Vancomycin-resistant enterococci, 2013

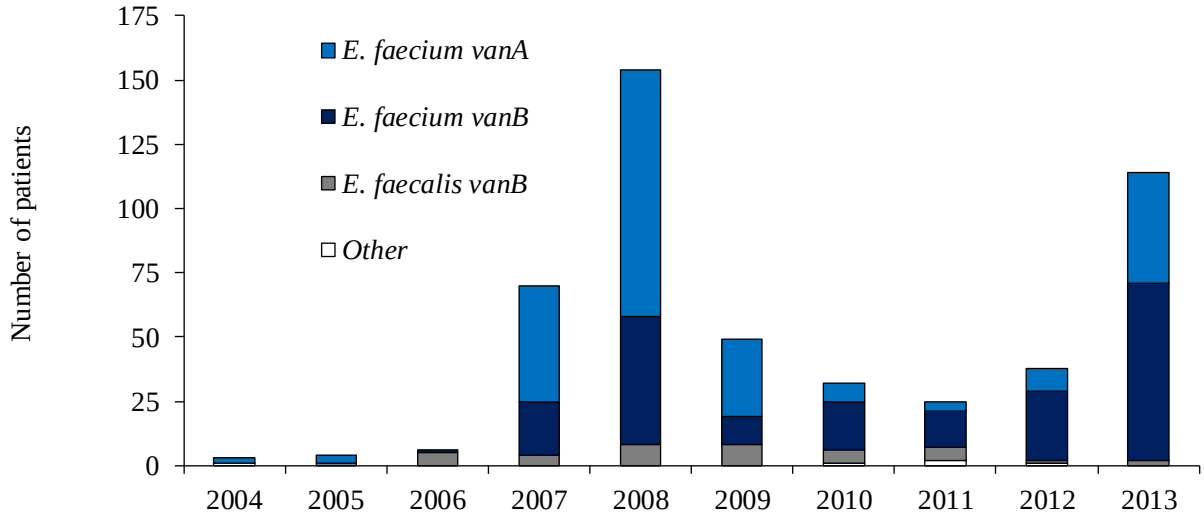
Hospital and community diagnostic laboratories are requested to refer all vancomycin-resistant *Enterococcus faecium* and *E. faecalis* (VRE) isolates to ESR for the national surveillance of these resistant organisms. At ESR, the isolates are confirmed as vancomycin resistant, the *van* gene is identified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

VRE from 111 patients were confirmed in 2013. The majority (102, 91.9%) of VRE were isolated from rectal swabs or faecal specimens as the result of screening for the organism. The remaining VRE were isolated from urine (5, 4.5%), blood (1, 0.9%) or other miscellaneous diagnostic specimens (3, 2.7%).

While 111 patients were identified with VRE in 2013, this report includes results for 114 VRE isolates as two distinct VRE strains were isolated from each of three patients: one patient had both a vanA *E. faecium* strain and a vanB *E. faecium* strain, another patient had two distinct (as identified by PFGE) vanA *E. faecium* strains, and a third patient had two distinct vanB *E. faecium* strains. Among the 114 VRE isolates, 69 (60.5%) were vanB *E. faecium*, 43 (37.7%) were vanA *E. faecium*, and 2 (1.8%) were vanB *E. faecalis*.

The species and van genotype distribution of the VRE confirmed in 2013 and the preceding 9 years is shown in Figure 1. The number of patients confirmed with VRE in 2013 (111) was nearly 3-times the number in 2012 (38), and 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, 2004-2013



In 2013, the majority (89, 78.1%) of the VRE were isolated from patients in Auckland hospitals: 48.2% (55) Auckland City Hospital, 28.9% (33) Middlemore Hospital, and 0.9% (1) North Shore Hospital. VRE from patients in Christchurch Public Hospital

accounted for almost all the remaining (19, 16.7%) VRE confirmed in 2013. A more detailed breakdown of the location of the patients is shown in Table 1.

