AUSTRALIAN GROUP ON ANTIMICROBIAL RESISTANCE

Australian *Staphylococcus aureus* Surveillance Outcome Program (ASSOP)

Bloodstream Infection Report

2022 Final Report

July 2023

Contents

Key findings:

Staphylococcus aureus

- A total of 3,214 *Staphylococcus aureus* (*S. aureus*) bacteraemia episodes were reported from 1 January to 31 December 2022, 77.5% of which were community-onset (CO). Of all episodes 15.0% were methicillin resistant.
- The 30-day all-cause mortality was 17.5%. There was a significant difference in mortality between methicillin-resistant *S. aureus* (MRSA) (21.4%) and methicillin-susceptible *S. aureus* (MSSA) (16.8%) $P = 0.02$ and between healthcare-associated MRSA (HA-MRSA) (34.5%) and community- associated MRSA (CA-MRSA) (19.9%) $P = 0.02$. There was no significant difference in mortality between hospital-onset (HO) (19.5%) and CO (17.0%) bacteraemia.
- The 30-day all-cause mortality for *S. aureus* was significantly lower amongst children (<18 years) (2.3%, 5/219) compared to adults (18.9%, 459/2,426) $P < 0.01$.
- Osteomyelitis/septic arthritis (20.8%) and skin and skin structure infections (19.7%) were the most common principal clinical manifestations.
- The hospital length of stay was more than 30 days in 24.6% of patients (21.5% in MRSA, 25.2% in MSSA although not significantly different $P = 0.09$).
- Antimicrobial resistance (AMR) to the non-β-lactams in MRSA has continued to decline overall, largely due to the substantial decline in the multi-resistant ST239-III clone.
- One MRSA from NSW was confirmed to have a daptomycin MIC of 1.5 mg/L. This isolate was an ST93-IV and carried the A302V MprF mutation and the A23V Cls2 mutation.
- CA-MRSA strains were the dominant cause of MRSA bacteraemia.
- Two HA-MRSA clones were identified; ST22-IV (EMRSA-15) which was the dominant clone and ST239-III (Aus 2/3 EMRSA). No HA-MRSA isolates harboured the Panton-Valentine leucocidin (PVL) associated genes.
- The majority of EMRSA-15 bacteraemias were community-onset.
- Sixty-four CA-MRSA clones were identified; the dominant CA-MRSA clone was ST93-IV (Queensland clone).
- Overall, 42.8% of CA-MRSA isolates harboured the PVL associated genes.
- The Queensland clone of CA-MRSA (ST93-IV), which harbours the PVL associated genes, was seen in all states and territories except Tasmania and is now the most common CA-MRSA clone in all other regions except New South Wales.
- The multi-resistant ST45-V CA-MRSA clone is prominent in New South Wales and is associated with both CO and HO bacteraemia.

Implications of key findings for health care

Methicillin resistance in *Staphylococcus aureus*

The proportion of *S. aureus* that are methicillin resistant throughout Australia has remained fairly stable over the years 2013–2022, although there are notable variations at state and territory level.

The total number of *S. aureus* bacteraemias identified by AGAR in 2022, excluding isolates from four hospitals that contributed in 2021 or 2022 only, was similar to 2021 (2,947 in 2021; 2,936 in 2022). Numbers decreased in New South Wales (770 to 713, down 7.4%), Victoria (615 to 593, down 3.6%) and Western Australia (513 to 497, down 3.1%). Numbers increased in Tasmania (115 to 159, up 38.3%), the Northern Territory (86 to 98, up 14.0%), the Australian Capital Territory (102 to 115, up 12.7%), Queensland (514 to 527, up 2.5%). The number from South Australia were similar for both years (232 to 234). Overall, the proportion of MRSA decreased by 1.5 percentage points, from 16.6% to 15.1%, hospital-onset MRSA infections increased from 22.3% to 23.8%.

Relative to 2021, there were no significant differences in the proportion of MRSA in all states and territories. The proportion of MRSA decreased in all states and territories except in the Northern Territory where there was a slight increase (40.7% in 2021, 42.9% in 2022).

Since 2013, there have been significant increases in the proportion of CA-MRSA clones nationally, notably in New South Wales. The proportion of HA-MRSA clones declined nationally, and in all states and territories except Tasmania.

In 2022, CA-MRSA clones accounted for 12.2% (388/3,182) of all *S. aureus*; in 2021 it was 13.7% (401/2,931). ST93-IV was the most prevalent CA-MRSA clone (104/388, 26.8%), and was found in all states and territories except Tasmania. ST45-V continues to dominate in New South Wales.

HA-MRSA clones accounted for only 1.9% (61/3,182 of all *S. aureus* in 2022. ST22-IV was the most common HA-MRSA clone (55/61, 90.2%), found in all states and territories.

Epidemiology of clinical manifestations

The most common clinical manifestation continues to be osteomyelitis/septic arthritis 22.6% (606/2,684) in 2021 and 20.8% (615/2,960) in 2022. Device-related bacteraemia accounted for 16.8% (452/2,684) in 2021 and 14.7% (434/2,960) in 2022. *S. aureus* bacteraemia was commonly associated with intra-vascular catheters and/or devices and prosthetic joints.

Variation across states and territories

AMR rates vary considerably across states and territories. Methicillin resistance in *S. aureus* ranged from 5.7% in Tasmania to 42.9% in the Northern Territory.

Variations between hospital and community settings

Overall *S. aureus* bacteraemias were more commonly community onset (77.5%: MRSA 75.5%, MSSA 77.9%

These variations have implications for choice of empiric antimicrobial therapy and guidelines in community- versus hospital-onset infections, accounting for infections in aged care home residents (which are included in the community-onset group in the AGAR data, but not distinguished as such in this report).

International comparisons

Australia ranks thirteenth of thirty-one countries for rates of resistance to methicillin in *S. aureus* compared to all European countries contributing to the European Antimicrobial Resistance Surveillance Network (EARS-Net) program (http://atlas.ecdc.europa.eu/public/index.aspx).

1. Background and objectives

The Australian Group on Antimicrobial Resistance (AGAR) commenced in 1985 and was established to collect national data on antimicrobial resistance (AMR) in bacteria causing important and life-threatening infections.

Historically, the main focus of AGAR was AMR in *Staphylococcus aureus*. The scope broadened over time to include surveillance studies on *Escherichia coli, Enterobacter species, Klebsiella species, Haemophilus influenzae, Streptococcus pneumoniae* and *Enterococcus species*. AGAR now concentrates on three groups of pathogens within the programs: Australian *Staphylococcus aureus* Surveillance Outcome Program (ASSOP), Australian Enterococcal Surveillance Outcome Program (AESOP) and the Gram-Negative Surveillance Outcome Program (GnSOP).

AGAR's focus on bacteraemia allows examination of laboratory-confirmed, invasive infections and comparison of rates over time for hospitals, states and territories. AGAR compares Australian data with EARS-Net, enabling benchmarking and trend projections. AGAR has collected ongoing data on the prevalence of AMR in Australia over a long period using standardised methods.

The 2022 ASSOP report presents analyses of AMR associated with episodes of *S. aureus* bacteraemia (blood stream infection) that were reported by 33 participating Australian public and private laboratories servicing 55 hospitals across Australia in 2022.

The 55 hospitals that currently contribute to AGAR, including five private hospitals, are listed in Table 1. In 2022, three additional hospitals (two from NSW and one from Queensland) contributed data.

AGAR publishes detailed annual reports on each program on its website (www.agargroup.org.au), and in the Communicable Diseases Intelligence (CDI) journal.

AGAR is part of the Antimicrobial Use and Resistance in Australia (AURA) surveillance system funded by the Australian Government Department of Health and Aged Care.

Table 1: Hospitals that contributed to AGAR, by state and territory, AGAR, 2022

State or territory	Hospital
New South Wales	Children's Hospital Westmead
	Concord Repatriation General Hospital
	Gosford Hospital
	John Hunter Hospital
	Liverpool Hospital
	Nepean Hospital
	Prince of Wales Hospital
	Royal North Shore Hospital
	Royal Prince Alfred Hospital
	St Vincent's Hospital, Sydney*
	Sydney Children's Hospital
	Westmead Hospital
	Wollongong Hospital
Victoria	Alfred Hospital
	Austin Hospital (Austin Health)
	Monash Children's Hospital†
	Monash Medical Centre (Dandenong Hospital)†
	Monash Medical Centre (Monash Health)
	Royal Melbourne Hospital
	Royal Women's and Children's Hospital
	St Vincent's Hospital*
Queensland	Gold Coast Hospital
	Greenslopes Private Hospital§ #
	Mater Private Hospital Townsville§ #
	Prince Charles Hospital**
	Princess Alexandra Hospital**
	Queensland Children's Hospital**
	Royal Brisbane and Women's Hospital
South Australia	Flinders Medical Centre
	Royal Adelaide Hospital
	Women's and Children's Hospital‡
Western Australia	Fiona Stanley Hospital
	Joondalup Hospital*
	North-west regional Western Australia (Broome, Derby, Fitzroy Crossing, Halls Creek, Karratha, Kununurra, Newman, Onslow, Paraburdoo, Port Hedland, Roebourne, Tom Price, Wyndham) §§
	Perth Children's Hospital§§
	Royal Perth Hospital##
	Sir Charles Gairdner Hospital
	St John of God Hospital, Murdoch#
Tasmania	Launceston General Hospital
	Royal Hobart Hospital
Northern Territory	Alice Springs Hospital
	Royal Darwin Hospital
Australian Capital Territory	Canberra Hospital

* Public/Private hospital
† Microbiology services provided by Monash Medical Centre (Monash Health)
§ Microbiology services provided by Sullivan Nicolaides Pathology
\# Private hospital

** Microbiology services provided by Pathology Queensland Central Laboratory
‡ Microbiology services provided by SA Pathology, Royal Adelaide Hospital
§§ Microbiology services provided by PathWest Laboratory Medicine WA, Queen Elizabeth II Medical Centre
Microbiology services provided by PathWest Laboratory Medicine WA, Fiona Stanley Hospital

1.1. Australian *Staphylococcus aureus* Surveillance Outcome Program

Globally *S. aureus* is one of the most frequent causes of hospital-acquired and community-acquired blood stream infections.[1] Although there are a wide variety of manifestations of serious invasive infection caused by *S. aureus*, in the great 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]

Despite standardised treatment protocols for SAB, including prolonged antimicrobial therapy and prompt source control[3], mortality can range from as low as 2.5% to as high as 40%.[4-6] Mortality rates are known to vary significantly with patient age, clinical manifestation, co-morbidities and methicillin resistance.[7, 8] A prospective study of SAB conducted by 27 laboratories in Australia and New Zealand found increased 30-day all-cause 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.[9]

AGAR began surveillance of AMR in *S. aureus* in 1986.[10] In 2013, AGAR commenced the Australian *Staphylococcus aureus* Sepsis Outcome Program (ASSOP).[11] The term “Sepsis” in the program was changed in 2021 to “Surveillance” to better reflect AGAR’s surveillance of episodes of bacteraemia rather than sepsis.

The primary objective of ASSOP 2022 was to determine the proportion of SAB isolates demonstrating AMR with particular emphasis on:

- Assessing susceptibility to methicillin
- Molecular epidemiology of methicillin-resistant *S. aureus* (MRSA).

2. Summary of methods

Fifty-five hospitals, in all states and territories of Australia, were enrolled in the 2022 AGAR programs. The AGAR laboratories collected all isolates from unique patient episodes of bacteraemia from 1 January 2022 to 31 December 2022. Approval to conduct the prospective data collection, including de-identified demographic data, was given by the research ethics committees associated with each participating hospital.

In patients with more than one isolate, a new episode was defined as a new positive blood culture more than two weeks after the initial positive culture. An episode was defined as community onset if the first positive blood culture was collected 48 hours or less after admission, and as hospital onset if collected more than 48 hours after admission.

AGAR meets the data security requirements of the AURA Surveillance System. These arrangements ensure that data conform to appropriate standards of data management and quality, and that data are used in accordance with appropriate approvals. The Australian Society for Antimicrobials (ASA), as data custodian for AGAR data, is responsible for:

- Approving access to, and use of AGAR data;
- Ensuring that AGAR data are protected from unauthorised access, alteration or loss;
- Ensuring compliance with relevant legislation and policies regarding administration, quality assurance, and data access and release.

2.1. Data fields

Laboratory data collected for each episode included an accession number, the date of blood culture collection, the organism isolated (genus and species), and the antimicrobial susceptibility test results (minimum inhibitory concentrations (MICs)) for each species. The patient's date of birth, sex and postcode of residence were also provided. If the patient was admitted to hospital, the date of admission was also provided. Depending on the laboratory's level of participation, limited clinical and outcome data were also provided. The data included the patient's discharge date, the principal clinical manifestation, device-related infection (yes or no) and the outcome (died, all-cause or survived) at seven and 30 days (see Appendix A).

2.2. Species identification

Isolates were identified to species level, if possible, using the routine method for each institution. This included the Vitek® 2 and BD Phoenix™ automated microbiology systems, and if available, matrix assisted laser desorption ionization-time of flight (MALDI-TOF) mass spectrometry (Bruker MALDI biotyper® or Vitek® MS).

