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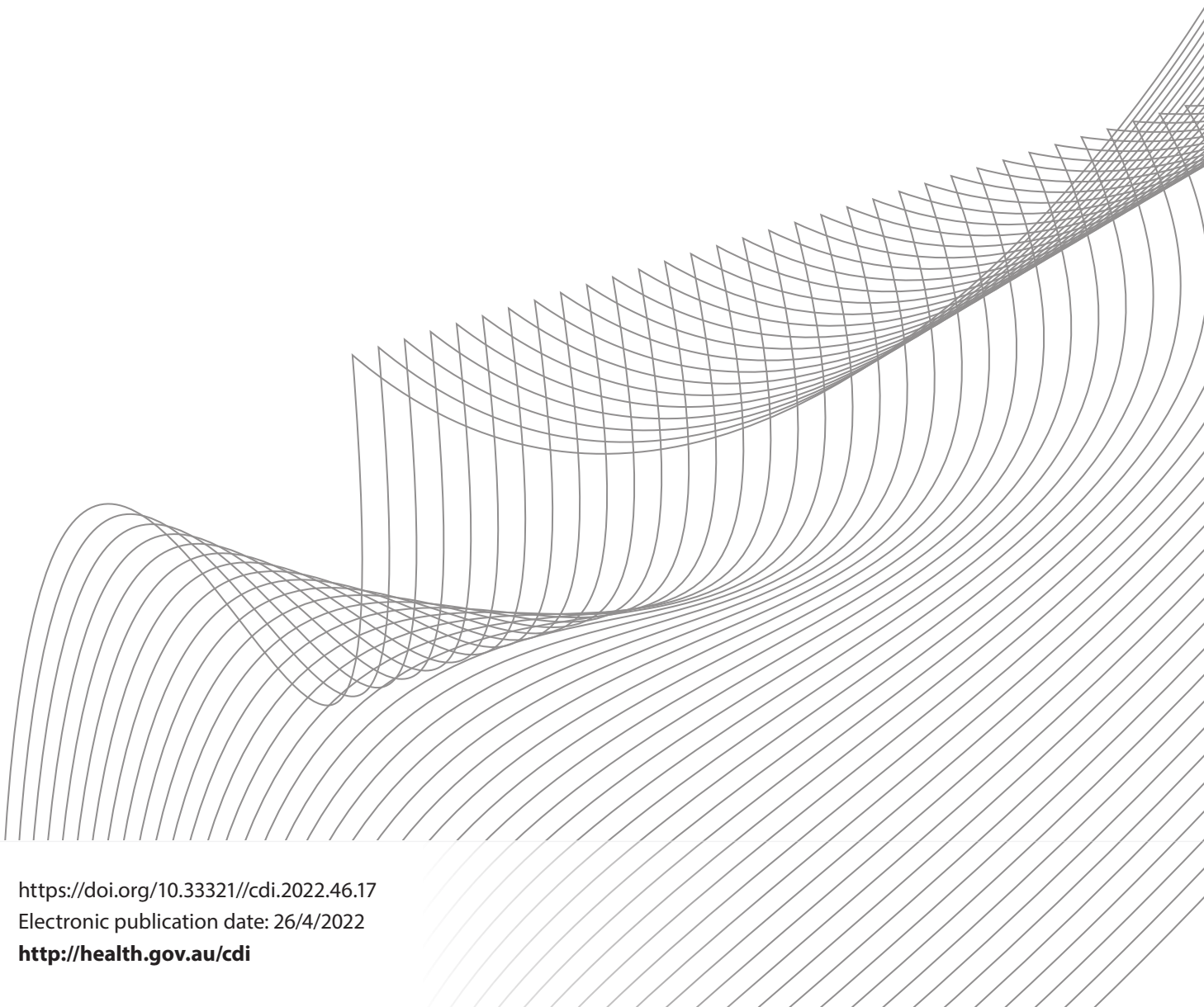
Australian Group on Antimicrobial Resistance (AGAR) Australian Enterococcal Sepsis Outcome Programme (AESOP) Annual Report 2020

Geoffrey W Coombs, Denise A Daley, Nicholas W T Yee, Princy Shoby, Shakeel Mowlaboccus, on behalf of the Australian Group on Antimicrobial Resistance



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Annual report

Australian Group on Antimicrobial Resistance (AGAR) Australian Enterococcal Sepsis Outcome Programme (AESOP) Annual Report 2020

