Australian Group on Antimicrobial Resistance (AGAR) Australian Enterococcal Surveillance Outcome Program (AESOP)

Bloodstream Infection Annual Report 2021

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# Abstract

From 1 January to 31 December 2021, forty-eight institutions around Australia participated in the Australian Enterococcal Surveillance Outcome Programme (AESOP). The aim of AESOP 2021 was to determine the proportion of enterococcal bacteraemia isolates in Australia that were antimicrobial resistant, and to characterise the molecular epidemiology of the Enterococcus faecium isolates. Of the 1,297 unique episodes of enterococcal bacteraemia investigated, 94.4% were caused by either E. faecalis (54.1%) or E. faecium (40.3%). Ampicillin resistance was detected in one E. faecalis isolate and in 89.3% of E. faecium isolates. Vancomycin non-susceptibility was not detected in E. faecalis but was detected in 37.9% of E. faecium. Overall, 39.6% of E. faecium harboured the vanA and/or vanB genes. For the vanA/vanB positive E. faecium isolates, 35.8% harboured the vanA gene and 64.2% the vanB gene. Although the percentage of vancomycin-resistant E. faecium bacteraemia isolates was significantly lower than that reported in the 2020 AESOP report (presumably due to the COVID-19 elective surgery restrictions placed on hospitals), it remains substantially higher than that recorded in most European countries. Isolates of E. faecium consisted of 73 multi-locus sequence types (STs); 77.2% of isolates were classified into seven major STs each containing more than ten isolates. All major STs belonged to clonal cluster (CC) 17, a major hospital-adapted polyclonal E. faecium cluster. The major STs (ST17, ST1424, ST796, ST78, ST80, ST1421 and ST555) were found across most regions of Australia. The predominant ST was ST17 which was identified in all regions except the Northern Territory. Overall, 46.5% of isolates belonging to the seven major STs harboured the vanA or vanB gene. The AESOP 2021 has shown that 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 and is the fourth and fifth leading cause of sepsis in North America and Europe respectively. In the 1970s, healthcare-associated enterococcal infections were primarily due to Enterococcus faecalis, but there has been a steady increasing prevalence of E. faecium nosocomial infections.1–3 Worldwide, the increase in nosocomial E. faecium infections has primarily been due to the expansion of polyclonal hospital-adapted clonal complex (CC) 17 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 pathogens (Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter species) requiring new therapies.4

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 1995.5 In 2011, AGAR commenced the Australian Enterococcal Sepsis Outcome Programme,6,7 now known as the Australian Enterococcal Surveillance Outcome Programme (AESOP). The objective of AESOP 2021 was to determine the proportion of E. faecalis and E. faecium bacteraemia isolates demonstrating antimicrobial resistance, with particular emphasis on:

* assessing susceptibility to ampicillin;
* assessing susceptibility to glycopeptides; and
* the molecular epidemiology of E. faecium.

# Methodology

## Participants

Thirty laboratories servicing 48 institutions from all Australian states and mainland territories.

## Collection period

From 1 January to 31 December 2021, the 30 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 bacteraemia 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, dates 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 by the Vitek® 2 (bioMérieux). Antimicrobial susceptibility testing was performed using the Vitek® 2 (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)8 and European Committee on Antimicrobial Susceptibility Testing (EUCAST)9 MIC 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) 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). Sequence reads were analysed using the Nullarbor pipeline.10

Confidence intervals 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 2021, there were 1,297 unique episodes of enterococcal bacteraemia identified. Although nine Enterococcus species were identified, E. faecalis and E. faecium predominated: 702 isolates (54.1%) were E. faecalis and 523 isolates (40.3%) were E. faecium. Seventy-two enterococci were identified either as E. gallinarum (23 isolates), E. casseliflavus (20 isolates), E. raffinosus (9 isolates), E. hirae (7 isolates), E. avium (6 isolates), E. durans (5 isolates), E. mundtii (1 isolate) or Enterococcus sp. [not speciated] (1 isolate).

A significant difference was observed in patient sex (p < 0.0001), with 852 (65.7%) being male (95% confidence interval [95% CI]: 62.4–68.9). The average age of patients was 64 years, ranging from 0 to 100 years, with a median age of 69 years. The majority of episodes, 696/1,297 (53.7%) were community-onset (95% CI: 49.9–57.5); however, a significant difference (p < 0.0001) in place of onset was observed between E. faecium and E. faecalis, with only 32.1% (95% CI: 25.2–39.7) of E. faecium episodes being community-onset compared to 68.7% (95% CI: 65.1–72.1) for E. faecalis. All-cause mortality at 30 days, where outcome was known, was 18.9% (95% CI: 13.8–24.9). There was a significant difference in mortality between E. faecalis and E. faecium episodes (14.5% vs. 25.2% respectively, p < 0.01). There was also a significant difference between vancomycin-susceptible and vancomycin non-susceptible E. faecium episodes (21.3% vs 31.0% respectively, p = 0.03).

