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# Vancomycin-resistant enterococci, 2023


## Summary

Vancomycin-resistant enterococci are under passive surveillance in New Zealand, with voluntary participation by all diagnostic laboratories in New Zealand.

In 2023, a total of 391 vancomycin-resistant *Enterococcus faecium* and *Enterococcus faecalis* (VRE) from 387 patients were confirmed. This is significantly more VRE in a year than New Zealand has ever identified previously. The majority of VRE samples in 2023 were from screening samples, with only 18 of the 391 isolates obtained from a clinical specimen.

*Enterococcus faecium* remains the dominant vancomycin-resistant enterococcal species in New Zealand (388/391, 99.2%).

Isolates showed a mix of resistance genes; 11.5% *vanA* (45/391), 88.2% *vanB* (345/391) and 0.3% *vanN* (1/391).

Isolates were predominantly referred from Waikato and Tauranga Hospitals (290/391, 74.2%), following the identification of an outbreak.

The majority of VRE in New Zealand in 2023 belonged to one cluster of *E. faecium* with *vanB* (259/374, 69.3%), which was first identified in New Zealand in 2022. The second largest cluster involved eight isolates.

This report highlights the importance and need for well-resourced and supported infection prevention and control strategies to contain and eliminate VRE from New Zealand healthcare facilities.


## Methods

Hospital and community diagnostic laboratories are requested to refer all vancomycin-resistant *E. faecium* and *E. faecalis* to ESR for the national surveillance of the antimicrobial susceptibility in these organisms.

Information on the hospital the patient was in was supplied for some isolates. 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.

A PCR to identify and distinguish *E. faecalis* and *E. faecium* was used to identify non-*E. faecium*, non-*E. faecalis* isolates[1]. These isolates may contain the *vanC* gene that confers intrinsic, low-level resistance to vancomycin.

Vancomycin and teicoplanin minimum inhibitory concentrations (MICs) were tested by gradient strip on Mueller-Hinton agar. Possible vancomycin-resistant isolates, with MICs just below the resistant breakpoint, were tested using the macro method[2]. Susceptibility to ampicillin, ciprofloxacin, high-level gentamicin, linezolid,

nitrofurantoin (*E. faecalis* only), quinupristin-dalfopristin (*E. faecium* only), high-level streptomycin and tetracycline were determined by disc testing. Susceptibility to daptomycin was determined by broth microdilution using ISO 20776-1 (2006). Susceptibility testing results were interpreted according to European Committee on Antimicrobial Susceptibility Testing (EUCAST)[3] breakpoints, except for tetracycline and daptomycin, which were interpreted using Clinical and Laboratory Standards Institute breakpoints[4].

The *van* genes were determined from whole genome sequencing (WGS) data or identified by PCR[5,6,7,8,9,10]. 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 an in-house developed pipeline linking 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[11], 7-gene MLST[12], AMRFinderPlus[13], core genome MLST (cgMLST) using Chewbacca[14], FastANI[15] to assess average nucleotide identity between genomes, and reference-free (kmer based) single nucleotide polymorphism (SNP)-clustering using split kmer analysis (SKA)[16]. A cgMLST pairwise allelic difference threshold of ≤25 was used to investigate possible clusters[17]. A threshold of 7 SKA SNPs was used to identify clusters likely to have resulted from putative transmission links[17].

## Results

*E. faecium* continue to be the dominant vancomycin-resistant enterococcal species in New Zealand. A total of 396 viable, non-duplicate enterococci were referred to ESR in 2023 as potential vancomycin-resistant enterococci: 388 *E. faecium*, three *E. faecalis*, four *E. gallinarum* and one *Enterococcus* spp. Three *E. gallinarum* contained *vanC* and one contained both *vanA* and *vanC.* The *Enterococcus spp.* also contained *vanC*. This report contains information on the 391 vancomycin-resistant *E. faecium* and *E. faecalis* (VRE) confirmed in 2023, that were cultured from 387 patients.