2.3. Susceptibility testing

Susceptibility testing of isolates is described in Appendix B. The analysis used breakpoints from the Clinical and Laboratory Standards Institute (CLSI) M100–Ed33[12] and the European Committee on Antimicrobial Susceptibility Testing (EUCAST) v13.1.[13]

2.4. PCR screening and whole genome sequencing

All MRSA were subjected to whole genome sequencing using the Illumina NextSeq™ 500 platform. The multi-locus sequence type (ST) was determined using the PubMLST *S. aureus* sequence definition database. SCC*mec* elements were identified using KmerFinder v3.2 and the SCC*mec* database curated from the Center for Genomic Epidemiology website. The PVL associated genes, *lukF-PV* and *lukS-PV*, were identified using nucleotide sequences from the NCBI database and a BLAST interface.

2.5. Statistical analysis

Confidence intervals for proportions, Fisher's exact test for categorical variables, and chi-squared test for trend were calculated, if appropriate, using MedCalc for Windows, version 19.7.4 (MedCalc Software, Ostend Belgium).

3. Results

3.1. Isolates recovered

Of 3,214 SAB episodes, 481 (15.0%; 95% confidence interval [CI] 13.8-16.3) were methicillin resistant, ranging from 5.7% (95% CI 2.7-10.5) in Tasmania to 42.9% (95% CI: 32.9-53.3) in the Northern Territory (Table 2). There was no significant difference in the proportion of MRSA amongst children (12.2%, 95% CI: 8.6-16.6) and adults (15.2%, 95% CI: 13.9-16.5), *P* = 0.2 (data not shown).

Table 2: Number of each species recovered, by state and territory, AGAR, 2022

Organism	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Staphylococcus aureus	982	593	536	234	497	159	98	115	3214
methicillin resistant, percent	17.8	11.8	11.8	17.1	14.7	5.7	42.9	7.8	15.0
methicillin susceptible, percent	82.2	88.2	88.2	82.9	85.3	94.3	57.1	92.2	85.0

NSW = New South Wales, Vic = Victoria, Qld = Queensland, SA = South Australia, WA = Western Australia, Tas = Tasmania, NT = Northern Territory, ACT = Australian Capital Territory

3.2. Place of onset of bacteraemia

A total of 3,133 (97.5%) of patients with SAB bacteraemia were admitted to hospital.

Information on place of onset of SAB was available for all episodes (Table 3).

Most SABs were community-onset (77.5%; 95% CI 76.0-78.9). The proportion of MRSA episodes that were community-onset was higher amongst children (85.3%, 29/34) than adults (74.7%, 334/447), although not statistically significant, *P* = 0.22.

Table 3: *Staphylococcus aureus* and methicillin result, by place of onset, AGAR, 2022

Organism	Community-onset % (*n*)	Hospital-onset % (*n*)	Total, 100%
Staphylococcus aureus	77.5 (2,491)	22.5 (723)	3,214
Methicillin resistant	75.5 (363)	24.5 (118)	481
Methicillin susceptible	77.9 (2,128)	22.1 (605)	2,733

3.3. Onset versus 30-day all-cause mortality

Information on 30-day all-cause mortality collected by the sending laboratories, when place of onset was known was available for 2,645 episodes (82.3%) (Table 4).

The 30-day all-cause mortality for *S. aureus* was significantly lower amongst children (2.3%, 5/219) compared to adults (18.9%, 459/2,426) ($P < 0.01$). There was a significant difference in 30-day all-cause mortality between MSSA (16.8%) and MRSA (21.4%) episodes ($P = 0.02$), and between healthcare-associated MRSA (HA-MRSA) (34.5%) and community-associated MRSA (CA-MRSA) (19.9%) clones ($P = 0.2$).

Table 4: Onset setting and 30-day all-cause mortality (blood culture isolates), AGAR, 2022

	Community onset		Hospital onset		Total	
Organism	**Number**	**Deaths % (*n*)**	**Number**	**Deaths % (*n*)**	**Number**	**Deaths % (*n*)**
Staphylococcus aureus	2,055	17.0 (349)	590	19.5 (115)	2,645	17.5 (464)
Methicillin resistant	318	20.8 (66)	97	23.7 (23)	415	21.4 (89)
CA-MRSA	261	19.9 (52)	66	19.7 (13)	327	19.9 (65)
HA-MRSA	31	32.3 (10)	27	37.0 (10)	58	34.5 (20)
Methicillin susceptible	1,737	16.3 (283)	493	18.7 (92)	2,230	16.8 (375)

CA-MRSA = community-associated methicillin-resistant *Staphylococcus aureus*; HA-MRSA = healthcare-associated methicillin-resistant *Staphylococcus aureus*

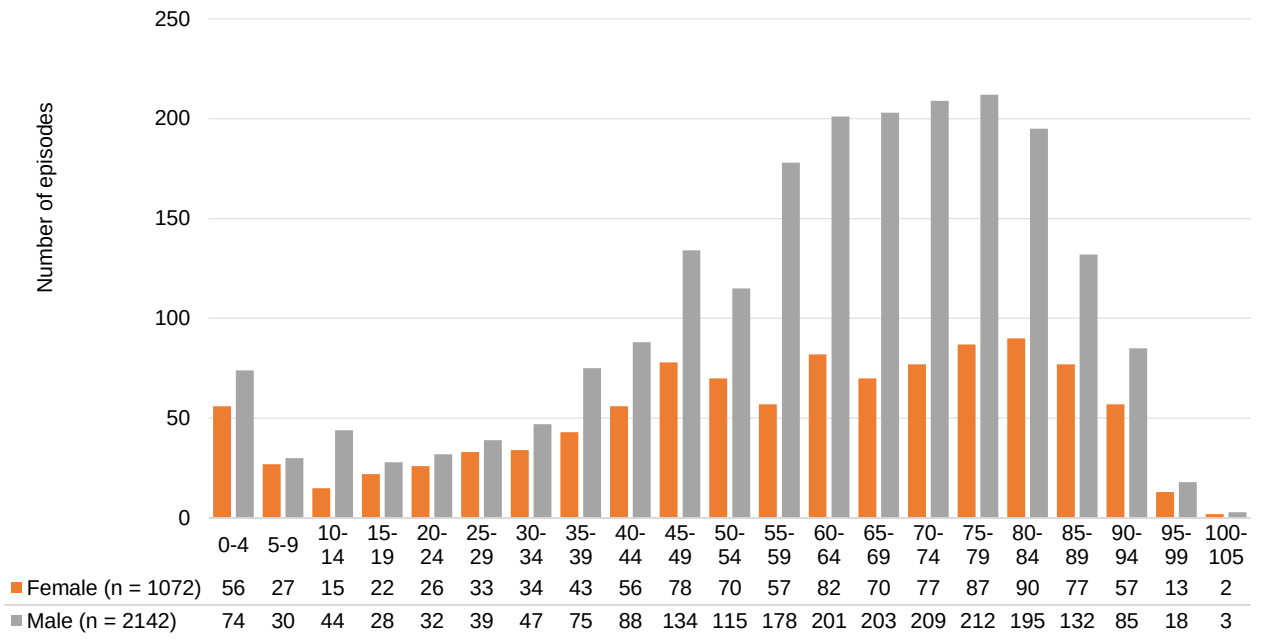
Note: Thirty methicillin-resistant *Staphylococcus aureus* were not available for whole genome sequencing.

3.4. Patient age and sex

Age and sex were available for all patients with SAB. The proportion of males was 66.6%.

Increasing age was a surrogate risk factor for SAB (Figure 1); only 19.4% of *S. aureus* episodes were in patients aged less than 40 years. The proportion of patients aged 0–19 years was 9.2% (*n* = 296).

Figure 1:
Number of episodes of bacteraemia due to *Staphylococcus aureus*, by patient age group and sex, AGAR, 2022



	0-4	5-9	10-14	15-19	20-24	25-29	30-34	35-39	40-44	45-49	50-54	55-59	60-64	65-69	70-74	75-79	80-84	85-89	90-94	95-99	100-105
Female (n = 1072)	56	27	15	22	26	33	34	43	56	78	70	57	82	70	77	87	90	77	57	13	2
Male (n = 2142)	74	30	44	28	32	39	47	75	88	134	115	178	201	203	209	212	195	132	85	18	3

3.5. Principal clinical manifestation

The principal clinical manifestations, which represent the most likely primary site or source for the origin of the blood stream infection, are described below.

The principal clinical manifestation was known for 2,960 (92.1%) episodes of SAB (Table 5). Overall, the most frequent principal clinical manifestation was osteomyelitis/septic arthritis (20.8%) followed by skin and skin structure infection (19.7%). Of the clinical manifestations in children 39.8% (106/266) were due to osteomyelitis/septic arthritis (data not shown).

Of the hospital-onset SABs where data were available, the most common principal clinical manifestation was device-related infection without metastatic focus (31.6%, 208/658). Of the community-onset SABs where data were available, the most common principal clinical manifestation was osteomyelitis/septic arthritis (23.9%, 551/2,302).

Table 5: Principal clinical manifestation for *Staphylococcus aureus* bacteraemia, by patient sex, AGAR, 2022

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)
Osteomyelitis/septic arthritis	19.5 (191)	21.4 (424)	20.8 (615)
Skin and skin structure infection	20.2 (198)	19.5 (386)	19.7 (584)
Device-related infection without metastatic focus	15.2 (149)	14.4 (285)	14.7 (434)
No identifiable focus	13.4 (131)	15.0 (297)	14.5 (428)
Other clinical syndrome	8.6 (84)	10.1 (201)	9.6 (285)
Endocarditis left-sided	6.1 (60)	5.3 (106)	5.6 (166)
Pneumonia/empyema	4.7 (46)	4.0 (80)	4.3 (126)
Deep abscess(es) excluding those in the CNS	4.0 (39)	3.1 (62)	3.4 (101)
Endocarditis right-sided	2.1 (21)	2.2 (43)	2.2 (64)
Device-related infection with metastatic focus	2.4 (23)	2.0 (39)	2.1 (62)
CNS infection (meningitis, abscess(es))	1.6 (16)	1.8 (35)	1.7 (51)
Febrile neutropenia	2.0 (20)	1.2 (24)	1.5 (44)
Total	978	1,982	2,960

CNS = central nervous system

The most common principal clinical manifestation for methicillin-susceptible *S. aureus* (MSSA) was osteomyelitis/septic arthritis (21.3%, 536/2,521), whereas for MRSA it was skin and skin structure infection (21.9%, 96/439) (Table 6).

Table 6: Principal clinical manifestation for *Staphylococcus aureus* bacteraemia, by methicillin susceptibility, AGAR, 2022

Principal clinical manifestation	Methicillin-resistant % (*n*)	Methicillin-susceptible % (*n*)	Total % (*n*)
Osteomyelitis/septic arthritis	18.0 (79)	21.3 (536)	20.8 (615)
Skin and skin structure infection	21.9 (96)	19.4 (488)	19.7 (584)
Device-related infection without metastatic focus	11.8 (52)	15.2 (382)	14.7 (434)
No identifiable focus	14.1 (62)	14.5 (366)	14.5 (428)
Other clinical syndrome	11.8 (52)	9.2 (233)	9.6 (285)
Endocarditis left-sided	4.1 (18)	5.9 (148)	5.6 (166)
Pneumonia/empyema	5.7 (25)	4.0 (101)	4.3 (126)
Deep abscess(es) excluding those in the CNS	4.8 (21)	3.2 (80)	3.4 (101)
Endocarditis right-sided	3.6 (16)	1.9 (48)	2.2 (64)
Device-related infection with metastatic focus	1.6 (7)	2.2 (55)	2.1 (62)
CNS infection (meningitis, abscess(es))	1.4 (6)	1.8 (45)	1.7 (51)
Febrile neutropenia	1.1 (5)	1.5 (39)	1.5 (44)
Total	439	2,521	2,960

CNS = central nervous system

3.6. Length of hospital stay following bacteraemic episode

Information on length of hospital stay following SAB was available for 3,002 (93.5%) episodes. Overall, 24.6% of patients remained in hospital for more than 30 days (Table 7).

Table 7: Length of hospital stay following *Staphylococcus aureus* bacteraemia, by methicillin susceptibility and place of onset, AGAR, 2022

Species	Length of stay following bacteraemia				Total
	<7 days % (*n*)	7–14 days % (*n*)	15–30 days % (*n*)	>30 days % (*n*)	
Staphylococcus aureus	19.9 (598)	25.1 (754)	30.3 (911)	24.6 (739)	3,002
Methicillin resistant	19.5 (87)	21.0 (94)	38.0 (170)	21.5 (96)	447
Community onset	21.1 (72)	19.4 (66)	38.7 (132)	20.8 (71)	341
Hospital onset	14.2 (15)	26.4 (28)	35.8 (38)	23.6 (25)	106
Methicillin susceptible	20.0 (511)	25.8 (660)	29.0 (741)	25.2 (643)	2,555
Community onset	21.3 (423)	26.5 (526)	27.5 (547)	24.7 (492)	1,988
Hospital onset	15.5 (88)	23.6 (134)	34.2 (194)	26.6 (151)	567

3.7. Susceptibility testing results

The following sections present the results of susceptibility testing and the findings for antimicrobial resistance by place of onset and multi-drug resistance. Susceptibility testing methods are described in Appendix B.

Percentages of non-susceptibility

Overall percentages of resistance or non-susceptibility using CLSI and EUCAST breakpoints are shown in Table 8. Methicillin resistance (as defined by EUCAST) by state and territory is shown in Figure 2; Detailed resistance by state and territory can be found in Appendix C.

