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Australian Group on Antimicrobial Resistance (AGAR) Australian *Staphylococcus aureus* Surveillance Outcome Program (ASSOP) Bloodstream Infection Annual Report 2024

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Abstract

From 1 January to 31 December 2024, fifty-five institutions across Australia participated in the Australian *Staphylococcus aureus* Surveillance Outcome Program (ASSOP). The aim of ASSOP 2024 was to determine the proportion of *Staphylococcus aureus* bacteraemia (SAB) isolates in Australia that were antimicrobial resistant, with particular emphasis on methicillin resistance, and to characterise the molecular epidemiology of methicillin-resistant *S. aureus* (MRSA). A total of 3,358 SAB episodes were reported, of which 78.5% were community-onset. Overall, 14.9% of *S. aureus* were methicillin resistant. The 30-day all-cause mortality associated with methicillin-resistant SAB was 13.7%, which was not significantly different to the 14.1% 30-day all-cause mortality associated with methicillin-susceptible SAB ($p = 0.9$). With the exception of the β-lactams and erythromycin, antimicrobial resistance in methicillin-susceptible *S. aureus* (MSSA) was infrequent. However, in addition to the β-lactams, 34.8% of MRSA were resistant to erythromycin; 28.9% to ciprofloxacin; 13.1% to gentamicin; 11.0% to tetracycline; and 2.7% to cotrimoxazole. A daptomycin-resistant MRSA from New South Wales was identified. The isolate had a daptomycin minimum inhibitory concentration (MIC) of 6.0 mg/L, and was identified as ST5-V, with a S337L MprF mutation. When applying the European Committee on Antimicrobial Susceptibility Testing (EUCAST) breakpoints, teicoplanin resistance was detected in three MSSA isolates. Linezolid or vancomycin resistance was not detected. Resistance to the non-β-lactam antimicrobials was largely attributable to the predominant healthcare-associated MRSA (HA-MRSA) clone ST22-IV [2B] (EMRSA-15), and to the community-associated MRSA (CA-MRSA) clone ST45-V [5C2&5], which has acquired resistance to multiple antimicrobials including ciprofloxacin, clindamycin, erythromycin, gentamicin, and tetracycline. Overall, 89.6% of methicillin-resistant SAB episodes were caused by CA-MRSA clones. Although polyclonal, approximately 72% of CA-MRSA clones were characterised as ST93-IV [2B] (Queensland clone), ST5-IV [2B], ST45-V [5C2&5], ST8-IV [2B], ST30-IV [2B], ST1-IV [2B], ST6-IV [2B], ST97-IV [2B] and Panton-Valentine leucocidin positive ST22-IV [2B]. As CA-MRSA is well established in the Australian community, it is important to monitor antimicrobial resistance patterns in community- and healthcare-associated SAB, as this information will guide therapeutic practices in treating *S. aureus* bacteraemia.

Keywords: Australian Group on Antimicrobial Resistance (AGAR); antimicrobial resistance surveillance; *Staphylococcus aureus*; methicillin-susceptible *Staphylococcus aureus* (MSSA); methicillin-resistant *Staphylococcus aureus* (MRSA); bacteraemia

Background

Globally, *Staphylococcus aureus* is one of the most frequent causes of hospital-acquired and community-acquired bloodstream infections.[1] Although there are a wide variety of manifestations of serious invasive infection caused by *S. aureus*, in the majority of cases the organism can be detected in blood cultures. Therefore, *S. aureus* bacteraemia (SAB) is considered a very useful marker for serious invasive infection.[2] In 2009, the Infectious Diseases Society of America highlighted *S. aureus* as one of the key problem bacteria or ESKAPE pathogens (*Enterococcus faecium*, *S. aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* species) requiring new therapies.[3] In 2024, the World Health Organisation listed methicillin-resistant *S. aureus* (MRSA) in its bacterial priority list of pathogens.[4]

Although prolonged antimicrobial therapy and prompt source control are used to treat SAB,[5] mortality ranges from as low as 2.5% to as high as 40%.[6-10] Mortality rates, however, are known to vary significantly with patient age, clinical manifestation, comorbidities and methicillin resistance. A prospective study of SAB conducted in 27 laboratories in Australia and New Zealand found a 30-day all-cause mortality of 20.6%.[11] On univariate analysis, increased mortality was significantly associated with older age; European ethnicity; methicillin resistance; infections not originating from a medical device; sepsis syndrome; pneumonia/empyema; and treatment with a glycopeptide or other non-β-lactam antibiotic.

The Australian Group on Antimicrobial Resistance (AGAR), a network of laboratories located across Australia, commenced surveillance of antimicrobial resistance (AMR) in *S. aureus* in 1986.[12] In 2013, AGAR commenced the Australian *Staphylococcus aureus* Sepsis Outcome Program, now known as the Australian *Staphylococcus aureus* Surveillance Outcome Program (ASSOP).[13] The primary objective of ASSOP 2024 was to determine the proportion of SAB isolates displaying antimicrobial resistance, with particular emphasis on:

1. susceptibility to methicillin; and
2. the molecular epidemiology of MRSA.

Methodology

Participants

Thirty-two laboratories servicing 55 institutions from all Australian states and mainland territories.

Collection period

From 1 January to 31 December 2024, the 32 laboratories collected all *S. aureus* isolated from blood cultures. When isolated from a patient's blood culture within 14 days of the first positive culture, *S. aureus* with the same antimicrobial susceptibility profiles were excluded. A new SAB episode in the same patient was recorded if it was identified in a blood culture collected more than 14 days after the last positive culture. Data were collected on age, sex, dates of admission and discharge (if admitted), and mortality at 30 days from date of first positive blood culture. To avoid interpretive bias, no attempt was made to assign attributable mortality. Each SAB episode was designated healthcare onset if the first positive blood culture(s) in the episode were collected > 48 hours after admission.

