AUSTRALIAN GROUP ON ANTIMICROBIAL RESISTANCE

Australian *Staphylococcus aureus* Surveillance Outcome Program (ASSOP)

Bloodstream Infection Report

2021 Final Report

Contents

Key findings:

Staphylococcus aureus

- A total of 2,928 *Staphylococcus aureus* (*S. aureus*) bacteraemia episodes were reported from 1 January to 31 December 2021, 78.4% of which were community-onset (CO). Of all episodes 16.9% were methicillin resistant.
- The 30-day all-cause mortality was 14.5%. There was no significant difference in mortality for methicillin-resistant *S. aureus* (MRSA) (15.0%) and methicillin-susceptible *S. aureus* (MSSA) (14.4%) or in hospital-onset (HO) (15.8%) and CO (14.1%) bacteraemia.
- The 30-day all-cause mortality for *S. aureus* was significantly lower among children (<18 years) (0.8%, 2/236) compared to adults (16.0%, 342/2,139) $P < 0.01$)
- Osteomyelitis/septic arthritis (22.6%) and skin and skin structure infections (19.0%) were the most common principal clinical manifestations.
- The hospital length of stay was more than 30 days in 23.6% of patients (25.2% in MRSA, 23.2% in MSSA).
- Resistance in MRSA has continued to decline overall, largely due to the substantial decline in the multi-resistant ST239-III clone.
- Community-associated methicillin-resistant *S. aureus* (CA-MRSA) strains were the dominant cause of MRSA bacteraemia.
- Three healthcare-associated methicillin-resistant *S. aureus* (HA-MRSA) clones were identified; the dominant HA-MRSA clone was ST22-IV (EMRSA-15). No HA-MRSA isolates harboured the Panton-Valentine leucocidin (PVL) associated genes.
- The majority of EMRSA-15 bacteraemias were community-onset.
- Sixty-seven CA-MRSA clones were identified; the dominant CA-MRSA clone was ST93-IV (Queensland clone).
- Overall, 37.9% 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; it is now the most common CA-MRSA clone in Queensland, South Australia, Western Australia and the Northern Territory.
- The multi-resistant ST45-V CA-MRSA clone remains prominent in New South Wales, Victoria and the Australian Capital Territory and is associated with both CO and HO infections.

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 antimicrobial resistance in *Staphylococcus aureus*. The scope broadened over time to include studies on *Escherichia coli, Enterobacter species, Klebsiella species, Haemophilus influenzae, Streptococcus pneumoniae* and *Enterococcus species*. It now concentrates on the 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 the European Antimicrobial Resistance Surveillance Network, enabling benchmarking and trend projections. AGAR has collected ongoing data on the prevalence of antimicrobial resistance in Australia over a long period using standardised methods.

This report presents analyses of antimicrobial resistance (AMR) associated with episodes of *S. aureus* bacteraemia (blood stream infection) that were reported by 30 participating Australian public and private laboratories servicing 48 hospitals across Australia in 2021.

The 48 hospitals that currently contribute to AGAR, including five private hospitals, are listed in Table 1. In 2021, three hospitals, two from Queensland and one from New South Wales were unable to participate due to staff shortages as a result of the COVID-19 pandemic and one new hospital from Victoria contributed data.

AGAR publishes detailed annual reports on each program on its website (www.agargroup.org.au), and also 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, 2021

State or territory	Hospital
New South Wales	Children's Hospital Westmead
	Concord Repatriation General Hospital
	John Hunter Hospital
	Liverpool Hospital
	Nepean Hospital
	Royal North Shore 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
	Prince Charles Hospital§
	Princess Alexandra Hospital§
	Royal Brisbane and Women's Hospital
	Greenslopes Private 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, Carnarvon, Derby, Exmouth, Fitzroy Crossing, Halls Creek, Karratha, Kununurra, Newman, Port Hedland, 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 Pathology Queensland Central Laboratory
# Microbiology services provided by Sullivan Nicolaides Pathology
** Microbiology services provided by SA Pathology, Royal Adelaide Hospital
†† Private 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 a 30-day all-cause mortality of 20.6%. 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.[9]

AGAR began surveillance of antimicrobial resistance 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 2021 was to determine the proportion of SAB isolates demonstrating antimicrobial resistance with particular emphasis on:

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

2. Summary of methods

Forty-eight hospitals, in each state and territory of Australia, were enrolled in the 2021 AGAR programs. The AGAR laboratories collected all isolates from unique patient episodes of bacteraemia from 1 January 2021 to 31 December 2021. 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 of 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 the blood culture was collected, the organism isolated (genus and species), and the antimicrobial susceptibility test results (minimum inhibitory concentrations) 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 dates of admission and discharge were recorded. Depending on the laboratory's level of participation, limited clinical and outcome data were also provided. These included 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® 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–Ed32[12] and the European Committee on Antimicrobial Susceptibility Testing (EUCAST) v12.0.[13]

2.4. PCR screening and whole genome sequencing

All MRSA were subjected to whole genome sequencing using the Illumina NextSeq™ 500 platform. Data were analysed using the Nullarbor bioinformatic pipeline.[14] The pipeline was used to identify the multi-locus sequence type, SCC*mec* and Panton-Valentine leucocidin in the MRSA isolates.

2.5. Statistical analysis

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 19.7.4 (MedCalc Software, Ostend Belgium).

3. Results

3.1. Isolates recovered

Of 2,928 SAB episodes, 495 (16.9%; 95% confidence interval [CI] 15.6-18.3) were methicillin resistant, ranging from 7.8% (95% CI 5.6 -10.5) in Tasmania to 43.0% (95% CI: 38.6-47.5) in the Northern Territory (Table 2). There was a significant difference in the proportion of MRSA among children (12.0%, 95% CI: 9.3-15.2) and adults (17.4%, 95% CI: 14.2-21.3), *P* = 0.02 (data not shown).

Table 2: Number of each species recovered, by state and territory, AGAR, 2021

Organism	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Total
Staphylococcus aureus	770	615	495	232	513	115	86	102	2,928
methicillin resistant, percent	19.7	12.7	13.1	18.1	19.1	7.8	43.0	13.7	16.9
methicillin susceptible, percent	80.3	87.3	86.9	81.9	80.9	92.2	57.0	86.3	83.1

3.2. Place of onset of bacteraemia

A total of 2,882 (98.4%) 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 (78.4%; 95% CI 76.9-79.9). The proportion of MRSA episodes that were community-onset was lower among children (67.6%, 23/34) than adults (78.5%, 362/461).

Table 3: *Staphylococcus aureus* and methicillin result, by place of onset, AGAR, 2021

Organism	Community-onset % (*n*)	Hospital-onset % (*n*)	Total, 100%
Staphylococcus aureus	78.4 (2,296)	21.6 (632)	2,928
Methicillin resistant	77.8 (385)	22.2 (110)	495
Methicillin susceptible	78.5 (1,911)	21.5 (522)	2,433

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 2,375 episodes (81.1%) (Table 4).

The 30-day all-cause mortality for *S. aureus* was significantly lower among children (0.8%, 2/236) compared to adults (16.0%, 342/2,139) ($P < 0.01$). There was no significant difference in 30-day all-cause mortality between MSSA (14.4%) and MRSA (15.0%) episodes, or between healthcare-associated MRSA (HA-MRSA) (22.6%) and community-associated MRSA (CA-MRSA) (13.5%) clones.

Table 4: Onset setting and 30-day all-cause mortality (blood culture isolates), AGAR, 2021

	Community onset		Hospital onset		Total	
Organism	Number	Deaths % (*n*)	Number	Deaths % (*n*)	Number	Deaths % (*n*)
Staphylococcus aureus	1,843	14.1 (260)	532	15.8 (84)	2,375	14.5 (344)
Methicillin resistant	319	12.9 (41)	89	22.5 (20)	408	15.0 (61)
CA-MRSA	261	11.9 (31)	64	20.3 (13)	325	13.5 (44)
HA-MRSA	43	18.6 (8)	20	30.6 (6)	63	22.2 (14)
Methicillin susceptible	1,524	14.4 (219)	443	14.4 (64)	1,967	14.4 (283)

