ESR
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Vancomycin-resistant enterococci, 2020

Hospital and community diagnostic laboratories are requested to refer all vancomycin-resistant *Enterococcus faecium* and *Enterococcus faecalis* (VRE) isolates to ESR for the national surveillance of these organisms. At ESR, each referred isolate is confirmed as phenotypically vancomycin resistant, by gradient strip on Mueller-Hinton agar. Susceptibility to teicoplanin was also determined by gradient strip. 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. Gradient strip minimum inhibitory concentrations and disc zones of inhibition were interpreted according to European Committee on Antimicrobial Susceptibility Testing (EUCAST)[1] breakpoints, except for tetracycline that was interpreted using Clinical and Laboratory Standards Institute[2] breakpoints. The *van* gene was identified by PCR[3,4,5,6,7,8], and isolates were typed by pulsed-field gel electrophoresis (PFGE). The index isolate of each new PFGE profile identified among vancomycin-resistant *E. faecium* is typed by multilocus sequence typing (MLST).[9]

A total of 47 enterococci were referred to ESR in 2020 as potential vancomycin-resistant enterococci: 40 *E. faecium*, four *E. faecalis,* two *E. casseliflavus* and one *E. raffinosus*. Of these, three *E. faecalis* were excluded from the dataset as they were not phenotypically vancomycin resistant. A further three isolates were excluded as they were duplicates, including two isolates that were referred by two different laboratories. The two *E. casseliflavus* and one *E. raffinosus* contained the *vanA* gene, but are not included in the analysis below.

VRE from 36 patients were confirmed in 2020. While 36 patients were identified with VRE, this report includes results for 38 VRE isolates, as two distinct VRE strains were isolated from each of two patients.

The site of isolation was reported for all 38 isolates. The majority (32/38, 84.2%) were isolated from screening specimens (i.e., rectal swabs and faecal specimens). The remaining VRE were from urine (3/38, 7.8%), blood (1/38, 2.6%) or other clinical specimens (2/38, 5.3%).

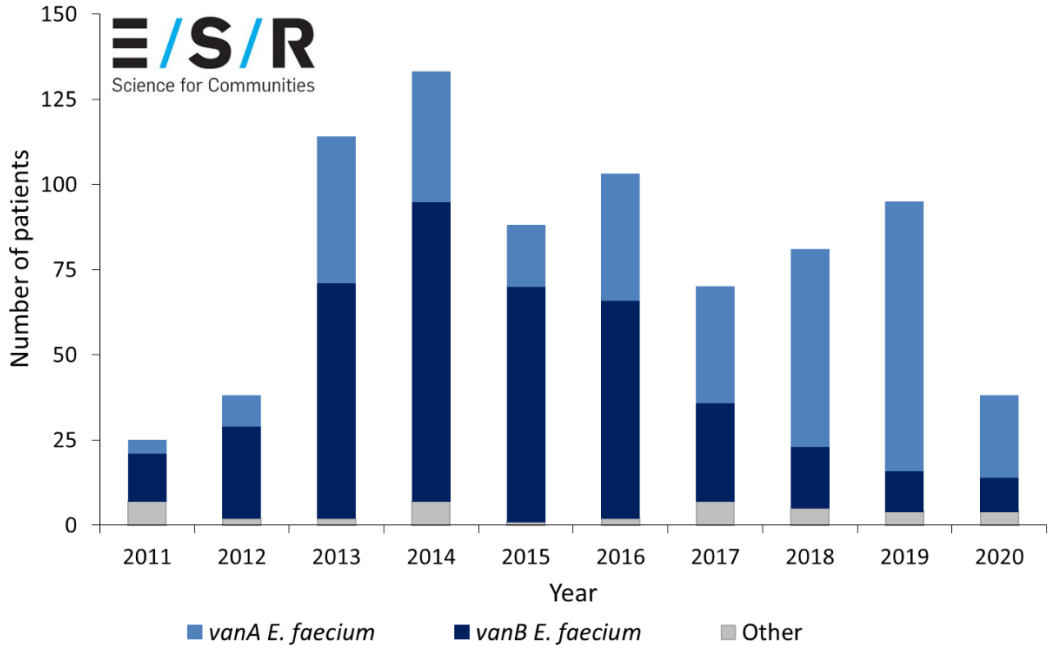
The species and *van* genotype distribution of the 38 VRE confirmed in 2020 was as follows:

- 24 *vanA E. faecium*;
- 10 *vanB E. faecium*;
- 2 *vanA* and *vanB E. faecium*;
- 1 *vanN E. faecium*;
- 1 *vanA E. faecalis.*

The number of patients with VRE confirmed each year over the last 10 years is shown in Figure 1.

INSTITUTE OF ENVIRONMENTAL SCIENCE AND RESEARCH LIMITED
Kenepuru Science Centre: 34 Kenepuru Drive, Kenepuru, Porirua 5022 | PO Box 50348, Porirua 5240, New Zealand
T: +64 4 914 0700 F: +64 4 914 0770
www.esr.cri.nz

Figure 1: Species and *van* genotype of VRE isolated in New Zealand, 2011-2020



In 2020 the lowest number of VRE were isolated in New Zealand since 2012. Since 2015 the prevalence of *vanA E. faecium* has been increasing and *vanB E. faecium* has been decreasing. However, in 2020 the percentage of *vanA E. faecium* dropped (63.2%, compared to 83.2% in 2019) and the percentage of *vanB E. faecium* increased (26.3%, compared to 12.6% in 2019). In 2020 there were still more *vanA E. faecium* than *vanB E. faecium.*

In 2020 the majority (24/38, 63.2%) of VRE were isolated from patients in Auckland hospitals: Middlemore Hospital (12/38, 31.6%), Auckland City Hospital (8/38, 21.1%) and North Shore Hospital (4/38, 10.5%). Dunedin Hospital accounted for the next largest number of isolates (4/38, 10.5%).

