

Vancomycin-resistant enterococci received by ESR from 1 January 2023 to 30 November 2023

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Hospital and community diagnostic laboratories in Aotearoa New Zealand are requested to refer all vancomycin-resistant *Enterococcus faecium* and *Enterococcus faecalis* (VRE) to ESR for the national surveillance of these organisms. Isolates received at ESR to 30 November are summarised in Table 1.

Table 1: Species and van genes found in vancomycin-resistant enterococci submitted to ESR from 1 January 2023 to 30 November 2023

Species/van gene	Number of isolates	Number in Waikato Hospital cluster*
<i>Enterococcus faecium</i>	402	293
<i>vanA</i>	43	-
<i>vanB</i>	357	293
<i>vanA and vanB</i>	1	
<i>vanN</i>	1	
<i>Enterococcus faecalis</i>	4	-
<i>vanA</i>	3	-
<i>vanB</i>	1	-
<i>Enterococcus gallinarum</i>	1	-
<i>Enterococcus species</i>	1	-
<i>vanB</i>	1	-
Total	408[#]	293

May include some duplicate isolates.

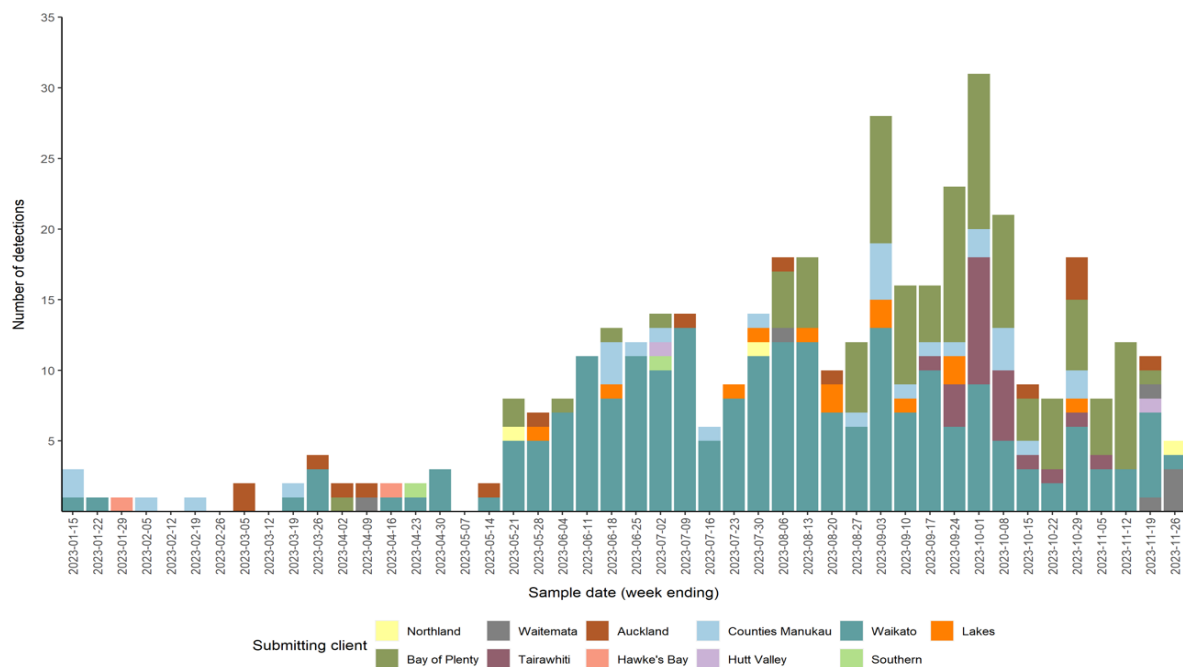
* A large outbreak of *E. faecium* with *vanB*, originally found in Waikato Hospital, was detected in 2023.

Most isolates were submitted from the Waikato and Bay of Plenty Te Whatu Ora districts (Table 2 and Figure 1).

Table 2: Patient Te Whatu Ora (TWO) district for all vancomycin-resistant enterococci submitted to ESR from 1 January 2023 to 30 November 2023

Patient TWO district	Number of isolates	Number <i>vanA</i> isolates	Number <i>vanB</i> isolates	Number confirmed in Waikato Hospital cluster
Waikato	217	11	203	176
Bay of Plenty	97	2	95	83
Canterbury	2	2	-	-
Counties Manukau	28	20	8	-
Hawkes Bay	2	-	2	-
Hutt Valley	2	1	1	-
Tairāwhiti	22	-	22	21
Lakes	13	-	13	8
Auckland	12	6	6	1
Northland	3	1	2	1
Southern	2	1	1	-
Waitemata	5	5	-	2
Grand Total	408	46	359	293

Figure 1: Patient TWO district by sample date for all vancomycin-resistant enterococci submitted to ESR from 1 January 2023 to 30 November 2023



To look at the genetic relatedness of isolates two methods have been used: multilocus sequence typing (MLST) and whole genome sequencing (WGS). MLST was used to provide an indication of genetic relatedness of bacterial isolates. This method assesses genetic variability in 450-500 bp internal fragments of each of seven genes. Whole genome sequencing looks at a nearly all the genetic material in an isolate, so the resolution is higher.