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

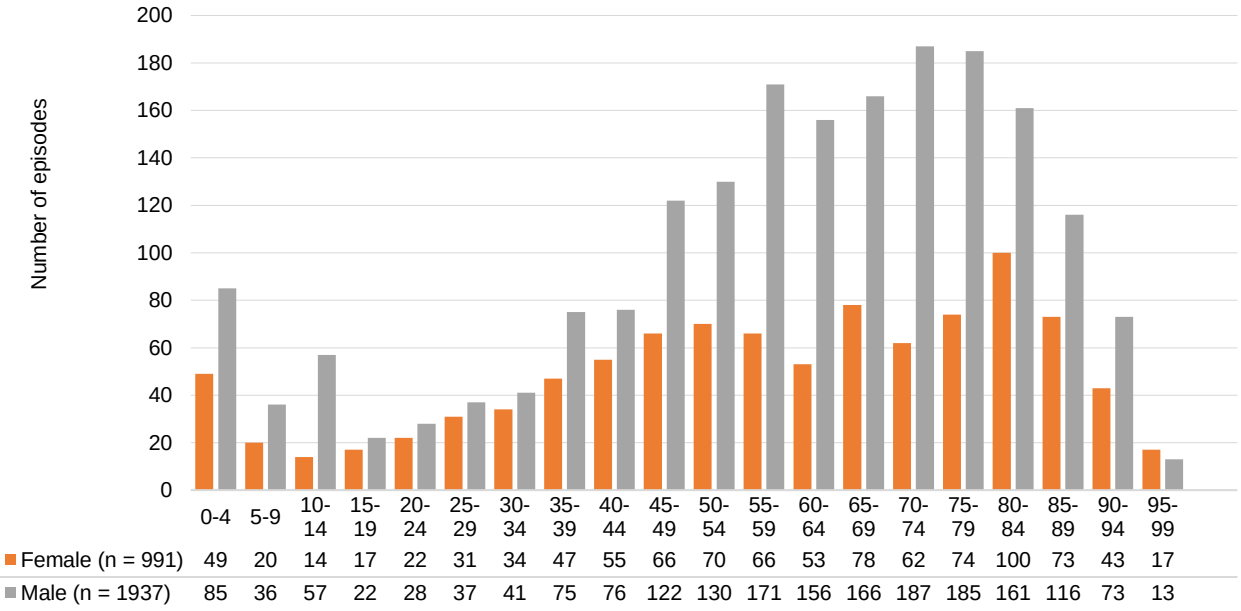
Notes:
Twenty methicillin-resistant *Staphylococcus aureus* were not available for whole genome sequencing.

3.4. Patient age and sex

Age and sex were available for all patients with staphylococcal bacteraemia. The proportion of males was 66.2%.

Increasing age was a surrogate risk factor for bacteraemia (Figure 1); 21.0% of *S. aureus* episodes were in patients aged less than 40 years. The proportion of patients aged 0–19 years was 10.2% (*n* = 300).

Figure 1:
Number of episodes of bacteraemia due to *Staphylococcus aureus*, by patient age group and sex, AGAR, 2021



	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
Female (n = 991)	49	20	14	17	22	31	34	47	55	66	70	66	53	78	62	74	100	73	43	17
Male (n = 1937)	85	36	57	22	28	37	41	75	76	122	130	171	156	166	187	185	161	116	73	13

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.

Staphylococcus aureus

The principal clinical manifestation was known for 2,684 (91.7%) episodes of SAB (Table 5). Overall, the most frequent principal clinical manifestation was osteomyelitis/septic arthritis (22.6%) followed by skin and skin structure infection (19.0%). Almost half (42.8%, 118/276) of the clinical manifestations in children 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 (34.8%, 202/581). Of the community-onset SABs where data were available, the most common principal clinical manifestation was osteomyelitis/septic arthritis (26.3%, 553/2,103).

Table 5: Principal clinical manifestation for *Staphylococcus aureus* bacteraemia, by patient sex, AGAR, 2021

Principal clinical manifestation	Female % (*n*)	Male % (*n*)	Total % (*n*)
Osteomyelitis/septic arthritis	20.2 (183)	23.8 (423)	22.6 (606)
Skin and skin structure infection	17.0 (154)	20.0 (355)	19.0 (509)
Device-related infection without metastatic focus	18.4 (167)	16.0 (285)	16.8 (452)
No identifiable focus	15.1 (137)	11.9 (212)	13.0 (349)
Other clinical syndrome	6.5 (59)	7.9 (140)	7.4 (199)
Endocarditis left-sided	5.0 (45)	6.0 (107)	5.7 (152)
Pneumonia/empyema	4.4 (40)	3.7 (65)	3.9 (105)
Deep abscess(es) excluding those in the CNS	2.9 (26)	4.0 (71)	3.6 (97)
Device-related infection with metastatic focus	2.1 (19)	2.3 (40)	2.2 (59)
Febrile neutropenia	3.3 (30)	1.3 (23)	2.0 (53)
CNS infection (meningitis, abscess(es))	1.8 (16)	2.0 (36)	1.9 (52)
Endocarditis right-sided	3.4 (31)	1.1 (20)	1.9 (51)
Total	907	1,777	2,684

CNS = central nervous system

The most common principal clinical manifestation for methicillin-susceptible *S. aureus* (MSSA) was osteomyelitis/septic arthritis (23.8%, 532/2,233), whereas for MRSA it was skin and skin structure infection (26.4%, 119/451) (Table 6).

Table 6: Principal clinical manifestation for *Staphylococcus aureus* bacteraemia, by methicillin susceptibility, AGAR, 2021

Principal clinical manifestation	Methicillin-resistant % (*n*)	Methicillin-susceptible % (*n*)	Total % (*n*)
Osteomyelitis/septic arthritis	16.4 (74)	23.8 (532)	22.6 (606)
Skin and skin structure infection	26.4 (119)	17.5 (390)	19.0 (509)
Device-related infection without metastatic focus	13.7 (62)	17.5 (390)	16.8 (452)
No identifiable focus	11.1 (50)	13.4 (299)	13.0 (348)
Other clinical syndrome	8.6 (39)	7.2 (160)	7.4 (199)
Endocarditis left-sided	6.4 (29)	5.5 (123)	5.7 (152)
Pneumonia/empyema	4.9 (22)	3.7 (83)	3.9 (105)
Deep abscess(es) excluding those in the CNS	6.0 (27)	3.1 (70)	3.6 (97)
Device-related infection with metastatic focus	1.3 (6)	2.4 (53)	2.2 (59)
Febrile neutropenia	1.3 (6)	2.1 (47)	2.0 (53)
CNS infection (meningitis, abscess(es))	2.2 (10)	1.9 (42)	1.9 (52)
Endocarditis right-sided	1.6 (7)	2.0 (44)	1.9 (51)
Total	451	2,233	2,684

CNS = central nervous system

3.6. Length of hospital stay following bacteraemic episode

Information on length of hospital stay following bacteraemia was available for 2,666 (91.1%) episodes. Overall, 23.6% of patients remained in hospital for more than 30 days (Table 7).

There was no significant difference between MRSA and MSSA and length of hospital stay.

Table 7: Length of hospital stay following *Staphylococcus aureus* bacteraemia, by methicillin susceptibility and place of onset, AGAR, 2021

Species	Length of stay following bacteraemia				Total
	<7 days % (*n*)	7–14 days % (*n*)	15–30 days % (*n*)	>30 days % (*n*)	
Staphylococcus aureus	18.3 (487)	27.4 (731)	30.8 (820)	23.6 (630)	2,666
Methicillin resistant	16.0 (73)	25.6 (117)	33.3 (152)	25.2 (115)	457
Community onset	17.0 (61)	26.4 (94)	34.8 (125)	22.0 (79)	359
Hospital onset	12.2 (12)	23.5 (23)	27.6 (27)	36.7 (36)	98
Methicillin susceptible	18.7 (414)	27.8 (614)	30.2 (668)	23.2 (513)	2,209
Community onset	20.6 (356)	29.7 (512)	28.9 (498)	20.8 (359)	1,725
Hospital onset	12.0 (58)	21.1 (102)	35.1 (170)	31.8 (154)	484

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 in national priority indicator species

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

Table 8: Antimicrobial resistances for *Staphylococcus aureus* using both CLSI and EUCAST breakpoints, AGAR, 2021

