Vancomycin-resistant enterococci, 2015

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).

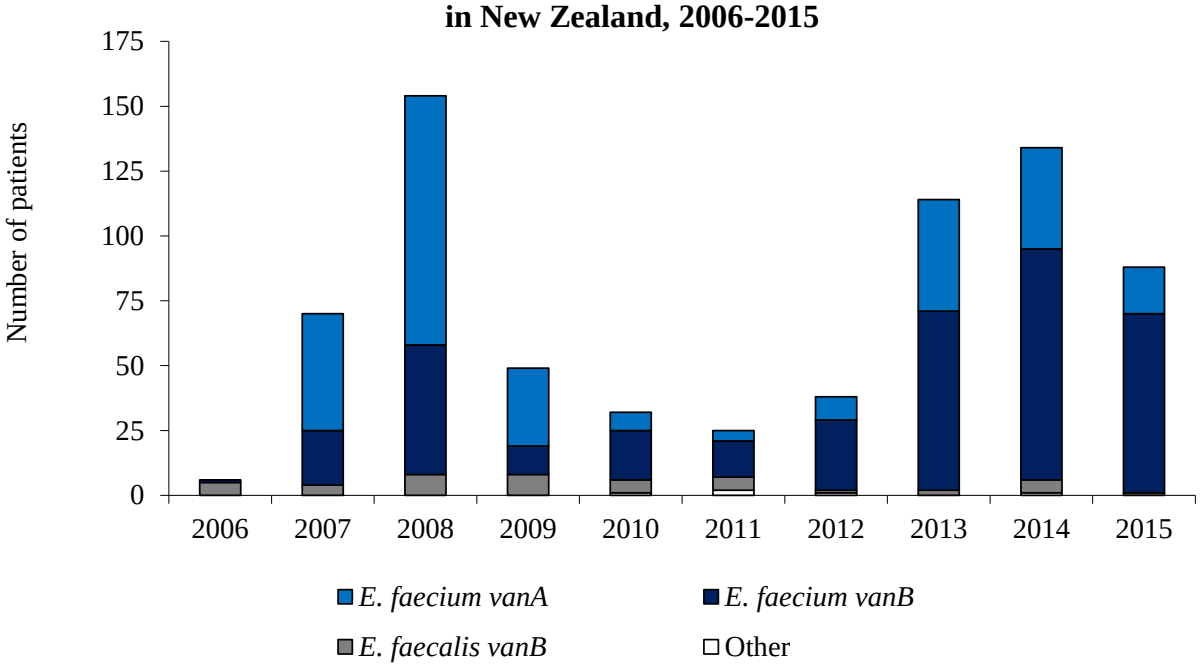
VRE from 88 patients were confirmed in 2015. The majority (81, 92.0%) were isolated from screening specimens (ie, rectal swabs and faecal specimens). The remaining VRE were isolated from urine (3, 3.4%) or other miscellaneous diagnostic specimens (4, 4.5%). There were no VRE isolated from blood or another invasive site.

The species and van genotype distribution of the 88 VRE confirmed in 2015 was:

- 18 vanA *E. faecium*;
- 69 vanB *E. faecium*; and
- 1 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 2015.

Figure 1. Species and van genotype of VRE isolated in New Zealand, 2006-2015



In 2015, the majority (71, 77.2%) of the VRE were isolated from patients in Auckland hospitals, mainly North Shore Hospital (55, 59.8%). VRE isolated from patients in Christchurch Hospital accounted for most of the remaining (16, 17.4%) VRE confirmed in 2015. Patients who were in more than one hospital are counted in each hospital in the above and 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 2015. Among the vanA *E. faecium* isolates, one strain, PFGE profile EfAV, was dominant and accounted for 44.4% (8/18) of the vanA *E. faecium* isolates. This strain was first identified in 2014, with all cases that year isolated from Christchurch Hospital patients. In 2015, all isolates of this strain were also from Christchurch Hospital patients. Strain EfAV is multilocus sequence type (MLST) ST80 which belongs in MLST clonal complex (CC) 17.