Prior to 2023 the highest annual number of VRE in New Zealand was 133 isolates in 2014. Of the 391 VRE, 88.2% contained *vanB* (345), 11.5% contained *vanA* (45) and 0.3% contained *vanN* (1). Two of the *E. faecalis* isolates contained *vanA* and the other contained *vanB*. The number of VRE confirmed each year over the last 10 years is shown in Figure 1.

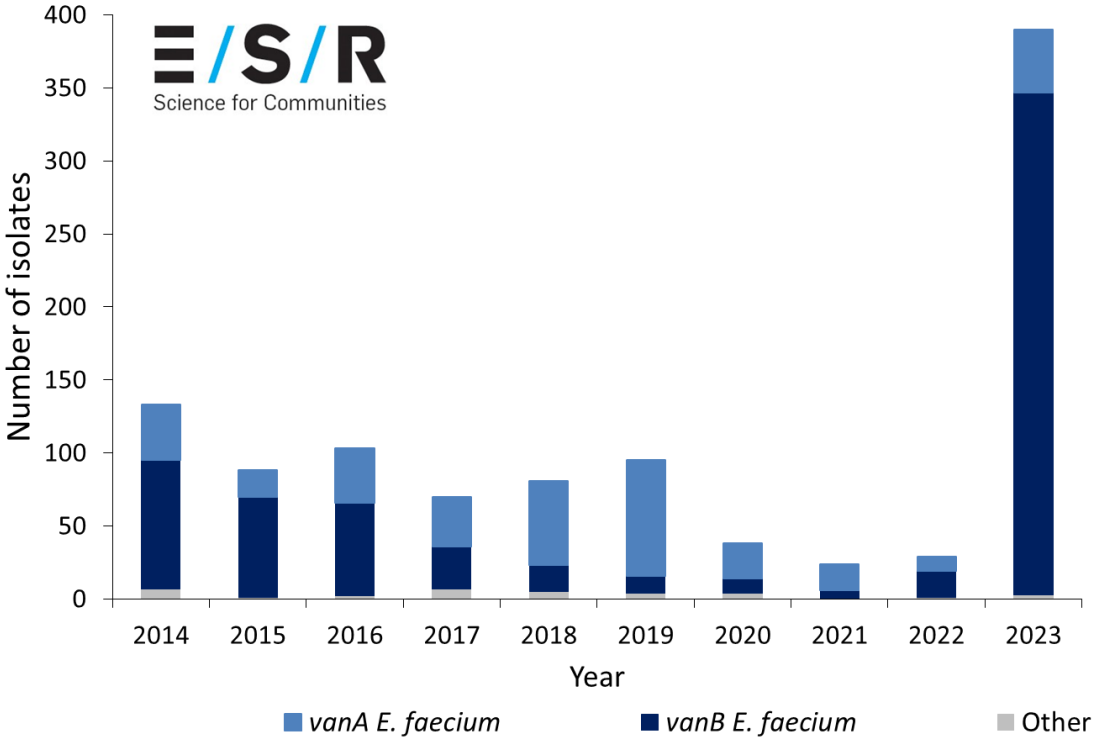


**Figure 1: Species and *van* genotype of vancomycin-resistant *E. faecium* and *E. faecalis* (VRE) isolated in New Zealand, 2014-2023**

The site of isolation was reported for all 391 isolates. The majority (373/391, 95.4%) were isolated from screening specimens (i.e. rectal swabs and faecal specimens). The remaining VRE were from urine (9/391, 2.3%), blood (2/391, 0.5%) or other clinical specimens (7/391, 1.8%).

In 2023 New Zealand had the highest percentage of *vanB* VRE ever reported. Between 2010 and 2016, *vanB* VRE were more prevalent than *vanA* VRE. However, between 2015-2019 the percentage of VRE attributed to *vanB* decreased (Figure 1), with the lowest percentage (12.6%) found in 2019. Since 2022 *vanB* VRE have been more prevalent than *vanA* VRE, and accounted for 88.2% of VRE in 2023.

