ESR
Science for Communities

Vancomycin-resistant enterococci, 2017

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).

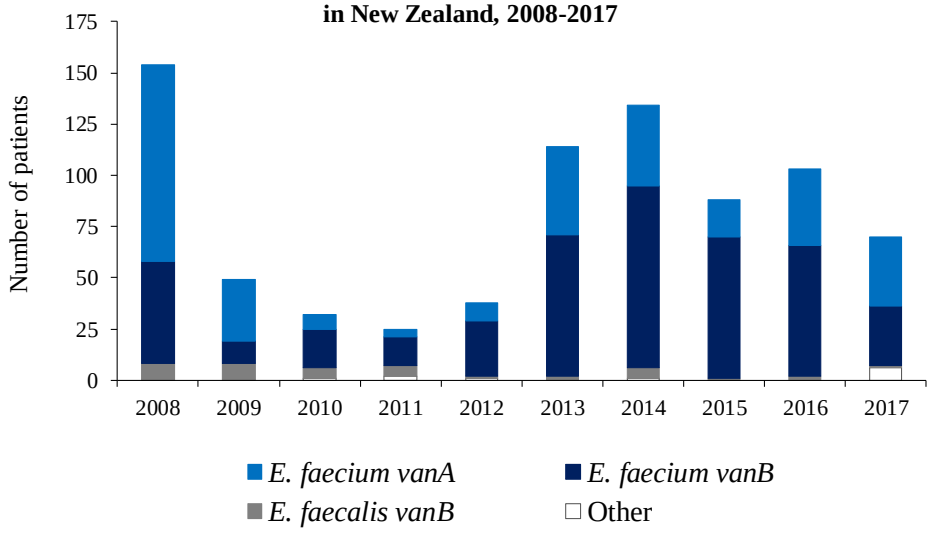
VRE from 67 patients were confirmed in 2017. While 67 patients were identified with VRE, this report includes results for 70 VRE isolates as two distinct VRE strains were isolated from one patient and three distinct VRE strains were isolated from another patient. The majority (60, 85.7%) of the 70 VRE were isolated from screening specimens (ie, rectal swabs and faecal specimens). The remaining VRE were isolated from urine (4, 5.7%), blood (3, 4.3%), or other miscellaneous diagnostic specimens (3, 4.3%).

The species and van genotype distribution of the 70 VRE confirmed in 2017 was:

- 34 vanA *E. faecium*;
- 29 vanB *E. faecium*;
- 2 vanD *E. faecium*;
- 4 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. There was a marked decrease in the number of patients from whom VRE were isolated in 2017 compared with the four preceding years. Also in contrast to the situation each year between 2010 and 2016 when vanB *E. faecium* was the dominant VRE genotype and species, in 2017 vanA *E. faecium* were prevalent.

Figure 1. Species and van genotype of VRE isolated in New Zealand, 2008-2017



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

In 2017, the majority (45, 60.8%) of the VRE were isolated from patients in Auckland hospitals: Auckland City Hospital (23, 31.1%), Middlemore Hospital (11, 14.9%) and North Shore Hospital (11, 14.9%). Dunedin Hospital accounted for the next largest number of patients (10, 13.5%) 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 2017. Among the vanA *E. faecium* isolates, two strains were prevalent: PFGE profiles EfBA and EfBC. Both these strains belong to MLST clonal complex (CC) 17 – a hospital-adapted *E. faecium* lineage. Strain EfBA was first identified among VRE in New Zealand in 2016 and is notable as it is missing one of the seven genes, *pstS*, used in the MLST scheme, although it has now been assigned as MLST ST1421 (see Table 1, footnote 4). *E. faecium* isolates missing the *pstS* gene, including ST1421, have been described among vanA *E. faecium* in Australia where they have become increasingly prevalent since 2015. Strain EfBC (ST612) was newly identified in 2017 and isolated from a small number of patients in hospitals in the Auckland area and Tauranga.

Among the vanB *E. faecium* isolates, two strains predominated: PFGE profiles EfAP and EfBB. Both these strains belong to MLST clonal complex (CC) 17. Strain EfAP is ST796, an MLST type common among vanB *E. faecium* in parts of Australia. Strain EfAP was first identified in New Zealand in 2012. In 2017, strain EfAP was identified from patients in Auckland hospitals and several hospitals in the South Island, albeit only in very small numbers from any one hospital (Table 1). Strain EfBB (ST555) was newly identified in 2017 and isolated solely from patients in Dunedin Hospital.

