Vancomycin-resistant enterococci, 2016

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).

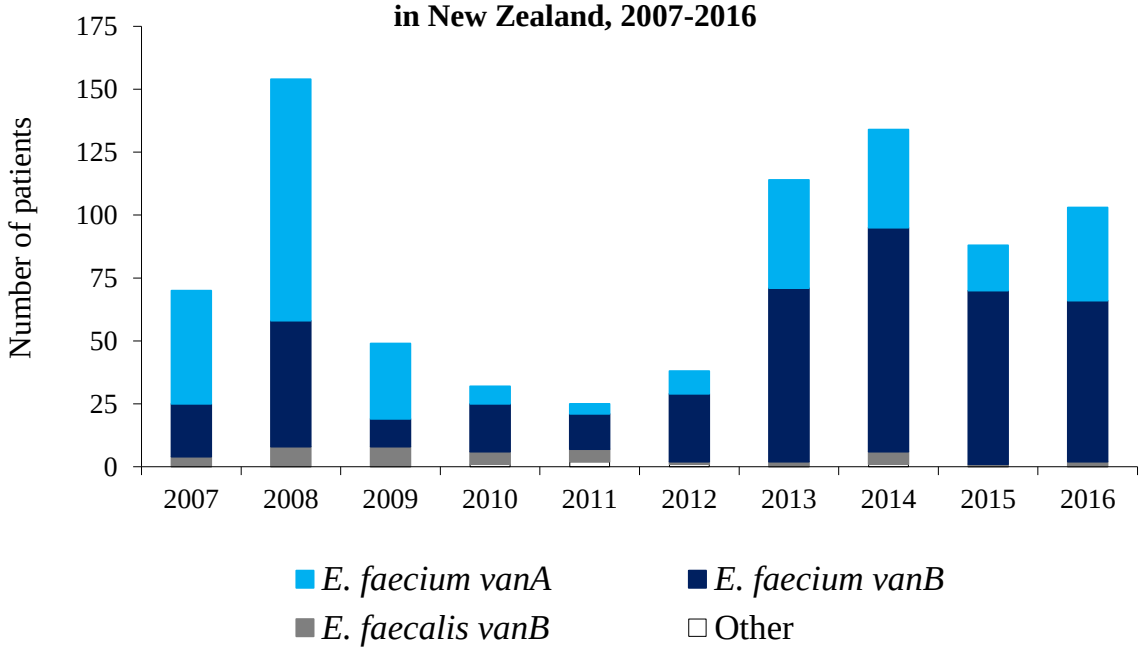
VRE from 99 patients were confirmed in 2016. While 99 patients were identified with VRE, this report includes results for 103 VRE isolates as two distinct VRE strains were isolated from two patients and three distinct VRE strains were isolated from a third patient. The majority (90, 87.4%) of the 103 VRE were isolated from screening specimens (ie, rectal swabs and faecal specimens). The remaining VRE were isolated from urine (7, 6.8%), blood (4, 3.9%), or other miscellaneous diagnostic specimens (2, 1.9%).

The species and van genotype distribution of the 103 VRE confirmed in 2016 was:

- 37 vanA *E. faecium*;
- 64 vanB *E. faecium*; and
- 2 vanB *E. faecalis.*

The number of patients with VRE confirmed each year over the last 10 years is shown in Figure 1. As has been the situation since 2010, vanB *E. faecium* was the dominant van genotype and VRE species in 2016.

Figure 1. Species and van genotype of VRE isolated in New Zealand, 2007-2016



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In 2016, the majority (75, 69.4%) of the VRE were isolated from patients in Auckland hospitals: Auckland City Hospital (34, 31.5%), Middlemore Hospital (24, 22.2%) and North Shore Hospital (17, 15.7%). VRE isolated from patients in Dunedin Hospital accounted for most of the remaining (12, 11.1%) VRE confirmed in 2016. 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 2016. Among the vanA *E. faecium* isolates, three strains were prevalent: PFGE profiles EfAX, EfAZ and EfBA. These three strains were all newly identified in 2016 and together accounted for 67.6% of the vanA *E. faecium* isolates. All three strains belong to MLST clonal complex (CC) 17. Notably the actual multilocus sequence type could not be determined for strain EfBA, as it is missing one of the seven genes used in the MLST scheme. Such *E. faecium* isolates have also been recently described in Australia (see Table 1, footnote 4). Strains EfAX and EfAZ were identified exclusively from patients in the Auckland area, with 13 of the 14 isolates of strain EfAX isolated from patients in Middlemore Hospital.