Laboratory testing

Participating laboratories performed antimicrobial susceptibility testing using the Vitek® 2 (bioMérieux, France) or the BD Phoenix™ (Becton Dickinson, USA) automated microbiology systems according to the manufacturer's instructions. Identification of *S. aureus* was achieved by matrix-assisted laser desorption ionisation (MALDI) using either the Vitek® MS (bioMérieux, France) or the MALDI Biotyper® (Bruker Daltonics, Germany). Appropriate growth on chromogenic agar or polymerase chain reaction (PCR) for the presence of the *nuc* gene may have been performed for confirmation.

Minimum inhibitory concentration (MIC) data and isolates were referred to the ASSOP reference laboratory at Murdoch University. The European Committee on Antimicrobial Susceptibility Testing (EUCAST)[14] MIC breakpoints were utilised for interpretation. Daptomycin-, linezolid-, and teicoplanin-resistant isolates were retested by Etest® (bioMérieux) using the method recommended by the manufacturer. The control strain used for the Etest® was *S. aureus* ATCC® 29213. All *S. aureus* with a penicillin MIC ≤ 0.12 mg/L, without a β-lactamase result provided by the referring laboratory, were confirmed by disc diffusion using a 10U penicillin disk. High-level mupirocin resistance was determined by the BD Phoenix™ or by using a 200 µg mupirocin disc on all isolates with a mupirocin MIC > 8 mg/L by Vitek® 2. Cotrimoxazole-resistant isolates were confirmed using a 25 µg cotrimoxazole disc. All disc susceptibility testing was performed using Clinical and Laboratory Standards Institute (CLSI) methodology and breakpoints.[15]

Multi-resistance was defined as resistance to three or more of the following non-β-lactam antimicrobials: ciprofloxacin; co-trimoxazole; erythromycin/clindamycin; fusidic acid; gentamicin; linezolid; high-level mupirocin; rifampicin; tetracycline; teicoplanin; and vancomycin.

Whole genome sequencing (WGS) was performed by the ASSOP reference laboratory at Murdoch University using the NovaSeq platform (Illumina, San Diego, USA). Sequence reads were analysed using the Nullarbor pipeline.[16] The SCC*mec* type was determined using KmerFinder v3.2 and the SCC*mec* database curated from the Center for Genomic Epidemiology database.[17–20] Point mutations associated with daptomycin resistance were screened using an in-house custom database.[21]

Confidence intervals for proportions, Fisher's exact test for categorical variables, and chi-square test for trend were calculated, if appropriate, using MedCalc for Windows, version 23.3.1 (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 2024, there were 3,358 unique episodes of SAB identified. A significant difference ($p < 0.01$) was observed in patient sex, with 2,221 patients (66.1%) being male (95% confidence interval [95% CI]: 63.4–70.0). The mean age of patients was 58 years, ranging from 0 to 103 years, with a median age of 61 years. Overall, 2,636 episodes (78.5%) were community-onset (95% CI: 75.5–81.6). All-cause mortality at 30 days (where known) was 14.0% (95% CI: 12.6–15.5). Methicillin-resistant SAB mortality was 13.7% (95% CI: 10.2–18.0); methicillin-susceptible SAB mortality was 14.1% (95% CI: 12.5–15.7).

Methicillin-susceptible *Staphylococcus aureus* (MSSA) antimicrobial susceptibility

Overall, 2,857 of the 3,358 isolates (85.1%) were methicillin susceptible. Where results were available, 2,075/2,840 MSSA isolates (73.1%) were penicillin resistant (MIC > 0.12 mg/L). All available penicillin-susceptible isolates (MIC ≤ 0.12 mg/L) were retested by penicillin disc diffusion (zone-edge test). By disc diffusion, 99 isolates reported as penicillin-susceptible by either the Vitek® 2 or BD Phoenix™ automated microbiology systems were considered penicillin-resistant. Fifty-five penicillin-susceptible isolates were not available for confirmation. Apart from erythromycin resistance (16.5%), resistance to the non-β-lactam antimicrobials amongst MSSA was infrequent (Table 1).

Six isolates were identified by Vitek® 2 as daptomycin resistant (MIC > 1.0 mg/L). Of these six isolates, one was unavailable for confirmation. By Etest®, all five isolates were considered daptomycin susceptible (MICs 0.125–1.0 mg/L).

Forty-two isolates were identified by Vitek® 2 or BD Phoenix™ as teicoplanin resistant (MIC > 2.0 mg/L). By Etest®, 35 isolates had a teicoplanin MIC ≤ 2.0 mg/L and were therefore considered teicoplanin susceptible. Three isolates with a MIC of 3.0 mg/L were confirmed as teicoplanin resistant. The four remaining isolates were unavailable for confirmation of teicoplanin resistance. All MSSA were linezolid and vancomycin susceptible. Eighty MSSA isolates (2.8%) were fusidic acid resistant. Overall, 2,001 of the 2,857 MSSA (70.0%) had mupirocin susceptibility testing performed, of which 25 (1.2%) were high-level mupirocin resistant. Eighteen of the 25 high-level mupirocin-resistant isolates were referred from Queensland, with the remainder from New South Wales (n = 3), Western Australia (n = 3), and the Australian Capital Territory (n = 1). Fourteen of the 25 mupirocin-resistant MSSA were also resistant to fusidic acid. Of the 2,840 MSSA isolates tested, 44 (1.5%) were constitutively resistant to clindamycin; however, 384 (13.5%) were classified as having constitutive and inducible clindamycin resistance. Seventy-three isolates were reported as cotrimoxazole resistant (73/2,811; 2.6%) by Vitek® 2 or BD Phoenix™; by disc susceptibility testing, only eight of these isolates were confirmed as cotrimoxazole resistant (8/2,807; 0.3%). Four MSSA were unavailable for confirmation.