Species and antimicrobial	Isolates (*n*)	CLSI		EUCAST	
		Intermediate % (*n*)	Resistant % (*n*)	Susceptible, increased exposure % (*n*)	Resistant % (*n*)
Staphylococcus aureus					
Benzylpenicillin*	2,876	–†	82.9 (2,385)	–†	82.9 (2,385)
Cefoxitin (methicillin)§	2,928	–†	16.9 (495)	–†	16.9 (495)
Ciprofloxacin	2,923	0.6 (18)	8.1 (236)	91.3 (2,669)	8.7 (254)
Clindamycin (constitutive)	2,920	0.1 (2)	2.3 (68)	–†	2.9 (85)
Clindamycin (constitutive + inducible resistance)	2,921	0.1 (2)	12.5 (366)	–†	13.6 (396)
Daptomycin	2,926	–†	0.0 (1)	–†	0.0 (1)
Erythromycin	2,922	27.2 (796)	15.8 (461)	0.6 (17)	16.3 (477)
Fusidic acid	2,923	–**	–**	–†	2.6 (77)
Gentamicin	2,923	1.5 (45)	2.1 (61)	–†	4.9 (144)
Linezolid	2,927	–†	0.0 (0)	–†	0.0 (0)
Mupirocin (high-level)‡	2,179	–†	1.1 (25)	–†	1.1 (25)
Rifampicin	2,920	0.1 (2)	0.2 (5)	–§§	0.3 (10)
Teicoplanin	2,913	0.0 (0)	0.0 (0)	–*	0.1 (3)
Tetracycline/doxycycline##	2,923	0.2 (7)##	4.0 (117)	0.7 (21)	4.5 (132)
Trimethoprim/sulfamethoxazole	2,906	0.1 (2)	0.7 (19)	0.1 (4)	0.7 (19)
Vancomycin	2,927	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)

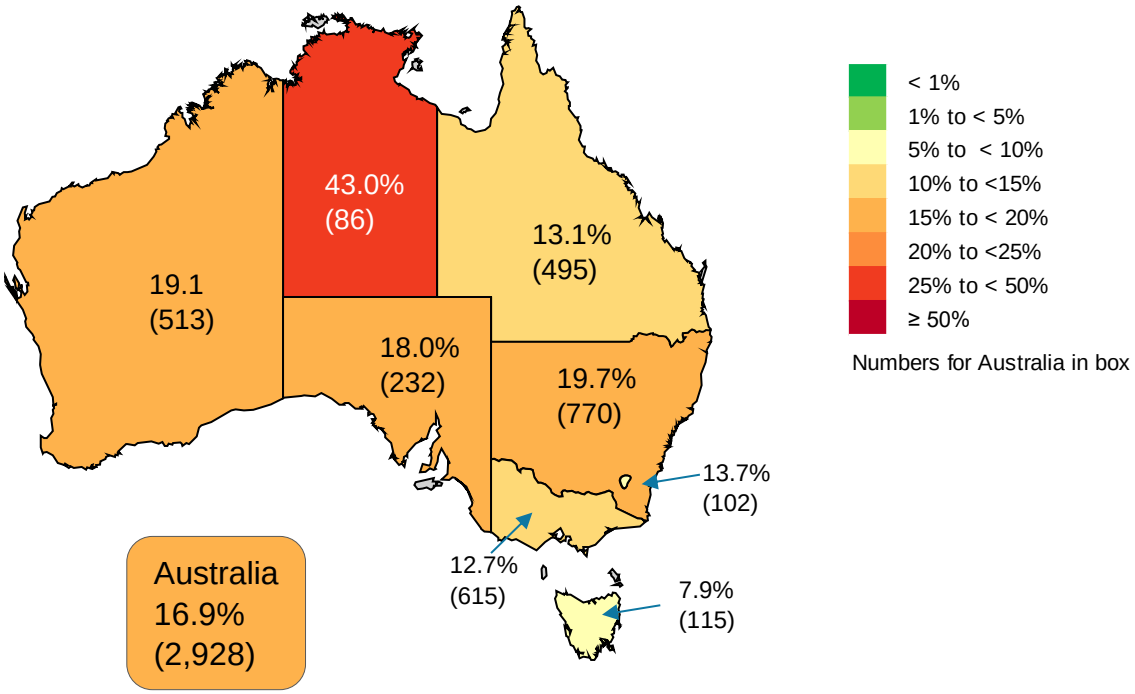
** No guidelines for indicated species (FUSc)

‡ 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

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 resistance as defined by EUCAST to methicillin, Australia, AGAR, 2021



Antimicrobial resistance by place of onset

Antimicrobial resistances using both 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, 2021

	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	2,288	–*	78.8	–*	78.8	631	–*	81.8	–*	81.8
Benzylpenicillin†	2,261	–*	81.9	–*	81.9	615	–*	86.8	–*	86.8
Cefoxitin (methicillin)§	2,296	–*	16.8	–*	16.8	632	–*	17.4	–*	17.4
Ciprofloxacin	2,292	0.8	7.6	91.6	8.4	631	0.0	9.7	90.3	9.7
Clindamycin (constitutive)	2,289	0.0	2.3	–*	2.8	631	0.2	2.5	–*	3.2
Clindamycin (inducible + constitutive resistance)	2,289	0.0	12.6	–*	13.5	631	0.2	12.4	–*	13.6
Daptomycin	2,295	–*	0.0	–*	0.0	631	–*	0.0	–*	0.0
Erythromycin	2,291	26.1	15.3	0.6	15.8	631	31.5	17.4	0.6	18.2
Fusidic acid	2,292	–**	–**	–*	2.6	631	–**	–**	–*	2.9
Gentamicin	2,292	1.5	2.3	–*	5.1	631	1.6	1.3	–*	4.1
Linezolid	2,295	–*	0.0	–*	0.0	632	–*	0.0	–*	0.0
Mupirocin (high-level)‡	1,717	–*	1.3	–*	1.3	462	–*	0.6	–*	0.6
Rifampicin	2,289	0.0	0.2	–§§	0.3	631	0.2	0.2	–§§	0.3
Teicoplanin	2,283	0.0	0.0	–*	0.0	630	0.0	0.0	–*	0.2
Tetracycline/doxycycline##	2,292	0.1	4.0	0.5	4.5	631	0.6	4.0	1.4	4.8
Trimethoprim/sulfamethoxazole	2,279	–*	0.7	0.2	0.7	627	–*	0.6	0.0	0.6
Vancomycin	2,295	0.0	0.0	–*	0.0	632	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 (FUSc)
‡ 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
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.[15] 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 and11. 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, 2021

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	149	50	17	23	60.4	27	15	13	4	0	0	0	0	0	39.6
Vic	78	27	25	14	84.6	6	6	0	0	0	0	0	0	0	15.4
Qld	65	36	9	12	87.7	5	2	1	0	0	0	0	0	0	12.3
SA	39	13	13	7	84.6	4	1	1	0	0	0	0	0	0	15.4
WA	98	70	9	9	89.8	6	1	3	0	0	0	0	0	0	10.2
Tas	9	3	1	2	n/a	3	0	0	0	0	0	0	0	0	n/a
NT	36	20	5	8	91.7	3	0	0	0	0	0	0	0	0	8.3
ACT	13	4	2	3	n/a	1	1	2	0	0	0	0	0	0	n/a
Total	487	223	81	78	78.4	55	26	20	4	**0**	**0**	**0**	**0**	**0**	**21.6**

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, 2021

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	617	490	47	66	97.7	9	2	2	1	0	0	0	0	0	2.3
Vic	536	431	41	46	96.6	15	3	0	0	0	0	0	0	0	3.4
Qld	422	334	23	50	96.4	13	1	1	0	0	0	0	0	0	3.6
SA	182	145	19	16	98.9	2	0	0	0	0	0	0	0	0	1.1
WA	414	337	22	45	97.6	10	0	0	0	0	0	0	0	0	2.4
Tas	105	93	6	6	100.0	0	0	0	0	0	0	0	0	0	0.0
NT	49	39	1	6	93.9	3	0	0	0	0	0	0	0	0	6.1
ACT	87	72	5	9	98.9	1	0	0	0	0	0	0	0	0	1.1
Total	2412	1941	164	244	97.4	53	6	3	1	**0**	**0**	**0**	**0**	**0**	2.6

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 among *Staphylococcus aureus* tested against methicillin, fluoroquinolones and rifampicin, AGAR, 2021

Resistance pattern	N	% of total
Fully susceptible	2333	80.5
Single resistance	390	13.5
Methicillin	312	10.8
Fluoroquinolones	73	2.5
Rifampicin	5	0.2
Resistance to two antimicrobial groups	175	6.0
Methicillin + fluoroquinolones	171	5.9
Methicillin + rifampicin	3	0.1
Fluoroquinolones + rifampicin	1	0.0
Resistance to three antimicrobial groups	1	0.0
Methicillin + fluoroquinolones + rifampicin	1	0.0

Note: Only data from isolates tested against all five antimicrobial groups were included (*n* = 2,899).

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, 2021

Species	Category	Total		Community onset		Hospital onset	
		Number	Deaths, % (n)	Number	Deaths, % (n)	Number	Deaths, % (n)
Staphylococcus aureus	Total	2,350	14.5 (340)	1,823	14.0 (256)	527	15.9 (84)
	Non-MDR (≤2)	2,148	14.1 (303)	1,670	13.8 (230)	478	15.3 (73)
	MDR (>2)	602	15.9 (96)	472	13.8 (65)	136	22.8 (31)

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

Notes:

1. Antimicrobial categories (agents) for each species are listed under Tables 9 and 10. For *Staphylococcus aureus,* anti-staphylococcal β-lactams (cefoxitin) is also included.