One MRSA from NSW was confirmed to have a daptomycin MIC of 2.0mg/L. This isolate was an ST93-IV and carried the A302V MprF mutation and the A23V Cls2 mutation[14, 15].

Table 8: Antimicrobial resistances for *Staphylococcus aureus* using both CLSI and EUCAST breakpoints, AGAR, 2022

Species and antimicrobial	Isolates (*n*)	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Staphylococcus aureus					
Benzylpenicillin*	3,199	–†	78.6 (2,516)	–†	78.6 (2,516)
Cefoxitin (methicillin)§	3,214	–†	15.0 (481)	–†	15.0 (481)
Ciprofloxacin	3,203	0.8 (26)	6.3 (202)	92.9 (2,975)	7.1 (228)
Clindamycin (constitutive)	3,201	0.0 (0)	3.2 (101)	–†	3.4 (110)
Clindamycin (constitutive + inducible resistance)	3,201	0.0 (0)	12.6 (403)	–†	13.4 (428)
Daptomycin	3,209	–†	<0.1 (1)**	–†	<0.1 (1)
Erythromycin	3,147	26.6 (837)	15.5 (488)	–†	16.3 (512)
Fusidic acid	3,147	–‡	–‡	–†	2.7 (86)
Gentamicin	3,203	1.2 (39)	1.5 (48)	–†	4.6 (148)
Linezolid	3,210	–†	0.0 (0)	–†	0.0 (0)
Mupirocin (high-level) §§	2,442	–†	1.3 (32)	–†	1.3 (32)
Rifampicin	3,200	0.1 (3)	0.4 (12)	–	0.7 (22)##
Teicoplanin	3,206	0.0 (0)	0.0 (0)	–†	0.1 (3)
Tetracycline/doxycycline***	3,199	0.1 (2)	3.9 (126)	–†	5.0 (159)
Trimethoprim/sulfamethoxazole	3,201	–†	0.5 (16)	0.2 (5)	0.6 (18)
Vancomycin	3,210	0.0 (0)	0.0 (0)	–†	0.0 (0)

CLSI = Clinical and Laboratory Standards Institute; EUCAST = European Committee on Antimicrobial Susceptibility Testing

* Beta-lactamase adjusted

† No category defined

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

** Non-susceptible, resistance not defined

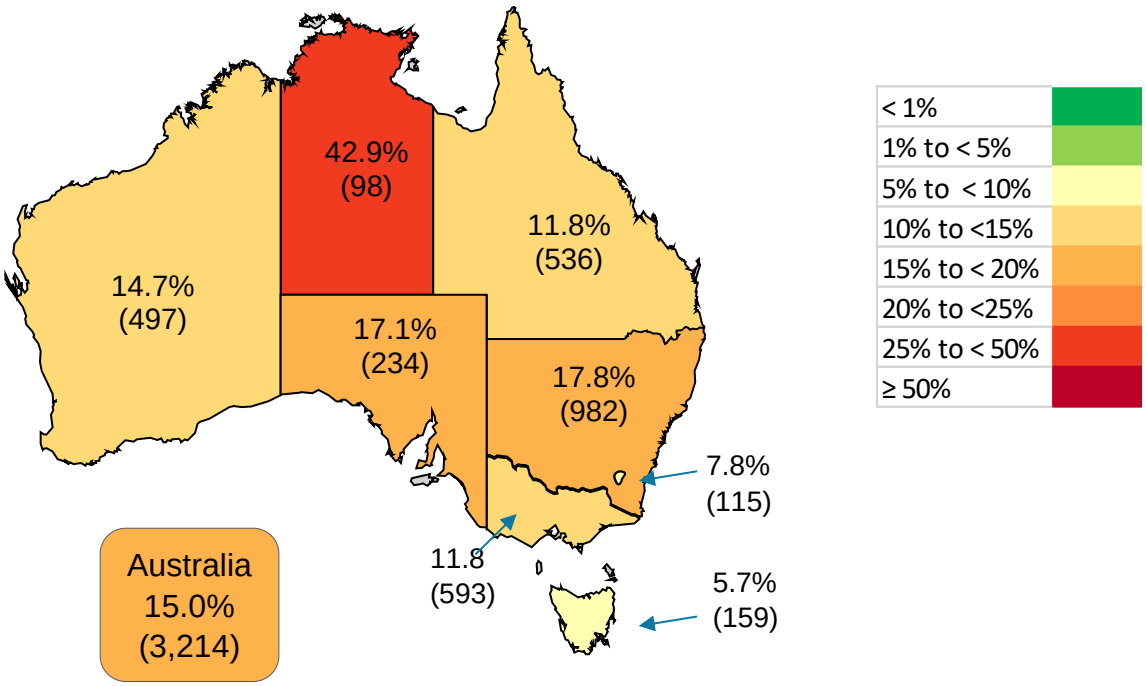
‡ No guidelines for indicated species

§§ Mupirocin high-level resistance screen

The rifampicin concentration range on the Phoenix card and one Vitek card (AST-P612) restricts the ability to accurately determine susceptibility for EUCAST (*n* = 1,242)

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

Figure 2: Percentage of *Staphylococcus aureus* from patients with bacteraemia with methicillin-resistance as defined by EUCAST, Australia, AGAR, 2022



Antimicrobial resistance by place of onset

Antimicrobial resistances using CLSI and EUCAST breakpoints, by place of onset, if known, are shown in Table 9.

Table 9: Antimicrobial resistances for *Staphylococcus aureus* using both CLSI and EUCAST breakpoints, by place of onset, AGAR, 2022

	Community onset					Hospital onset				
	No.	CLSI		EUCAST		No.	CLSI		EUCAST	
Species and antimicrobial		% I	% R	%S-IE	%R		%I	% R	%S-IE	%R
Staphylococcus aureus										
Benzylpenicillin	2,483	–*	75.7	–*	75.7	717	–*	78.4	–*	78.4
Benzylpenicillin†	2,479	–*	78.3	–*	78.3	720	–*	79.9	–*	79.9
Cefoxitin (methicillin)§	2,491	–*	14.6	–*	14.6	723	–*	16.3	–*	16.3
Ciprofloxacin	2,485	0.8	5.5	93.7	6.3	718	1.0	9.1	90.0	10.0
Clindamycin (constitutive)	2,483	0.0	3.0	–*	3.3	718	0.0	3.6	–*	4.0
Clindamycin (inducible + constitutive resistance)	2,483	0.0	12.1	–*	12.8	718	0.0	14.2	–*	15.3
Daptomycin	2,487	–*	0.0	–*	0.0	722	–*	0.1	–*	0.1
Erythromycin	2,439	26.0	15.0	–*	15.8	708	28.8	17.1	–*	17.9
Fusidic acid	2,440	–**	–**	–*	2.6	707	–**	–**	–*	3.1
Gentamicin	2,485	1.1	1.3	–*	4.4	718	1.5	2.1	–*	5.3
Linezolid	2,488	–*	0.0	–*	0.0	722	–*	0.0	–*	0.0
Mupirocin (high-level)‡	1,902	–*	1.3	–*	1.3	540	–*	1.3	–*	1.3
Rifampicin	2,484	0.1	0.3	–*	0.6§§	716	0.1	0.6	–*	1.0 §§
Teicoplanin	2,486	0.0	0.0	–*	0.0	720	0.0	0.0	–*	0.0
Tetracycline/doxycycline##	2,481	0.1	3.7	–*	4.7	718	0.0	4.9	–*	5.8
Trimethoprim/sulfamethoxazole	2,484	–*	0.3	0.1	0.4	717	–*	1.1	0.3	1.1
Vancomycin	2,488	0.0	0.0	–*	0.0	722	0.0	0.0	–*	0.0

CLSI = Clinical and Laboratory Standards Institute; EUCAST = European Committee on Antimicrobial Susceptibility Testing; No. = Number; I = Intermediate; R = Resistant; S-IE = Susceptible, increased exposure

* No category defined
† Beta-lactamase adjusted
§ Resistance as determined by cefoxitin screen (Vitek) or cefoxitin MIC (Phoenix)
** No guidelines for indicated species
‡ Mupirocin high-level resistance screen
§§ The rifampicin concentration range on the Phoenix card and one Vitek card (AST-P612) restricts the ability to accurately determine susceptibility (community-onset, *n* = 936); hospital-onset, *n* = 306)
Doxycycline concentration range (Phoenix panel) restricts ability to accurately identify intermediate and resistant category

3.8. Multi-drug resistance

The most problematic pathogens are those with multiple acquired resistances. The definitions defined by Magiorakos et al.[16] were applied in this survey, where multi-drug resistance was defined as resistance to one or more agent in three or more antimicrobial categories. For each species, antimicrobials were excluded from the count if they were affected by natural resistance mechanisms.

Only isolates for which the full range of antimicrobial categories was tested were included for determination of multi-drug resistance. EUCAST breakpoints were primarily used in the analysis.

Multiple acquired resistances are shown in Tables 10 and 11. The agents included are listed in the notes after each table.

Table 10: Multiple acquired resistance in *Staphylococcus aureus* (methicillin-resistant), by state and territory, AGAR, 2022

State or territory	Number of categories (non-MDR)					Number of categories (MDR)									
	Total	0	1	2	%	3	4	5	6	7	8	9	10	11	%
NSW	171	66	31	25	71.3	29	4	12	4	0	0	0	0	0	28.7
Vic	70	34	13	5	74.3	10	6	1	1	0	0	0	0	0	25.7
Qld	63	30	10	16	88.9	5	1	1	0	0	0	0	0	0	11.1
SA	40	16	12	6	85.0	5	1	0	0	0	0	0	0	0	15.0
WA	73	53	6	13	98.6	0	0	1	0	0	0	0	0	0	1.4
Tas	9	4	2	2	n/a	1	0	0	0	0	0	0	0	0	n/a
NT	42	30	2	9	97.6	1	0	0	0	0	0	0	0	0	2.4
ACT	9	4	0	2	n/a	1	0	1	1	0	0	0	0	0	n/a
Total	477	237	76	78	82.0	52	12	16	6	0	0	0	0	0	18.0

MDR = multi-drug resistant; resistant to one or more agent in three or more antimicrobial categories.

n/a = not applicable, insufficient numbers (<30) to calculate percentage

Note: Antimicrobials were aminoglycosides (gentamicin), ansamycins (rifampicin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), fucidanes (fusidic acid), glycopeptides (vancomycin or teicoplanin), lincosamides (clindamycin), lipopeptides (daptomycin), macrolides (erythromycin), oxazolidinones (linezolid), and tetracyclines (tetracycline, Vitek®; doxycycline, Phoenix™).

Table 11: Multiple acquired resistance in *Staphylococcus aureus* (methicillin-susceptible), by state and territory, AGAR, 2022

State or territory	Number of categories (non-MDR)					Number of categories (MDR)									
	Total	0	1	2	%	3	4	5	6	7	8	9	10	11	%
NSW	745	567	88	65	96.6	21	4	0	0	0	0	0	0	0	3.4
Vic	523	411	48	36	94.6	27	1	0	0	0	0	0	0	0	5.4
Qld	470	373	35	48	97.0	13	1	0	0	0	0	0	0	0	3.0
SA	193	156	20	14	98.4	3	0	0	0	0	0	0	0	0	1.6
WA	421	331	37	40	96.9	11	1	1	0	0	0	0	0	0	3.1
Tas	149	126	5	14	97.3	4	0	0	0	0	0	0	0	0	2.7
NT	56	36	2	7	80.4	10	1	0	0	0	0	0	0	0	19.6
ACT	106	83	7	11	95.3	4	1	0	0	0	0	0	0	0	4.7
Total	2,663	2,083	242	235	96.1	93	9	1	0	0	0	0	0	0	3.9

MDR = multi-drug resistant; resistant to one or more agent in three or more antimicrobial categories

n/a = not applicable, insufficient numbers (<30) to calculate percentage

Note: Antimicrobials were aminoglycosides (gentamicin), ansamycins (rifampicin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim–sulfamethoxazole), fucidanes (fusidic acid), glycopeptides (vancomycin or teicoplanin), lincosamides (clindamycin), lipopeptides (daptomycin), macrolides (erythromycin), oxazolidinones (linezolid), and tetracyclines (tetracycline, Vitek®; doxycycline, Phoenix™).

For *S. aureus*, the most common resistance combination was resistance to methicillin and fluoroquinolones (Table 12).

Table 12: Resistance combinations amongst *Staphylococcus aureus* tested against methicillin, fluoroquinolones and rifampicin, AGAR, 2022

Resistance pattern	N	% of total
Fully susceptible	2,574	82.0%
Single resistance	412	13.1%
Methicillin	327	10.4%
Fluoroquinolones	75	2.4%
Rifampicin	10	0.3%
Resistance to two antimicrobial groups	151	4.8%
Methicillin + fluoroquinolones	143	4.6%
Methicillin + rifampicin	4	0.1%
Fluoroquinolones + rifampicin	4	0.1%
Resistance to three antimicrobial groups	3	0.1%
Methicillin + fluoroquinolones + rifampicin	3	0.1%

Note: Only data from isolates tested against all five antimicrobial groups were included (*n* = 3,140).

Multi-drug resistance by onset setting and 30-day all-cause mortality

Multi-drug resistances by onset setting (community or hospital) and 30-day all-cause mortality are shown in Table 13.