Only 5.9% of MSSA were multi-resistant.

Table 1: The number and proportion of methicillin-susceptible *Staphylococcus aureus* (MSSA) isolates resistant to penicillin and the non-β-lactam antimicrobials, EUCAST breakpoints,[a] AGAR, Australia, 2024

Antimicrobial	Isolates (*n*)	Susceptible % (n)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Benzylpenicillin	2,840	26.9 (765)	–[b]	73.1 (2,075)
Benzylpenicillin[c]	2,807	22.6 (633)	–[b]	77.4 (2,174)
Cefoxitin (methicillin)[d]	2,857	100.0 (2,857)	–[b]	0.0 (0)
Ciprofloxacin	2,840	–[b]	96.2 (2,733)	3.8 (107)
Clindamycin (constitutive)	2,840	98.5 (2,796)	–[b]	1.5 (44)
Clindamycin (constitutive + inducible resistance)	2,840	86.5 (2,456)	–[b]	13.5 (384)
Daptomycin	2,850	100.0 (2,850)	–[b]	0.0 (0)
Erythromycin	2,840	83.5 (2,370)	–[b]	16.5 (470)
Fusidic acid	2,840	97.2 (2,760)	–[b]	2.8 (80)
Gentamicin	2,799	93.6 (2,619)	–[b]	6.4 (180)
Linezolid	2,849	100.0 (2,849)	–[b]	0.0 (0)
Mupirocin (high-level)[e]	2,001	98.8 (1,976)	–[b]	1.2 (25)
Rifampicin[f]	1,164	99.0 (1,152)	–[b]	1.0 (12)
Teicoplanin	2,846	99.9 (2,843)	–[b]	0.1 (3)
Tetracycline/doxycycline[g]	2,825	97.5 (2,754)	–[b]	2.5 (71)
Trimethoprim/sulfamethoxazole (cotrimoxazole, SXT)[h]	2,807	99.6 (2,797)	0.1 (2)	0.3 (8)
Vancomycin	2,849	100.0 (2,849)	–[b]	0.0 (0)

a EUCAST: European Committee on Antimicrobial Susceptibility Testing.

b No category defined.

c Beta-lactamase adjusted.

d Resistance as determined by cefoxitin screen (Vitek) or cefoxitin MIC (Phoenix).

e Mupirocin high-level resistance screen (CLSI).

f The rifampicin concentration range on cards restricts category interpretation to non-resistant or resistant.

g Doxycycline concentration range (Phoenix panel) restricts ability to accurately identify intermediate and resistant category.

h SXT resistant isolates by MIC confirmed by disc diffusion (CLSI).

MRSA antimicrobial susceptibility

The proportion of *S. aureus* identified as MRSA was 14.9% (95% CI: 13.6–16.3). Of the 501 MRSA identified, 452 were cefoxitin-screen positive by Vitek® 2 and 49 had a cefoxitin MIC > 4 mg/L by BD Phoenix™. Two MRSA isolates were penicillin susceptible. Amongst the MRSA isolates, resistance to non-β-lactam antimicrobials was common (Table 2). All MRSA were susceptible to linezolid and vancomycin.

Of the three isolates reported by Vitek® 2 as daptomycin resistant (MIC > 1.0 mg/L), two isolates were available for confirmation by Etest®. One isolate was considered daptomycin susceptible (MIC 1.0 mg/L), whilst the second isolate, which was from New South Wales, had a daptomycin MIC of 6.0 mg/L. The isolate was identified as ST5-V and harboured a S337L MprF mutation.

By Vitek® 2, one isolate was reported as teicoplanin resistant (MIC = 16.0 mg/L); however, the teicoplanin MIC when tested by Etest® was 1.5 mg/L and was therefore considered susceptible. Of the 501 MRSA, 324 (64.7%) had mupirocin testing performed. Eight MRSA (2.5%) had high-level mupirocin resistance. The isolates were from Queensland (n = 4), New South Wales (n = 3) and Western Australia (n = 1).

Of the 494 MRSA tested, 78 (15.8%) were constitutively resistant to clindamycin by EUCAST criteria, whilst 138 (27.9%) were classified as having constitutive and inducible clindamycin resistance.

Fifty-two MRSA isolates were reported as cotrimoxazole resistant (52/489; 10.6%) by Vitek® 2 or BD Phoenix™; by disc susceptibility testing, only 13 of the isolates were confirmed as cotrimoxazole resistant (13/489; 2.7%).

Overall, 20.5% of MRSA were multi-resistant.

MRSA molecular epidemiology

WGS was performed on 433 of the 501 MRSA (86.4%). Based on molecular typing, 45 (10.4%) and 388 (89.6%) of the isolates were identified as healthcare-associated MRSA (HA-MRSA) and community-associated MRSA (CA-MRSA) respectively (Table 3).