Among the vanB *E. faecium* isolates, one strain, PFGE profile EfAP, was dominant and accounted for 75.0% of the vanB *E. faecium* in 2016. Strain EfAP is MLST ST796, an MLST type common among vanB *E. faecium* in the Melbourne area. Strain EfAP was first identified in New Zealand in 2012. In 2016, strain EfAP was the most common VRE strain in Auckland City Hospital and North Shore Hospital. Strain EfAP was also identified for the first time in 2016 among Dunedin Hospital patients where it was eventually isolated from 12 patients during the year (Table 1).

Table 1. Distribution of patients with VRE by healthcare facility, 2016

Species	*van* gene	Referred from	PFGE profile / 'strain'[1]	MLST/CC[2]	Number of patients[3]
E. faecium	A	Middlemore Hospital	**EfAX**	ST80/CC17	13
			EfAZ	ST18/CC17	3
			EfBA	CC17[4]	2
			EfAS	ST761/CC17	1
			distinct[5]		3
		Auckland City Hospital	**EfBA**	CC17	2
			EfAZ	ST18/CC17	1
			distinct		1
		Christchurch Hospital	**EfBA**	CC17	2
			EfAV	ST80/CC17	1
		North Shore Hospital	distinct		2
		Whangarei Hospital	distinct		1
		Waikato Hospital	distinct		1
		Wellington Hospital	**EfBA**	CC17	1
		Auckland community	**EfAX**	ST80/CC17	1
			EfAZ	ST18/CC17	1
			distinct		2
	B	Auckland City Hospital	EfAP	ST796/CC17	26
			distinct		4
		North Shore Hospital	EfAP	ST796/CC17	9
			EfAW	ST78/CC17	3
			EfAT	ST203/CC17	2
		Dunedin Hospital	EfAP	ST796/CC17	12
		Whangarei Hospital	distinct[6]		4
		Middlemore Hospital	distinct		2
		Waikato Hospital	EfAE	ST203/CC17	1
			EfAP	ST796/CC17	1
		Christchurch Hospital	distinct		1
		Auckland community	EfAT	ST203/CC17	1
			EfAW	ST78/CC17	1
		Dunedin community	EfAP	ST796/CC17	1
E. faecalis	B	North Shore Hospital	distinct		1
		Wellington community	EfZ		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 2016.

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/.

3 Patients who were in more than one hospital are counted in each hospital. Five of the 99 patients with VRE were in two hospitals, and another three patients had ≥2 VRE strains, resulting in a total 'patient' count of 108 in this table.

4 Strain EfBA could not be assigned a multilocus sequence type as it appears to be missing one (*pstS*) of the seven genes used in this typing scheme. Such strains have also been described among *E. faecium* in Australia (Carter G et al. Emergence of endemic MLST non-typeable vancomycin-resistant *Enterococcus faecium*. J Antimicrob Chemother 2016; 71: 3367-71). Sequencing of the other six genes used in the *E. faecium* MLST scheme indicates this strain belongs to CC17.

footnotes continued next page

5 PFGE profile distinct (ie, <90% similarity) from any of the profiles designated a strain name.
6 While the four vanB *E. faecium* isolated from Whangarei Hospital patients had PFGE profiles that were distinct from any of the designated strains, three of these four VRE had very closely related profiles.

The antimicrobial susceptibility among the 2016 VRE is shown in Table 2.

Table 2. Resistance among VRE, 2016

Antimicrobial agent[2]	**Percent resistance**		
	E. faecium		**All n=103**[1]
	vanA n=37	**vanB n=64**	
ampicillin	97.3	98.4	96.1
ciprofloxacin	97.3	98.4	96.1
gentamicin high-level	67.6	79.7	75.7
linezolid	0.0	0.0	0.0
nitrofurantoin[3]	-	-	0.0
quinupristin/dalfopristin[4]	46.0	0.0	16.8
streptomycin high-level	59.5	4.7	25.2
teicoplanin	100.0	1.6	36.9
tetracycline	75.7	93.8	86.4
multiresistant[5]	94.6	98.4	95.1

1 Susceptibility data not shown separately for the two vanB *E. faecalis* isolates, but this data is included in the data for all VRE. Besides the expected intrinsic resistance to quinupristin/dalfopristin, one of these vanB *E. faecalis* isolates had high-level gentamicin and streptomycin resistance, and the other isolate had high-level gentamicin resistance and tetracycline resistance.
2 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.
3 The EUCAST nitrofurantoin breakpoints are specifically for *E. faecalis*, so the overall rate of 0.0% resistance is only for the two *E. faecalis* isolates.
4 *E. faecalis* are considered intrinsically resistant to quinupristin/dalfopristin, so the overall rate of 16.8% resistance is only for the 101 *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*).