Geoffrey W Coombs, Denise A Daley, Nicholas W T Yee, Princy Shoby, Shakeel Mowlaboccus, on behalf of the Australian Group on Antimicrobial Resistance

Abstract

From 1 January to 31 December 2020, forty-nine institutions around Australia participated in the Australian Enterococcal Sepsis Outcome Programme (AESOP). The aims of AESOP 2020 were to determine the proportion of enterococcal bacteraemia isolates in Australia that were antimicrobial-resistant, and to characterise the molecular epidemiology of the *E. faecium* isolates. Of the 1,230 unique episodes of enterococcal bacteraemia investigated, 93.9% were caused by either *E. faecalis* (54.2%) or *E. faecium* (39.7%). Ampicillin resistance was not detected in *E. faecalis* but was detected in 88.2% of *E. faecium*. Vancomycin non-susceptibility was detected in 0.2% of *E. faecalis* and 32.6% of *E. faecium*. Overall, 35.2% of *E. faecium* harboured *vanA* and/or *vanB* genes. For the *vanA/B* positive *E. faecium* isolates, 38.8% harboured the *vanA* gene, 60.6% the *vanB* gene, and 0.6% harboured both *vanA* and *vanB*. Although the percentage of *E. faecium* bacteraemia isolates was significantly lower than that detected in the 2019 AESOP (presumably due to the COVID-19 elective surgery restrictions placed on hospitals), it remains substantially higher than that recorded in most European countries. The *E. faecium* isolates detected consisted of 71 multilocus sequence types (STs), with 81.7% of these isolates classified into eight major STs each containing ten or more isolates. All major STs belonged to clonal cluster 17 (CC17), a major hospital-adapted polyclonal *E. faecium* cluster. The major STs (ST17, ST1424, ST80, ST796, ST78, ST1421, ST555 and ST117) were found across most regions of Australia. The predominant clone was ST17, which was identified in all regions except the Northern Territory. Overall, 40.9% of isolates belonging to the eight major STs harboured the *vanA* or *vanB* gene. The AESOP 2020 has shown enterococcal bacteraemia episodes in Australia are frequently caused by polyclonal ampicillin-resistant high-level gentamicin-resistant *vanA*- or *vanB*-positive *E. faecium* which have limited treatment options.

Keywords: Australian Group on Antimicrobial Resistance (AGAR); antimicrobial resistance surveillance; *Enterococcus faecium*, *Enterococcus faecalis*, vancomycin-resistant enterococci (VRE), bacteraemia

Background

Globally, enterococcus is believed to account for approximately 10% of all bacteraemia cases; it is the fourth and fifth leading cause of sepsis in North America and Europe respectively.[1,2] Although, in the 1970s, healthcare-associated enterococcal infections were primarily due to *Enterococcus faecalis*, there has been a steady increasing prevalence of *E. faecium* nosocomial infections.[3–5] Worldwide, the increase in nosocomial *E. faecium* infections has primarily been due to the expansion of polyclonal hospital-adapted clonal complex 17 (CC17) strains. While innately resistant to many classes of antibiotics, *E. faecium* has further demonstrated a remarkable capacity to evolve new antimicrobial resistances. In 2009, the Infectious Diseases

Society of America highlighted *E. faecium* as one of the key problem bacteria or ESKAPE (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* species) pathogens requiring new therapies.[6]

The Australian Group on Antimicrobial Resistance (AGAR) is a network of laboratories located across Australia that commenced surveillance of antimicrobial resistance in *Enterococcus* species in 1995.[7] In 2011, AGAR commenced the Australian Enterococcal Sepsis Outcome Programme (AESOP).[8,9] The objective of AESOP 2020 was to determine the proportion of *E. faecalis* and *E. faecium* bacteraemia isolates demonstrating antimicrobial resistance, with particular emphasis on:

1. assessing susceptibility to ampicillin;

2. assessing susceptibility to glycopeptides; and

3. the molecular epidemiology of *E. faecium*.

Methodology

Participants

Thirty laboratories servicing 49 institutions from all Australian states and mainland territories.