Table 1 also shows the various VRE strains identified by PFGE typing in 2013. Among the vanA *E. faecium* isolates, two strains, PFGE profiles EfAS and EfAQ, were dominant and accounted for 34.9% (15/43) and 27.9% (12/43) of vanA *E. faecium* isolates, respectively. Strain EfAS was newly identified in 2013, with the index case being a Christchurch Hospital patient. This strain was subsequently identified from a further 12 patients in that hospital throughout 2013. Strain EfAQ was first identified in 2012 from a patient in Middlemore Hospital. In 2012, strain EfAQ was isolated from a further 12 patients in Auckland hospitals.

Among the vanB *E. faecium* isolates, one strain, PFGE profile EfAP, was predominant and accounted for 69.6% (48/69) of vanB *E. faecium* isolates. This strain was isolated from 43 patients in Auckland City Hospital, 3 patients in Middlemore Hospital, 1 patient in Waikato Hospital and 1 Auckland community patient. Strain EfAP was first identified in 2012, and was isolated from 16 patients in Auckland hospitals that year. It appears this strain originated in Australia. It is indistinguishable from a strain common in the Melbourne area (multilocus sequence type 796) and the New Zealand index patient had been hospitalised in Melbourne.

Table 1. VRE referred to ESR, 2013

Species	*van* gene	Referred from	PFGE profile/'strain'[1]	Number of patients
E. faecium	A	Middlemore Hospital	**EfAQ**	9
			EfAS	1
			distinct[2]	10
		Christchurch Hospital	EfAS	13
			distinct	2
		Auckland City Hospital	**EfAQ**	3
			EfAS	1
			distinct	2
		North Shore Hospital	distinct	1
		Waikato Hospital	distinct	1
	B	Auckland City Hospital	**EfAP**	43
			EfAC	6
		Middlemore Hospital	**EfAC**	4
			EfAP	3
			distinct	6
		Christchurch Hospital	EfAR	4
		Waikato Hospital	**EfAP**	1
		Tauranga Hospital	distinct	1
		Auckland community	**EfAP**	1
E. faecalis	B	Wellington Hospital	**EfZ**	2

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 that were identified prior to 2013.

2 Distinct isolates that share <90% PFGE profile similarity with any other VRE isolate.

The antimicrobial susceptibility among the 2013 vancomycin-resistant *E. faecium* isolates is shown in Table 2. The majority of vancomycin-resistant *E. faecium* isolates were multiresistant to ≥3 antibiotic classes in addition to glycopeptides.

Table 2. Resistance among vancomycin-resistant *E. faecium*, 2013[1]

Antimicrobial agent[2]	Percent resistance		
	vanA n=43	vanB n=69	All n=112
ampicillin	97.7	100	99.1
ciprofloxacin	100	100	100
gentamicin high-level	53.5	87.0	74.1
nitrofurantoin	46.5	26.1	33.9
quinupristin/dalfopristin	51.2	0.0	19.6
streptomycin high-level	53.5	17.4	31.3
teicoplanin	95.4[3]	1.5[4]	37.5
tetracycline	90.7	98.6	95.5
multiresistant[5]	97.7	98.6	98.2

1 Data not included for the two vanB *E. faecalis* isolates. These two isolates were indistinguishable by PFGE and were resistant to high-level gentamicin and streptomycin, with the expected intrinsic resistance to quinupristin/dalfopristin.

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] No isolate was resistant to linezolid.

3 Two vanA *E. faecium* isolates were not resistant to teicoplanin. One was susceptible and the other had intermediate resistance. VRE with a vanA genotype but a vanB phenotype are infrequently observed.

4 One vanB *E. faecium* isolate was resistant to teicoplanin. VRE with a vanB genotype but a vanA phenotype are infrequently.

5 Resistant ≥3 classes of antibiotics in addition to glycopeptides.

[1] Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing; twenty-third informational supplement. Wayne, PA, USA: CLSI, 2013. CLSI document M100-S23.