Table 13: Multi-drug resistance, by onset setting and 30-day all-cause mortality, AGAR, 2022

Species	Category	Total		Community onset		Hospital onset	
		Number	Deaths, % (n)	Number	Deaths, % (n)	Number	Deaths, % (n)
Staphylococcus aureus	Total	2,577	17.4 (449)	2,004	16.8 (336)	573	17.9 (113)
	Non-MDR (≤2)	2,080	17.0 (354)	1,623	16.4 (266)	457	17.7 (88)
	MDR (>2)	497	19.1 (95)	381	18.4 (70)	116	18.3 (25)

MDR = multi-drug resistant; resistant to one or more agent in three or more antimicrobial categories

Notes:

1. Antimicrobial categories (agents) are listed under Tables 10 and 11. For *Staphylococcus aureus,* anti-staphylococcal β-lactams (cefoxitin) is also included.

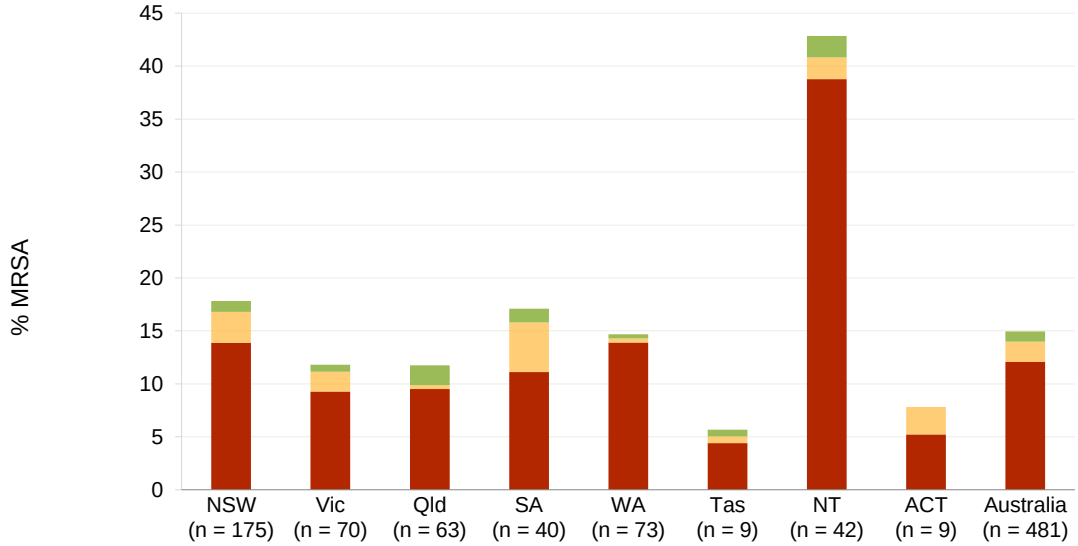
3.9. Whole genome sequencing

This section describes the whole genome sequencing results and the molecular epidemiology of MRSA. The benefits of molecular methods include increased accuracy in detecting the genetic mechanisms for AMR and clarifying the underlining epidemiology.

3.9.1. Molecular epidemiology of methicillin-resistant *Staphylococcus aureus*

Of the 481 MRSA reported, 449 (93.3%) were available for typing by whole genome sequencing. There were marked differences amongst the states and territories in the percentage and types of MRSA clones. Prevalence of MRSA ranged from 5.7% (9/159) in Tasmania to 42.9% (42/98) in the Northern Territory (Figure 3).

Figure 3: Methicillin-resistant *Staphylococcus aureus* as a percentage of all *S. aureus* isolates, by state and territory, and nationally, AGAR, 2022



	NSW (n = 175)	Vic (n = 70)	Qld (n = 63)	SA (n = 40)	WA (n = 73)	Tas (n = 9)	NT (n = 42)	ACT (n = 9)	Australia (n = 481)
Not available (n = 32)	1.0	0.7	1.9	1.3	0.4	0.6	2.0	0.0	1.0
Healthcare associated (n = 61)	3.0	1.9	0.4	4.7	0.4	0.6	2.0	2.6	1.9
Community associated (n = 388)	13.8	9.3	9.5	11.1	13.9	4.4	38.8	5.2	12.1

MRSA = methicillin-resistant *Staphylococcus aureus*

Notes:
1. *S. aureus* were categorised as MRSA based on cefoxitin screen (Vitek) or cefoxitin MIC (Phoenix).
2. Thirty-two MRSA were not available for whole genome sequencing so association could not be determined

Healthcare-associated MRSA

Based on the MLST and SCC*mec* type, two HA-MRSA clones were identified: ST22-IV (EMRSA-15) and ST239-III (Aus 2/3 EMRSA) (Tables 14 and15).

PVL-associated genes were not identified in HA-MRSA.

The most frequently isolated HA-MRSA clone, PVL-negative ST22-IV, was identified in all states and territories. ST239-III was identified in three states: New South Wales, South Australia and the Australian Capital Territory (Table 15).

Community-associated MRSA

Based on the MLST and SCC*mec* type, 64 CA-MRSA clones were identified. There were 35 STs with a single isolate. PVL was detected in 13 CA-MRSA clones. Overall, 42.8% (166/388) of CA MRSA were PVL positive (Table 14). The most frequently isolated CA-MRSA clone, ST93-IV (Queensland clone), was isolated in all states and territories except Tasmania (Table 16).

Four PVL-positive ST22-IV isolates were identified: two in Victoria, and one each in Queensland and Western Australia. PVL positive ST22-IV are frequently isolated in the South Asian subcontinent; they are not related to EMRSA-15, and are not considered to be a HA-MRSA clone.[17]

Of the hospital-onset MRSA, 74.3% (84/113) were caused by CA-MRSA.

Table 14: MRSA clones, association, place of onset and PVL carriage, AGAR, 2022

Clone	Clonal complex (CC)	Total, *n*	Community onset, % (*n*)*	Hospital onset, % (*n*)*	PVL positive, % (*n*)*
Healthcare-associated					
ST22-IV (EMRSA-15)	CC22	55	54.5 (30)	45.5 (25)	0.0 (0)
ST239-III (Aus2/3 EMRSA)	CC8	6	–† (2)	–† (4)	–† (0)
Total HA-MRSA		61	52.5 (32)	47.5 (29)	0.0 (0)
Community-associated					
ST93-IV	CC93	104	88.5 (92)	11.5 (12)	99.0 (103)
ST5-IV	CC5	48	81.3 (39)	18.8 (9)	45.8 (22)
ST45-V	CC45	38	71.1 (27)	28.9 (11)	0.0 (0)
ST1-IV	CC1	25	68.0 (17)	32.0 (8)	4.0 (1)
ST30-IV	CC30	21	85.7 (18)	14.3 (3)	61.9 (13)
ST97-IV	CC97	21	61.9 (13)	38.1 (8)	0.0 (0)
ST953-IV	CC97	11	90.9 (10)	9.1 (1)	0.0 (0)
ST8-IV	CC8	11	81.8 (9)	18.2 (2)	72.7 (8)
ST6-IV	CC6	8	–† (4)	–† (4)	–† (0)
ST78-IV	CC78	6	–† (4)	–† (2)	–† (0)
ST5-V	CC5	6	–† (3)	–† (3)	–† (0)
ST45-IV	CC45	5	–† (2)	–† (3)	–† (0)
ST872-IV	CC1	5	–† (3)	–† (2)	–† (0)
ST834-IV	CC1	4	–† (3)	–† (1)	–† (0)
ST88-IV	CC88	4	–† (3)	–† (1)	–† (0)
ST59-V	CC59	4	–† (4)	–† (0)	–† (3)
ST22-IV (PVL positive)	CC22	4	–† (4)	–† (0)	–† (4)
ST1232-V	CC398	4	–† (2)	–† (2)	–† (4)
ST59-IV	CC59	3	–† (2)	–† (1)	–† (0)
ST6151-IV	CC93	3	–† (2)	–† (1)	–† (3)
ST8430-IV	CC1	2	–† (2)	–† (0)	–† (0)
ST3074-IV	CC5	2	–† (1)	–† (1)	–† (0)
ST8534-IV	CC8	2	–† (2)	–† (0)	–† (2)
ST8536-IV	CC1	2	–† (2)	–† (0)	–† (0)
ST6959-IV	CC5	2	–† (1)	–† (1)	–† (0)
ST398-V	CC398	2	–† (1)	–† (1)	–† (0)
ST149-IV	CC5	2	–† (2)	–† (0)	–† (0)
ST188-IV	CC188	2	–† (1)	–† (1)	–† (0)
ST72-IV	CC72	2	–† (2)	–† (0)	–† (0)
ST6145-V	CC45	1	–† (1)	–† (0)	–† (0)

Clone	Clonal complex (CC)	Total, *n*	Community onset, % (*n*)*	Hospital onset, % (*n*)*	PVL positive, % (*n*)*
ST8547-IV	CC2250	1	–† (0)	–† (1)	–† (0)
ST8539-IV	CC30	1	–† (1)	–† (0)	–† (1)
ST6963-IV	CC22	1	–† (1)	–† (0)	–† (0)
ST87-IV	CC59	1	–† (0)	–† (1)	–† (0)
ST5669-IV	CC30	1	–† (1)	–† (0)	–† (0)
ST8537-IV	CC22	1	–† (1)	–† (0)	–† (0)
ST7014-V	CC45	1	–† (1)	–† (0)	–† (0)
ST8543-IV	CC1	1	–† (0)	–† (1)	–† (0)
ST8-V	CC8	1	–† (1)	–† (0)	–† (0)
ST8550-IV	CC93	1	–† (1)	–† (0)	–† (1)
ST913-IV	CC913	1	–† (1)	–† (0)	–† (0)
ST6865-V	CC5	1	–† (1)	–† (0)	–† (0)
ST5977-IV	CC5	1	–† (1)	–† (0)	–† (0)
ST5213-IV	CC1	1	–† (1)	–† (0)	–† (0)
ST1649-IV	CC6	1	–† (0)	–† (1)	–† (0)
ST8538-IV	CC45	1	–† (1)	–† (0)	–† (0)
ST30-V	CC30	1	–† (1)	–† (0)	–† (0)
ST8542-IV	CC59	1	–† (1)	–† (0)	–† (0)
ST188-V	CC188	1	–† (0)	–† (1)	–† (0)
ST8544-IV	CC97	1	–† (0)	–† (1)	–† (0)
ST8420-IV	CC1	1	–† (1)	–† (0)	–† (0)
ST8548-V	CC1	1	–† (1)	–† (0)	–† (0)
ST3628-V	CC5	1	–† (1)	–† (0)	–† (0)
ST6607-IV	CC6	1	–† (1)	–† (0)	–† (0)
ST8525-V	CC45	1	–† (1)	–† (0)	–† (0)
ST672-IV	CC672	1	–† (1)	–† (0)	–† (0)
ST8532-IV	CC22	1	–† (1)	–† (0)	–† (0)
ST5662-IV	CC5	1	–† (1)	–† (0)	–† (0)
ST8533-IV	CC1	1	–† (1)	–† (0)	–† (1)
ST2250-IV	CC2250	1	–† (1)	–† (0)	–† (0)
ST762-IV	CC1	1	–† (1)	–† (0)	–† (0)
ST2493-IV	CC1	1	–† (1)	–† (0)	–† (0)
ST779-IV	CC779	1	–† (1)	–† (0)	–† (0)
ST7891-IV	CC1	1	–† (1)	–† (0)	–† (0)
Total CA-MRSA		388	78.4 (304)	21.6 (84)	42.8 (166)
MRSA typed		449	74.8 (336)	25.2 (113)	37.0 (166)

MRSA = methicillin-resistant *Staphylococcus aureus*; PVL = Panton-Valentine leucocidin

* Percentage of the clone
† Insufficient numbers (<10) to calculate percentage

Table 15: Healthcare-associated MRSA clones, by state and territory, AGAR, 2022

Clone	Percentage of clone (number)								
	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
ST22-IV (EMRSA-15)	86.2 (25)	90.9 (10)	–* (2)	100.0 (11)	–* (2)	–* (1)	–* (2)	–* (2)	90.2 (55)
ST239-III (Aus2/3 EMRSA)	13.8 (4)	9.1 (1)	–* (0)	0.0 (0)	–* (0)	–* (0)	–* (0)	–* (1)	9.8 (6)
Total	29	11	2	11	2	1	2	3	61

MRSA = methicillin-resistant *Staphylococcus aureus*.
* Insufficient numbers (<10) to calculate percentage

Table 16: Major community-associated MRSA clones (> 10 isolates) by state and territory and PVL carriage, AGAR, 2022

