Vancomycin-resistant enterococci, 2014

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).

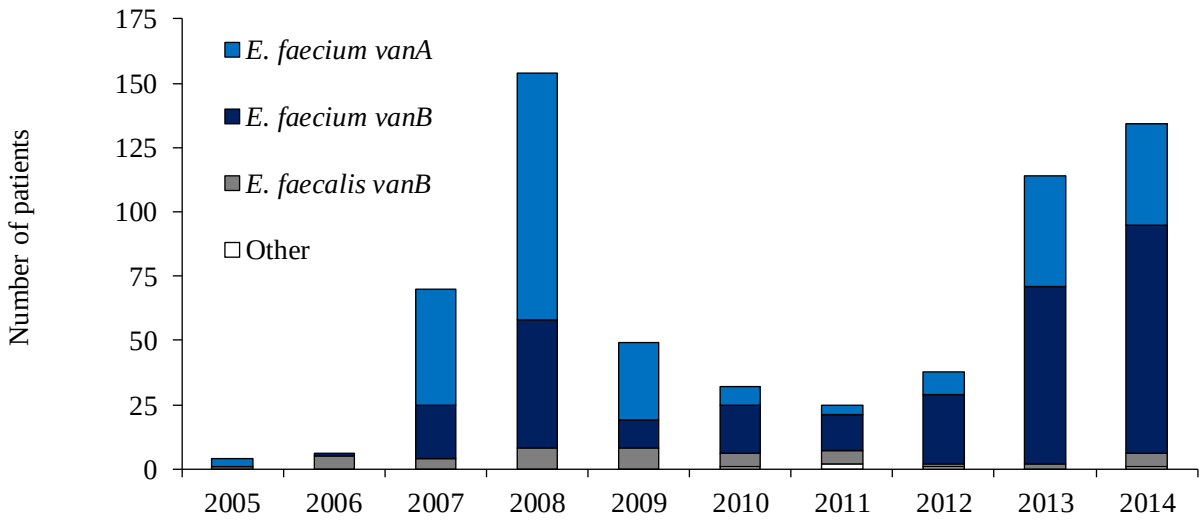
VRE from 132 patients were confirmed in 2014. While 132 patients were identified with VRE, this report includes results for 133 VRE isolates as two distinct vanB *E. faecium* strains were isolated from one of the patients. The site of isolation was reported for 130 (97.7%) of the isolates, and the majority (119, 91.5%) were isolated from screening specimens (ie, rectal swabs and faecal specimens). The remaining VRE were isolated from urine (5, 3.8%), blood (2, 1.5%) or other miscellaneous diagnostic specimens (4, 3.1%).

The species and van genotype distribution of the 133 VRE confirmed in 2014 was:

- 38 vanA *E. faecium*
- 88 vanB *E. faecium*
- 1 vanA + vanB *E. faecium*
- 1 vanA *E. faecalis*
- 5 vanB *E. faecalis*

The number of patients with VRE confirmed each year over the last 10 years is shown in Figure 1. The number of VRE confirmed in 2014 was the highest annual number since 2008 when there were outbreaks of several VRE strains in Auckland hospitals.

Figure 1. Species and van genotype of VRE isolated in New Zealand, 2005-2014



As has been the pattern in earlier years, in 2014 the majority (103, 75.7%) of the VRE were isolated from patients in Auckland hospitals: 52.9% (72) North Shore Hospital, 11.8% (16) Middlemore Hospital, and 11.0% (15) Auckland City Hospital. VRE from patients in Christchurch Hospital accounted for most of the remaining (26, 19.1%) VRE confirmed in 2014. A more detailed breakdown of the location of the patients is shown in Table 1.

Table 1 also shows the various VRE strains identified in 2014. Among the vanA *E. faecium* isolates, one strain, PFGE profile EfAS, was dominant and accounted for 47.4% (18/38) of the vanA *E. faecium* isolates. The *E. faecium* isolate that had both vanA and vanB was also strain EfAS. This strain was first identified in 2013, with the index case and most other cases that year isolated from Christchurch Hospital patients. In 2014 the strain was isolated from a further 19 patients, 18 of whom were Christchurch Hospital patients. Strain EfAS is multilocus sequence type (ST) 761 which belongs in MLST clonal complex (CC) 17.

Among the vanB *E. faecium* isolates, three strains, PFGE profiles EfAP, EfAT and EfAU, were predominant and accounted for 87.5% (77/88) of the vanB *E. faecium* isolates. Strain EfAP was first identified in 2012 and appears to have originated in Australia. It is indistinguishable from a strain common in the Melbourne area: ST796 which belongs in CC17. In 2014 strain EfAP accounted for 62.5% (55/88) of vanB *E. faecium* and was exclusively isolated from patients in Auckland hospitals, predominantly North Shore Hospital (Table 1). Strains EfAT and EfAU were newly identified in 2014 and, like the EfAP strain, predominantly isolated from patients in North Shore Hospital. Both strains EfAT and EfAU are ST203, also an MLST type common among vanB *E. faecium* in the Melbourne area. ST203 also belongs in CC17.

