ST17 Waikato Hospital and the ST2529 North Shore Hospital outbreak strains are highly clonal,

with limited genetic variability since they were first detected in September 2022 and November 2023 respectively.

In New Zealand, VREfm is dominated by the hospital-adapted CC17 lineage. This globally disseminated lineage has near-universal ampicillin resistance, high rates of fluoroquinolone resistance, and frequent multidrug resistance (Lee T et al., 2019).

Phenotypic and genotypic analysis of New Zealand VREfm are consistent with both global trends and previous local observations (PHF Science, 2023). Phenotypic resistance found in New Zealand VREfm was typical of CC17 lineages as were the chromosomal mutations and mobile genetic elements.

Resistance to high-level gentamicin and high-level streptomycin increased among *vanB* VREfm in New Zealand in 2024. This was primarily due to the expansion of a strain belonging to the CC17 lineage, ST2529, that had high-level aminoglycoside resistance as well as resistance to ampicillin and ciprofloxacin. Encouragingly, resistance to both linezolid and daptomycin resistance is still rare in New Zealand VREfm and VREfs, however, interpretation of daptomycin trends is limited as routine testing was only introduced in 2023.

Discrepancies between phenotypic and genotypic resistance for some antimicrobials highlight gaps and warrant further investigation. This is especially relevant for daptomycin and tetracycline, which had the lowest concordance between phenotypic and genotypic results in this study. CLSI breakpoints have been used for interpretation of daptomycin and tetracycline susceptibility testing however, the absence of EUCAST breakpoints against enterococci for these agents highlight the uncertainty around breakpoint interpretation.

Although resistance to daptomycin was uncommon among the 292 isolates tested, over 68.5% of phenotypically susceptible isolates had mutations, most frequently within the *liaRS* operon, a locus associated with the emergence of daptomycin resistance. However, the high prevalence of these mutations among susceptible isolates indicates that the mutations on their own are insufficient to confer phenotypic resistance. In addition, one phenotypically resistant isolate lacked detectable mutations in the regions examined, suggesting that additional or uncharacterised mechanisms contribute to daptomycin resistance. Together, these findings highlight the discordance between genotype and phenotype and underscore the complexity of predicting resistance from

genomic data for certain antimicrobials. It also highlights the need for phenotypic susceptibility testing until we have a better understanding of these data.

VRE continues to be considered non-endemic in New Zealand. In 2024, New Zealand hospitals continue to implement a 'stamp it out' approach to VRE, which emphasizes the need for ongoing genomic surveillance to support intensive infection prevention strategies.

APPENDIX A:

Table A1: Distribution of VREfm with *vanA* by healthcare facility and multilocus sequence type, 2024

Healthcare Facility	Sequence type (No.)												Total
	ST117	ST1299	ST1421	ST1424	ST17	ST18	ST2675	ST2701	ST736	ST761	ST787	ST80	
Middlemore Hospital			1	19		1	1					13	35
Auckland City Hospital	1			9						2		7	19
North Shore Hospital					1							7	8
Waikato Hospital				3								2	5
Christchurch Hospital		1										4	5
Waitākere Hospital				1							1	2	4
Wellington Hospital				2								1	3
Hutt Hospital		2											2
Te Nikau Hospital								1					1
Private HCF Auckland				1								1	2
Dunedin Hospital					1								1
Whangārei Hospital				1									1
Southland Hospital									1				1
Total	1	3	1	36	2	1	1	1	1	2	1	37	87

Table A2: Distribution of VREfm with *vanB* by healthcare facility and multilocus sequence type, 2024

Healthcare Facility	Sequence type (No.)																			Total
	ST1052	ST17	ST18	ST2142	ST2217	ST2293	ST2529	ST2582	ST2584	ST2588	ST26	ST2667	ST2686	ST2687	ST375	ST623	ST78	ST80	ST874	
Waikato Hospital		143					1	1	2		1		1					14	1	164
Whangārei Hospital		3					43										1			47
North Shore Hospital		1					38										1			40
Tauranga Hospital		30		1						1				1				6		39
Middlemore Hospital		6					11										2			19
Gisborne Hospital		16																		16
Palmerston North Hospital		13																2		15
Auckland City Hospital		5					8										1			14
Whakātane Hospital	1	8				1						1				1		1		13
Rotorua Hospital		7															1	4		12
Waitākere Hospital							5													5
ARC ¹ Northern region							4													4
Community – Midland region		3													1					4
Hutt Hospital		3															1			4
Thames Hospital		4																		4

Healthcare Facility	Sequence type (No.)																			Total
	ST1052	ST17	ST18	ST2142	ST2217	ST2293	ST2529	ST2582	ST2584	ST2588	ST26	ST2667	ST2686	ST2687	ST375	ST623	ST78	ST80	ST874	
ARC ¹ – Midland region		3																		3
Tokoroa Hospital		3																		3
Kaitaia Hospital							2													2
Private HCF ² Midland region		1	1																	2
Wellington Hospital		2																		2
Taranaki Base Hospital		1																		1
Dargaville Hospital							1													1
Te Kūiti Hospital		1																		1
Taumarunui Hospital		1																		1
Gore Hospital		1																		1
Dunedin Hospital					1															1
Christchurch Hospital		1																		1
Total	1	256	1	1	1	1	113	1	2	1	1	1	1	1	1	1	7	27	1	419

1. ARC = Aged Residential Care facility

2. HCF = Healthcare Facility

APPENDIX B:

SEQUENCING CRITERIA FOR 2024 VRE:

Sequencing will only be performed on VRE isolates referred by Waikato Hospital Laboratory if the following criteria are met and communicated to the AMR lab team:

- There is a specific request from the IPC team to sequence the patient's isolate due to an unknown epi link with the ongoing ST17 *vanB* Waikato Hospital outbreak strain.
- The isolate contains a different *van* gene (i.e. not *vanB*)
- The isolate is phenotypically vancomycin resistant but without any *van* genes detected by PCR performed by Waikato Hospital Laboratory
- The isolate has a different antibiogram to the ST17 *vanB* outbreak strain – (the antibiogram of isolates is uniform - resistant to ampicillin, ciprofloxacin, quinupristin/dalfopristin, streptomycin, tetracycline and vancomycin, susceptible to daptomycin, high-level gentamicin, linezolid and teicoplanin).
- The patient is in a Healthcare facility outside Waikato Hospital

APPENDIX C:

Table C1: Antimicrobial classes and antimicrobials tested in 2024 for VRE:

Antimicrobial class	Antimicrobial
Aminoglycosides	High-level gentamicin High-level streptomycin
Fluoroquinolones	Ciprofloxacin
Glycopeptides	Teicoplanin Vancomycin
Lipopeptide	Daptomycin
Nitrofurantoin	Nitrofurantoin
Oxazolidinones	Linezolid
Penicillin	Ampicillin
Tetracyclines	Tetracycline

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**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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