Clone	Percentage (*n*)								
	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
ST93-IV (Qld CA-MRSA)	15.4 (21)	20.0 (11)	37.3 (19)	42.3 (11)	24.6 (17)	–* (0)	60.5 (23)	–* (2)	26.8 (104)
Number PVL-positive	21	11	19	10	17	0	23	2	103
Number PVL-negative	0	0	0	1	0	0	0	0	1
ST5-IV	7.4 (10)	7.3 (4)	9.8 (5)	15.4 (4)	20.3 (14)	–* (1)	26.3 (10)	–* (0)	12.4 (48)
Number PVL-positive	0	1	0	2	11	0	8	0	22
Number PVL-negative	10	3	5	2	3	1	2	0	26
ST45-V	20.6 (28)	12.7 (7)	2.0 (1)	0.0 (0)	0.0 (0)	–* (0)	2.6 (1)	–* (1)	9.8 (38)
Number PVL-positive	0	0	0	0	0	0	0	0	0
Number PVL-negative	28	7	1	0	0	0	1	1	38
ST1-IV	6.6 (9)	0.0 (0)	5.9 (3)	11.5 (3)	13.0 (9)	–* (1)	0.0 (0)	–* (0)	6.4 (25)
Number PVL-positive	1	0	0	0	0	0	0	0	1
Number PVL-negative	8	0	3	3	9	1	0	0	24
ST30-IV	8.8 (12)	7.3 (4)	3.9 (2)	3.8 (1)	1.4 (1)	–* (0)	0.0 (0)	–* (1)	5.4 (21)
Number PVL-positive	7	2	1	1	1	0	0	1	13
Number PVL-negative	5	2	1	0	0	0	0	0	8
ST97-IV	6.6 (9)	3.6 (2)	9.8 (5)	0.0 (0)	4.3 (3)	–* (1)	0.0 (0)	–* (1)	5.4 (21)
Number PVL-positive	0	0	0	0	0	0	0	0	0
Number PVL-negative	9	2	5	0	3	1	0	1	21
ST953-IV	0.0 (0)	0.0 (0)	0.0 (0)	0.0 (0)	15.9 (11)	–* (0)	0.0 (0)	–* (0)	2.8 (11)
Number PVL-positive	0	0	0	0	0	0	0	0	0
Number PVL-negative	0	0	0	0	11	0	0	0	11
ST8-IV	5.9 (8)	3.6 (2)	2.0 (1)	0.0 (0)	0.0 (0)	–* (0)	0.0 (0)	–* (0)	2.8 (11)
Number PVL-positive	5	2	1	0	0	0	0	0	8
Number PVL-negative	3	0	0	0	0	0	0	0	3

Clone	Percentage (*n*)								
	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Other clones (n = 56)	28.7 (39)	45.5 (25)	29.4 (15)	26.9 (7)	20.3 (14)	–* (4)	10.5 (4)	–* (1)	28.1 (109)
Number PVL-positive	4	8	4	1	2	0	0	0	19
Number PVL-negative	35	17	11	6	12	4	4	1	90
Total	136	55	51	26	69	7	38	6	388
PVL-positive	38	24	25	14	31	0	31	3	166
PVL-negative	98	31	26	12	38	7	7	3	222

CA-MRSA = community-associated methicillin-resistant *Staphylococcus aureus*; MRSA = methicillin-resistant *Staphylococcus aureus*; PVL = Panton-Valentine leucocidin

* Insufficient numbers (<10) to calculate percentage

3.10. Trend analysis (2013–2022)

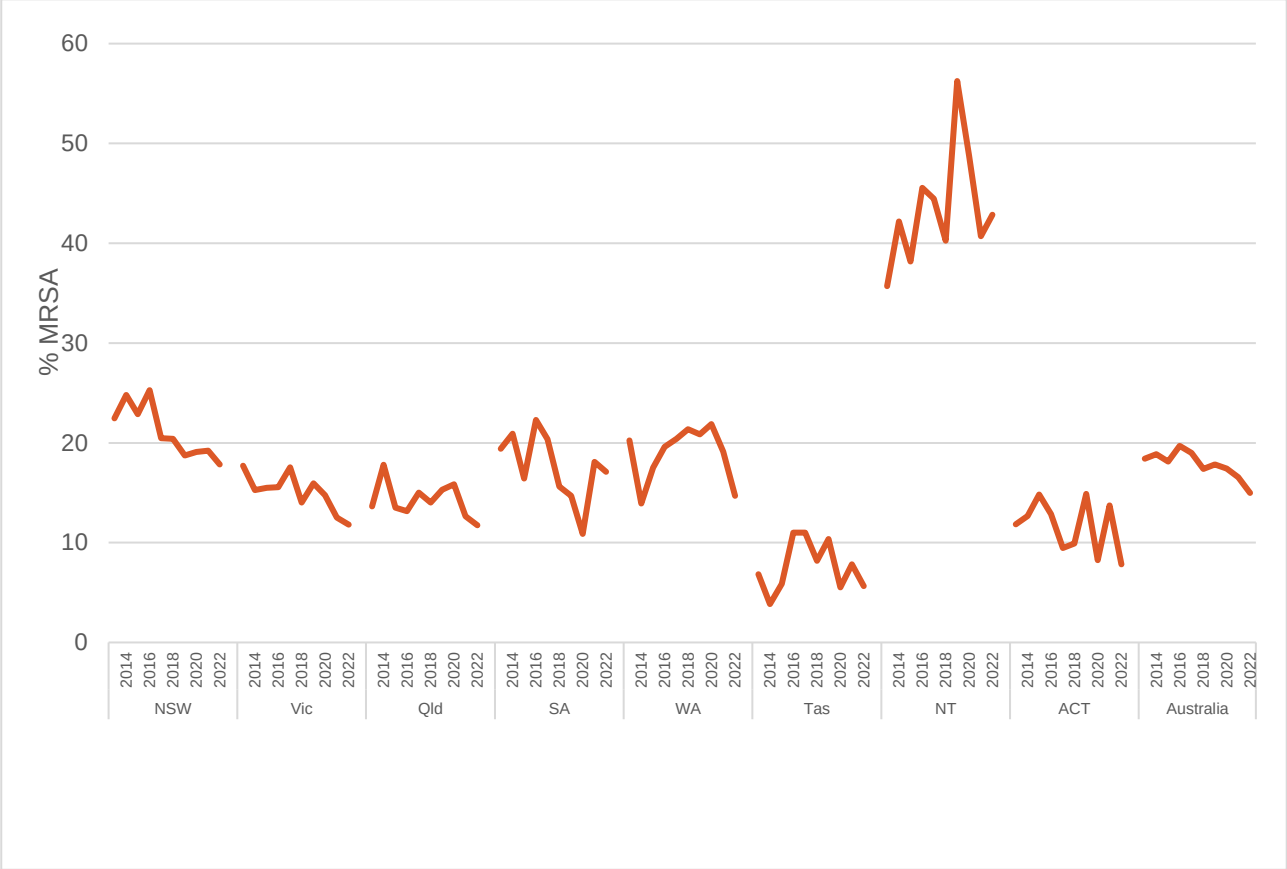
A primary objective of the ASSOP 2022 survey was to determine the proportion of SAB isolates demonstrating resistance to methicillin and other important anti-staphylococcal agents. The following sections describe the major trends observed for the period 2013–2022.

3.10.1. Methicillin-resistant *Staphylococcus aureus*

Since 2016, the proportion of *S. aureus* that was methicillin-resistant began to decline nationally, although there were notable variations at state and territory level (Figure 4). Relative to 2021, there were no statistically significant differences in the proportion of MRSA in the states and territories.

Over the past five years (2018-2022) there was a significantly decreasing trend in MRSA in Australia (χ^2 for linear trend = 8.68, $P < 0.01$), notably in Western Australia (χ^2 for linear trend = 7.17, $P = 0.01$) (Table 17).

Figure 4: Proportion of methicillin-resistant *Staphylococcus aureus*, by state and territory, and nationally, AGAR, 2013–2022



MRSA = methicillin-resistant *Staphylococcus aureus*

Notes:

1. Percentage resistance determined using EUCAST 2023 breakpoints for all years.
2. Number of contributors per year – 2013 and 2014, *n* = 27; 2015, *n* = 36; 2016, *n* = 35; 2017, *n* = 41, 2018, *n* = 41; 2019, n = 46, 2020, *n* = 45, 2021, *n* = 48, 2022, *n* = 55.

Table 17: *Staphylococcus aureus*, percentage resistant to methicillin (EUCAST) and number tested, state and territory, AGAR, 2013–2022

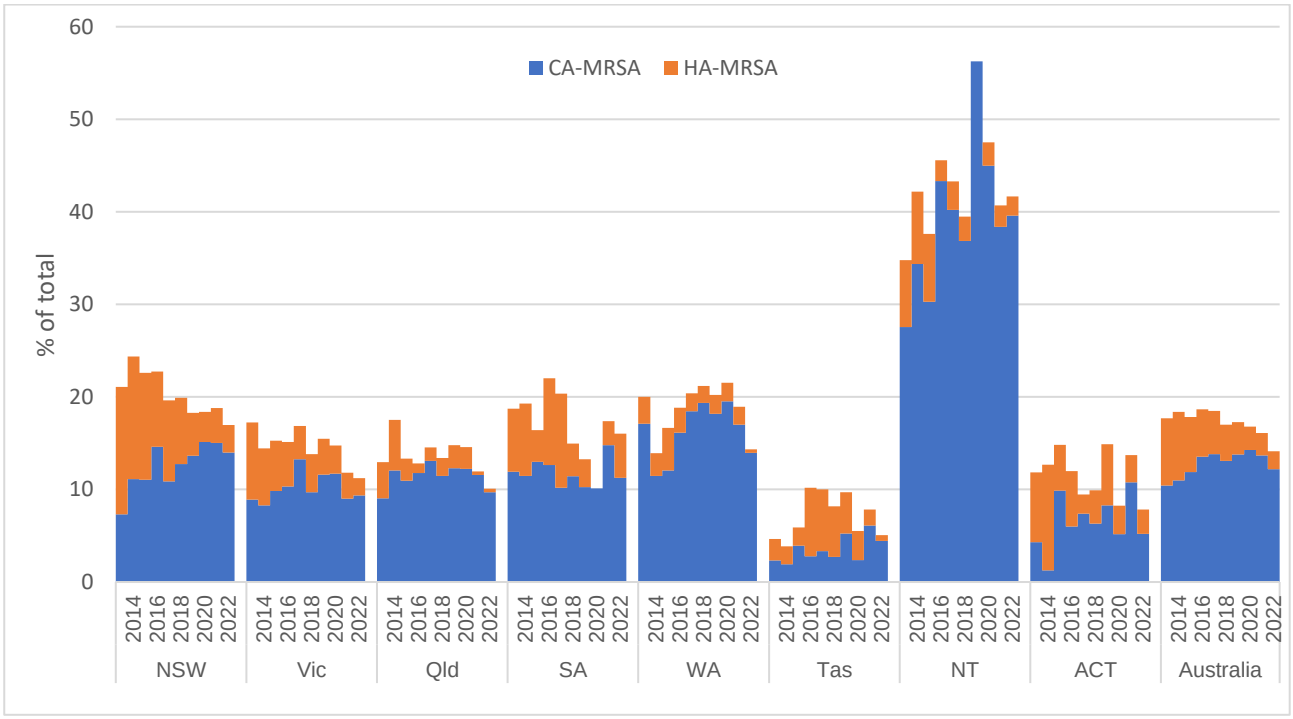
State and territory	Percentage resistant, (*n*) by year										Trend 2018–2022*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	
NSW	22.4 (459)	24.8 (516)	22.9 (590)	25.3 (637)	20.5 (679)	20.4 (647)	18.7 (907)	19.1 (807)	19.2 (770)	17.8 (982)	↔
Vic	17.7 (373)	15.3 (426)	15.5 (407)	15.6 (418)	17.5 (365)	14.0 (414)	15.9 (546)	14.8 (461)	12.5 (615)	11.8 (593)	↔
Qld	13.6 (513)	17.8 (550)	13.5 (503)	13.2 (494)	15.0 (553)	14.0 (571)	15.3 (647)	15.9 (473)	12.6 (514)	11.8 (536)	↔
SA	19.4 (237)	20.9 (196)	16.4 (262)	22.3 (278)	20.4 (167)	15.6 (256)	14.7 (238)	10.9 (239)	18.1 (232)	17.1 (234)	↔
WA	20.3 (311)	13.9 (323)	17.5 (394)	19.6 (413)	20.4 (466)	21.4 (487)	20.8 (499)	21.9 (448)	19.1 (513)	14.7 (497)	▼
Tas	6.8 (44)	3.8 (52)	5.9 (51)	11.0 (109)	11.0 (91)	8.2 (110)	10.4 (135)	5.5 (127)	7.8 (115)	5.7 (159)	↔
NT	35.7 (70)	42.2 (64)	38.2 (110)	45.6 (90)	44.4 (99)	40.3 (77)	56.3 (64)	48.8 (82)	40.7 (86)	42.9 (98)	↔
ACT	11.8 (93)	12.7 (79)	14.8 (81)	12.9 (101)	9.5 (95)	9.9 (111)	14.9 (121)	8.2 (97)	13.7 (102)	7.8 (115)	↔
Australia	18.4 (2,100)	18.9 (2,206)	18.1 (2,398)	19.7 (2,540)	19.0 (2,515)	17.4 (2,673)	17.8 (3,157)	17.4 (2,734)	16.6 (2,947)	15.0 (3,214)	▼

* Chi-squared test for trend for past five years (2018–2022), significant decrease ▼ *p*-value <0.05, ↔ no significant difference

Note: Percentage resistance determined using EUCAST 2023 breakpoints for all years.

Since 2013, there were significant increases in the proportion of CA-MRSA clones nationally (χ^2 for linear trend = 8.729, $P < 0.01$); notably in New South Wales (Figure 5). The proportion of HA-MRSA clones significantly declined nationally (χ^2 for linear trend = 190.1, $P < 0.01$), and in all states and territories except for Tasmania.