## *Enterococcus faecalis* phenotypic susceptibility results

Apart from erythromycin, tetracycline, ciprofloxacin and high-level gentamicin, acquired resistance was rare amongst E. faecalis isolates (Table 1). Fifty-nine E. faecalis isolates (8.4%) were initially reported as linezolid non-susceptible (CLSI breakpoint > 2 mg/L). Two isolates were unavailable for linezolid susceptibility test confirmation. By Etest®, 20 of the 57 referred isolates had a linezolid MIC of ≤ 2 mg/L and were therefore considered linezolid susceptible. Thirty-five isolates with linezolid MICs of 4 mg/L, although intermediate by CLSI criteria, were considered susceptible by EUCAST criteria. Of the remaining two isolates (both linezolid MIC 6.0 mg/L), one isolate harboured the optrA gene. No linezolid resistance genes (cfr, cfr(B), optrA, poxtA) nor known mutations in the 23S rRNA were identified in the other isolate.

Nine isolates were initially reported as daptomycin resistant (≥ 8 mg/L) by CLSI criteria. One isolate was unavailable for confirmation. By Etest®, seven of the eight referred isolates had a daptomycin MIC < 8 mg/L. The remaining isolate, with a MIC of 8.0 mg/L, had no known mutations identified.

****Table 1: The number and proportion of *E. faecalis* isolates non-susceptible to ampicillin, penicillin and the non-β-lactam antimicrobials, AGAR, 2021****

| Species and antimicrobial | Isolates (n) | CLSIa | | EUCASTb | |
| --- | --- | --- | --- | --- | --- |
| Intermediate % (*n*) | Resistant % (*n*) | Susceptible, increased exposure % (*n*) | Resistant % (*n*) |
| ***Enterococcus faecalis*** |  |  |  |  |  |
| Ampicillin | 698 | –c | 0.1 (1) | 0.0 (0) | 0.1 (1) |
| Benzylpenicillin | 587 | –c | 0.9 (5) | –d | –d |
| Ciprofloxacin | 419 | 2.4 (10) | 5.0 (21) | –c | 2.0 (8)e |
| Daptomycin | 650 | 42.5 (276) | 0.3 (2) | –d | –d |
| Linezolid | 697 | 5.2 (36) | 0.3 (2) | –c | 0.3 (2) |
| Teicoplanin | 699 | 0.0 (0) | 0.0 (0) | –c | 0.1 (1) |
| Vancomycin | 699 | 0.0 (0) | 0.0 (0) | –c | 0.0 (0) |

a CLSI: Clinical and Laboratory Standards Institute.

b EUCAST: European Committee on Antimicrobial Susceptibility Testing.

c No guidelines for indicated species.

d No category defined.

e The ciprofloxacin ECOFF (4 mg/L, *E. faecalis*) was used to distinguish between isolates with and without acquired resistance mechanisms, as breakpoints apply to uncomplicated urinary tract infections only.

## *Enterococcus 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, 198 isolates (37.9%) were phenotypically vancomycin non-susceptible (MIC > 4 mg/L). By CLSI and EUCAST criteria respectively, 54 (10.3%) and 69 (13.2%) isolates were teicoplanin non-susceptible. Nineteen isolates (3.6%) were initially reported as linezolid non-susceptible (CLSI breakpoint > 2 mg/L). Two isolates were unavailable for confirmation. By Etest®, nine of the seventeen referred isolates had a linezolid MIC ≤ 2 mg/L and therefore were considered susceptible. Six isolates with a MIC of 4.0 mg/L by Etest®, although intermediate by CLSI criteria, were considered susceptible by EUCAST criteria. Of the remaining two isolates, one (linezolid MIC 24 mg/L) harboured the poxtA gene and in the other (linezolid MIC 16 mg/L) the 23S rRNA G2576T mutation was detected.

Two isolates were initially reported as daptomycin non-susceptible (MICs > 4 mg/L). By Etest®, one isolate had a daptomycin MIC of 4.0 mg/L and was considered susceptible. The other isolate was confirmed as resistant by CLSI criteria (daptomycin MIC 8.0 mg/L) and a L39N mutation was detected in the liaF gene.

