ESR
Science for Communities

Vancomycin-resistant enterococci, 2018

Hospital and community diagnostic laboratories are requested to refer all vancomycin-resistant *Enterococcus faecium* and *E. faecalis* (VRE) isolates to ESR for the national surveillance of these resistant organisms. At ESR, the isolates are confirmed as vancomycin resistant, the *van* gene is identified by PCR, the isolates' susceptibility to a range of antibiotics is determined, and the isolates are typed by pulsed-field gel electrophoresis (PFGE). In addition, the index isolate of each new PFGE profile identified among vancomycin-resistant *E. faecium* is typed by multilocus sequence typing (MLST).

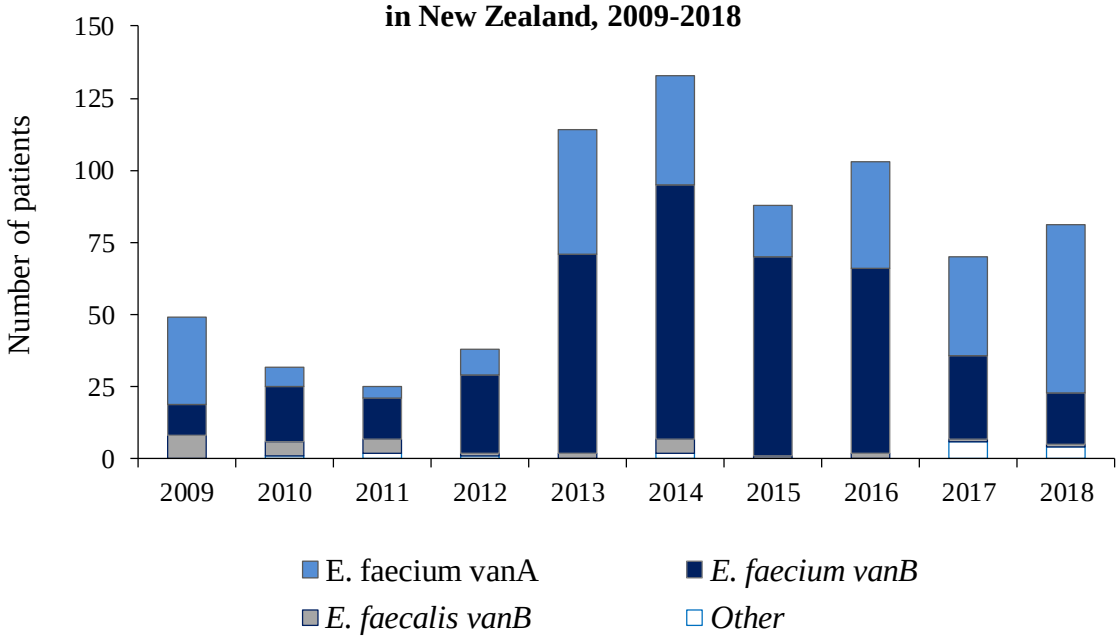
VRE from 73 patients were confirmed in 2018. While 73 patients were identified with VRE, this report includes results for 81 VRE isolates, as two distinct VRE strains were isolated from each of eight patients. The site of isolation was reported for 80 (98.8%) of the isolates. The majority (72, 90.0%) were isolated from screening specimens (ie, rectal swabs and faecal specimens). The remaining VRE were from blood (3, 3.8%), urine (2, 2.5%), or other miscellaneous specimens (3, 3.8%).

The species and *van* genotype distribution of the 81 VRE confirmed in 2017 was:

- 58 *vanA E. faecium*;
- 18 *vanB E. faecium*;
- 2 *vanA* and *vanB E. faecium*
- 1 *vanN E. faecium*;
- 1 *vanA E. faecalis*; and
- 1 *vanB E. faecalis.*

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

Figure 1. Species and *van* genotype of VRE isolated in New Zealand, 2009-2018



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A similar number of VRE were found in 2017 and 2018. However, the prevalence of *vanA E. faecium* increased, accounting for 72.8% of all VRE in New Zealand in 2018. This is in contrast to the prevalence of *vanB E. faecium* between 2010 and 2016. Australia has also reported increasing an increased proportion of *vanA* in recent years.

In 2018 the majority (65, 78.3%) of the VRE were isolated from patients in Auckland hospitals: Middlemore Hospital (30, 36.1%), Auckland City Hospital (23, 27.7%) and North Shore Hospital (12, 14.5%). Wellington Hospital accounted for the next largest number of patients (5, 6.0%) from whom VRE were isolated. Patients who were in more than one hospital are counted in each hospital in the above data, in any following hospital distribution data and in Table 1, which shows a more detailed breakdown of the location of the patients.

Table 1 also shows the various VRE strains identified in 2018. Most *vanA E. faecium* (32, 54.2%) had distinct pulsed field gel electrophoresis (PFGE) profiles. Of those that could be assigned to a strain the most common strains were EfBE, EfBD and EfBA, all of which below to the MLST clonal complex (CC) 17 – a hospital-adapted *E. faecium* lineage. Strain EfBE (ST761) and strain EfBD (ST80) were newly identified in 2018. The eight isolates of strain EfBE were found only in the Auckland region whereas the ten EfBD isolates were found in both Auckland (9) and Christchurch (1).