Table 2: The number and proportion of methicillin-resistant *Staphylococcus aureus* (MRSA) isolates resistant to penicillin and the non-β-lactam antimicrobials, EUCAST breakpoints,[a] AGAR, Australia, 2024

Antimicrobial	Isolates (*n*)	Susceptible % (n)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Benzylpenicillin	493	1.0 (5)	—[b]	99.0 (488)
Benzylpenicillin[c]	495	0.4 (2)	—[b]	99.6 (493)
Cefoxitin (methicillin)[d]	501	0.0 (0)	—[b]	100.0 (501)
Ciprofloxacin	494	—[b]	71.1 (351)	28.9 (143)
Clindamycin (constitutive resistance)	494	84.2 (416)	—[b]	15.8 (78)
Clindamycin (constitutive + inducible resistance)	494	72.1 (356)	—[b]	27.9 (138)
Daptomycin	496	99.8 (495)	—[b]	0.2 (1)
Erythromycin	494	65.2 (322)	—[b]	34.8 (172)
Fusidic acid	494	95.1 (470)	—[b]	4.9 (24)
Gentamicin	490	86.9 (426)	—[b]	13.1 (64)
Linezolid	497	100.0 (497)	—[b]	0.0 (0)
Mupirocin (high-level resistance)[e]	324	97.5 (316)	—[b]	2.5 (8)
Rifampicin[f]	187	97.9 (305)	—[b]	2.1 (4)
Teicoplanin	494	100.0 (494)	—[b]	0.0 (0)
Tetracycline/doxycycline[g]	492	89.0 (438)	—[b]	11.0 (54)
Trimethoprim/sulfamethoxazole (cotrimoxazole, SXT)[h]	487	96.7 (471)	0.6 (3)	2.7 (13)
Vancomycin	496	100.0 (496)	—[b]	0.0 (0)

[a] EUCAST: European Committee on Antimicrobial Susceptibility Testing.

[b] No category defined.

[c] Beta-lactamase adjusted.

[d] Resistance as determined by cefoxitin screen (Vitek) or cefoxitin MIC (Phoenix).

[e] Mupirocin high-level resistance screen (CLSI).

[f] The rifampicin concentration range on cards restricts category interpretation to non-resistant or resistant.

[g] Doxycycline concentration range (Phoenix panel) restricts ability to accurately identify intermediate and resistant category.

[h] SXT resistant isolates by MIC confirmed by disc diffusion (CLSI).

Table 3: Proportion of healthcare-associated and community-associated methicillin-resistant *Staphylococcus aureus*, AGAR, Australia, 2024 by clone, onset, and detection of Panton-Valentine leucocidin (PVL)-associated genes

Clone[a]	Clonal complex	Total, *n*	Community onset, % (*n*)[b]	Hospital onset, % (*n*)[b]	PVL positive, % (*n*)[b]
Healthcare-associated					
ST22-IV (EMRSA-15)	22	38	63.2 (24)	36.8 (14)	0.0 (0)
ST239-III (Aus2/3 EMRSA)	239	7	—[c] (6)	—[c] (1)	—[c] (0)
Total HA-MRSA		**45**	**66.7 (30)**	**33.3 (15)**	**0.0 (0)**
Community-associated					
ST93-IV	93	115	87.0 (100)	13.0 (15)	94.8 (109)
ST5-IV	5	46	71.7 (33)	28.3 (13)	43.5 (20)
ST45-V	45	21	66.7 (14)	33.3 (7)	0.0 (0)
ST8-IV	8	20	80.0 (16)	20.0 (4)	90.0 (18)
ST30-IV	30	19	94.7 (18)	5.3 (1)	89.5 (17)
ST1-IV	1	18	88.9 (16)	11.1 (2)	11.1 (2)
ST6-IV	6	15	73.3 (11)	26.7 (4)	13.3 (2)
ST97-IV	97	14	78.6 (11)	21.4 (3)	0.0 (0)
ST22-IV (PVL positive)	22	11	81.8 (9)	18.2 (2)	100.0 (11)
ST88-IV	22	7	—[c] (4)	—[c] (3)	—[c] (1)
ST953-IV	97	6	—[c] (5)	—[c] (1)	—[c] (0)
ST78-IV	78	6	—[c] (4)	—[c] (2)	—[c] (0)
ST1232-V	398	6	—[c] (3)	—[c] (3)	—[c] (4)
ST188-IV	88	5	—[c] (2)	—[c] (3)	—[c] (0)
ST672-unk	672	5	—[c] (4)	—[c] (1)	—[c] (0)
ST398-V	398	4	—[c] (2)	—[c] (2)	—[c] (0)
ST59-IV	59	4	—[c] (3)	—[c] (1)	—[c] (1)
ST45-IV	45	3	—[c](2)	—[c] (1)	—[c] (0)
ST5-VI	5	3	—[c] (3)	—[c] (0)	—[c] (0)
ST5-V	5	3	—[c] (1)	—[c] (2)	—[c] (1)
ST45-unk	45	3	—[c] (1)	—[c] (2)	—[c] (0)
ST6151-IV	93	3	—[c] (3)	—[c] (0)	—[c] (3)
ST2250-IV	2250	3	—[c] (3)	—[c] (0)	—[c] (0)
ST872-IV	1	3	—[c] (3)	—[c] (0)	—[c] (0)
ST59-V	59	3	—[c] (2)	—[c] (1)	—[c] (2)
ST6145-V	45	3	—[c] (3)	—[c] (0)	—[c] (0)
ST508-IV	45	2	—[c] (1)	—[c] (1)	—[c] (0)
ST152-IV	8	2	—[c] (1)	—[c] (1)	—[c] (1)
ST10232-IV	97	2	—[c] (2)	—[c] (0)	—[c] (0)
ST672-V	672	2	—[c] (1)	—[c] (1)	—[c] (0)