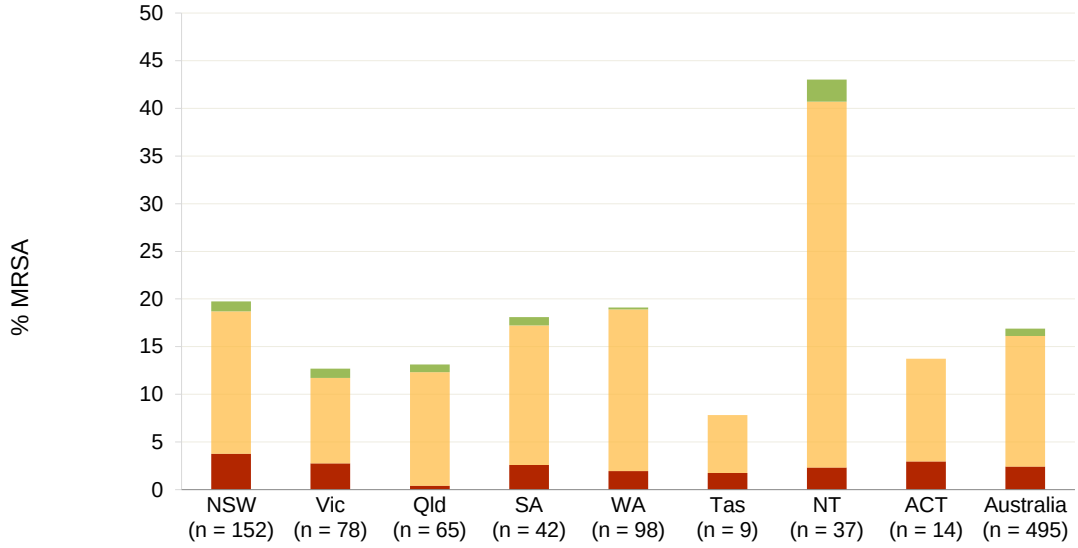
3.9. Whole genome sequencing

This section describes the 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 495 MRSA reported, 472 (95.4%) were available for typing by whole genome sequencing. There were marked differences among the states and territories in the percentage and types of MRSA clones. Prevalence of MRSA ranged from 7.8% (9/115) in Tasmania to 43.0% (37/86) 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, 2021



	NSW (n = 152)	Vic (n = 78)	Qld (n = 65)	SA (n = 42)	WA (n = 98)	Tas (n = 9)	NT (n = 37)	ACT (n = 14)	Australia (n = 495)
Not available (n = 23)	1.0	1.0	0.8	0.9	0.2	0.0	2.3	0.0	0.8
Community associated (n = 401)	14.9	8.9	11.9	14.7	17.0	6.1	38.4	10.8	13.7
Healthcare associated (n = 71)	3.8	2.8	0.4	2.6	1.9	1.7	2.3	2.9	2.4

MRSA = methicillin-resistant *Staphylococcus aureus*

Notes:
1. *S. aureus* were categorised as MRSA based on cefoxitin screen ((Vitek) or cefoxitin MIC (Phoenix).
2. Twenty-three 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, three HA-MRSA clones were identified: ST22-IV (EMRSA-15), ST239-III (Aus 2/3 EMRSA) and ST5-I (Cordoba) (Tables 14 and15).

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

The most frequently isolated HA-MRSA clone, ST22-IV, was identified in all states and territories. ST239-III was identified in two states; New South Wales and South Australia (Table 15).

Community-associated MRSA

Based on the MLST and SCC*mec* type, 67 CA-MRSA clones were identified. There were 40 STs with a single isolate. PVL was detected in 15 CA-MRSA clones. Overall, 37.9% (152/401) of CA MRSA were PVL positive (Table 14). The most frequently isolated CA-MRSA clone, ST93-IV (Qld CA-MRSA), was isolated in all states except Tasmania (Table 16).

Nine PVL positive ST22-IV isolates were identified: three in South Australia, two in Victoria and Queensland, and one each in New South Wales and the Australian Capital Territory. 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.[16]

Of the hospital-onset MRSA, 78.1% (82/105) were caused by CA-MRSA.

Table 14: MRSA clones, association, place of onset and PVL carriage, AGAR, 2021

Clone	Clonal complex	Total, *n*	Community onset, % (*n*)*	Hospital onset, % (*n*)*	PVL positive, % (*n*)*
Healthcare-associated					
ST22-IV (EMRSA-15)	22	64	68.8 (44)	31.3 (20)	0.0 (0)
ST239-III (Aus2/3 EMRSA)	8	6	–† (4)	–† (2)	–† (0)
ST5-I (Cordoba)	5	1	–† (0)	–† (1)	–† (0)
Total HA-MRSA		71	67.6 (48)	32.4 (23)	0.0 (0)
Community-associated					
ST93-IV	93	99	91.9 (91)	8.1 (8)	94.9 (94)
ST45-V	45	62	80.6 (50)	19.4 (12)	0.0 (0)
ST5-IV	5	48	81.3 (39)	18.8 (9)	37.5 (18)
ST1-IV	1	28	75.0 (21)	25.0 (7)	7.1 (2)
ST30-IV	30	20	85.0 (17)	15.0 (3)	80.0 (16)
ST97-IV	97	15	66.7 (10)	33.3 (5)	0.0 (0)
ST22-IV	22	9	–† (5)	–† (4)	–† (9)
ST88-IV	88	8	–† (5)	–† (3)	–† (0)
ST59-IV	59	7	–† (1)	–† (6)	–† (0)
ST6-IV	6	7	–† (6)	–† (1)	–† (3)
ST8-IV	8	7	–† (6)	–† (1)	–† (0)
ST953-IV	97	7	–† (6)	–† (1)	–† (0)
ST72-IV	8	5	–† (4)	–† (1)	–† (0)
ST78-IV	8	5	–† (3)	–† (2)	–† (0)
ST188-IV	188	4	–† (3)	–† (1)	–† (0)
ST6145-V	45	4	–† (3)	–† (1)	–† (0)
ST872-IV	1	4	–† (3)	–† (1)	–† (0)
ST5-V	5	3	–† (2)	–† (1)	–† (0)
ST5-VI	5	3	–† (1)	–† (2)	–† (0)
ST149-IV	5	2	–† (1)	–† (1)	–† (2)
ST2250-IV	2250	2	–† (2)	–† (0)	–† (0)
ST45-IV	45	2	–† (1)	–† (1)	–† (0)
ST59-V	59	2	–† (1)	–† (1)	–† (0)
ST5-unk	5	2	–† (1)	–† (1)	–† (0)
ST7696-V	45	2	–† (2)	–† (0)	–† (0)
ST7709-IV	97	2	–† (2)	–† (0)	–† (0)

ST8-novel	8	2	–† (2)	–† (0)	–† (0)
ST121-V	121	1	–† (1)	–† (0)	–† (0)
ST1232-V	398	1	–† (1)	–† (0)	–† (0)
ST1524-IV	5	1	–† (1)	–† (0)	–† (1)
ST188-V	188	1	–† (0)	–† (1)	–† (0)
ST1-novel	1	1	–† (1)	–† (0)	–† (0)
ST2048-IV	395	1	–† (0)	–† (1)	–† (0)
ST2884-V	88	1	–† (1)	–† (0)	–† (0)
ST3628-V	5	1	–† (1)	–† (0)	–† (1)
ST3921-IV	30	1	–† (1)	–† (0)	–† (0)
ST398-V	398	1	–† (1)	–† (0)	–† (0)
ST4301-IV	22	1	–† (1)	–† (0)	–† (0)
ST508-IV	45	1	–† (0)	–† (1)	–† (0)
ST5213-IV	1	1	–† (0)	–† (1)	–† (0)
ST5662-IV	5	1	–† (1)	–† (0)	–† (0)
ST6149-IV	97	1	–† (1)	–† (0)	–† (1)
ST6151-IV	93	1	–† (1)	–† (0)	–† (0)
ST672-V	672	1	–† (1)	–† (0)	–† (1)
ST6963-IV	22	1	–† (1)	–† (0)	–† (0)
ST72-V	8	1	–† (1)	–† (0)	–† (0)
ST73-IV	5	1	–† (1)	–† (0)	–† (0)
ST7684-IV	6	1	–† (0)	–† (1)	–† (1)
ST7685-V	Singleton	1	–† (1)	–† (0)	–† (0)
ST7697-IV	5	1	–† (1)	–† (0)	–† (1)
ST7698-IV	5	1	–† (1)	–† (0)	–† (0)
ST7699-V	45	1	–† (1)	–† (0)	–† (0)
ST7700-IV	1	1	–† (0)	–† (1)	–† (1)
ST7701-IV	5	1	–† (1)	–† (0)	–† (0)
ST7702-IV	1	1	–† (0)	–† (1)	–† (0)
ST7703-IV	1	1	–† (1)	–† (0)	–† (0)
ST7704-novel	398	1	–† (1)	–† (0)	–† (0)
ST7705-IV	22	1	–† (1)	–† (0)	–† (0)
ST7706-IV	398	1	–† (1)	–† (0)	–† (0)
ST7707-IV	1	1	–† (0)	–† (1)	–† (0)
ST7708-IV	93	1	–† (1)	–† (0)	–† (0)
ST7711-IV	1	1	–† (1)	–† (0)	–† (1)
ST7-IV	7	1	–† (1)	–† (0)	–† (0)
ST80-IV	80	1	–† (0)	–† (1)	–† (0)
ST834-IV	Singleton	1	–† (1)	–† (0)	–† (0)
ST87-IV	59	1	–† (1)	–† (0)	–† (0)
ST88-novel	88	1	–† (1)	–† (0)	–† (0)
Total CA-MRSA		401	79.6 (319)	20.4 (82)	37.9 (152)
MRSA typed		472	77.8 (367)	22.2 (105)	32.2 (152)