In 2023 the majority (290/391, 74.2%) of VRE were referred by Waikato Hospital (201/391, 51.4%) and Tauranga Hospital (89/391, 22.8%) (Figure 2). The next largest number of submissions were from Middlemore Hospital (28/391, 7.2%) and Gisborne Hospital (22/391, 5.6). A total of 51 VRE were submitted by all other New Zealand healthcare facilities in 2023.

Low numbers of VRE submissions were received in early 2023, rising to a peak in September (Figure 2). In the first half of the year, submissions from Waikato Hospital were largely responsible for the high numbers of VRE. Submissions from Tauranga Hospital increased in August. By the end of 2023, VRE were identified in healthcare facilities throughout New Zealand, although most facilities had low numbers of isolates.

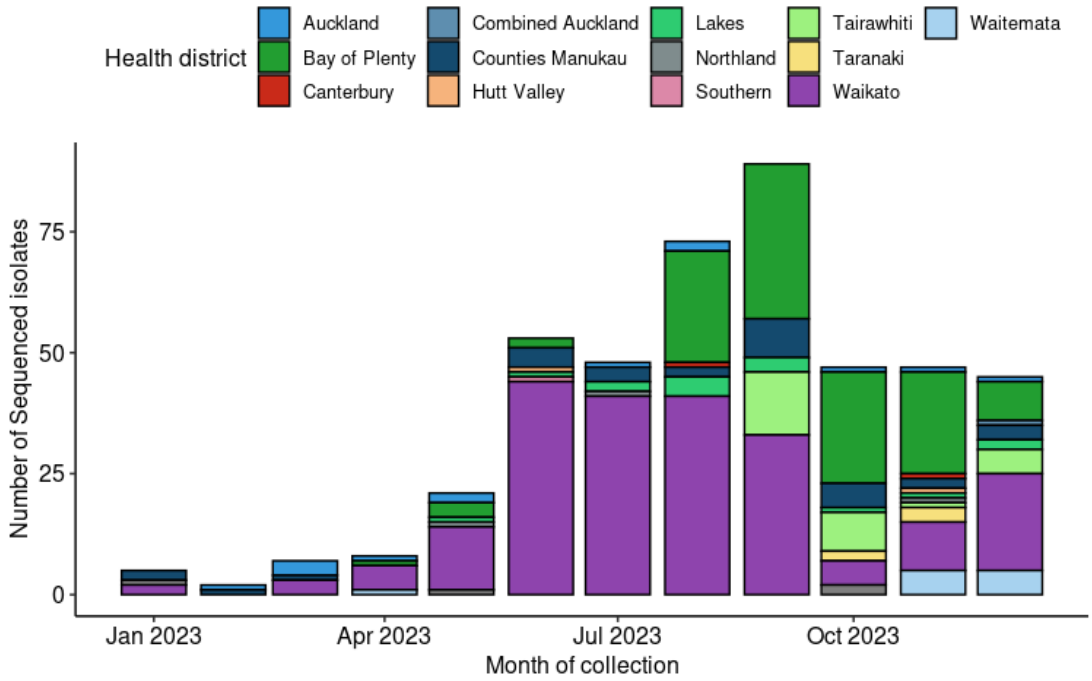


**Figure 2: Epidemic curve by health district for vancomycin-resistant *E. faecium* and *E. faecalis* (VRE) in New Zealand 2023**

The 7-gene multilocus sequence types for vancomycin-resistant *E. faecium* with *vanA* and *vanB* 2023 are shown in Table 1 and Table 2 respectively. The sequence type of one *E. faecium* with *vanB* could not be determined from the data available. The majority of sequence types identified belonged to clonal complex 17 (CC17), a hospital-adapted *E. faecium* lineage. The most common sequence type was ST17 (278/375, 74.1%), with all being *E. faecium* and all except one containing *vanB*. The sequence type of the two *vanA E. faecalis* isolates was ST6, the sequence type of the *vanB E. faecalis* was a single locus variant of ST81 and the *vanN E. faecium* isolate was ST2426.