Figure 5: Proportion of methicillin-resistant *Staphylococcus aureus*, by state and territory and association, AGAR, 2013–2022

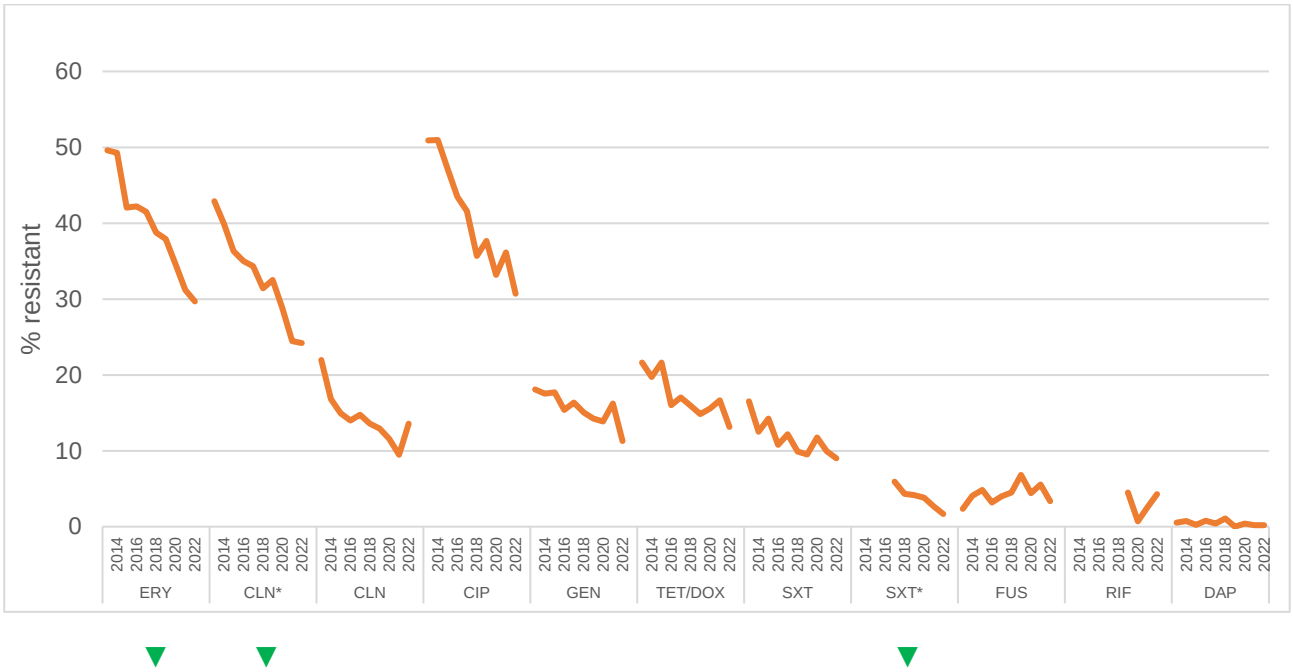


MRSA = methicillin-resistant *Staphylococcus aureus*; CA-MRSA = community-associated MRSA; HA-MRSA = healthcare-associated MRSA

Relative to 2021, the percentage resistance to antimicrobial agents tested against MRSA in 2022 remained stable, except for gentamicin (16.2% in 2021, 11.3% in 2022, P = 0.03).

Rates of resistance in MRSA over the past five years (2018–2022) decreased for erythromycin (χ^2 for linear trend = 13.21, P = <0.01), clindamycin (inducible + constitutive resistance [χ^2 for linear trend = 12.37, P < 0.01] and trimethoprim-sulfamethoxazole (χ^2 for linear trend = 6.82, P < 0.01) (Figure 6).

Figure 6: Methicillin-resistant *Staphylococcus aureus* resistance to key antimicrobials (EUCAST), Australia, AGAR, 2013–2022



CIP = ciprofloxacin; CLN = clindamycin; CLN* = clindamycin (inducible and constitutive); DAP = daptomycin; ERY = erythromycin; EUCAST = European Committee on Antimicrobial Susceptibility Testing; FUS = fusidic acid; GEN = gentamicin; RIF = rifampicin; SXT = trimethoprim–sulfamethoxazole, TET/DOX = tetracyclines (tetracycline, Vitek®; doxycycline, and Phoenix™)

Notes:

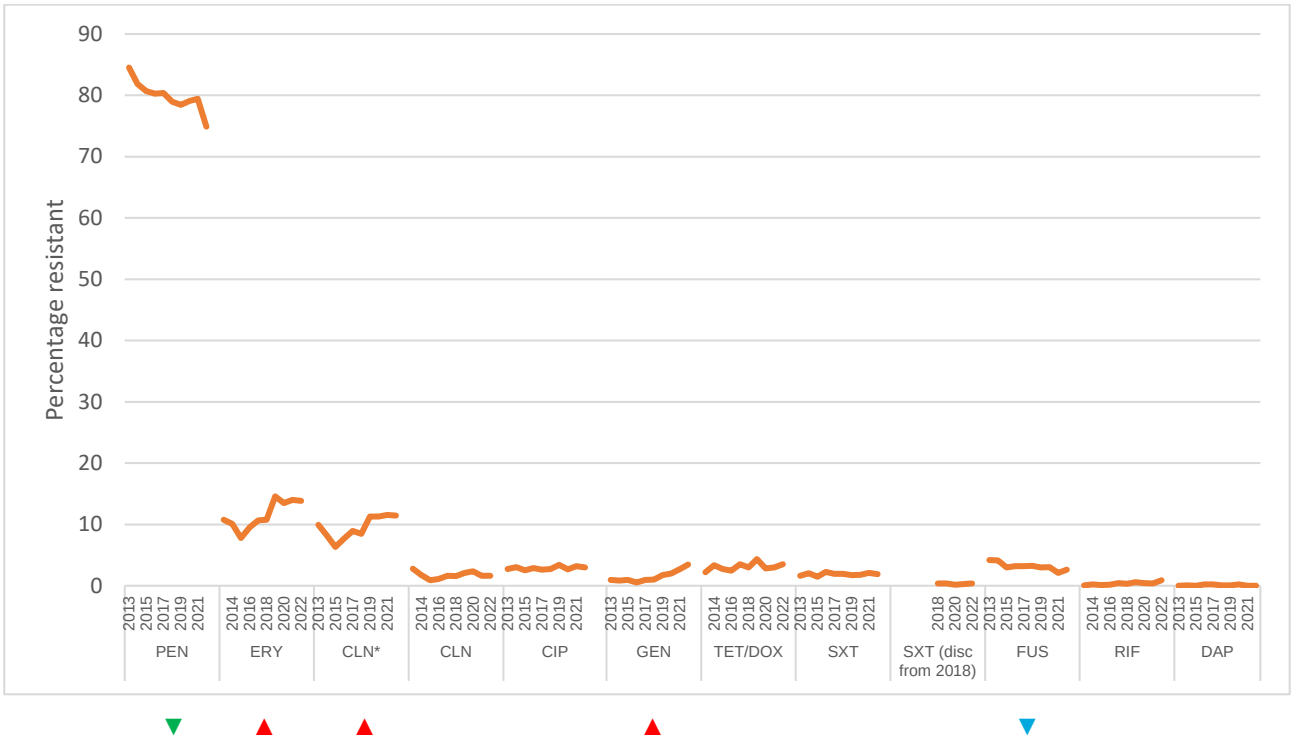
1. Percentage resistance determined using EUCAST 2023 breakpoints for all years.
2. Green arrows indicate antimicrobial agents with significant decrease (P < 0.01) over the past five years (2018 to 2022).
3. Trimethoprim–sulfamethoxazole resistance (as determined by Vitek or Phoenix) was not confirmed by an alternative method in 2013–2015.
4. Rifampicin concentration on the Phoenix™ and one Vitek® card (AST-P612) restricts the ability to accurately determine susceptibility (EUCAST) from 2013 to 2018.

3.10.2 Methicillin-susceptible *Staphylococcus aureus*

The percentage resistance for MSSA in 2022 was similar to 2021 for the antimicrobial agents tested, except for benzylpenicillin (79.4% in 2021, 74.9% in 2022, $P < 0.01$) Figure 7).

Rates of resistance in MSSA over the past five years (2018–2022) increased for gentamicin (χ^2 for linear trend = 39.18, $P < 0.01$), clindamycin (inducible + constitutive) (χ^2 for linear trend = 8.81, $P < 0.01$) and erythromycin (χ^2 for linear trend = 5.28, $P = 0.02$), and decreased for penicillin (adjusted for β-lactamase production) (χ^2 for linear trend = 8.63, $P < 0.01$) and fusidic acid (χ^2 for linear trend = 3.87, $P = 0.05$) (Figure 7).

Figure 7: Methicillin-susceptible *Staphylococcus aureus* resistance to key antimicrobials (EUCAST), Australia, AGAR, 2013–2022



CIP = ciprofloxacin; CLN = clindamycin; CLN* = clindamycin (inducible + constitutive); DAP = daptomycin; ERY = erythromycin; EUCAST = European Committee on Antimicrobial Susceptibility Testing; FUS = fusidic acid; GEN = gentamicin; RIF = rifampicin; SXT = trimethoprim–sulfamethoxazole, TET/DOX = tetracyclines (tetracycline, Vitek®; doxycycline, Phoenix™)

Notes:

1. Percentage resistance determined using EUCAST 2023 breakpoints for all years.
2. Green arrows indicate antimicrobial agents with significant decrease ($P < 0.01$) over the past five years (2018–2022).
3. Red arrows indicate antimicrobial agents with significant increase ($P < 0.05$) over the past five years (2018 to 2022).
4. Blue arrows indicate antimicrobial agents with significant decrease ($P < 0.05$) over the past five years (2018 to 2022).
5. Trimethoprim–sulfamethoxazole resistance (as determined by Vitek or Phoenix) was not confirmed by an alternative method in 2013–2017.
6. Rifampicin concentration on the Phoenix™ and one Vitek® card (AST-P612) restricts the ability to accurately determine susceptibility (EUCAST) from 2013 to 2018.

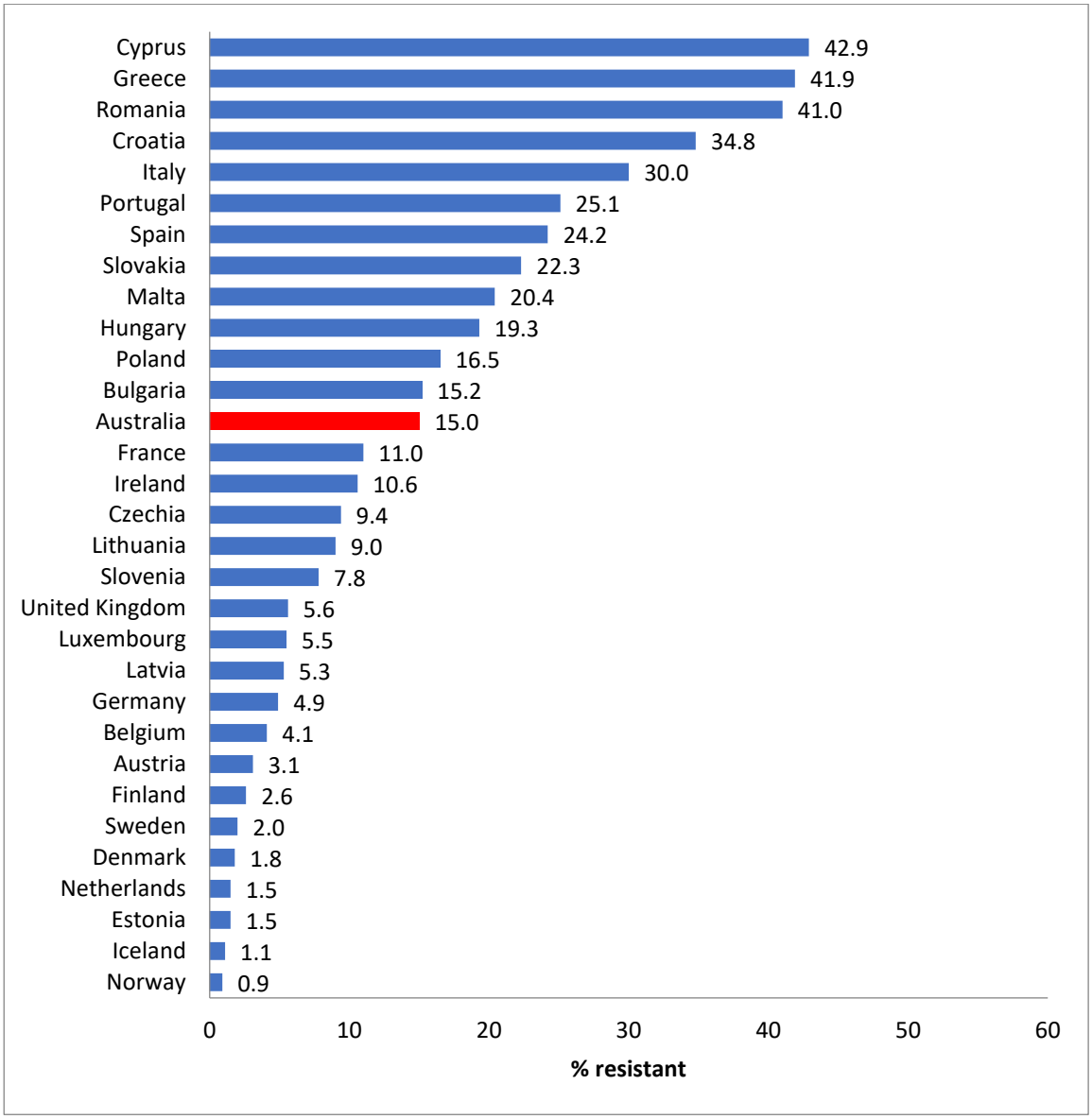
4. International comparisons

Data from AGAR can be compared with data from the EARs-Net program[18], and the World Health Organization (WHO) Central Asian and European Surveillance of Antimicrobial Resistance (CAESAR) network[19], as all these surveillance systems review resistance in bacterial pathogens isolated from blood cultures. Data for 2022 from EARS-Net and CAESAR was not available at the time of this report.