****Table 2: The number and proportion of *E. faecium* isolates non-susceptible to ampicillin, penicillin and the non-β-lactam antimicrobials, AGAR, 2021****

| Species and antimicrobial | Isolates (n) | CLSIa | | EUCASTb | |
| --- | --- | --- | --- | --- | --- |
| Intermediate % (*n*) | Resistant % (*n*) | Susceptible, increased exposure % (*n*) | Resistant % (*n*) |
| ***Enterococcus faecium*** |  |  |  |  |  |
| Ampicillin | 521 | –c | 89.3 (465) | 0.0 (0) | 89.3 (465) |
| Benzylpenicillin | 436 | –c | 90.1 (393) | –d | –d |
| Ciprofloxacin | 323 | 2.8 (9) | 88.2 (285) | –c | –e |
| Linezolid | 520 | 1.3 (7) | 0.4 (2) | –c | 0.4 (2) |
| Teicoplanin | 522 | 1.1 (6) | 10.3 (54) | –c | 13.2 (69) |
| Vancomycin | 522 | 1.5 (8) | 36.4 (190) | –c | 37.9 (198) |

a CLSI: Clinical and Laboratory Standards Institute.

b EUCAST: European Committee on Antimicrobial Susceptibility Testing.

c No guidelines for indicated species.

d No category defined.

e The ciprofloxacin concentration range available on Vitek and Phoenix cards restricts the ability to determine non-wild type (ECOFF 8 mg/L) *E. faecium*.

## Genotypic vancomycin susceptibility results

For 336 (47.9%) of the 702 E. faecalis isolates, vanA/vanB polymerase chain reaction (PCR) results were available. No vanA/vanB genes were detected.

The presence of vanA/vanB genes was determined by PCR and/or WGS on 508 (97.1%) of the 523 E. faecium isolates. Overall, 201 of the 508 isolates (39.6%) harboured a vanA and/or vanB gene. Of the vancomycin non-susceptible E. faecium isolates (Vitek® 2 vancomycin MIC > 4 mg/L), 71 harboured vanA and 124 harboured vanB. The vanA or vanB gene was detected in six vancomycin-susceptible E. faecium isolates. One isolate, with a vancomycin MIC of ≤ 0.5 mg/L and teicoplanin MIC of 1.0 mg/L, harboured vanA. The five vanB-positive isolates had vancomycin MICs ranging from ≤ 0.5 mg/L to 3.0 mg/L.

## *E. faecium* molecular epidemiology

Of the 523 episodes, 496 E. faecium isolates (94.8%) were available for typing by WGS. The 496 isolates were classified into 73 sequence types (STs), including seven STs with ten or more isolates (Table 3). Of the 66 STs with fewer than ten isolates, 45 STs were each represented by only one isolate. Overall, 383 (77.2%) of the 496 isolates were grouped into the seven major STs. Using eBURST, all major STs were grouped into CC17.

Geographical distribution of the STs varied (Table 3). Among the seven major STs, ST17 (124 isolates) was identified in all regions except the Northern Territory; ST1424 (86 isolates) was identified in all regions except Western Australia and the Northern Territory; ST796 (53 isolates) was identified in all regions except Queensland, Western Australia and the Australian Capital Territory; ST78 (43 isolates) was identified in all regions except Queensland and the Northern Territory; ST80 (40 isolates) was identified in all regions except the Northern Territory; ST1421 (24 isolates) was identified only in New South Wales, Victoria, Queensland and the Australian Capital Territory; and ST555 (13 isolates) was identified in all regions except Queensland and the Australian Capital Territory.

The vanA gene was detected in four major STs (69 isolates from ST17, ST1424, ST80 and ST1421) (Table 4).The vanB gene was detected in all seven major STs (126 isolates). One minor ST (ST117) harboured vanA and eight minor STs (ST18, ST203, ST233, ST538, ST789, ST1543, ST2082 and ST2217) harboured vanB.

****Table 3: The number and proportion of major *Enterococcus faecium* sequence types, AGAR, 2021, by state and territory****