**Table 1. Distribution of vancomycin-resistant *E. faecium* with *vanA* by healthcare facility and multilocus sequence type, 2023**

| | Sequence type | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **Referred from** | **ST80** | **ST1424** | **ST18** | **ST761** | **ST17** | **ST117** | **ST1421** | **ST1887** | **ST2454** | **Total** |
| Middlemore Hospital | 14 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | 17 |
| Waikato Hospital | 4 | 6 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 14 |
| Auckland City Hospital | 2 | 0 | 0 | 2 | 0 | 0 | 0 | 1 | 0 | 5 |
| Christchurch Hospital | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| Community | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| Dunstan Hospital | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| Gisborne Hospital | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| Hutt Hospital | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| Whakatāne Hospital | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| Whangārei Base Hospital | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| **Total** | **23** | **9** | **4** | **2** | **1** | **1** | **1** | **1** | **1** | **43** |

The genomic relationships between VRE isolates in New Zealand were analysed via core genome MLST (cgMLST). This approach allows a relatively coarse level of genomic clustering but is appropriate to use at a species-wide level, consequently it allows an overview of the complete dataset. A minimum spanning tree showing genomic relationships between all isolates shows the presence of multiple closely related clusters, each centred in single geographic region (Figure 3).

In 2023, 13 VRE clusters with three or more isolates were identified (Table 3). These 13 clusters involved 311 isolates, out of the 375 isolates with available whole genome sequencing data. The main cluster consisted of 259 *E. faecium* with *vanB* that were ST17 or closely related sequence types. This strain was initially detected in 2022, when seven isolates were found[18]. The ST17 cluster started in Waikato Hospital and subsequently spread to Tauranga and Gisborne Hospitals. ST17 isolates were also found in patients the Auckland and Northland regions, but transmission was not detected. The next largest cluster, with eight isolates, was caused by ST80 *E. faecium* with *vanB.*

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**Table 2. Distribution of *E. faecium* with *vanB* by healthcare facility and multilocus sequence type, 2023**

| Referred from | Sequence type | | | | | | | | | | | | | | | Total |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | ST17 | ST80 | ST78 | ST2529 | ST117 | ST796 | ST779 | ST1693 | ST2455[1] | ST2500[1] | ST2503[1] | ST2504[1] | ST2505[1] | ST2530 | ST2581 | |
| Waikato Hospital | 137 | 22 | 1 | 0 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 168 |
| Tauranga Hospital | 86 | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 89 |
| Gisborne Hospital | 21 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 21 |
| Middlemore Hospital | 6 | 0 | 2 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 9 |
| Whakatāne Hospital | 9 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 9 |
| Rotorua Hospital | 7 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 8 |
| Auckland City Hospital | 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 6 |
| North Shore Hospital | 1 | 0 | 0 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 6 |
| Community | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 2 |
| Hāwera Hospital | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 |
| Taupō Hospital | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 |
| Hastings Hospital | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| Hutt Hospital | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| Kaitāia Hospital | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| Thames Hospital | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| Whangārei Base Hospital | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| **Total** | **277** | **27** | **6** | **4** | **2** | **2** | **1** | **1** | **1** | **1** | **1** | **1** | **1** | **1** | **1** | **327[2]** |

1 Single locus variants of ST17 at the *atpA* locus. Determined to be part of the Waikato Hospital cluster by cgMLST and SKA analysis.

2 The sequence type of one isolate from Waikato Hospital could not be determined from available data. Sixteen isolates from Waikato Hospital, assumed to be part of the Waikato Hospital Cluster, were not sequenced so the sequence type could not be determined.