Collection period

From 1 January to 31 December 2020, the 39 laboratories collected all enterococcal species isolated from blood cultures. Enterococci of the same species and antimicrobial susceptibility profiles isolated from a patient's blood culture within 14 days of the first positive culture were excluded. A new enterococcal sepsis episode in the same patient was recorded if it was confirmed by a further culture of blood taken more than 14 days after the initial positive culture. Data were collected on age, sex, date of admission and discharge (if admitted), and mortality at seven and 30 days from date of blood culture collection. To avoid interpretive bias, no attempt was made to assign attributable mortality. Each episode of bacteraemia was designated as "hospital-onset" if the first positive blood culture(s) in an episode was collected > 48 hours after admission.

Laboratory testing

Enterococcal isolates were identified to the species level by the participating laboratories using matrix-assisted laser desorption ionization (MALDI)—MALDI Biotyper (Bruker Daltonics, USA) or Vitek-MS (bioMérieux, France)—or Vitek2® (bioMérieux). Antimicrobial susceptibility testing was performed using the Vitek2® (bioMérieux) or BD Phoenix™ (Becton Dickinson, USA) automated microbiology systems according to the manufacturer's instructions. Minimum inhibitory concentration (MIC) data and isolates were referred to the Antimicrobial Resistance and Infectious Diseases (AMRID) Research Laboratory at Murdoch University. Clinical and Laboratory Standards Institute (CLSI)[10] and European Committee on Antimicrobial Susceptibility Testing (EUCAST)[11] breakpoints were utilised for interpretation. Linezolid and daptomycin non-susceptible isolates and vancomycin-susceptible isolates which harboured the *vanA* or *vanB* genes were retested by Etest® (bioMérieux, France), using the Mueller-Hinton agar recommended by the manufacturer. The control strain used was *E. faecalis* ATCC® 29212. Genotyping was performed by whole genome sequencing (WGS) using the NextSeq® 500 platform (Illumina, USA). Sequencing results were analysed using the Nullarbor pipeline.[12]

Confidence intervals (CI) for proportions, Fisher's exact test for categorical variables, and chi-square test for trend, were calculated as appropriate, using MedCalc for Windows, version 12.7 (MedCalc Software, Belgium).

Approval to conduct the prospective data collection was given by the research ethics committee associated with each participating laboratory.

Results

From 1 January to 31 December 2020, there were 1,230 unique episodes of enterococcal bacteraemia identified. Although nine *Enterococcus* species were identified, *E. faecalis* and *E. faecium* predominated: 667 isolates (54.2%) were *E. faecalis* and 488 isolates (39.7%) were *E. faecium*. Seventy-five enterococci were identified either as *E. gallinarum* (20 isolates), *E. casseliflavus* (19 isolates), *E. raffinosus* (12 isolates), *E. avium* (12 isolates), *E. hirae* (8 isolates), *E. durans* (2 isolates), *E.cecorum* (1 isolate) or *Enterococcus* sp. [not speciated] (1 isolate).

A significant difference was observed in patient sex ($p < 0.0001$), with 801 (65.1%) being male (95% CI: 62.4–67.8). The average age of patients was 63 years, ranging from 0 to 100 years, with a median age of 69 years. The majority of episodes, 688/1,230 (55.9%), were community-onset (95% CI: 53.1–58.7); however, a significant difference ($p < 0.0001$) in place of onset was seen between *E. faecium* and *E. faecalis*, with only 33.2% (95% CI: 30.6-36.1) of *E. faecium* episodes being community-onset compared to 66.8% (95% CI: 64.0–69.5) for *E. faecalis*. All-cause mortality at 30 days, where outcome was known, was 18.1% (95% CI: 15.7–20.1). There was no significant difference in mortality between *E. faecalis* and *E. faecium* episodes (17.4% vs. 19.5% respectively, $p = 0.4$), or between vancomycin-susceptible and vancomycin non-susceptible *E. faecium* episodes (19.4% vs 19.8% respectively, $p = 0.9$).

E. faecalis phenotypic susceptibility results

Apart from erythromycin, tetracycline, ciprofloxacin and high-level gentamicin, acquired resistance was rare amongst *E. faecalis* isolates (Table 1). One isolate was resistant to vancomycin (MIC ≥ 32 mg/L). Twenty-four *E. faecalis* isolates (3.6%) were initially reported as linezolid non-susceptible (CLSI breakpoint > 2 mg/L). By Etest®, 17 of the 24 isolates had a linezolid MIC of ≤ 2 mg/L and were therefore considered linezolid susceptible. The remaining seven isolates, with MICs of 4 mg/L—although intermediate by CLSI criteria—were considered susceptible by EUCAST criteria. Of the seven isolates, only one isolate harboured the *optrA* gene. The G2576T 23S rRNA mutation was detected in two isolates and the G2576T and G2505A 23S rRNA mutations were detected in one isolate. The remaining three isolates did not possess any known mutations in 23S rRNA. The *cfr*, *cfrB* and *poxtA* genes were not detected in the seven linezolid non-susceptible isolates.