The majority of VRE isolated in Aotearoa New Zealand in 2023 were ST17 (Figure 2 and Table 3).

Figure 2: Multilocus sequence type (ST) by sample date for all vancomycin-resistant enterococci submitted to ESR from 1 January 2023 to 30 November 2023

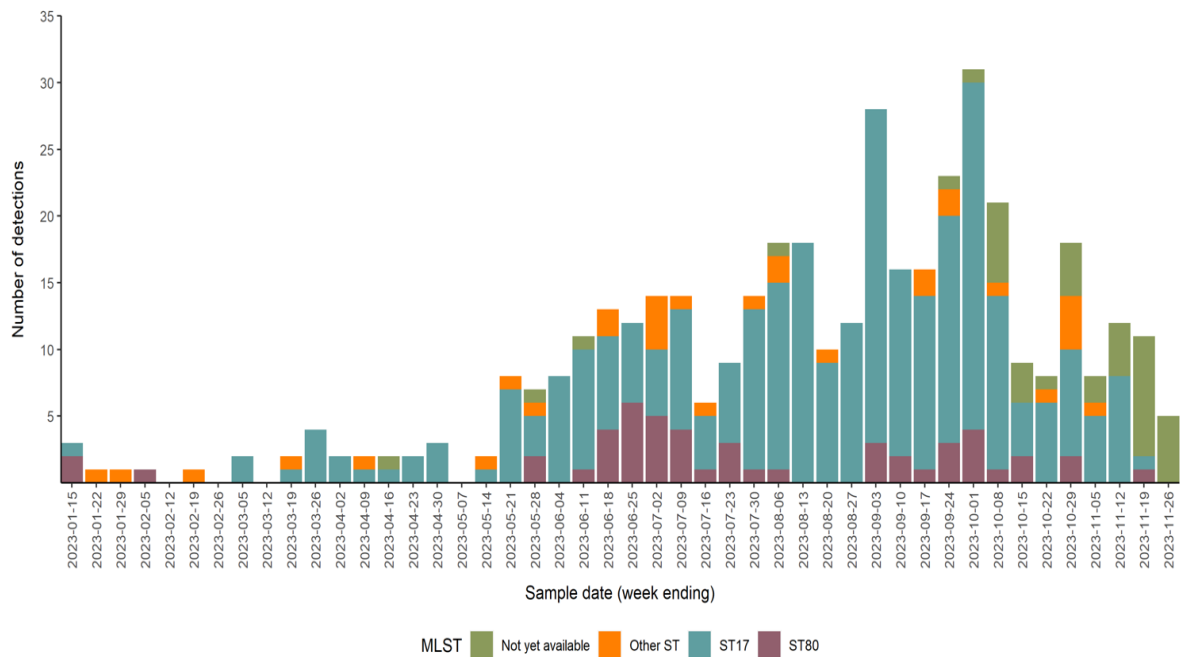


Table 3: Species, *van* gene and multilocus sequence type for all vancomycin-resistant enterococci submitted to ESR from 1 January 2023 to 30 November 2023

Species and <i>van</i> gene	MLST	Number of isolates
<i>Enterococcus faecium vanB</i>		357
	ST17	285
	ST80	26
	ST78	3
	ST796	2
	ST779	2
	ST18	1
	ST117	1
	ST203	1
	ST1424	1
	slvST17 [#]	1
	Not available yet	34
<i>Enterococcus faecium vanA</i>		43
	ST80	24
	ST1424	5
	ST18	3
	ST761	3
	ST17	2
	ST117	1
	ST1421	1
	ST1887	1
	Not available yet	3
<i>Enterococcus faecalis vanA</i>		3
	ST6	2
	ST108	1
<i>Enterococcus faecalis vanB</i>		1
	slvST81	1
<i>Enterococcus faecalis vanN</i>		1
	Not available yet	1

SLV = single locus variant

If more than ten isolates from a particular laboratory were referred in 2023 the sequences types of each isolate was plotted by sample date. Figures were used to assess if clusters of related isolates were present (Figures 3-7). The only large cluster identified was the ST17 cluster found.