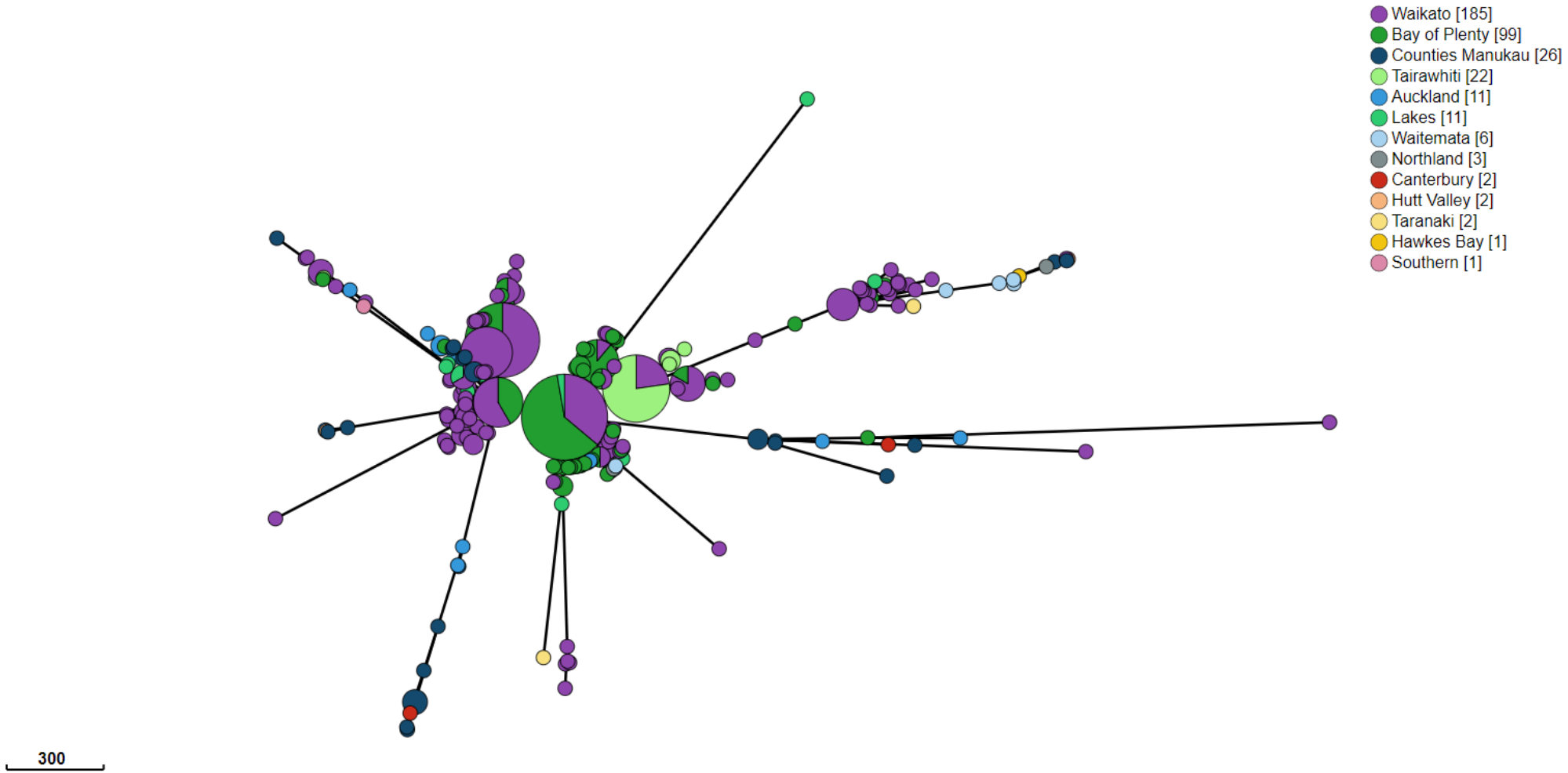


**Figure 3: Minimum spanning tree containing all 2023 vancomycin-resistant *E. faecium*. Each node represents one unique cgMLST type, with size scaled according to the number of genomes with that type. Nodes coloured by Te Whatu Ora district.**