Clone[a]	**Clonal complex**	**Total, *n***	**Community onset, % (*n*)[b]**	**Hospital onset, % (*n*)[b]**	**PVL positive, % (*n*)[b]**
ST8-V	8	2	—[c] (2)	—[c] (0)	—[c] (0)
ST2518-IV	1	1	—[c] (0)	—[c] (1)	—[c] (0)
ST10230-IV	8	1	—[c] (1)	—[c] (0)	—[c] (0)
ST10236-IV	88	1	—[c] (1)	—[c] (0)	—[c] (1)
ST45-I	45	1	—[c] (1)	—[c] (0)	—[c] (0)
ST10244-IV	78	1	—[c] (1)	—[c] (0)	—[c] (0)
ST3628-V	5	1	—[c] (1)	—[c] (0)	—[c] (0)
ST1649-IV	6	1	—[c] (1)	—[c] (0)	—[c] (0)
ST1413-V	121	1	—[c] (1)	—[c] (0)	—[c] (1)
ST10242-IV	72	1	—[c] (1)	—[c] (0)	—[c] (0)
ST72-V	72	1	—[c] (1)	—[c] (0)	—[c] (0)
ST10246-IV	97	1	—[c] (1)	—[c] (0)	—[c] (0)
ST7891-IV	1	1	—[c] (1)	—[c] (0)	—[c] (0)
ST672-IV	672	1	—[c] (1)	—[c] (0)	—[c] (0)
ST1482-IV	30	1	—[c] (1)	—[c] (0)	—[c] (1)
ST2689-IV	5	1	—[c] (1)	—[c] (0)	—[c] (0)
ST834-IV	1	1	—[c] (1)	—[c] (0)	—[c] (0)
ST1223-IV	1223	1	—[c] (1)	—[c] (0)	—[c] (0)
ST3921-IV	30	1	—[c] (1)	—[c] (0)	—[c] (1)
ST10241-IV	1	1	—[c] (1)	—[c] (0)	—[c] (0)
ST5025-IV	5	1	—[c] (0)	—[c] (1)	—[c] (0)
ST10235-V	672	1	—[c] (0)	—[c] (1)	—[c] (0)
ST1153-V	1153	1	—[c] (0)	—[c] (1)	—[c] (1)
ST10237-IV	8	1	—[c] (1)	—[c] (0)	—[c] (0)
ST5-unk	5	1	—[c] (1)	—[c] (0)	—[c] (0)
ST10231-IV	6	1	—[c] (0)	—[c] (1)	—[c] (0)
ST9284-V	45	1	—[c] (1)	—[c] (0)	—[c] (0)
ST10233-IV	5	1	—[c] (1)	—[c] (0)	—[c] (0)
ST9288-IV	1	1	—[c] (1)	—[c] (0)	—[c] (0)
ST9292-IV	250	1	—[c] (1)	—[c] (0)	—[c] (0)
Total CA-MRSA		**388**	**79.1 (307)**	**20.9 (81)**	**50.8 (197)**
MRSA typed		**433**	**77.8 (337)**	**22.2 (96)**	**45.5 (197)**

a MRSA: methicillin-resistant *Staphylococcus aureus*; HA-MRSA : healthcare-associated MRSA ; CA-MRSA : community-associated MRSA ; PVL: Panton-Valentine leucocidin.

b Percentage of the clone.

c Insufficient numbers (< 10) to calculate percentage.

Healthcare-associated methicillin-resistant *Staphylococcus aureus*

For the 45 HA-MRSA isolates, 15 episodes (33.3%) were classified as hospital-onset and 30 (66.7%) were classified as community-onset. Based on the multilocus sequence type (ST) and the SCC*mec* type, two HA-MRSA clones were identified: 38 isolates of ST22-IV [2B] (EMRSA-15) accounting for 8.8% of MRSA typed and 1.1% of *S. aureus* isolates; and seven isolates of ST239-III [3A] (Aus-2/3 EMRSA), accounting for 1.6% of MRSA typed and 0.2% of *S. aureus* isolates (Table 3).

ST22-IV [2B] (EMRSA-15) is the dominant HA-MRSA clone in Australia, and in 2024 accounted for 84.4% of HA-MRSA and was identified in all states and territories except Queensland and the Australian Capital Territory (Table 4). ST22-IV [2B] (EMRSA-15) is Panton-Valentine Leucocidin (PVL) negative; 91.9% and 32.4% of isolates of this clone were ciprofloxacin and erythromycin resistant, respectively. Overall, 36.8% of ST22-IV [2B] (EMRSA-15) isolates were hospital-onset.

ST239-III [3A] (Aus-2/3 EMRSA) accounted for 15.6% of HA-MRSA and was identified in New South Wales, South Australia and the Australian Capital Territory (Table 4). PVL-negative ST239-III [3A] (Aus-2/3 EMRSA) are typically resistant to ciprofloxacin, clindamycin, cotrimoxazole, erythromycin, gentamicin, and tetracycline. Six of the seven ST239-III [3A] (Aus-2/3 EMRSA) isolates were community-onset.