EARS-Net is based on routine clinical antimicrobial susceptibility data from local and clinical laboratories reported to European Centre for Disease and Prevention (ECDC) by appointed representatives from the Member States. The data originate from national AMR surveillance initiatives and/or laboratory networks. Only data from invasive isolates (blood and cerebrospinal fluid) are included in EARS-Net and CAESAR.

Australia ranked thirteenth in the rate of resistance to methicillin in *S. aureus* compared to the thirty-one contributing European countries (Figure 8).

Figure 8: Comparison of *Staphylococcus aureus* rates of resistance to methicillin in Australia (AGAR, 2022) and European countries (2021), blood culture isolates



Source: EARS-Net 2021 (Europe)[20], CAESAR 2021 (United Kingdom)[19]

5. Limitations of the study

Although this study is considered comprehensive in its coverage of Australia, and the methods follow international standards, the data and their interpretation have several limitations:

- The data are not denominator controlled, and there is currently no consensus on an appropriate denominator for such surveys; hospital size, patient throughput, patient complexity and local antibiotic use patterns all influence the types of resistance that are likely to be observed
- Although data have been collected from 55 hospitals across Australia, it is not clear how representative the sample is of Australia as a whole, because the proportion of the population that is served by the laboratories that participate in AGAR is not accurately known. Further, it is likely that the proportion of the population served differs in each state and territory
- Concentration ranges of some antimicrobial agents in both the Vitek® and Phoenix™ cards limit the ability to accurately identify 'susceptible' for some combinations of antimicrobial agents and species
- Data are classified into hospital- and community-onset infections; healthcare-associated community-onset infections may be included in the community-onset group
- Association with relevant mobile genetic element/s (for example, plasmid/s) is not included in this report.

6. Discussion and conclusions

The 2022 AGAR data show that SAB episodes in Australia had their onset overwhelmingly in the community (77.5%). The most frequent principal clinical manifestations were osteomyelitis/septic arthritis and skin and skin structure infections. Strategies to reduce blood stream infections should take this information on clinical manifestation (sources of bacteraemia) into account.

The overall rates of MRSA fell from 16.6% in 2021[21] to 15.0% in the 2022 study. This compares with the 2021 EU/EEA population-weighted mean MRSA percentage of 14.3%, ranging from 0.9% in the Norway to 42.9% in Cyprus.[19, 20]

The rate of community-onset SABs that are methicillin-resistant has remained steady. CA-MRSA clones are an increasing source of hospital-onset bacteraemia (particularly ST93-IV, ST45-V ST5-IV). While HA-MRSA are decreasing significantly, HA-MRSA in particular ST22-IV, were more frequently found in community-onset bacteraemia. The molecular characterisation of MRSA contained within this report aids in identifying opportunities for control of MRSA bacteraemia in the Australian setting.

The rapidly changing picture of MRSA in Australia, drawing from 15 years of AGAR surveillance, is further explored in *Methicillin-resistant Staphylococcus aureus* in Australia. MRSA bacteraemia – *2013 to 2018*.[17] This technical paper will be updated as appropriate by AGAR and the Commission to provide further information on the issue.

In this survey, multidrug resistance did not appear to play a contributory role in the rates of all-cause mortality *S. aureus* bacteraemia.

It should be noted, outbreaks of multidrug-resistant organisms occur in hospitals and other institutional care settings, and substantial transmission occurs before invasive blood stream infections develop. AGAR bacteraemia data need to be assessed with other sources of information to provide broader insights into antimicrobial resistance in Australia. The AURA Surveillance System enables these assessments via Australian Passive AMR Surveillance (APAS) and National Alert System for Critical Antimicrobial Resistances (CARAlert) data, which complement AGAR data.

AGAR surveillance remains core to Australia's response to the problem of increasing AMR. AGAR data contribute to understanding AMR in Australian human health settings, and to informing the national response to AMR. AGAR contributes internationally through annual contribution of data on *S. aureus* from blood to the World Health Organization (WHO) Global Antimicrobial Resistance and Use Surveillance System (GLASS).

Abbreviations

Abbreviation	Term
AGAR	Australian Group on Antimicrobial Resistance
AMR	Antimicrobial resistance
AURA	Antimicrobial Use and Resistance in Australia
APAS	Australian Passive AMR Surveillance
ASA	Australian Society of Antimicrobials
CA-MRSA	Community-associated Methicillin resistant *Staphylococcus aureus*
CARAlert	Critical Antimicrobial Resistances Alert System
CC	Clonal complex
CI	Confidence interval
CO	Community-onset
CLSI	Clinical and Laboratory Standards Institute
EARS-Net	European Antimicrobial Resistance Surveillance Network
EUCAST	European Committee on Antimicrobial Susceptibility Testing
GLASS	Global Antimicrobial Resistance and Use Surveillance System
HA-MRSA	Hospital-associated Methicillin resistant *Staphylococcus aureus*
HO	Hospital-onset
MDR	Multi-drug resistant
MIC	Minimum inhibitory concentration
MLST	Multi-locus sequence type
MRSA	Methicillin resistant *Staphylococcus aureus*
MSSA	Methicillin susceptible *Staphylococcus aureus*
PVL	Panton-Valentine leucocidin
ST	Sequence type
WGS	Whole genome sequencing
WHO	World Health Organization

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Participating members of AGAR:

Hospital	AGAR members
Alfred Hospital, Vic	Adam Jenney and Jacqueline Williams
Alice Springs Hospital, NT	James McLeod
Austin Hospital, Vic	Marcel Leroi and Elizabeth Grabsch
Canberra Hospital, ACT	Peter Collignon and Susan Bradbury
Children's Hospital Westmead, NSW	Alison Kesson and Andrew Jarrett
Concord Hospital, NSW	Thomas Gottlieb and John Huynh
Dandenong Hospital, Vic	Tony Korman and Kathryn Cisera
Fiona Stanley Hospital, WA	Denise Daley and Shakeel Mowlaboccus
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Gold Coast University Hospital, Qld	Petra Derrington and Cheryl Curtis
Gosford Hospital, NSW	Gabrielle O'Kane and Nola Hitchick
Greenslopes Private Hospital, QLD	Jennifer Robson and Marianne Allen
John Hunter Hospital, NSW	Hemalatha Varadhan and Bree Harris
Joondalup Hospital, WA	Shalinie Perera and Ian Meyer
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Liverpool Hospital, NSW	Michael Maley and Helen Ziochos
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Prince of Wales Hospital, NSW	Monica Lahra and Peter Huntington
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Appendix A. Study design

Fifty-five institutions participated in the 2022 survey, forty-eight adult and seven children's hospitals. All states and territories were represented. The hospital peer group/type[22] represented were:

Principal referral hospitals (*n* = 27)
Public acute group A hospitals (*n* = 5)
Children's hospitals (*n* = 6)
Combined Women's and children's hospitals (*n* = 1)
Private acute group A hospitals (*n* = 2)
Private acute group B hospitals (*n* = 1)
Regional and district hospitals from north-west regional Western Australia (*n* = 13)

- Public acute group C hospitals (*n* = 5)
- Public acute group D hospitals (*n* = 6)
- Very small hospitals (*n* = 2)

The 33 laboratories that serviced the hospitals participating in AGAR collected all isolates from different patient episodes of bacteraemia. In patients with more than one isolate, a new episode was defined as a new positive blood culture more than two weeks after the initial positive culture.

An episode was defined as community onset if the first positive blood culture was collected ≤48 hours after admission, and as hospital onset if collected >48 hours after admission.

All laboratories that participated in AGAR obtained basic laboratory information for each patient episode plus varying demographic information, depending on the level at which they are enrolled in the program. There are two levels of enrolment: Bronze and Silver (Table A1). At Bronze level, participating laboratories provided date of collection, date of birth, sex, postcode, and admission date. At Silver level, participating laboratories provided discharge date, device-related infection, principal clinical manifestation, intensive care unit admission, outcome at seven and 30 days, and date of death if appropriate.

Table A1: Level of ASSOP participation of hospitals that contributed data on *Staphylococcus aureus* bacteraemia, by state and territory, 2022

State or territory	Number of hospitals	Level of participation	
		Bronze	Silver
New South Wales	13	1	12
Victoria	8	0	8
Queensland	7	0	7
South Australia	3	0	3
Western Australia	19*	2	17*
Tasmania	2	0	2
Northern Territory	2	1	1
Australian Capital Territory	1	0	1
Total	55	4	51

*Includes 13 regional and district hospitals from northwest Western Australia

Appendix B. Methods

Species identification

Isolates were identified using the routine methods for each institution. These included the Vitek® and Phoenix™ automated microbiology systems, and, if available, mass spectrometry (MALDI - TOF).

Susceptibility testing

Testing was performed using two commercial semi-automated methods: Vitek® 2 (bioMérieux) (*n* = 31) and Phoenix (BD) (*n* = 3), which are calibrated to the ISO (International Organization for Standardization) reference standard method of broth microdilution. Commercially available Vitek 2 (AST-P612 and AST-P656) or Phoenix (PMIC-84) cards were used by all participants throughout the survey period.

The CLSI M100[12] and the EUCAST v13.1[13] breakpoints from January 2023 were used in the analysis.

S. aureus were classified as MRSA if cefoxitin screen positive (Vitek®) or cefoxitin MIC > 4 mg/L (Phoenix™) and *mec*A or SCC*mec* was detected. Cefoxitin screen negative isolates that were oxacillin-resistant underwent *mec*A/nuc PCR or WGS. If mecA or SCCmec was detected, the isolate was reported as MRSA. All *S. aureus* with penicillin MIC ≤ 0.12 mg/L and no β-lactamase results provided were tested for penicillinase by disc diffusion. A sharp zone edge around a penicillin disc (1 unit, EUCAST or 10 unit, CLSI) was recorded as a penicillinase producer.[12, 13]

Additional tests were performed on *S. aureus* to confirm unusual resistances or to provide additional information for antimicrobials where issues have been reported with Vitek/Phoenix panels.[23-25]

- E-test MIC if:
  - Linezolid MIC >4 mg/L, or if MIC not provided
  - Daptomycin MIC > 1 mg/L or if MIC not provided
  - Vancomycin MIC > 2 mg/L or if MIC not provided
  - Teicoplanin MIC > 2 mg/L or if MIC not provided
- High-level mupirocin
  - Mupirocin > 2 mg/L (Vitek AST-P612)
- Trimethoprim/sulfamethoxazole disc (SXT 25 µg)
  - Trimethoprim/sulfamethoxazole resistant (Vitek or Phoenix)

Clinical and outcome data

Device related infection

Device-related bacteraemia is defined as a bacteraemia derived from central (which includes portacaths, PICC lines) or peripheral (venous and arterial) intravascular devices, from catheter-associated urinary tract infection (including nephrostomy tubes and stents), or ventilator-associated respiratory tract infection or bacteraemias associated with biliary stents.

Principal clinical manifestation

For ASSOP surveys, the principal clinical manifestation for each patient episode is categorised as:

- CNS infection (meningitis, abscess (es))
- Deep abscess (es) excluding those in the CNS
- Device-related infection with metastatic focus
- Device-related infection without metastatic focus
- Endocarditis left-sided
- Endocarditis right-sided
- Febrile neutropenia
- No identifiable focus
- Osteomyelitis/septic arthritis

- Other clinical syndrome
- Pneumonia/empyema
- Skin and skin structure infection

Length of hospital stay following bacteraemia
Length of hospital stay following bacteraemia is calculated from the date of blood culture collection to patient discharge or death.

All-cause mortality
All-cause mortality refers to outcome (died, survived, unknown) at 7- and 30-days from blood culture date of collection.

Antimicrobials tested

The antimicrobials tested are shown in Table B1.

Table B1: Antimicrobials available on susceptibility testing cards and interpretive guidelines for CLSI and EUCAST when applied to *Staphylococcus aureus*

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v13.0†		
	S	SDD	I	R	S, SD	S, IE	R
Benzylpenicillin	≤0.12		–§	≥0.25	≤0.125	–§	>0.125
Chloramphenicol	≤8		16	≥32	–#	–#	–#
Ciprofloxacin	≤1		2	≥4	≤0.001	0.002–1	>1
Clindamycin	≤0.5		1–2	≥4	≤0.25	–§	>0.25
Daptomycin	≤1		–#	–#	≤1	–§	>1
Doxycycline (Phoenix™ card)	≤4		8**	≥16**	≤1	–§	**>1**
Erythromycin	≤0.5		1–4	≥8	≤1	–§	**>1**
Fusidic acid	–#		–#	–#	≤1	–§	>1
Gentamicin	≤4		8	≥16	≤2	–§	>2
Linezolid	≤4		–§	≥8	≤4	–§	>4
Oxacillin	≤2		–§	≥4	–#	–#	–#
Quinupristin-dalfopristin	≤1		2	≥4	≤1	–§	**>1**
Rifampicin	≤1		2	≥4	≤0.06‡	–§	>0.06‡
Teicoplanin	≤8		16	≥32	≤2	–§	>2
Tetracycline	≤4		8	≥16	≤1	–§	**>1**
Trimethoprim–sulfamethoxazole	≤2/38		–§	≥4/76	≤2	4	>4
Vancomycin	≤2		4–8	≥16	≤2	–§	>2

CLSI = Clinical and Laboratory Standards Institute; EUCAST = European Committee on Antimicrobial Susceptibility Testing; I = intermediate (CLSI); R = resistant; S = susceptible (CLSI); S, IE = susceptible, increased exposure (EUCAST); S, SD = sensitive, standard dosing (EUCAST); SDD = sensitive dose dependent (CLSI)

Note: Information in **blue** boldface type is new or modified since 2022.