Most *vanB E. faecium* isolates also had distinct PFGE profiles. There were a small number of isolates assigned to each of EfAW, EfAU, EfAT, EfAP and EfAB, which belong to CC17. All strains had been found in New Zealand in previous years.

Table 1. Distribution of patients with VRE by healthcare facility, 2018

Species	*van* gene	Referred from	PFGE profile / 'strain'[1]	MLST/CC[2]	Number of patients[3]
E. faecium	A	Middlemore Hospital	**EfBD**	**ST80/CC17**	5
			EfBE	**ST761/CC17**	3
			EfBA	ST1421/CC17	2
			EfAS		2
			EfAV		1
			distinct[4]		8
		Auckland City Hospital	**EfBE**	**ST761/CC17**	3
			EfBD	**ST80/CC17**	2
			EfBA	ST1421[4]/CC17	2
			distinct		11
		North Shore Hospital	**EfBD**	**ST80/CC17**	2
			EfBE	**ST761/CC17**	2
			distinct		2
		Wellington Hospital	distinct		5
		Auckland community	EfY	ST192/CC17	1
			distinct		1
		Tauranga Hospital	distinct		2
		Christchurch Hospital	**EfBD**	**ST80/CC17**	1
		Dunedin Hospital	distinct		1
		Hawkes Bay Hospital	EfBA	ST1421[4]/CC17	1
		Kaitaia Hospital	distinct		1
	B	North Shore Hospital	EfAT	ST203/CC17	1
			EfAW	ST78/CC17	1
			distinct		4
		Middlemore Hospital	EfAU	ST203/CC17	2
			EfAB	ST17/CC17	1
			EfAP	ST796/CC17	1
			distinct		1
		Auckland City Hospital	EfAT	ST203/CC17	1
			distinct		2
		Waikato Hospital	EfAP	ST796/CC17	1
			distinct		1
		Auckland community	EfAP	ST796/CC17	1
		Whangarei Hospital	distinct		1
		Dunedin Hospital	EfAB	ST17/CC17	1
	A&B	Auckland City Hospital	EfAP	ST796/CC17	1
		Middlemore Hospital	EfAP	ST796/CC17	1
	N	Middlemore Hospital	distinct		1
E. faecalis	A	Auckland City Hospital	distinct		1
	B	Middlemore Hospital	distinct		1

Footnotes on next page

Footnotes for Table 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. PFGE profile designations in boldface are profiles of strains newly identified in 2018.

2 MLST, multilocus sequence type; CC, MLST clonal complex. MLST only determined for PFGE profiles identified among 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 Patients who were in more than one hospital are counted in each hospital. Of the 81 patients with VRE, two had the same strain isolated in two hospitals. As a result, the total 'patient' count in this table is 83.

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

The antimicrobial susceptibility among the 2018 VRE is shown in Table 2.

Table 2. Resistance among VRE in New Zealand, 2018

	Percent resistance (%)		
	***E. faecium*[2]**		
Antimicrobial agent[1]	***vanA*** **n = 58**	***vanB*** **n = 18**	**All[3]** **n = 81**
ampicillin	96.6	94.4	92.6
ciprofloxacin	96.6	94.4	93.8
gentamicin high-level	46.6	61.1	50.6
linezolid	3.5	0.0	2.5
nitrofurantoin[4]	-	-	0.0[4]
quinupristin/dalfopristin[5]	31.0	11.1	25.9[5]
streptomycin high-level	55.2	44.4	50.6
teicoplanin	98.3	0.0	74.1
tetracycline	56.9	77.8	63.0
multiresistant[6]	86.2	100.0	87.6

1 Teicoplanin susceptibilities were determined by Etest minimum inhibitory concentrations (MICs). Ampicillin, ciprofloxacin, gentamicin, linezolid, nitrofurantoin (*E. faecalis* only), quinupristin/dalfopristin (*E. faecium* only), streptomycin and tetracycline susceptibilities were determined by disc testing. MICs and zones of inhibition were interpreted according to the current European Committee on Antimicrobial Susceptibility Testing (EUCAST) clinical breakpoints, except for tetracycline zones which were interpreted according to the current Clinical and Laboratory Standards Institute's (CLSI) breakpoints.

2 Susceptibility data not shown separately for the *E. faecium* isolates with both *vanA*&B or those with *vanN*, but this data is included in the results for all VRE. The isolates with both *vanA* and *vanB* were resistant to ampicillin, ciprofloxacin, high-level gentamicin and tetracycline. The isolate with *vanN* was resistant to quinupristin/dalfopristin only.

3 Susceptibility data not shown separately for the two *E. faecalis* isolates. One was resistant to ciprofloxacin, high-level gentamicin, high-level streptomycin and tetracycline. The other was resistant to tetracycline only.

4 The EUCAST nitrofurantoin breakpoints are specifically for *E. faecalis*, so the overall rate of resistance is only for the two *E. faecalis* isolates.

5 *E. faecalis* are considered intrinsically resistant to quinupristin/dalfopristin, so the overall rate of resistance is only for the 79 *E. faecium* isolates.

6 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*).