Table 4: The number and proportion of healthcare-associated methicillin-resistant *Staphylococcus aureus* (MRSA) clones, AGAR, Australia, 2024, by jurisdiction

	Percentage (*n*)[a]								
Clone	**ACT**	**NSW**	**NT**	**Qld**	**SA**	**Tas.**	**Vic.**	**WA**	**Australia**
ST22-IV (EMRSA-15)	–[b] (0)	77.8 (14)	–[b] (1)	–[b] (0)	–[b] (6)	–[b] (1)	–[b] (9)	–[b] (7)	84.4 (38)
ST239-III (Aus2/3 EMRSA)	–[b] (1)	22.2 (4)	–[b] (0)	–[b] (0)	–[b] (2)	–[b] (0)	–[b] (0)	–[b] (0)	15.6 (7)
Total	**1**	**18**	**1**	**0**	**8**	**1**	**9**	**7**	**45**

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 Insufficient numbers (< 10) to calculate percentage.

Community-associated methicillin-resistant *Staphylococcus aureus*

For the 388 CA-MRSA isolates, 81 episodes (20.9%) were classified as hospital-onset and 307 (79.1%) as community-onset. Based on the multilocus sequence type and the SCC*mec* type, 60 CA-MRSA clones were identified (Table 3). Overall, 71.9% of CA-MRSA were classified into nine clones each represented by more than ten isolates:

- 115 isolates of ST93-IV [2B] (Queensland clone) (26.6% of MRSA typed and 3.4% of *S. aureus*);
- 46 isolates of ST5-IV [2B] (10.6% and 1.4%);
- 21 isolates of ST45-V [5C2&5] (4.8% and 0.6%);
- 20 isolates of ST8-IV [2B] (4.6% and 0.6%);
- 19 isolates of ST30-IV [2B] (4.4% and 0.6%);
- 18 isolates of ST1-IV [2B] (4.2% and 0.5%);
- 15 isolates of ST6-IV [2B] (3.5% and 0.4%);
- 14 isolates of ST97-IV [2B] (3.2% and 0.4%); and
- 11 isolates of PVL-positive ST22-IV [2B] (2.5% and 0.3%).

ST93-IV [2B] (Queensland clone) accounted for 29.6% of CA-MRSA, ranging from 18.3% in Victoria to 44.6% of CA-MRSA in Western Australia. ST93-IV was not identified in Tasmania (Table 5). Typically PVL positive, 87.0% of ST93-IV [2B] isolates were community-onset.

ST5-IV [2B] accounted for 11.9% of CA-MRSA and was isolated in all regions of Australia except the Australian Capital Territory (Table 5). Overall, 43.5% of the isolates were PVL positive and 71.7% were community-onset.

ST45-V [5C2&5] accounted for 5.4% of CA-MRSA and was isolated in all regions except South Australia, Tasmania, the Northern Territory and the Australian Capital Territory (Table 5). All isolates were PVL negative and 66.7% were community-onset.

ST8-IV [2B] accounted for 5.2% of CA-MRSA and was isolated in all regions except Tasmania and the Northern Territory (Table 5). Overall, 90.0% of the isolates were PVL positive and 80.0% were community-onset.

ST30-IV [2B] accounted for 4.9% of CA-MRSA and was isolated in all regions of Australia except Tasmania and the Northern Territory (Table 5). Overall, 89.5% of the isolates were PVL positive and 94.7% were community-onset.

ST1-IV [2B] accounted for 4.6% of CA-MRSA and was isolated in all regions of Australia except the Australian Capital Territory (Table 5). Overall, 11.1% of the isolates were PVL positive and 88.9% were community-onset.

ST6-IV [2B] accounted for 3.9% of CA-MRSA and was isolated in all regions of Australia except South Australia (Table 5). Overall, 13.3% isolates of the isolates were PVL positive and 73.3% were community-onset.

ST97-IV [2B] accounted for 3.6% of CA-MRSA and was isolated in all regions of Australia except South Australia, Tasmania, the Northern Territory and the Australian Capital Territory. All ST97-IV [2B] isolates were PVL negative and 78.6% were community-onset.

PVL-positive ST22-IV [2B] accounted for 2.8% of CA-MRSA and was isolated in all regions of Australia except Tasmania and the Northern Territory. This clone is not related to the HA-MRSA clone PVL-negative ST22-IV [2B] (EMRSA-15). Overall, 81.8% of PVL-positive ST22-IV [2B] were community-onset.

Overall, 82.7% of CA-MRSA were non-multi-resistant, with 54.9% of CA-MRSA resistant to the β-lactams only. Multi-resistance was primarily due to the ST45-V [5C2&5] clone.

The AMR profiles of the nine predominant CA-MRSA clones are shown in Table 6.

Panton-Valentine leucocidin

Overall, 197 MRSA isolates (45.5% of MRSA and 50.8% of CA-MRSA) were PVL positive. The PVL-associated genes (*lukF*-PV and *lukS*-PV) were not detected in the HA-MRSA clones (Table 3).

Table 5: The number and proportion of the major community-associated methicillin-resistant *Staphylococcus aureus* (MRSA) clones (> 10 isolates), AGAR by jurisdiction and detection of Panton-Valentine leucocidin (PVL)-associated genes,[a] Australia, 2024