Twelve isolates were initially reported as daptomycin non-susceptible (> 2 mg/L) by CLSI criteria. By Etest®, 11 of the 12 isolates had a daptomycin MIC < 2 mg/L. The remaining isolate with an MIC of 8.0 mg/L was confirmed as daptomycin resistant. Polymorphisms in the *liaF, liaS, liaR, cls* and *gdpD* genes were investigated and the N237D mutation in Cls was detected.

E. faecium phenotypic susceptibility results

The majority of *E. faecium* isolates were non-susceptible to multiple antimicrobials including ampicillin, erythromycin, tetracycline, ciprofloxacin, nitrofurantoin and high-level gentamicin (Table 2). Overall, 158 isolates (32.6%) were phenotypically vancomycin non-susceptible (MIC > 4 mg/L). Fifty-seven (11.7%) and fifty-nine (12.1%) isolates were teicoplanin non-susceptible by CLSI and EUCAST criteria respectively. Nine isolates (1.9%) were initially reported as linezolid non-susceptible (CLSI breakpoint > 2 mg/L). By Etest®, eight of the nine isolates had a linezolid MIC of ≤ 2 mg/L and therefore were considered susceptible. One isolate with an MIC of 4.0 mg/L by Etest®, although intermediate by CLSI criteria, was considered susceptible by EUCAST criteria. The isolate did not have any known mutations in 23S rRNA and did not harbour *optrA, cfr, cfrB* or *poxtA*.

Five isolates were initially reported as daptomycin non-susceptible (MIC > 4 mg/L). By Etest®, two of the five isolates had a daptomycin MIC of 4.0 mg/L and were considered susceptible. The

Table 1: The number and proportion of *E. faecalis* non-susceptible to ampicillin, penicillin and the non-β-lactam antimicrobials, Australia, 2020

Antimicrobial	Tested (N)	Breakpoint guideline	Breakpoint (mg/L)[a]			Susceptible	Intermediate	Resistant
			S	I	R	% (n)	% (n)	% (n)
Ampicillin	666	CLSI	≤ 8		≥ 16	100 (666)	—[b]	0 (0)
		EUCAST	≤ 4	8	> 8	100 (666)	0 (0)	0 (0)
Benzylpenicillin	608	CLSI	≤ 8		≥ 16	98.7 (600)	—[b]	1.3 (8)
Ciprofloxacin	406	CLSI	≤ 1	2	≥ 4	88.2 (358)	4.9 (20)	6.9 (28)
Daptomycin	650	CLSI	≤ 2	4	≥ 8	56.9 (370)	42.9 (279)	0.2 (1)
Erythromycin	523	CLSI	≤ 0.5	1–4	≥ 8	10.9 (57)	49.0 (256)	40.1 (210)
Gentamicin (high-level)	469	CLSI	< 256		≥ 256	82.1 (385)	—[b]	17.9 (84)
Linezolid	663	CLSI	≤ 2	4	≥ 8	98.5 (656)	1.1 (7)	0 (0)
		EUCAST	≤ 4		> 4	100 (666)	—[b]	0 (0)
Nitrofurantoin	664	CLSI	≤ 32	64	≥ 128	98.3 (653)	1.5 (10)	0.2 (1)
Teicoplanin	666	CLSI	≤ 8	16	≥ 32	99.8 (665)	0 (0)	0.2 (1)
		EUCAST	≤ 2		> 2	99.8 (665)	—[b]	0.2 (1)
Tetracycline/doxycycline[c]	505	CLSI	≤ 4	8	≥ 16	29.3 (148)	10.5 (53)	60.2 (304)
Vancomycin	666	CLSI	≤ 4	8–16	≥ 32	99.8 (665)	0 (0)	0.2 (1)
		EUCAST	≤ 4		≥ 4	99.8 (665)	—[b]	0.2 (1)

a S: susceptible; I: intermediate; R: resistant.

b No category defined.

c The calling range of the Phoenix susceptibility cards only allows a susceptible or non-susceptible result.

other three isolates were confirmed as resistant by CLSI criteria. Polymorphisms in the *liaF, liaS, liaR, cls* and *gdpD* genes were investigated. The following mutations were detected: L39N in LiaF (isolate 1: MIC 6.0 mg/L; isolate 3: MIC 32.0 mg/L), T120N in LiaS and W73C in LiaR (isolate 2: MIC 6.0 mg/L).