Table 1. Distribution of patients with VRE by healthcare facility, 2017

Species	*van* gene	Referred from	PFGE profile / 'strain'[1]	MLST/CC[2]	Number of patients[3]
E. faecium	A	Auckland City Hospital	EfBA	ST1421[4]/CC17	9
			EfBC	ST612/CC17	2
			EfY	ST192/CC17	1
			distinct[5]		7
		Middlemore Hospital	**EfBC**	ST612/CC17	2
			EfBA	ST1421/CC17	1
			distinct		3
		North Shore Hospital	EfY	ST192/CC17	2
			distinct		2
		Tauranga Hospital	**EfBC**	ST612/CC17	1
			distinct		1
		Whangarei Hospital	EfBA	ST1421/CC17	1
		Waikato Hospital	distinct		1
		Hawke's Bay Hospital	distinct		1
		Taranaki Base Hospital	distinct		1
		Christchurch Hospital	distinct		1
		Auckland community	distinct		1
	B	Dunedin Hospital	**EfBB**	ST555/CC17	7
			EfAP	ST796/CC17	3
		North Shore Hospital	EfAP	ST796/CC17	2
			distinct		5[6]
		Waikato Hospital	distinct		4
		Auckland City Hospital	EfAP	ST796/CC17	1
			distinct		2
		Middlemore Hospital	EfAP	ST796/CC17	1
			distinct		1
		Christchurch Hospital	EfAP	ST796/CC17	1
			distinct		1
		Wellington Hospital	distinct		1
		Southland Hospital	EfAP	ST796/CC17	1
	D	Middlemore Hospital	-[7]		2
E. faecalis	A	Auckland City Hospital	distinct		1
		Middlemore Hospital	distinct		1
		Tauranga Hospital	distinct		1
		Greymouth Hospital	EfA		1
	B	Hawke's Bay 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. PFGE profile designations in boldface are profiles of strains newly identified in 2017.

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/.

footnotes continued next page

3 Patients who were in >1 hospital are counted in each hospital. Of the 67 patients with VRE, three were in 2 hospitals, one had 2 VRE strains, and another had 3 VRE strains with 1 of the strains isolated from the patient while in 2 hospitals. As a result, the total 'patient' count in this table is 74.
4 In the 2016 annual report, it was noted that strain EfBA could not be assigned a multilocus sequence type as it was missing one (*pstS*) of the seven genes used in this typing scheme. A sequence type, ST1421, has now been assigned for the allelic profile (atpA 1, ddl 1, gdh 1, purK 1, gyd 1, pstS 0, adk 1) of strain EfBA.
5 PFGE profile distinct (ie, <90% similarity) from any of the profiles designated a strain name.
6 While 5 of the vanB *E. faecium* isolated from North Shore Hospital patients had PFGE profiles that were distinct from any of the profiles designated a strain name, 4 of 5 VRE had indistinguishable or very closely related PFGE profiles.
7 The 2 vanD *E. faecium* isolates were not typed.

The antimicrobial susceptibility among the 2017 VRE is shown in Table 2.

Table 2. Resistance among VRE, 2017

Antimicrobial agent[1]	**Percent resistance**			
	***E. faecium*[2]**		***E. faecalis*** **n = 5[3]**	**All** **n = 70**
	vanA **n = 34**	**vanB** **n = 29**		
ampicillin	97.1	100	0.0	91.4
ciprofloxacin	94.1	96.6	60.0	92.9
gentamicin high-level	61.8	86.2	60.0	70.0
linezolid	5.9	0.0	20.0	4.3
nitrofurantoin[4]	-	-	0.0	0.0[4]
quinupristin/dalfopristin[5]	35.3	0.0	-	17.1[5]
streptomycin high-level	35.3	24.1	40.0	30.0
teicoplanin	94.1	0.0	80.0	52.9
tetracycline	82.4	96.6	80.0	88.6
multiresistant[6]	97.1	96.6	60.0	94.3

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 2 vanD *E. faecium* isolates, but this data is included in the data for all VRE. These 2 vanD *E. faecium* isolates were both resistant to ampicillin, ciprofloxacin and tetracycline.
3 Susceptibility data not shown separately for the 4 vanA and the 1 vanB *E. faecalis* isolates.
4 The EUCAST nitrofurantoin breakpoints are specifically for *E. faecalis*, so the overall rate of 0.0% resistance is only for the 5 *E. faecalis* isolates.
5 *E. faecalis* are considered intrinsically resistant to quinupristin/dalfopristin, so the overall rate of 17.1% resistance is only for the 65 *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*).