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, 2021

Clone	Percentage of clone (number)								
	NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
ST22-IV (EMRSA-15)	79.3 (23)	100.0 (17)	–* (2)	–* (5)	100.0 (10)	–* (2)	–* (2)	–* (3)	90.1 (64)
ST239-III (Aus2/3 EMRSA)	17.2 (5)	0.0 (0)	–* (0)	–* (1)	0.0 (0)	–* (0)	–* (0)	–* (0)	8.5 (6)
ST5-1 (Cordoba)	3.4 (1)	0.0 (0)	–* (0)	–* (0)	0.0 (0)	–* (0)	–* (0)	–* (0)	1.4 (1)
Total	**29**	**17**	**2**	**6**	**10**	**2**	**2**	**3**	**71**

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, 2021

	Percentage (*n*)								
Clone	**NSW**	**Vic**	**Qld**	**SA**	**WA**	**Tas**	**NT**	**ACT**	**Australia**
ST93-IV (Qld CA-MRSA)	10.4 (12)	12.7 (7)	30.5 (18)	23.5 (8)	37.9 (33)	–* (0)	60.6 (20)	9.1 (1)	24.7 (99)
Number PVL positive	12	7	17	7	31	0	20	0	94
Number PVL negative	0	0	1	1	2	0	0	1	5
ST45-V	31.3 (36)	29.1 (16)	5.1 (3)	2.9 (1)	2.3 (2)	–* (0)	0.0 (0)	36.4 (4)	15.5 (62)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	36	16	3	1	2	0	0	4	62
ST5-IV	7.0 (8)	7.3 (4)	16.9 (10)	8.8 (3)	17.2 (15)	–* (3)	15.2 (5)	0.0 (0)	12.0 (48)
Number PVL positive	0	2	0	1	10	2	3	0	18
Number PVL negative	8	2	10	2	5	1	2	0	30
ST1-IV	7.0 (8)	1.8 (1)	10.2 (6)	14.7 (5)	3.4 (3)	–* (2)	6.1 (2)	9.1 (1)	7.0 (28)
Number PVL positive	0	0	2	0	0	0	0	0	2
Number PVL negative	8	1	4	5	3	2	2	1	26
ST30-IV	8.7 (10)	7.3 (4)	3.4 (2)	0.0 (0)	3.4 (3)	–* (1)	0.0 (0)	0.0 (0)	5.0 (20)
Number PVL positive	9	3	1	0	2	1	0	0	16
Number PVL negative	1	1	1	0	1	0	0	0	4
ST97-IV	6.1 (7)	7.3 (4)	5.1 (3)	0.0 (0)	1.1 (1)	–* (0)	0.0 (0)	0.0 (0)	3.7 (15)
Number PVL positive	0	0	0	0	0	0	0	0	0
Number PVL negative	7	4	3	0	1	0	0	0	15
Other clones (n = 61)	29.6 (34)	34.5 (19)	28.8 (17)	50.0 (17)	34.5 (30)	–* (1)	18.2 (6)	45.5 (5)	32.2 (129)
Number PVL positive	5	6	4	4	1	0	1	1	22
Number PVL negative	29	13	13	13	29	1	5	4	107
Total	**115**	**55**	**59**	**34**	**87**	**7**	**33**	**11**	**401**
PVL positive	26	18	24	12	44	3	24	1	152
PVL negative	89	37	35	22	43	4	9	10	249

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 (2013–2021)

3.10.1. Staphylococcus aureus

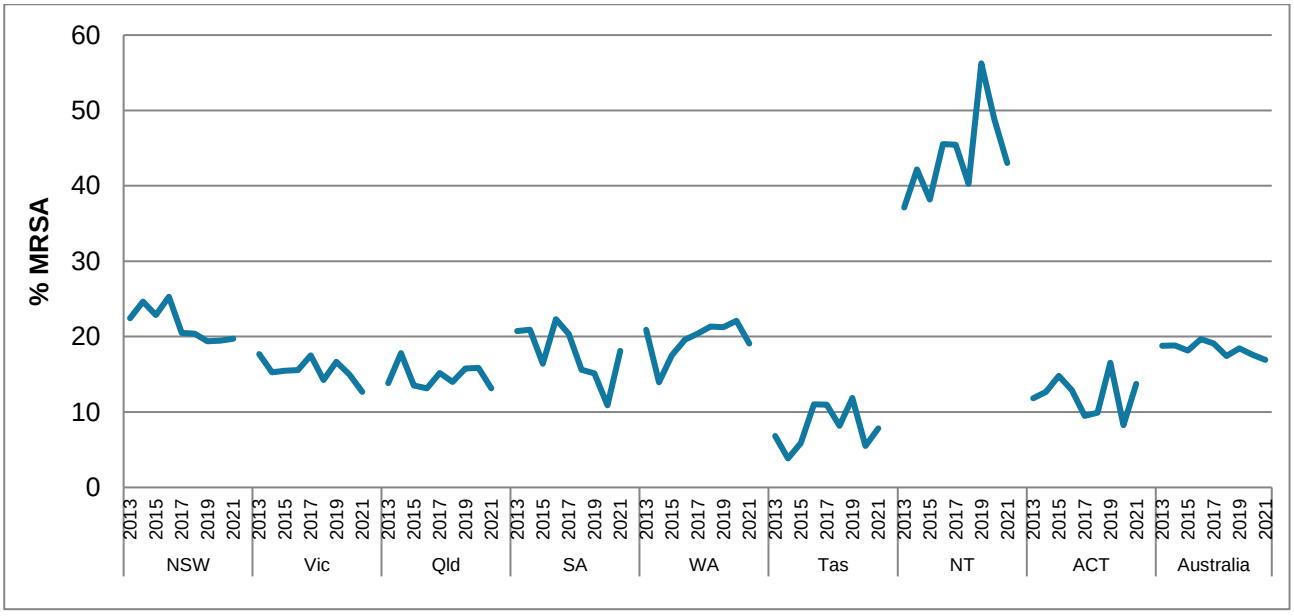
A primary objective of the ASSOP 2021 survey was to determine the proportion of *S. aureus* bacteraemia isolates demonstrating resistance to methicillin and other important anti-staphylococcal agents. The following sections describe the major trends observed for the period 2013–2021.

Methicillin-resistant *Staphylococcus aureus*

The proportion of *S. aureus* that was methicillin resistant throughout Australia remained stable over the years 2013–2021, although there were notable variations at state and territory level (Figure 4). Relative to 2020, there were no significant differences in the proportion of MRSA in the states and territories, except for South Australia (10.9% in 2020, 18.1% in 2021, *P* = 0.03).

Over the past five years (2017-2021) there were no significant trends either nationally or at state/territory level (Table 17).