Genotypic vancomycin susceptibility results

For 348 of the 667 *E. faecalis* isolates (52.2%), *vanA*/*vanB* polymerase chain reaction (PCR) results were available. One isolate, which had a vancomycin and teicoplanin MIC of ≥ 32 mg/L, harboured *vanA*. The *vanB* gene was not detected.

The presence of *vanA*/*B* genes was determined by PCR and/or WGS on 483 (99.0%) of the 488 *E. faecium* isolates. Overall, 170 of the 483 isolates (35.2%) harboured a *vanA* and/or *vanB* gene. Of the vancomycin non-susceptible *E. faecium* isolates (Vitek2® vancomycin MIC > 4mg/L), 57 harboured *vanA* and 99 harboured *vanB*. One isolate harboured both *vanA* and *vanB* genes. The *vanA* or *vanB* gene was detected in twelve vancomycin-susceptible *E. faecium* isolates. Nine isolates harboured *vanA*. The nine *vanA*-positive isolates had vancomycin MIC values of 4.0 mg/L [3 isolates], 2.0 mg/L [2 isolates], 1.0 mg/L [2 isolates] and ≤ 0.5 mg/L [2 isolates]; all had teicoplanin MIC ≤ 1 mg/L. Three isolates harboured *vanB* with vancomycin MIC values of 4.0 mg/L [1 isolate] and 1.0 mg/L [2 isolates].

Table 2: The number and proportion of *E. faecium* non-susceptible to ampicillin, penicillin and the non-β-lactam antimicrobials, Australia, 2020

Antimicrobial	Tested (N)	Breakpoint guideline	Breakpoint (mg/L)[a]			Susceptible	Intermediate	Resistant
			S	I	R	% (n)	% (n)	% (n)
Ampicillin	485	CLSI	≤ 8		≥ 16	11.8 (57)	—[b]	88.2 (428)
		EUCAST	≤ 4	8	> 8	11.8 (57)	0 (0)	88.2 (428)
Benzylpenicillin	441	CLSI	≤ 8		≥ 16	11.1(49)	—[b]	88.9 (392)
Ciprofloxacin	319	CLSI	≤ 1	2	≥ 4	9.1 (29)	0.8 (9)	88.1 (281)
Daptomycin[c]	62	CLSI	≤ 4[c]		≥ 8	95.2 (59)	0 (0)	4.8 (3)
Erythromycin	379	CLSI	≤ 0.5	1–4	≥ 8	7.9 (30)	48 (12.7)	79.4 (301)
Gentamicin (high-level)	340	CLSI	< 256		≥ 256	58.8 (200)		41.2 (140)
Linezolid	487	CLSI	≤ 2	4	≥ 8	99.6 (485)	0.4 (2)	0 (0)
		EUCAST	≤ 4		> 4	100 (487)	—[b]	0 (0)
Nitrofurantoin	413		≤ 32	64	≥ 128	16.5 (68)	117 (28.3)	55.2 (228)
Teicoplanin	485	CLSI	≤ 8	16	≥ 32	88.3 (429)	0.6 (3)	11.1 (54)
		EUCAST	≤ 2		> 2	87.9 (427)	—[b]	13.0 (63)
Tetracycline/doxycycline[d]	374	CLSI	≤ 4	8	≥ 16	30.7 (115)	5.1 (19)	64.2 (240)
Vancomycin	485	CLSI	≤ 4	8–16	≥ 32	67.4 (327)	0.6 (3)	32.0 (155)
		EUCAST	≤ 4		≥4	67.4 (327)	—[b]	32.6 (158)

a S: susceptible; I: intermediate; R: resistant.

b No category defined.

c Susceptible dose dependent.

d The calling range of the Phoenix susceptibility cards only allows a susceptible or non-susceptible result.