Figure 3: Multilocus sequence type of isolates submitted by Waikato Hospital during 2023 by sample date

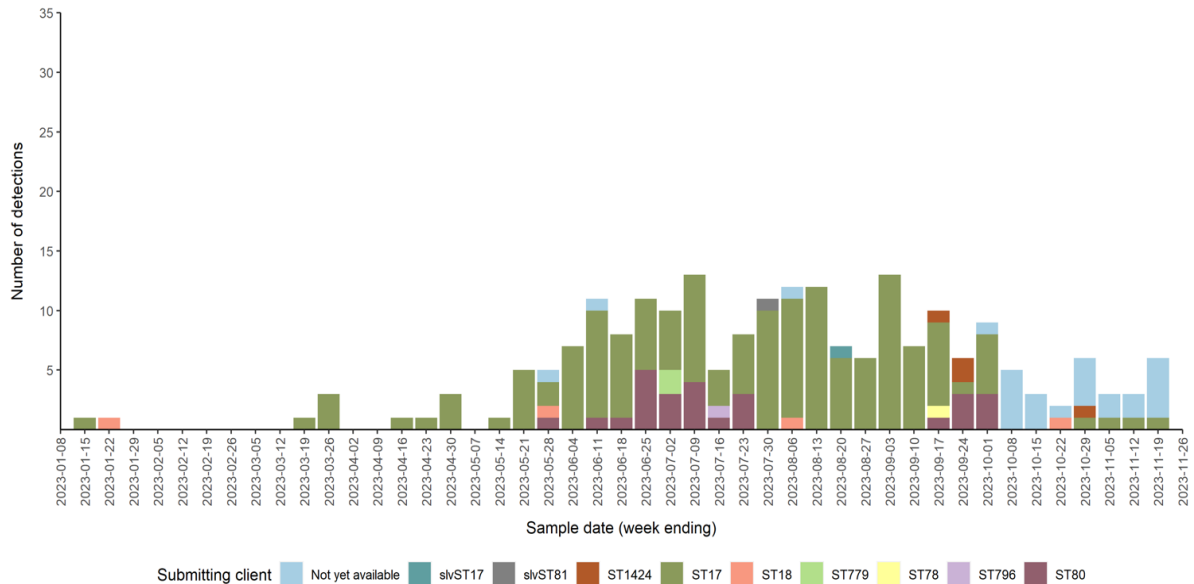
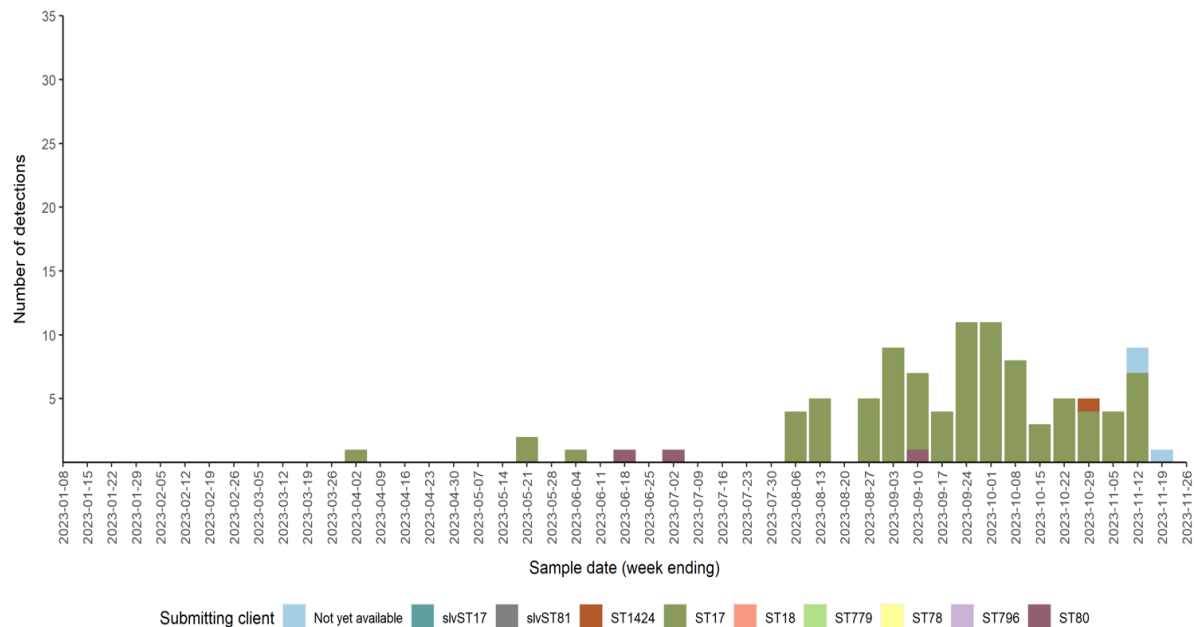


Figure 4: Multilocus sequence type of isolates submitted by PathLab Bay of Plenty (from BoP TWO district) during 2023 by sample date



Whole genome sequencing (WGS) for all VRE referred to ESR was performed using Illumina technology. Relationships among isolates were determined by calculating pairwise single nucleotide polymorphism (SNP) differences between isolates, and the results were visualised using Microreact software (www.microreact.org). Data for ST17 isolates are shown in Figure 9, which shows a large cluster of ST17 isolates that were primarily submitted by Waikato, Bay of Plenty and Tairāwhiti Te Whatu Ora districts. The cluster was defined as isolates that differed from each other by up to 7 SNPs.

Figure 9: Microreact tree highlighting the genetic variability in ST17 vancomycin-resistant enterococci referred to ESR in 2023