|  | Percentage, % (*n*)a | | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| MLSTb | ACT | NSW | NT | Qld | SA | Tas | Vic | WA | Australia |
| ST17 | 7.1 (1) | 14.0 (19) | –c (0) | 58.1 (25) | 34.0 (17) | 29.4 (5) | 14.4 (24) | 54.1 (33) | 25.0 (124) |
| ST1424d | 42.9 (6) | 39.0 (53) | –c (0) | 4.7 (2) | 4.0 (2) | 17.6 (3) | 12.0 (20) | 0.0 (0) | 17.3 (86) |
| ST796 | 0.0 (0) | 1.5 (2) | –c (4) | 0.0 (0) | 8.0 (4) | 11.8 (2) | 24.6 (41) | 0.0 (0) | 10.7 (53) |
| ST78 | 14.3 (2) | 3.7 (5) | –c (0) | 0.0 (0) | 14.0 (7) | 5.9 (1) | 15.6 (26) | 3.3 (2) | 8.7 (43) |
| ST80 | 21.4 (3) | 3.7 (5) | –c (0) | 16.3 (7) | 8.0 (4) | 5.9 (1) | 9.6 (16) | 6.6 (4) | 8.1 (40) |
| ST1421d | 7.1 (1) | 15.4 (21) | –c (0) | 2.3 (1) | 0.0 (0) | 0.0 (0) | 0.6 (1) | 0.0 (0) | 4.8 (24) |
| ST555 | 0.0 (0) | 0.7 (1) | –c (1) | 0.0 (0) | 6.0 (3) | 5.9 (1) | 3.0 (5) | 3.3 (2) | 2.6 (13) |
| Other types (n = 66) | 7.1 (1) | 22.1 (30) | –c (3) | 18.6 (8) | 26.0 (13) | 23.5 (4) | 20.4 (34) | 32.8 (20) | 22.8 (113) |
| **Total** | **14** | **136** | **8** | **43** | **50** | **17** | **167** | **61** | **496** |

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

b MLST: multi-locus sequence type.

c Insufficient numbers (< 10) to calculate percentage.

d pstS-null.

****Table 4: The number and proportion of major *Enterococcus faecium* sequence types harbouring vanA/B genes, AGAR, 2021****

| MLSTb | Percentagea (*n*) | | | | Total, n |
| --- | --- | --- | --- | --- | --- |
| *vanA* | *vanB* | *vanA* and *vanB* | *vanA* or *vanB* not detected |
| ST17 | 1.6 (2) | 4.0 (5) | 0.0 (0) | 94.4 (117) | 124 |
| ST1424 | 51.2 (44) | 0.0 (0) | 0.0 (0) | 48.8 (42) | 86 |
| ST796 | 0.0 (0) | 100.0 (53) | 0.0 (0) | 0.0 (0) | 53 |
| ST78 | 0.0 (0) | 100.0 (43) | 0.0 (0) | 0.0 (0) | 43 |
| ST80 | 7.5 (3) | 5.0 (2) | 0.0 (0) | 87.5 (35) | 40 |
| ST1421 | 62.5 (15) | 0.0 (0) | 0.0 (0) | 37.5 (9) | 24 |
| ST555 | 0.0 (0) | 84.6 (11) | 0.0 (0) | 15.4 (2) | 13 |
| Other types (n =66) | 4.4 (5) | 10.6 (12) | 0.0 (0) | 85.0 (96) | 113 |
| **Total** | **13.9 (69)** | **25.4 (126)** | **0.0 (0)** | **60.7 (301)** | **496** |

a Percentage of total with *van* genes.

b MLST: multi-locus sequence type.

# Discussion

Enterococci are intrinsically resistant to a broad range of antimicrobials including the cephalosporins and sulphonamides. Because of 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 2021 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 14.3% (95% CI: 14.1–14.6).11 The 2020 national percentages ranged from 0.0% in Luxembourg to 66.4% in Lithuania.[[1]](#footnote-2)

In AESOP 2021, a total of 40.3% of enterococcal bacteraemia episodes were due to E. faecium, of which 37.9% (95% CI: 33.7–42.2) were phenotypically vancomycin non-susceptible by Vitek® 2 or BD Phoenix™. However, 39.6% of E. faecium isolates tested (201/508) harboured a vanA/vanB gene, of which 35.8% were vanA-positive. Overall, 72 E. faecium isolates (14.2%) harboured the vanA gene. Prior to the 2021 AESOP, we have reported a significant increase in vanA-positive E. faecium in Australia, from 6% in 2013 to 22.3% in 2019.12–18 The decrease in vanA-positive E. faecium in 2020 and 2021 (13.7% and 14.2% respectively)19 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 2021 AESOP survey confirms that the incidence of vancomycin-resistant E. faecium bacteraemia in Australia continues to be a significant problem.

Five (3.9%) of the 129 vanB-positive E. faecium and one (1.4%) of the 72 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 polyclonal, consistent with the known plasticity of the enterococcal genome. The seven major E. faecium STs form part of CC17, a global hospital-derived lineage that has successfully adapted to hospital environments. CC17 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 2021, seven E. faecium STs predominated: ST17 (of which 1.6% of isolates harboured vanA, 4.0% vanB genes); ST1424 (51.2% vanA, 0% vanB); ST796 (100% vanB); ST78 (100% vanB), ST80 (7.5% vanA, 5.0% vanB); ST1421 (62.5% vanA, 0% vanB) and ST555 (0% vanA, 84.6% vanB).

# Conclusions

The AESOP 2021 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 (37.9%) 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 will assist in preventing their nosocomial transmission.

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