**Table 3. Clusters of vancomycin-resistant *E. faecium* found in New Zealand 2023**

| Species | *van* gene | ST[1] | Number in cluster[2] | Referred from (Number of isolates) |
|---|---|---|---|---|
| *E. faecium* | *vanB* | 17 | 259[3] | Waikato Hospital (138), Tauranga Hospital (82), Gisborne Hospital (21), Whakatāne Hospital (9), Rotorua Hospital (3), Auckland City Hospital (1), Kaitāia Hospital (1), North Shore Hospital (1), Community (1), Taupō Hospital (1), Thames Hospital (1) |
| *E. faecium* | *vanB* | 80 | 8 | Waikato Hospital (7)<br>Rotorua Hospital (1) |
| *E. faecium* | *vanB* | 17 | 6 | Middlemore Hospital (6) |
| *E. faecium* | *vanB* | 17 | 5 | Rotorua Hospital (3)<br>Waikato Hospital (2) |
| *E. faecium* | *vanB* | 17 | 5 | Auckland City Hospital (4)<br>Tauranga Hospital (1) |
| *E. faecium* | *vanA* | 1424 | 5 | Waikato Hospital (3)<br>Gisborne Hospital (1)<br>Whakatāne Hospital (1) |
| *E. faecium* | *vanB* | 17 | 4 | Tauranga Hospital (3)<br>Taupō Hospital (1) |
| *E. faecium* | *vanA* | 80 | 4 | Middlemore Hospital (4) |
| *E. faecium* | *vanB* | 80 | 4 | Waikato Hospital (4) |
| *E. faecium* | *vanB* | 2529 | 4 | North Shore Hospital (4) |
| *E. faecium* | *vanA* | 1424 | 3 | Waikato Hospital (3) |
| *E. faecium* | *vanA* | 761 | 2 | Auckland City Hospital (2) |
| *E. faecium* | *vanA* | 18 | 2 | Waikato Hospital (2) |

1 Includes closely related sequence types
2 Clusters determined from the 375 isolates with available whole genome sequencing data.
3 ST17 Waikato Hospital *vanB* outbreak strain. There were an additional 16 isolates referred by Waikato Hospital that were not sequenced that were assumed to be genetically related to the outbreak strain.

The antimicrobial susceptibility among the 2023 VRE isolates is shown in Table 4. Resistance to ampicillin and ciprofloxacin is common in strains belonging to the CC17 lineage, which was observed in *E. faecium* from New Zealand in 2023 (Table 4). All isolates tested for susceptibility to vancomycin were vancomycin-resistant, except two ST17 *E. faecium* with *vanB* that had vancomycin MICs of 4 µg/mL and one ST80 *E. faecium* with *vanA* that had a vancomycin MIC of 2 µg/mL. Both *vanB* isolates were categorised as vancomycin-resistant using the macro method. The vancomycin-susceptible isolate with *vanA* appeared to have all the van regulatory genes, and the reason for it being phenotypically susceptible was not determined. In general, the presence of the *vanA* gene cluster conferred high-level teicoplanin resistance whereas isolates with *vanB* were teicoplanin-susceptible.