* The breakpoints selected to identify resistance are described in the *Performance Standards for Antimicrobial Susceptibility Testing.* 33rd *ed. CLSI supplement* M100, 2023
† EUCAST breakpoint tables for interpretation of MICs and zone diameters, version 13.1, 2023 (www.eucast.org)
§ No category defined
# No guidelines for indicated species
** The concentration range available on the current Phoenix™ card restricts the ability to identify intermediate and resistant categories
‡ The rifampicin concentration on the Vitek® AST-P612 and Phoenix™ PMIC-84 cards does not allow any category interpretation

Molecular confirmation of resistance

For ASSOP and AESOP WGS was performed by the Antimicrobial Resistance Infectious Diseases (AMRID) Research Laboratory at Murdoch University using the Illumina NextSeq™ 500 platform. The Nullarbor bioinformatic pipeline[26] was used to identify the multi-locus sequence type and Panton-Valentine leucocidin (MRSA). For MRSA SCC*mec* was determined using KmerFinder v3.2 and the SCCmec database curated from the Center for Genomic Epidemiology database (www.genomicepidemiology.org).

Quality control

Quality control strains used were those recommended by CLSI and EUCAST standards.

Data validation

Various checks were made to ensure that the data were valid. These included:

- Null values in the mandatory fields
- Missing MIC data
- Patient age if ≥100 or <0 days
- Confirm dates when:
  - Specimen collected after patient discharged or died
  - Patient discharged or died before admitted
  - Patient admitted before born
  - Patient admitted more than two days after specimen collected
  - Patient admitted more than six months before specimen collected

Appendix C. Susceptibility to antimicrobial agents

Overall percentages of resistance or non-susceptibility for *S. aureus* are shown in Table C1. For some antimicrobials, the concentration range tested did not distinguish between intermediate susceptibility (I) and resistant (R), and the term non-susceptible (NS) was used to describe these isolates.

Table C1: Susceptibility (CLSI and EUCAST) to antimicrobial agents in *Staphylococcus aureus*, by state and territory, 2022

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Benzylpenicillin†										
Staphylococcus aureus	n	974	592	535	234	493	158	98	115	3,199
	%R	81.2, 81.2	77.5, 77.5	75.9, 75.9	80.8, 80.8	80.5, 80.5	69.0, 69.0	88.8, 88.8	67.8, 67.8	78.6, 78.6
Ciprofloxacin										
Staphylococcus aureus	n	974	593	536	234	495	158	98	115	3,203
	%R	10.0, 10.7	7.6, 8.4	2.1, 3.4	8.5, 9.0	3.6, 4.2	1.9, 3.2	3.1, 4.1	4.3, 4.3	6.3, 7.1
Methicillin-resistant *S. aureus*	n	173	70	63	40	73	9	42	9	479
	%R	42.8, 43.9	41.4, 41.4	11.1, 14.3	37.5, 37.5	8.2, 8.2	n/a, n/a	7.1, 7.1	n/a, n/a	29.4, 30.7
Methicillin-susceptible *S. aureus*	n	801	523	473	194	422	149	56	106	2,724
	%R	2.9, 3.5	3.1, 4.1	0.8, 1.9	2.6, 3.1	2.8, 3.6	0.7, 0.7	0.0, 1.8	0.0, 0.0	2.2, 3.0
Clindamycin (inducible + constitutive resistance)										
Staphylococcus aureus	n	974	593	535	234	494	158	98	115	3,201
	%R	12.8, 13.4	11.8, 12.1	14.8, 15.3	6.0, 6.0	10.3, 12.8	12.0, 12.7	26.5, 26.5	16.5, 17.4	12.6, 13.4
Methicillin-resistant *S. aureus*	n	173	70	63	40	73	9	42	9	479
	%R	24.9, 26.6	24.3, 24.3	33.3, 34.9	17.5, 17.5	12.3, 15.1	n/a, n/a	19.0, 19.0	n/a, n/a	23.0, 24.2
Methicillin-susceptible *S. aureus*	n	801	523	472	194	421	149	56	106	2,722
	%R	10.2, 10.6	10.1, 10.5	12.3, 12.7	3.6, 3.6	10.0, 12.4	11.4, 12.1	32.1, 32.1	15.1, 16.0	10.8, 11.5
Daptomycin										
Staphylococcus aureus	n	978	593	536	233	497	159	98	115	3,209
	%NS/%R	0.1, 0.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Methicillin-resistant *S. aureus*	n	174	70	63	40	73	9	42	9	480
	%NS/%R	0.6, 0.6	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a, n/a	0.0, 0.0	n/a, n/a	0.2, 0.2
Methicillin-susceptible *S. aureus*	n	804	523	473	193	424	150	56	106	2,729
	%NS/%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Erythromycin										
Staphylococcus aureus	n	919	593	536	233	495	158	98	115	3,147
	%R	16.2, 17.0	15.9, 16.2	15.5, 15.7	17.2, 17.2	11.5, 13.5	12.0, 12.7	26.5, 26.5	17.4, 20.0	15.5, 16.3
Methicillin-resistant *S. aureus*	n	172	70	63	40	73	9	42	9	478
	%R	29.7,	31.4,	36.5,	40.0,	16.4,	n/a,	19.0,	n/a,	28.7,

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
		31.4	31.4	36.5	40.0	19.2	n/a	19.0	n/a	29.7
Methicillin-susceptible *S. aureus*	n	747	523	473	193	422	149	56	106	2,669
	%R	13.1, 13.7	13.8, 14.1	12.7, 12.9	12.4, 12.4	10.7, 12.6	11.4, 12.1	32.1, 32.1	16.0, 18.9	13.2, 13.9
Fusidic acid										
Staphylococcus aureus	n	918	593	536	234	495	158	98	115	3,147
	%R	–#, 3.7	–#, 1.9	–#, 3.4	–#, 3.4	–#, 1.8	–#, 1.9	–#, 2.0	–#, 0.9	–#, 2.7
Methicillin-resistant *S. aureus*	n	172	70	63	40	73	9	42	9	478
	%R	–#, 5.2	–#, 2.9	–#, 3.2	–#, 7.5	–#, 0.0	–#, n/a	–#, 0.0	–#, n/a	–#, 3.3
Methicillin-susceptible *S. aureus*	n	746	523	473	194	422	149	56	106	2,669
	%R	–#, 3.4	–#, 1.7	–#, 3.4	–#, 2.6	–#, 2.1	–#, 2.0	–#, 3.6	–#, 0.9	–#, 2.6
Gentamicin										
Staphylococcus aureus	n	974	593	536	234	495	158	98	115	3,203
	%R	2.6, 6.3	0.3, 4.9	1.5, 3.4	2.6, 2.6	0.6, 2.8	0.6, 1.3	0.0, 12.2	2.6, 5.2	1.5, 4.6
Methicillin-resistant *S. aureus*	n	173	70	63	40	73	9	42	9	479
	%R	10.4, 20.8	2.9, 7.1	3.2, 4.8	5.0, 5.0	2.7, 4.1	n/a, n/a	0.0, 4.8	n/a, n/a	5.8, 11.3
Methicillin-susceptible *S. aureus*	n	801	523	473	194	422	149	56	106	2,724
	%R	0.9, 3.1	0.0, 4.6	1.3, 3.2	2.1, 2.1	0.2, 2.6	0.7, 1.3	0.0, 17.9	0.9, 2.8	0.7, 3.5
Linezolid										
Staphylococcus aureus	n	978	593	536	234	497	159	98	115	3,210
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Methicillin-resistant *S. aureus*	n	174	70	63	40	73	9	42	9	480
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a, n/a	0.0, 0.0	n/a, n/a	0.0, 0.0
Methicillin-susceptible *S. aureus*	n	804	523	473	194	424	150	56	106	2,730
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0
Mupirocin (high-level)**										
Staphylococcus aureus	n	528	408	536	234	493	115	13	115	2,442
	%R	2.1, 2.1	1.0, 1.0	2.6, 2.6	1.3, 1.3	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	1.3, 1.3
Methicillin-resistant *S. aureus*	n	96	53	63	40	73	8	4	9	346
	%R	3.1, 3.1	1.9, 1.9	4.8, 4.8	0.0, 0.0	0.0, 0.0	n/a, n/a	n/a, n/a	n/a, n/a	2.0, 2.0
Methicillin-susceptible *S. aureus*	n	432	355	473	194	420	107	9	106	2,096
	%R	1.9, 1.9	0.8, 0.8	2.3, 2.3	1.5, 1.5	0.0, 0.0	0.0, 0.0	n/a, n/a	0.0 0.0	1.2, 1.2
Oxacillin/methicillin										
Staphylococcus aureus	n	982	593	536	234	497	159	98	115	3,214
	%R	17.8, 17.8	11.8, 11.8	11.8, 11.8	17.1, 17.1	14.7, 14.7	5.7, 5.7	42.9, 42.9	7.8, 7.8	15.0, 15.0
Rifampicin‡										
Staphylococcus aureus	n	973	593	534	234	495	158	98	115	3,200
	%R	0.4, –‡	0.3, –‡	0.6, –‡	0.0, –‡	0.2, –‡	0.6, –‡	0.0, –‡	0.9, –‡	0.4, –‡

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Methicillin-resistant *S. aureus*	n	173	70	63	40	73	9	42	9	479
	%R	0.6, –‡	0.0, –‡	4.8, –‡	0.0, –‡	0.0, –‡	n/a, n/a	0.0, –‡	n/a, n/a	1.0, –‡
Methicillin-susceptible *S. aureus*	n	800	523	471	194	422	149	56	106	2,721
	%R	0.4, –‡	0.4, –‡	0.0, –‡	0.0, –‡	0.2, –‡	0.0, –‡	0.0, –‡	0.9, –‡	0.3, –‡
Teicoplanin										
Staphylococcus aureus	n	977	593	533	234	497	159	98	115	3,206
	%R	0.0, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.1
Tetracycline/doxycycline§§										
Staphylococcus aureus	n	974	593	536	234	495	158	98	115	3,203
	%R	6.0, 7.5	4.6, 4.9	2.6, 3.0	0.9, 4.7	3.8, 4.0	1.3, 1.3	1.0, 2.0	2.6, 5.2	3.9, 5.0
Methicillin-resistant *S. aureus*	n	173	70	63	40	73	9	42	9	479
	%R	19.1, 23.7	15.7, 15.7	6.3, 6.3	0.0, 0.0	4.1, 4.1	n/a, n/a	0.0, 2.4	n/a, n/a	10.9, 13.2
Methicillin-susceptible *S. aureus*	n	801	523	473	194	422	149	56	106	2,724
	%R	3.1, 4.0	3.1, 3.4	2.1, 2.5	1.0, 5.7	3.8, 4.0	1.3, 1.3	1.8, 1.8	1.9, 2.8	2.7, 3.5
Trimethoprim–sulfamethoxazole										
Staphylococcus aureus	n	972	593	536	234	495	158	98	115	3,201
	%R	0.8, 1.0	0.3, 0.3	0.4, 0.4	0.4, 0.4	0.2, 0.2	0.0, 0.0	1.0, 1.0	0.9, 0.9	0.5, 0.6
Methicillin-resistant *S. aureus*	n	172	70	63	40	73	9	42	9	478
	%R	2.9, 2.9	1.4, 1.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	n/a, n/a	2.4, 2.4	n/a, n/a	1.7, 1.7
Methicillin-susceptible *S. aureus*	n	800	523	473	194	422	149	56	106	2,723
	%R	0.4, 0.6	0.2, 0.2	0.4, 0.4	0.5, 0.5	0.2, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.3, 0.4
Vancomycin										
Staphylococcus aureus	n	978	593	536	234	497	159	98	115	3,210
	%R	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0

CLSI = Clinical and Laboratory Standards Institute; EUCAST = European Committee on Antimicrobial Susceptibility Testing; I = intermediate (CLSI) or susceptible, increased exposure (EUCAST); n/a = insufficient numbers (<10) to calculate; NS = non-susceptible (intermediate plus resistant); R = resistant; SDD = sensitive dose dependent (CLSI)

* Category analysed for each organism. If different for CLSI and EUCAST, they are separated by a comma.
† Benzylpenicillin resistance including beta-lactamase producers
§ No category defined
# No breakpoints defined for indicated species
** Mupirocin high-level resistance screen
‡ The rifampicin concentration range on the Phoenix™ card and Vitek® card (AST-P612) restricts the ability to accurately determine susceptibility for EUCAST
§§ The doxycycline concentration range available on the Phoenix card used restricts the ability to accurately identify intermediate and resistant (CLSI) categories