Figure 4: Proportion of methicillin-resistant *Staphylococcus aureus*, by state and territory, and nationally, AGAR, 2013–2021



MRSA = methicillin-resistant *Staphylococcus aureus*

Notes:

1. Percentage resistance determined using EUCAST 2022 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.

Table 17: *Staphylococcus aureus*, percentage resistant to methicillin (EUCAST) and number tested, state and territory, AGAR, 2013–2021

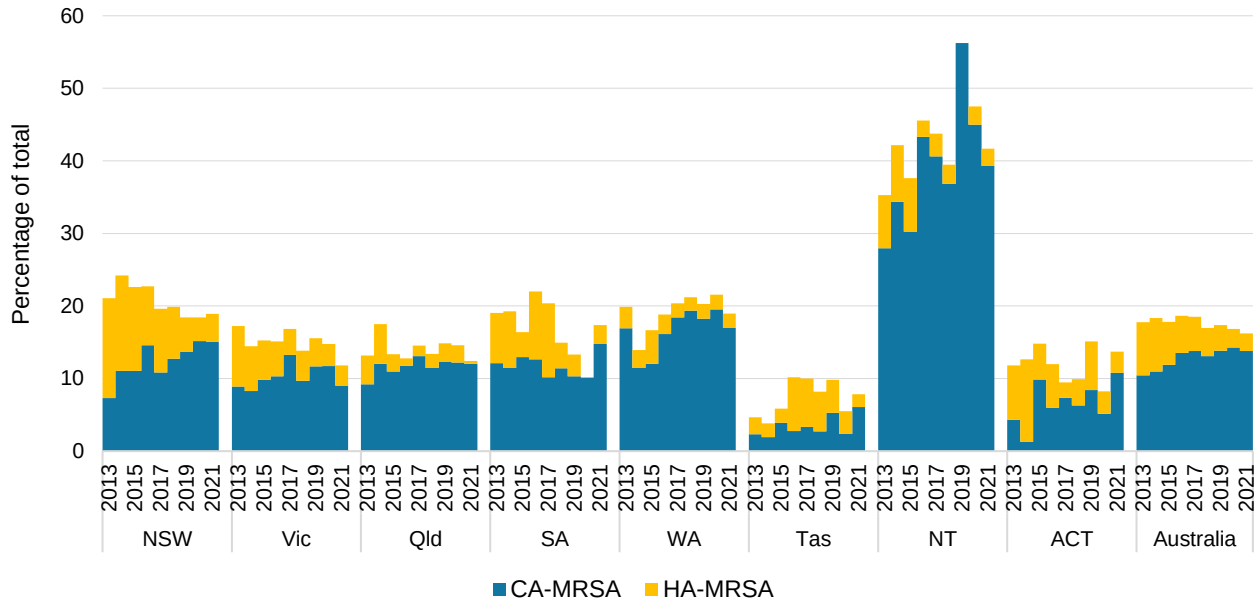
State and territory	Percentage resistant, (*n*) by year									Trend 2017–2021*
	2013	2014	2015	2016	2017	2018	2019	2020	2021	
NSW	22.4 (459)	24.7 (519)	22.9 (590)	25.3 (637)	20.5 (679)	20.4 (647)	19.4 (907)	19.5 (807)	19.7 (770)	↔
Vic	17.7 (373)	15.3 (426)	15.5 (407)	15.6 (418)	17.5 (365)	14.3 (414)	16.7 (546)	15.0 (461)	12.7 (615)	↔
Qld	13.8 (513)	17.8 (550)	13.5 (503)	13.2 (494)	15.2 (553)	14.0 (571)	15.8 (647)	15.9 (473)	13.1 (495)	↔
SA	20.8 (236)	20.9 (196)	16.4 (262)	22.3 (278)	20.4 (167)	15.6 (256)	15.1 (238)	10.9 (239)	18.1 (232)	↔
WA	20.9 (311)	13.9 (323)	17.5 (394)	19.6 (413)	20.4 (466)	21.4 (487)	21.2 (499)	22.1 (448)	19.1 (513)	↔
Tas	6.8 (44)	3.8 (52)	5.9 (51)	11.0 (109)	11.0 (91)	8.2 (110)	11.9 (135)	5.5 (127)	7.8 (115)	↔
NT	37.1 (70)	42.2 (64)	38.2 (110)	45.6 (90)	45.5 (99)	40.3 (77)	56.3 (64)	48.8 (82)	43.0 (86)	↔
ACT	11.8 (93)	12.7 (79)	14.8 (81)	12.9 (101)	9.5 (95)	9.9 (111)	16.5 (121)	8.2 (97)	13.7 (102)	↔
Australia	18.8 (2,099)	18.8 (2,209)	18.1 (2,398)	19.7 (2,540)	19.1 (2,515)	17.4 (2,673)	18.5 (3,157)	17.6 (2,734)	16.9 (2,928)	↔

* Chi-square test for trend for past five years (2017–2021), p-value <0.05, ↔ no significant difference

Note: Percentage resistance determined using EUCAST 2022 breakpoints for all years.

Since 2013, there were significant increases in the proportion of CA-MRSA clones nationally (X^2 for linear trend = 24.07, P < 0.01); notably in New South Wales, Western Australia and the Northern Territory (Figure 5). The proportion of HA-MRSA clones significantly declined nationally (X^2 for linear trend = 149.0, P < 0.01), in all states and territories except for Tasmania.

Figure 5: Proportion of methicillin-resistant *Staphylococcus aureus*, by state and territory and association, AGAR, 2013–2021



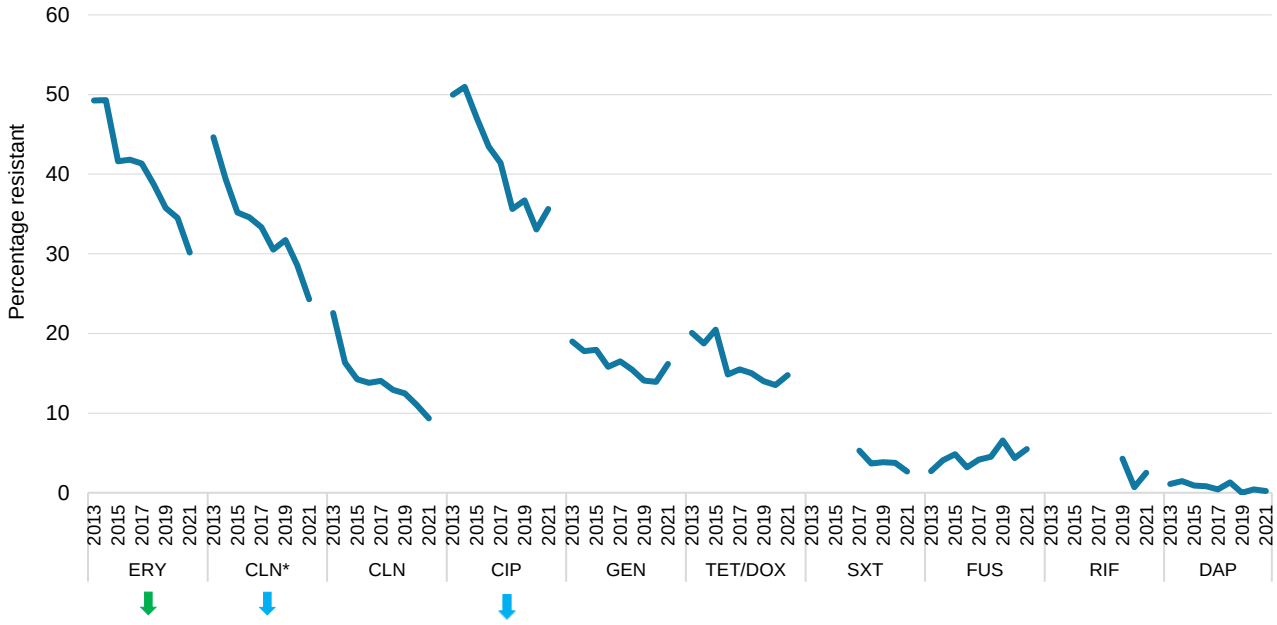
MRSA = methicillin-resistant *Staphylococcus aureus*; CA-MRSA = community-associated MRSA; HA-MRSA = healthcare-associated MRSA

Relative to 2020, the percentage resistance to antimicrobial agents tested against MRSA in 2021 remained stable, except for rifampicin (0.2% in 2020, 0.8% in 2021).

In 2021, one daptomycin-resistant MRSA isolate from Queensland was confirmed (MIC 1.5 mg/L) however no known mutations or resistance genes could be found.

Rates of resistance in MRSA over the past five years (2017–2021) decreased for erythromycin (χ^2 for linear trend = 14.74, *P* = <0.01), clindamycin (inducible + constitutive resistance [χ^2 for linear trend = 11.01, *P* <0.01], ciprofloxacin (χ^2 for linear trend = 4.15, *P* = 0.02) (Figure 6).