E. faecium molecular epidemiology

Of the 488 episodes, 470 *E. faecium* isolates (96.3%) were available for typing by WGS. The 470 isolates were classified into 71 sequence types (STs) including eight STs with ten or more isolates (Table 3). Of the 63 STs with fewer than ten isolates, 50 STs were each represented by only one isolate. Overall, 384 of the 470 isolates (81.7%) were grouped into the eight major STs. Using eBURST, all major STs were grouped into CC17.

Geographical distribution of the STs varied (Table 3). For the eight major STs, ST17 (116 isolates) was identified in all regions except the Northern Territory; ST1424 (94 isolates) was found in all regions except South Australia and the Northern Territory; ST80 (52 isolates) was found in all regions except Tasmania and the Northern Territory; ST796 (47 isolates) was found only in New South Wales, Victoria and Tasmania; ST78 (34 isolates) was found in all regions except Western Australia, Tasmania and the Northern Territory; ST1421 (20 isolates) was found only in New South Wales and the Australian Capital Territory; ST555 (11 isolates) was found in all regions except Western Australia, Tasmania, and the Australian Capital Territory; and ST117 (10 isolates) was found only in New South Wales and Western Australia.

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Table 3: The number and proportion of major *Enterococcus faecium* sequence types (STs), Australia, 2020, by jurisdiction[a]

ST	ACT		NSW		NT		Qld		SA		Tas.		Vic.		WA		Australia	
	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
ST17	1	3.2	24	13.8	0	0.0	19	55.9	17	45.9	2	25.0	15	12.5	38	62.3	116	24.7
ST1424	8	25.8	63	36.2	0	0.0	3	8.8	0	0.0	4	50.0	15	12.5	1	1.6	94	20.0
ST80	13	41.9	22	12.6	0	0.0	2	5.9	3	8.1	0	0.0	7	5.8	5	8.2	52	11.1
ST796	0	0.0	8	4.6	0	0.0	0	0.0	0	0.0	1	12.5	38	31.7	0	0.0	47	10.0
ST78	3	9.7	5	2.9	0	0.0	2	5.9	1	2.7	0	0.0	23	19.2	0	0.0	34	7.2
ST1421	1	3.2	19	10.9	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	20	4.3
ST555	0	0.0	2	1.1	3	60.0	1	2.9	2	5.4	0	0.0	3	2.5	0	0.0	11	2.3
ST117	0	0.0	3	1.7	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	7	11.5	10	2.1
Other	5	16.1	28	16.1	2	40.0	7	20.6	14	37.8	1	12.5	19	15.8	10	16.4	86	18.3
Total	**31**		**174**		**5**		**34**		**37**		**8**		**120**		**61**		**470**	

a ACT: Australian Capital Territory; NSW: New South Wales; NT: Northern Territory; Qld: Queensland; SA: South Australia; Tas.: Tasmania; Vic.: Victoria; WA: Western Australia.

The *vanA* gene was detected in four major STs (61 isolates: ST1424, ST80, ST1421 and ST117) (Table 4).The *vanB* gene was detected in six major STs (95 isolates: ST17, ST1424, ST80, ST796, ST78 and ST555). One ST796 isolate harboured both *vanA* and *vanB* genes. Three minor STs (each represented by one isolate) harboured *vanA* and five minor STs (each represented by one isolate) harboured *vanB*.

Discussion

Enterococci are intrinsically resistant to a broad range of antimicrobials including the cephalosporins and sulphonamides. By their ability to acquire additional resistance through the transfer of plasmids and transposons, and to disseminate easily in the hospital environment, enterococci have become difficult to treat and provide major infection control challenges.

As the AGAR programs are similar to those conducted in Europe, comparison of Australian antimicrobial resistance data with other countries is possible.