Among the vanB *E. faecium* isolates, two strains, PFGE profiles EfAT and EfAP, were predominant and collectively accounted for 78.3% [56.5% (39/69) and 21.7% (15/69), respectively] of the vanB *E. faecium* isolates. All of the patients with these two strains, and all but three of the patients with vanB *E. faecium*, were in Auckland hospitals (Table 1). Strains EfAT and EfAP are MLST types ST203 and ST796, respectively. ST796 is a single-locus variant of ST203 and both types belong to MLST CC17. These two MLST types are common among vanB *E. faecium* in the Melbourne area. Strain EfAP was first identified in New Zealand in 2012 and appears to have originated in Australia. EfAT was newly identified among VRE in New Zealand in 2014.

Table 1. Distribution of patients with VRE by healthcare facility, 2015

Species	*van* gene	Referred from	PFGE profile / 'strain'[1]	MLST/CC[2]	Number of patients[3]
E. faecium	A	Christchurch Hospital	EfAV	ST80/CC17	8
			EfAS	ST761/CC17	3
			distinct[4]		3
		Whangarei Hospital	distinct		1
		North Shore Hospital	distinct		1
		Wellington Hospital	EfAQ	ST80/CC17	1
		Nelson Hospital	distinct		1
	B	North Shore Hospital	EfAT	ST203/CC17	36
			EfAP	ST796/CC17	11
			EfAW	ST78/CC17	3
			distinct		4
		Middlemore Hospital	EfAP	ST796/CC17	4
			EfAB	ST17/CC17	1
			EfAT	ST203/CC17	1
			distinct		4
		Auckland City Hospital	EfAT	ST203/CC17	5
			EfAP	ST796/CC17	1
		Christchurch Hospital	distinct		2
		Wellington Hospital	distinct		1
E. faecalis	B	Wellington Hospital	EfZ		1

1 In-house pulsed-field gel electrophoresis (PFGE) profile designations. PFGE profiles were analysed with BioNumerics software version 6.6 (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 2015.

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 system described on the *E. faecium* MLST website at http://efaecium.mlst.net/.

3 Patients who were in more than one hospital are counted in each hospital. Four of the 88 patients with VRE (all vanB *E. faecium*) were in two hospitals, so the total patient count in this table is 92.

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

The antimicrobial susceptibility among the 2015 VRE is shown in Table 2. All vancomycin-resistant *E. faecium* isolates were multiresistant to ≥3 antimicrobial classes in addition to glycopeptides.

Table 2. Resistance among VRE, 2015[1]

Antimicrobial agent[2]	**Percent resistance**		
	E. faecium		**All n=88[1]**
	vanA n=18	**vanB n=69**	
ampicillin	100	100	98.9
ciprofloxacin	100	100	98.9
gentamicin high-level	22.2	21.7	22.7
linezolid	0.0	0.0	0.0
nitrofurantoin	77.8	79.7	78.4
quinupristin/dalfopristin	16.7	2.9	5.7[3]
streptomycin high-level	50.0	24.6	30.7
teicoplanin	88.9[4]	0.0	18.2
tetracycline	88.9	97.1	94.3
multiresistant[5]	100	100	98.9

1 Susceptibility data not shown separately for the one vanB *E. faecalis* isolate, but this data is included in the data for all VRE. Besides the expected intrinsic resistance to quinupristin/dalfopristin, this vanB *E. faecalis* isolate had high-level gentamicin and streptomycin resistance.

2 Teicoplanin susceptibilities were determined by Etest minimum inhibitory concentrations (MICs). Ampicillin, ciprofloxacin, gentamicin and linezolid susceptibilities were determined by Etest or disc testing. Nitrofurantoin, quinupristin/dalfopristin, streptomycin and tetracycline susceptibilities were determined by disc testing. MICs and zones of inhibition were interpreted according to the Clinical and Laboratory Standards Institute's criteria.[1]

3 *E. faecalis* are considered intrinsically resistant to quinupristin/dalfopristin, so this rate of 5.7% resistance is only for the 87 *E. faecium* isolates.

4 Two (11.1%) vanA *E. faecium* isolates demonstrated only intermediate teicoplanin resistance (MIC 16 mg/L).

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

[1] Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing; twenty-fifth informational supplement. Wayne, PA, USA: CLSI; 2015. CLSI document M100-S25.