Table 1. VRE referred to ESR, 2014

Species	*van* gene	Referred from	PFGE profile/'strain'[1]	MLST/CC[2]	Number of patients[3]
E. faecium	A	Christchurch Hospital	EfAS	ST761/CC17	17
			EfAV	ST80/CC17	3
			distinct[4]		4
		Auckland City Hospital	EfN	ST375/CC17	1
			EfAQ	ST80/CC17	1
			distinct		3
		Middlemore Hospital	distinct		5
		North Shore Hospital	distinct		3
		Wellington Hospital	EfAQ	ST80/CC17	1
		Nelson Hospital	EfAS	ST761/CC17	1
	A + B	Christchurch Hospital	EfAS	ST761/CC17	1
	B	North Shore Hospital	EfAP	ST796/CC17	48
			EfAT	ST203/CC17	14
			EfAU	ST203/CC17	6
			distinct		1
		Middlemore Hospital	EfAP	ST796/CC17	3
			EfAC	ST869/CC17	1
			EfAU	ST203/CC17	1
			distinct		5
		Auckland City Hospital	EfAP	ST796/CC17	6
			EfAB	ST17/CC17	1
			EfAT	ST203/CC17	1
			distinct		1
		Wellington Hospital	EfAE	ST203/CC17	1
		Christchurch Hospital	distinct		1
E. faecalis	A	Auckland City Hospital	EfA		1
	B	Wellington Hospital	EfZ		3
		Middlemore Hospital	distinct		1
		Hawkes Bay Hospital	distinct		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 2014.

2 MLST, multilocus sequence type; CC, MLST clonal complex. MLST only determined for PFGE profiles identified among vancomycin-resistant *E. faecium*.

3 Patients who were in more than one hospital are counted in each hospital. Four of the 132 patients with VRE were in two hospitals, so the total patient count in this table is 136.

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

The antimicrobial susceptibility among the 2014 VRE is shown in Table 2. The majority of VRE were multiresistant to ≥3 antimicrobial classes in addition to glycopeptides.

Twenty (52.6%) of the 38 vanA *E. faecium* isolates only demonstrated intermediate teicoplanin resistance (MICs 16 mg/L). A further two isolates were teicoplanin susceptible with MICs of 4 or 8 mg/L. However, these teicoplanin MICs of 4-16 mg/L found among vanA *E. faecium* were all elevated compared with the teicoplanin MICs of vanB *E. faecium* isolates which were ≤1 mg/L. Fourteen of the 20 vanA *E. faecium* isolates that had intermediate teicoplanin resistance belonged to the EfAS strain.

Linezolid resistance among VRE was detected for the first time in New Zealand in 2014. Linezolid-resistant vanA *E. faecium* were isolated from two patients who had recently returned from India where they had been hospitalised.

Table 2. Resistance among VRE, 2014[1]

Antimicrobial agent[2]	**Percent resistance**			
	E. faecium			***E. faecalis***
	vanA n=38	**vanB n=88**	**All n=127[3]**	**vanB n=5**
ampicillin	100	100	100	0.0
ciprofloxacin	100	100	100	0.0
gentamicin high-level	57.9	73.9	69.3	60.0
linezolid	5.3	0.0	1.6	0.0
nitrofurantoin	47.4	29.6	35.4	0.0
quinupristin/dalfopristin	55.3	0.0	16.5	-[4]
streptomycin high-level	73.7	3.4	24.4	80.0
teicoplanin	42.1[5]	0.0	12.6	0.0
tetracycline	92.1	89.8	90.6	40.0
multiresistant[6]	97.4	93.2	94.5	0.0

1 Data not shown for the one vanA *E. faecalis* isolate (which was not resistant to any of the antibiotics tested other than glycopeptides).

2 Ampicillin, ciprofloxacin, gentamicin, linezolid and teicoplanin susceptibilities were determined by Etest minimum inhibitory concentrations (MICs). 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 One *E. faecium* isolate with both vanA and vanB is only included in the data for all *E. faecium*.

4 *E. faecalis* are considered intrinsically resistant to quinupristin/dalfopristin.

5 Twenty (52.6%) vanA *E. faecium* isolates only demonstrated intermediate teicoplanin resistance (MICs 16 mg/L). A further two isolates were teicoplanin susceptible (MICs 4-8 mg/L).

6 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-fourth informational supplement. Wayne, PA, USA: CLSI, 2014. CLSI document M100-S24.