Table 1 shows the various VRE strains identified in 2020. Most *vanA E. faecium* (10/24, 41.7%) had distinct pulsed field gel electrophoresis (PFGE) profiles. Of those that could be assigned to a strain, the most common strains were EfBD and EfBE, both of which belong to the MLST clonal complex (CC) 17 – a hospital-adapted *E. faecium* lineage. There were no new strains identified in New Zealand in 2020.

Most *vanB E. faecium* isolates (5/10, 50.0%) belonged to the EfAP strain (Table 1). There were a small number of isolates assigned to each of EfAW and EfBB, which belong to CC17. All strains had been found in New Zealand in previous years.

We are currently undertaking a project to assess the ability of Illumina-based whole genome sequencing to type New Zealand VRE. It is hoped that the 2021 annual report will contain typing information from this new platform.

Table 1. Distribution of patients with VRE by healthcare facility, 2020

Species	*van* gene	Referred from	PFGE profile/'strain'[1]	MLST/CC[2]	Number of patients
E. faecium	*vanA*	Middlemore Hospital	EfBD	ST80/CC17	4
			EfBE	ST761/CC17	2
			EfBF	ST80/CC17	2
			EfBG	ST761/CC17	1
			distinct[3]		1
		Auckland City Hospital	EfBD	ST80/CC17	1
			EfBG	ST761/CC17	1
			distinct		2
		North Shore Hospital	distinct		3
		Wellington Hospital	distinct		2
		Auckland community	EfBE	ST761/CC17	1
		Rangitikei community	EfBC	ST612/CC17	1
		Christchurch Hospital	distinct		1
		Dunedin Hospital	EfBA	ST1421/CC17	1
		Southland Hospital	distinct		1
	vanB	Middlemore Hospital	EfAP	ST796/CC17	2
		Auckland City Hospital	EfAP	ST796/CC17	2
		Auckland community	distinct		2
		Dunedin Hospital	EfAP	ST796/CC17	1
			EfBB	ST555/CC17	1
		North Shore Hospital	EfAW	ST78/CC17	1
		Waikato Hospital	distinct		1
	vanN	Dunedin community	distinct		1
	vanA&*B*	Auckland City Hospital	EfAP	ST796/CC17	1
		Wellington Hospital	EfAP	ST796/CC17	1
E. faecalis	*vanA*	Auckland City Hospital	distinct		1

1 In-house pulsed-field gel electrophoresis (PFGE) profile designations. PFGE profiles were analysed with BioNumerics software version 7.6 (Applied Maths, St-Martens-Latem, Belgium) using the Dice coefficient and unweighted-pair group method with arithmetic averages, at settings of 0.5% optimisation and 1.5% position tolerance. The PFGE profiles of isolates designated as the same strain share ≥90% similarity.

2 MLST, multilocus sequence type; CC, MLST clonal complex. MLST only determined for vancomycin-resistant *E. faecium*. MLST performed according to the scheme described on the *E. faecium* MLST website at https://pubmlst.org/efaecium/, by either PCR and Sanger sequencing or whole genome sequencing.

3 PFGE profile distinct (ie, <90% similarity) from any of the profiles designated a strain name.

The antimicrobial susceptibility among the 2020 VRE is shown in Table 2.

Table 2. Resistance among VRE in New Zealand, 2020

Antimicrobial agent	Percent resistance (%)		
	E. faecium[1]		
	vanA **n = 24**	***vanB*** **n = 10**	**All[2] n = 38**
Ampicillin	100.0	90.0	92.1
Ciprofloxacin	91.7	90.0	89.5
Gentamicin high-level	50.0	70.3	57.9
Linezolid	8.3	0.0	5.3
Nitrofurantoin[3]	-	-	0.0[4]
Quinupristin/dalfopristin[4]	41.7	10.0	29.7[4]
Streptomycin high-level	66.7	20.0	47.4
Teicoplanin	100.0	0.0	71.1
Tetracycline	54.2	70.0	60.5
Multiresistant[5]	95.8	90.0	92.1

1 Susceptibility data not shown separately for the *E. faecium* with both *vanA and vanB or vanN,* but this data is included in the results for all VRE. The isolate *with vanA* and *vanB* was resistant to ampicillin, ciprofloxacin, gentamicin and teicoplanin. The isolate with *vanN* was only resistant to vancomycin.

2 Susceptibility data not shown separately for the *E. faecalis* isolates, but this data is included in the results for all VRE. The two *vanA E. faecalis* were resistant to ciprofloxacin, high-level gentamicin, tetracycline and teicoplanin. The *vanB E. faecalis* was resistant to high-level gentamicin, tetracycline and teicoplanin.

3 The overall rate of resistance is for the one *E. faecalis* isolate only, 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 37 *E. faecium* isolates.

5 Resistant to ≥3 classes of antibiotics in addition to glycopeptides (quinupristin/dalfopristin resistance not included for *E. faecalis* and nitrofurantoin resistance not included for *E. faecium*).

References

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[2] Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing. 30th ed. Wayne, USA: CLSI; 2020. CLSI supplement M100.

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