		Jurisdiction:[b] clone percentage (number)								
Clone	**PVL category[a]**	**ACT**	**NSW**	**NT**	**Qld**	**SA**	**Tas.**	**Vic.**	**WA**	**Australia**
ST93-IV	All	—[c] (3)	18.9 (17)	43.8 (14)	41.3 (26)	—[c] (7)	—[c] (0)	18.3 (15)	44.6 (33)	29.6 (115)
	PVL positive	2	15	13	25	7	0	14	33	109
	PVL negative	1	2	1	1	0	0	1	0	6
ST5-IV	All	—[c] (0)	—[c] (5)	31.3 (10)	19.0 (12)	—[c] (3)	—[c] (1)	—[c] (6)	—[c] (9)	11.9 (46)
	PVL positive	0	1	8	1	2	0	0	8	20
	PVL negative	0	4	2	11	1	1	6	1	26
ST45-V	All	—[c] (0)	11.1 (10)	—[c] (0)	—[c] (1)	—[c] (0)	—[c] (0)	—[c] (9)	—[c] (1)	5.4 (21)
	PVL positive	0	0	0	0	0	0	0	0	0
	PVL negative	0	10	0	1	0	0	9	1	21
ST8-IV	All	—[c] (3)	13.3 (12)	—[c] (0)	—[c] (2)	—[c] (1)	—[c] (0)	—[c] (1)	—[c] (1)	5.2 (20)
	PVL positive	3	11	0	2	0	0	1	1	18
	PVL negative	0	1	0	0	1	0	0	0	2
ST30-IV	All	—[c] (1)	—[c] (3)	—[c] (0)	—[c] (1)	—[c] (2)	—[c] (0)	13.4 (11)	—[c] (1)	4.9 (19)
	PVL positive	1	3	0	1	2	0	9	1	17
	PVL negative	0	0	0	0	0	0	2	0	2
ST1-IV	All	—[c] (0)	—[c] (2)	—[c] (2)	—[c] (3)	—[c] (4)	—[c] (1)	—[c] (3)	—[c] (3)	4.6 (18)
	PVL positive	0	1	0	0	0	0	1	0	2
	PVL negative	0	1	2	3	4	1	2	3	16
ST6-IV	All	—[c] (1)	—[c] (5)	—[c] (1)	—[c] (2)	—[c] (0)	—[c] (2)	—[c] (3)	—[c] (1)	3.9 (15)
	PVL positive	0	2	0	0	0	0	0	0	2
	PVL negative	1	3	1	2	0	2	3	1	13

Clone	PVL category[a]	Jurisdiction:[b] clone percentage (number)								
		ACT	NSW	NT	Qld	SA	Tas.	Vic.	WA	Australia
ST97-IV	All	—[c] (0)	—[c] (7)	—[c] (0)	—[c] (1)	—[c] (0)	—[c] (0)	—[c] (3)	—[c] (3)	3.6 (14)
	PVL positive	0	0	0	0	0	0	0	0	0
	PVL negative	0	7	0	1	0	0	3	3	14
ST22-IV (PVL positive)	All	—[c] (1)	—[c] (3)	—[c] (0)	—[c] (2)	—[c] (1)	—[c] (0)	—[c] (3)	—[c] (1)	2.8 (11)
	PVL positive	1	3	0	2	1	0	3	1	11
	PVL negative	0	0	0	0	0	0	0	0	0
Other clones	All	—[c] (3)	28.9 (26)	—[c] (5)	20.6 (13)	40.0 (12)	—[c] (1)	34.1 (28)	28.4 (21)	28.1 (109)
	PVL positive	0	3	0	2	5	0	6	2	18
	PVL negative	3	23	5	11	7	1	22	19	91
Total	**—**	**12**	**90**	**32**	**63**	**30**	**5**	**82**	**74**	**388**

a PVL: Panton-Valentine leucocidin.

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

c Insufficient numbers (< 10) to calculate percentage.

Table 6: Antimicrobial resistance combinations for the most predominant CA-MRSA clones,[a,b] AGAR, Australia, 2024

Resistance pattern[c]	ST93-IV	ST5-IV	ST45-V	ST30-IV	ST8-IV	ST1-IV	ST6-IV	ST97-IV	ST22-IV (PVL positive)[d]
Single resistance									
β-lactams only	78	32		15	9	14	8	11	
Resistance to methicillin and one antimicrobial									
Cip		1	2	1	1		3		
Ery	2	2			1		1	1	
Fus		2							
Gen					1			1	
Sxt		1							
Resistance to methicillin and two antimicrobials									
CipGen									5
CipTet			1						
EryCip				1	3				
EryFus		1							
EryIcr	28	3		1		2	2		
RifFus	1								
Resistance to methicillin and three antimicrobials									
CipTetGen			5					1	
EryCipGen			2						
EryIcrCip		2		1	2		1		1
EryIcrFus						1			
EryIcrTet	3					1			
Resistance to methicillin and four antimicrobials									
EryCipTetGen			1						
EryIcrCipFus			1						
EryIcrCipGen									3
EryIcrCipTet			2						

Resistance pattern[c]	ST93-IV	ST5-IV	ST45-V	ST30-IV	ST8-IV	ST1-IV	ST6-IV	ST97-IV	ST22-IV (PVL positive)[d]
Resistance to methicillin and five antimicrobials									
EryIcrCipSxtGen			1						
EryIcrCipTetFus			1						
EryIcrCipTetGen			4						
Resistance to methicillin and six antimicrobials									
EryIcrCipSxtTetFus					1				
Total	**112**	**44**	**20**	**19**	**18**	**18**	**15**	**14**	**9**

a CA-MRSA: community-acquired methicillin-resistant *Staphylococcus aureus*.

b Only data from isolates tested against all antimicrobial groups were included (n = 269).

c Cip: ciprofloxacin; Ery: erythromycin; Fus: fusidic acid; Gen: gentamicin; Icr: Inducible clindamycin; Rif: rifampicin; Sxt: cotrimoxazole; Tet: tetracycline.

d PVL: Panton-Valentine leucocidin.