**Table 4. Resistance among vancomycin-resistant *E. faecium* and *E. faecalis* in New Zealand, 2023**

| | Percent resistance (%) in *E. faecium* | | | |
|---|---|---|---|---|
| | | *vanB* | | Percent resistance (%) in all VRE[1, 2] |
| Antimicrobial agent | *vanA* n = 43 | All n = 104 | Waikato Hospital ST17 outbreak strain n = 35 | n = 151 |
| Ampicillin | 100.0 | 99.0 | 100.0 | 96.7 |
| Ciprofloxacin | 100.0 | 96.2 | 100.0 | 96.0 |
| Daptomycin | 0.0 | 0.0 | 0.0 | 0.0 |
| Gentamicin high-level | 44.2 | 10.6 | 5.7 | 21.2 |
| Linezolid | 11.6 | 0.0 | 0.0 | 3.3 |
| Nitrofurantoin[3] | - | - | - | 0.0[3] |
| Quinupristin/dalfopristin[4] | 41.9 | 60.6 | 100.0 | 54.3[4] |
| Streptomycin high-level | 46.5 | 77.9 | 100.0 | 68.2 |
| Teicoplanin | 97.7 | 1.9 | 0.0 | 30.5 |
| Tetracycline | 69.8 | 70.2 | 100.0 | 70.2 |
| Vancomycin | 97.7 | 98.1 | 97.1 | 98.0 |
| Multiresistant[5] | 79.1 | 97.1 | 100.0 | 90.7 |

1 Includes all 2023 vancomycin resistant *E. faceium* and E. *faecalis* with susceptibility data. Data were available for all isolates, except for those belonging to, or assumed to belong to, the Waikato Hospital ST17 outbreak strain where 35/275 were tested.

2 Includes all isolates with susceptibility data, including *E. faecium* with *vanA* (43), 104 *vanB* (104) and *vanN* (1), and *E. faecalis* with *vanA* (2) and *vanB* (1).

3 The overall rate of resistance is for three *E. faecalis* isolates, as the EUCAST nitrofurantoin breakpoints are specifically for *E. faecalis*.

4 *E. faecalis* are considered intrinsically resistant to quinupristin/dalfopristin, so the overall rate of resistance is only for the 148 *E. faecium* isolates.

5 Resistant to three classes of antibiotics, in addition to glycopeptides (quinupristin/dalfopristin resistance not included for *E. faecalis)*.

## Discussion

The number of vancomycin resistant *E. faecium* and *E. faecalis* identified in New Zealand in 2023 was nearly three times that recorded previously in a single year. The high number of isolates was primarily due to the spread of one ST17 strain of *E.faecium*. This strain was first detected in Waikato Hospital in 2022, when seven isolates were found[18]. In 2023 this ST17 outbreak strain was found in a large number of patients in Waikato Hospital. It subsequently spread and was transmitted between patients in Tauranga and Gisborne Hospitals. For this reason, the burden of VRE sat predominantly in the Te Manawa Taki region in 2023.

The utilisation of WGS-based methods to type VRE in 2023 has improved VRE surveillance in New Zealand. 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 The ST17 Waikato Hospital outbreak strain is highly clonal and there has been limited genetic variability found since it was first detected in September 2022.

Current surveillance of VRE in New Zealand indicates that clinical infections are uncommon. The majority of VRE samples continue to be detected from screening specimens. However, without sustained efforts to prevent and control VRE contamination and colonisation, clinical infections are likely to increase.

The high numbers of VRE identified in 2023, resulted in an increased number of VRE screening swabs being taken, both in facilities with high numbers of patients with VRE and in other New Zealand hospitals. The increase in VRE isolated in New Zealand in 2023, is likely due to both transmission within and between healthcare facilities and an increase in screening and testing leading to increased detection.

VRE continues to be considered non-endemic in New Zealand. In 2023, New Zealand hospitals continue to implement a ‘stamp it out’ approach to VRE. This requires ongoing and highly resource intensive infection prevention action, with particular attention to cleaning, transmission-based precautions and patient screening in an attempt to contain and eliminate VRE from New Zealand healthcare facilities. However, despite intensive efforts, VRE continues to spread, with associated significant negative impacts for patients, whānau and our healthcare facilities. Further coordination and resourcing of the New Zealand VRE outbreak response, including laboratory testing and insights from genomic surveillance, is essential and should be prioritised.

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