In the 2019 European Centre for Disease Prevention and Control (ECDC) enterococci surveillance program, the European Union/European Economic Area (EU/EEA) population-weighted mean percentage of *E. faecium* resistant to vancomycin was 18.3% (95% CI: 15.0–22.0), which represents a significant increase from 2015 when the percentage was 10.5%. The 2019 national percentages ranged from 0.0% in Iceland, Finland, and Malta to 50.0% in Cyprus.[13]

In AESOP 2020, a total of 39.7% of enterococcal bacteraemia episodes were due to *E. faecium* of which 32.6% (95% CI: 28.5–37.0) were phenotypically vancomycin non-susceptible by Vitek2® or BD Phoenix™. However 35.2% of *E. faecium* isolates tested (170/483) harboured a *vanA/vanB* gene, of which 38.8% were *vanA*-positive. Overall, 66 *E. faecium* isolates (13.7%) harboured the *vanA* gene. Prior to the 2020 AESOP we have reported a significant increase in *vanA*-positive *E. faecium* in Australia, from 6% in 2013 to 22.3% in 2019.[14–20] The decrease in *vanA*-positive *E. faecium* in 2020 was primarily due to a decrease in ST1421 and ST1424 isolates. The majority of *E. faecium* isolates were non-susceptible to multiple antimicrobials including ampicillin, erythromycin, tetracycline, ciprofloxacin and high level gentamicin. The 2020 AESOP survey confirms that the incidence of vancomycin-resistant *E. faecium* bacteraemia in Australia continues to be a substantial problem.

Table 4: The number and proportion of major *Enterococcus faecium* sequence types (STs) harbouring *vanA/vanB* genes, Australia, 2020

ST	Not detected		*vanA*		*vanA/vanB*		*vanB*		Total
	n	%	n	%	n	%	n	%	
ST17	113	97.4	0	0.0	0	0.0	3	2.6	**116**
ST1424	46	48.9	46	48.9	0	0.0	2	2.1	**94**
ST80	49	94.2	1	1.9	0	0.0	2	3.8	**52**
ST796	0	0.0	0	0.0	1	2.1	46	97.9	**47**
ST78	0	0.0	0	0.0	0	0.0	34	100.0	**34**
ST1421	11	55.0	9	45.0	0	0.0	0	0.0	**20**
ST555	3	27.3	0	0.0	0	0.0	8	72.7	**11**
ST117	5	50.0	5	50.0	0	0.0	0	0.0	**10**
Other	78	90.7	3	3.5	0	0.0	5	5.8	**86**
Total	**305**	**64.9**	**64**	**13.6**	**1**	**0.2**	**100**	**21.3**	**470**

Three (2.9%) of the 103 *vanB*-positive *E. faecium* and nine (14.1%) of the 64 *vanA*-positive *E. faecium* isolates had a vancomycin MIC at or below the CLSI and the EUCAST susceptible breakpoint (≤ 4 mg/L) and therefore would not have been identified using routine phenotypic antimicrobial susceptibility methods.

By WGS, *E. faecium* was shown to be very polyclonal, consistent with the known plasticity of the enterococcal genome. The eight major *E. faecium* STs form part of CC17, a global hospital-derived lineage that has successfully adapted to hospital environments. The CC17 lineage is characteristically ampicillin- and quinolone-resistant and subsequent acquisition of *vanA*- or *vanB*-containing transposons by horizontal transfer in CC17 clones has resulted in multi-resistant enterococci with pandemic potential.

In AESOP 2020, eight *E. faecium* STs predominated: ST17 (of which 0% of isolates harboured *vanA*, 2.6% *vanB* genes); ST1424 (48.9% *vanA*, 2.1% *vanB)*; ST80 (1.9% *vanA,* 3.8% *vanB)*; ST796 (0% *vanA,* 97.9% *vanB*, 2.1% *vanA* and *vanB*), ST78 (0% *vanA*, 100% *vanB*); ST1421 (45.0% *vanA,* 0% *vanB*); ST555 (0% *vanA,* 72.7% *vanB*) and ST117 (50.0% *vanA*, 0% *vanB*).

Conclusions

The AESOP 2020 study has shown that, although predominately caused by *E. faecalis,* enterococcal bacteraemia in Australia is frequently caused by ampicillin-resistant, high-level gentamicin-resistant vancomycin-resistant *E. faecium*. Furthermore, the percentage of *E. faecium* bacteraemia isolates resistant to vancomycin in Australia—although significantly lower than reported in the 2019 AESOP ($p < 0.002$)—remains significantly higher than that seen in most European countries. In addition to being a significant cause of healthcare-associated sepsis, the emergence of multiple multi-resistant hospital-adapted *E. faecium* strains has become a major infection control issue in Australian hospitals. Ongoing studies on the enterococcal genome will contribute to our understanding of the rapid and ongoing evolution of enterococci in the hospital environment and assist in preventing their nosocomial transmission.

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