Figure 6: Methicillin-resistant *Staphylococcus aureus* resistance to key antimicrobials (EUCAST), Australia, AGAR, 2013–2021



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:

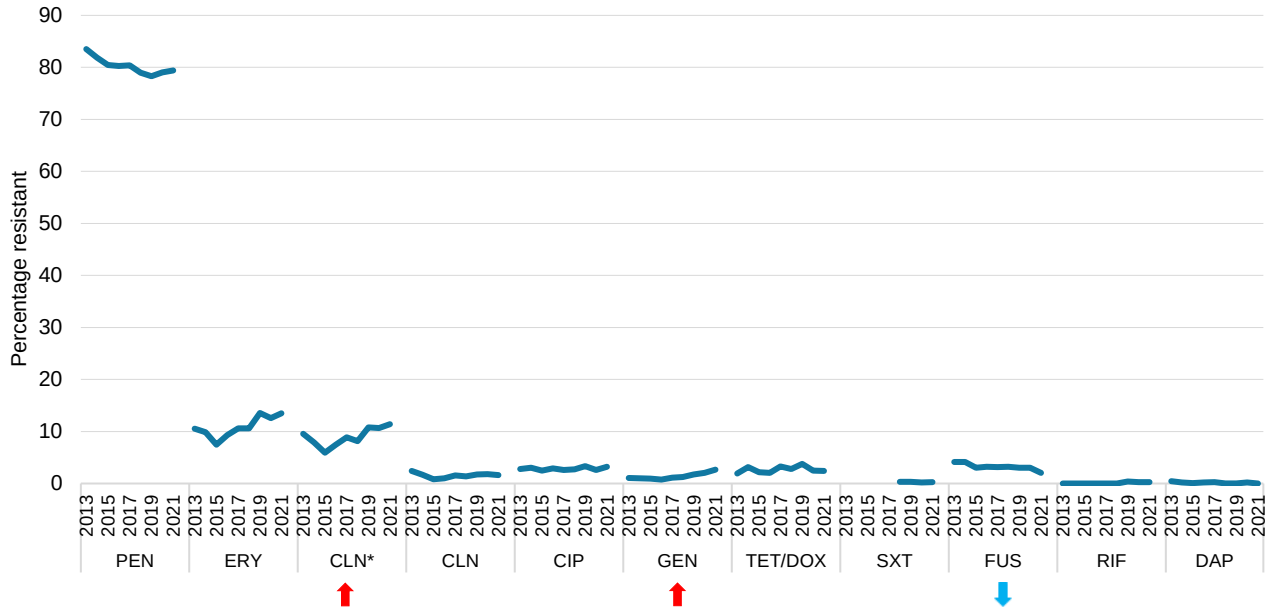
1. Percentage resistance determined using EUCAST 2022 breakpoints for all years.
2. Green arrows indicate antimicrobial agents with significant decrease (*P* < 0.01) over the past five years (2017 to 2021).
3. Blue arrows indicate antimicrobial agents with significant decrease (0.01 < *P* < 0.05) over the past five years (2017 to 2021).
4. Trimethoprim–sulfamethoxazole resistance (as determined by Vitek or Phoenix) was not confirmed by an alternative method in 2013–2016.

Methicillin-susceptible *Staphylococcus aureus*

The percentage resistance for MSSA in 2021 was similar to 2020 for the antimicrobial agents tested, except for fusidic acid (3.0% in 2020, 2.1% in 2021, $P = 0.04$).

Rates of resistance in MSSA over the past five years (2017–2021) increased for clindamycin (inducible + constitutive) (χ^2 for linear trend = 14.08, $P < 0.01$), and gentamicin (χ^2 for linear trend = 26.54, $P < 0.01$) and decreased for fusidic acid (χ^2 for linear trend = 4.90, $P = 0.03$) (Figure 7).

Figure 7: Methicillin-susceptible *Staphylococcus aureus* resistance to key antimicrobials (EUCAST), Australia, AGAR, 2013–2021



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 2022 breakpoints for all years.
2. Red arrows indicate antimicrobial agents with significant increase ($P < 0.05$) over the past five years (2017 to 2021).
3. Blue arrows indicate antimicrobial agents with significant decrease ($P < 0.05$) over the past five years (2017 to 2021).
4. Trimethoprim–sulfamethoxazole resistance (as determined by Vitek or Phoenix) was not confirmed by an alternative method in 2013–2017.

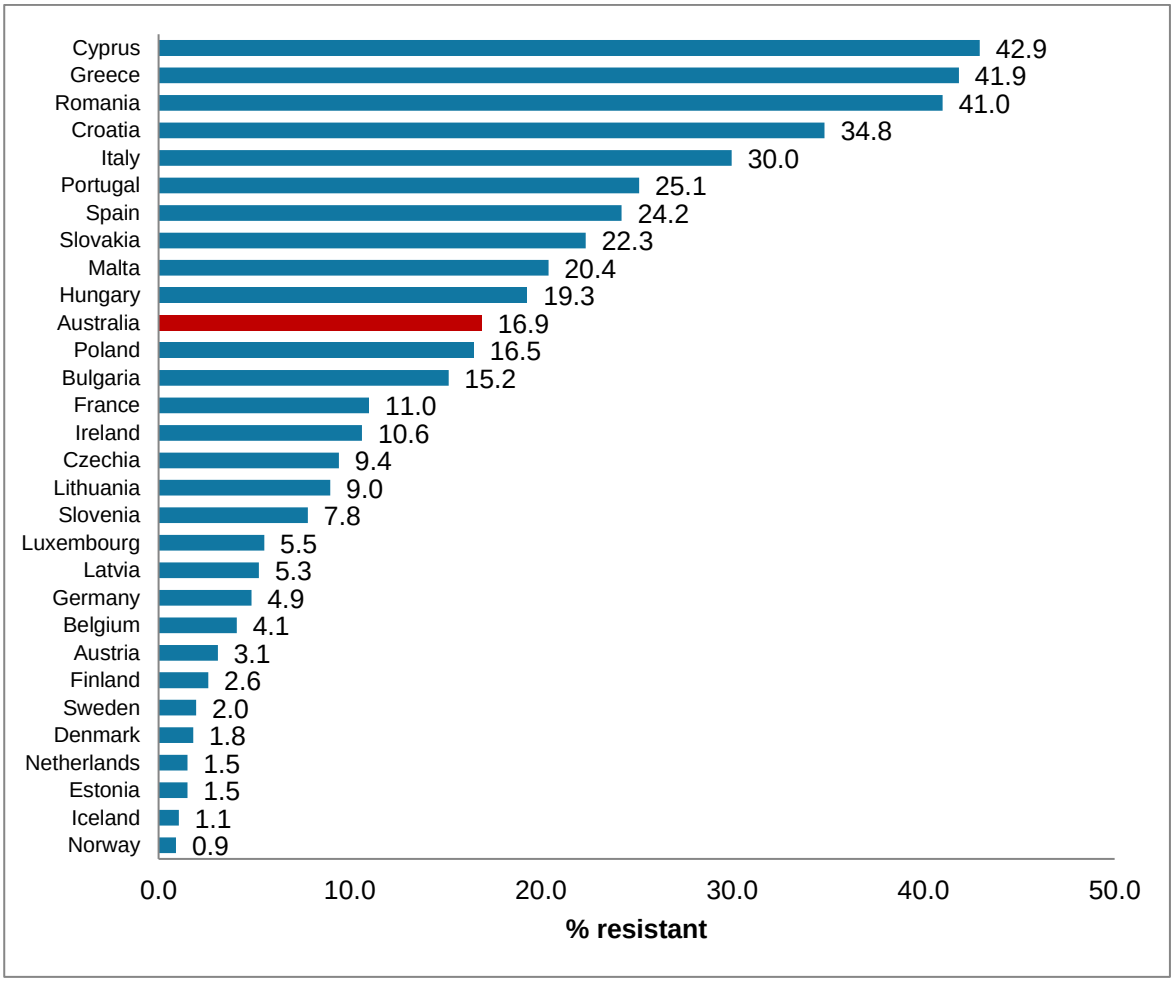
4. International comparisons

Data from AGAR can be compared with data from the European Antimicrobial Resistance Surveillance Network (EARs-Net) program.[17]

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

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

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



EU/EEA = European Union (EU) and European Economic Area (EEA) countries population-weighted mean percentages

Source: EARS-Net (Europe)[17, 18, 21]

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 48 hospitals across Australia, it is not yet 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

AGAR data show that in 2021 episodes of staphylococcal bacteraemia in Australia had their onset overwhelmingly in the community (78.4%). 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 slightly from 17.6% in 2020[19] to 16.9% in the 2021 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.[17, 20, 21]

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 strains 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*.[16] 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 that 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.