Discussion

The AGAR surveillance programs collect data on AMR, focussing on bloodstream infections caused by *S. aureus*, *Enterococcus* and gram-negative bacilli including the *Enterobacterales*, *Pseudomonas aeruginosa* and *Acinetobacter* species. All data collected in the AGAR programs are generated as part of routine patient care in Australia, with most data available through laboratory and hospital bed management information systems. Isolates are referred to a central laboratory where strain and AMR profile characterisation is performed. As the programs are similar to the AMR surveillance programs conducted in Europe, comparison of Australian AMR data with European countries is possible.[22]

In ASSOP 2024, methicillin resistance was identified in 14.9% of the 3,358 SAB episodes (95% CI: 13.6–16.3). In the 2023 European Centre for Disease Prevention and Control (ECDC) SAB surveillance program, nine of the 44 (20%) reporting countries had methicillin resistance rates below 5%. Rates equal to or above 25% were found in 10 countries (23%): Croatia, Cyprus, Greece, Italy, Kosovo, Macedonia, Montenegro, Romania, Spain, and Türkiye, with methicillin resistance rates over 50% in Cyprus and Kosovo.[23]

A decrease in methicillin-resistant SAB has been reported in several parts of the world,[24,25] and is believed to be due to the implementation of antimicrobial stewardship and a package of improved infection control procedures including hand hygiene; MRSA screening and decolonisation; patient isolation; and infection prevention care bundles.[26–29] In the ASSOP surveys, the percentage of methicillin-resistant SAB in Australia has decreased significantly over the last ten years, ranging from 18.1% in 2015 to 14.9% in 2024 (χ^2 for linear trend = 37.76; $p < 0.01$). There have also been significant decreases in HA-MRSA, from 33.3% in 2014 to 10.4% in 2024 (χ^2 for linear trend = 27.61; $p < 0.01$), and in hospital-onset MRSA, from 28.0% to 22.8% ($p < 0.01$) over the last ten ASSOP surveys.[30–39] Over the same time period, significant increases have been observed in CA-MRSA from 66.7% to 89.6% ($p < 0.01$) and in community-onset MRSA from 72.0% to 77.2% ($p < 0.01$). Because of the increased burden of CA-MRSA bacteraemia in the Australia community, a significant reduction in the overall proportion of SAB due to MRSA may prove problematic.

In ASSOP 2024, the all-cause mortality at 30 days was 14.0% (95% CI: 12.6–15.5). There was no significant difference in mortality observed between methicillin-resistant SAB (13.7%) and methicillin-susceptible SAB (14.1%) ($p = 0.9$). Using data from the 28 labs who contributed to ASSOP over the last ten years, the all-cause mortality at 30 days reported in the ASSOP has ranged from 13.5% in 2020 to 17.5% in 2022. Over the same period the all-cause mortality at 30 days for MRSA has ranged from 13.3% in 2020 to 22.7% in 2016, and for MSSA from 13.5% in 2020 to 16.8% in 2022.[31–39]

With the exception of the β-lactams and erythromycin, AMR in MSSA remains rare. However, for MRSA, in addition to the β-lactams, 34.8% of isolates were resistant to erythromycin; 28.9% to ciprofloxacin; 13.1% to gentamicin; and 11.0% to tetracycline. AMR was identified in the two major HA-MRSA clones: ST22-IV [2B] (EMRSA-15), which is typically ciprofloxacin and erythromycin resistant, and ST239-III [3A] (Aus-2/3 EMRSA) which is typically erythromycin, clindamycin, ciprofloxacin, cotrimoxazole, tetracycline and gentamicin resistant. In the early 1980s, the multi-resistant ST239-III [3A] (Aus-2/3 EMRSA) was the dominant HA-MRSA clone in Australian hospitals. However, in 2013, the first ASSOP survey identified ST22-IV [2B] (EMRSA-15) as having replaced ST239-III [3A] (Aus-2/3 EMRSA) as the predominant HA-MRSA clone and this change had occurred throughout most of the country. In ASSOP 2024, 8.8% of MRSA were characterised as ST22-IV [2B] (EMRSA-15), and 1.6% as ST293-III [3A].

In ASSOP 2024, PVL-positive ST93-IV [2B] (Queensland clone) remained the predominant CA-MRSA clone (29.6% of CA-MRSA) in Australia. CA-MRSA, in particular the ST45-V [5C2&5] clone (5.4% of CA-MRSA), has acquired multiple AMR determinants including resistance to ciprofloxacin, erythromycin, clindamycin, gentamicin and tetracycline.

Approximately 20.9% of SAB episodes caused by CA-MRSA were hospital-onset. As transmission of CA-MRSA in Australian hospitals is thought to be rare,[40,41] it is likely that many of the hospital-onset CA-MRSA SAB infections reported in ASSOP 2024 were caused by the patient's own colonising strain acquired prior to admission. In Australia, CA-MRSA clones such as PVL-positive ST93-IV [2B] (Queensland clone) are well established in the community and therefore it is important to monitor AMR patterns in community- and healthcare-associated SAB, as this information will guide therapeutic practices in treating *S. aureus* sepsis.

Conclusion

ASSOP 2024 has demonstrated AMR in SAB in Australia continues to be a significant problem.
The percentage of SAB episodes that are methicillin resistant is higher in Australia than in most EU/EEA countries; CA-MRSA prevalent in Australia but not in most EU/EEA countries. In Australia, MRSA remains a public health priority particularly in the community. Continuous surveillance of SAB and its outcomes, and the implementation of comprehensive MRSA management strategies targeting hospitals and long-term care facilities, remain essential.

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