It is clear that 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

Abbreviations

Abbreviation	Term
AGAR	Australian Group on 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
CI	Confidence interval
CO	Community-onset
CLSI	Clinical and Laboratory Standards Institute
EUCAST	European Committee on Antimicrobial Susceptibility Testing
HA-MRSA	Hospital-associated Methicillin resistant *Staphylococcus aureus*
HO	Hospital-onset
MDR	Multi-drug resistant
MIC	Minimum inhibitory concentration
MLST	Multi-locus sequence type
WGS	Whole genome sequencing
MRSA	Methicillin resistant *Staphylococcus aureus*
MSSA	Methicillin susceptible *Staphylococcus aureus*
WHO	World Health Organization

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Participating members of AGAR:

Institution	AGAR members
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Alice Springs Hospital, NT	James McLeod
Austin Hospital, Vic	Marcel Leroi and Elizabeth Grabsch
Canberra Hospital, ACT	Peter Collignon and Susan Bradbury
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Concord Hospital, NSW	Thomas Gottlieb and John Huynh
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Appendix A. Study design

Forty-eight institutions participated in the 2021 survey, 42 adult and six children's hospitals. All states and territories were represented. The hospital peer group/type[22] represented were:

Principal referral hospitals (*n* = 25)
Public acute group A hospitals (*n* = 2)
Children's hospitals (*n* = 5)
Combined Women's and children's hospitals (*n* = 1)
Private acute group A hospitals (*n* = 2)
Regional and district hospitals from north-west regional Western Australia (*n* = 11)

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

The laboratories that participated 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.

Table A1: Level of participation of laboratories that contributed data on *Staphylococcus aureus* bacteraemia, by state and territory, 2021

State or territory	Number of institutions	Level of participation	
		Bronze	Silver
New South Wales	10	1	9
Victoria	8	0	8
Queensland	5	0	5
South Australia	3	0	3
Western Australia	17*	2	15*
Tasmania	2	0	2
Northern Territory	2	1	1
Australian Capital Territory	1	0	1
Total	48	4	44

*Includes 11 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* = 27) 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 v12.0[13] breakpoints from January 2022 were used in the analysis.

S. aureus were classified as MRSA if cefoxitin screen positive (Vitek) or cefoxitin MIC > 4 mg/L (Phoenix). Cefoxitin screen negative isolates that were oxacillin resistant underwent mecA/nuc PCR. If mecA 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

Antimicrobial agent	Breakpoint (mg/L)						
	CLSI M100*				EUCAST v12.0†		
	S	SDD	I	R	S, SD	S, IE	R
Benzylpenicillin							
	≤0.12		–§	≥0.25	≤0.125	–§	>0.125
Chloramphenicol (Phoenix card)							
	≤8		16	≥32	≤8	–§	>8
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	2	>2
Erythromycin							
	≤0.5		1–4	≥8	≤1	2	>2
Fusidic acid							
	–#		–#	–#	≤1	–§	>1
Gentamicin							
	≤4		8	≥16	≤2	–§	>2
Linezolid							
	≤4		–§	≥8	≤4	–§	>4
Oxacillin							
	≤2		–§	≥4	–#	–#	–#
Rifampicin							
	≤1		2	≥4	≤0.06‡		>0.06
Teicoplanin							
	≤8		16	≥32	≤2	–§	>2
Tetracycline							
	≤4		8	≥16	≤1	2	>2
Trimethoprim							
	≤8		–§	≥16	–#	–#	–#
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)

* The breakpoints selected to identify resistance are described in the *Performance Standards for Antimicrobial Susceptibility Testing. 32nd ed. CLSI supplement* M100, 2022
† EUCAST breakpoint tables for interpretation of MICs and zone diameters, version 12.0, 2022 (www.eucast.org)
§ No category defined
# No guidelines for indicated species
** The concentration range available on the current Vitek® card restricts the ability to identify the susceptible category. For analysis, breakpoints of ≤4 mg/L for susceptible and ≥8 mg/L for resistant were applied
‡ The rifampicin concentration on the cards restricts category interpretation to non-resistant or resistant

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[14] 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, 2021

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	769	614	447	230	513	115	86	102	2,876
	%R	83.5, 83.5	82.2, 82.2	88.6, 88.6	83.9, 83.9	80.9, 80.9	75.7, 75.7	86.0, 86.0	71.6, 71.6	82.9, 82.9
Ciprofloxacin										
Staphylococcus aureus	n	769	615	495	229	513	114	86	102	2,923
	%R	13.0, 13.4	8.9, 9.8	3.2, 4.6	9.6, 10.0	4.9, 5.1	2.6, 2.6	4.7, 5.8	10.8, 10.8	8.1, 8.7
Methicillin-resistant *S. aureus*	n	152	78	65	41	98	9	37	14	494
	%R	52.6, 53.9	53.8, 55.1	10.8, 10.8	36.6, 36.6	14.3, 14.3	n/a, n/a	8.1, 10.8	64.3, 64.3	34.8, 35.6
Methicillin-susceptible *S. aureus*	n	617	537	430	188	415	105	49	88	2,429
	%R	3.2, 3.4	2.4, 3.2	2.1, 3.7	3.7, 4.3	2.7, 2.9	1.0, 1.0	2.0, 2.0	2.3, 2.3	2.6, 3.2
Clindamycin (inducible + constitutive resistance)										
Staphylococcus aureus	n	769	615	495	228	512	114	86	102	2,921
	%R	13.3, 15.2	11.1, 11.7	15.2, 15.8	7.5, 9.2	12.5, 13.3	8.8, 8.8	17.4, 17.4	14.7, 14.7	12.5, 13.6
Methicillin-resistant *S. aureus*	n	152	78	65	41	98	9	37	14	494
	%R	26.3, 30.3	17.9, 17.9	23.1, 24.6	17.1, 17.1	18.4, 19.4	n/a, n/a	21.6, 21.6	35.7, 35.7	22.7, 24.3
Methicillin-susceptible *S. aureus*	n	617	537	430	187	414	105	49	88	2,427
	%R	10.0, 11.5	10.1, 10.8	14.0, 14.4	5.3, 7.5	11.1, 11.8	4.8, 4.8	14.3, 14.3	11.4, 11.4	10.5, 11.4
Daptomycin										
Staphylococcus aureus	n	769	615	495	231	513	115	86	102	2,926
	%NS§/R	0.0, 0.0	0.0, 0.0	0.2, 0.2	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.0	<0.1, <0.1
Methicillin-resistant *S. aureus*	n	151	78	65	42	98	9	37	14	494
	%NS§/R	0.0, 0.0	0.0, 0.0	1.5, 1.5	0.0, 0.0	0.0, 0.0	n/a, n/a	0.0, 0.0	0.0, 0.0	0.2, 0.2
Methicillin-susceptible *S. aureus*	n	618	537	430	186	415	106	49	88	2,432
	%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	769	615	495	229	512	114	86	102	2,922
	%R	19.0, 19.8	12.8, 13.7	17.2, 17.4	17.5, 17.5	13.1, 13.9	11.4, 11.4	17.4, 17.4	15.7, 15.7	15.8, 16.3

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	152	78	65	41	98	9	37	14	494
	%R	36.8, 37.5	20.5, 21.8	33.8, 33.8	39.0, 39.0	18.4, 19.4	n/a, n/a	21.6, 21.6	35.7, 35.7	29.6, 30.2
Methicillin-susceptible *S. aureus*	n	617	537	430	188	414	105	49	88	2,428
	%R	14.6, 15.4	11.7, 12.5	14.7, 14.9	12.8, 12.8	11.8, 12.6	7.6, 7.6	14.3, 14.3	12.5, 12.5	13.0, 13.5
Fusidic acid										
Staphylococcus aureus	n	769	615	495	229	513	114	86	102	2,923
	%R	–#, 2.5	–#, 2.6	–#, 3.6	–#, 3.1	–#, 2.1	–#, 1.8	–#, 4.7	–#, 0.0	–#, 2.6
Methicillin-resistant *S. aureus*	n	152	78	65	41	98	9	37	14	494
	%R	–#, 7.2	–#, 3.8	–#, 4.6	–#, 9.8	–#, 2.0	–#, n/a	–#, 8.1	–#, 0.0	–#, 5.5
Methicillin-susceptible *S. aureus*	n	617	537	430	188	415	105	49	88	2,429
	%R	–#, 1.3	–#, 2.4	–#, 3.5	–#, 1.6	–#, 2.2	–#, 1.0	–#, 2.0	–#, 0.0	–#, 2.1
Gentamicin										
Staphylococcus aureus	n	769	615	495	229	513	114	86	102	2,923
	%R	4.7, 8.6	0.5, 3.7	0.6, 2.8	3.9, 4.4	1.2, 2.7	0.0, 0.9	2.3, 10.5	2.0, 6.9	2.1, 4.9
Methicillin-resistant *S. aureus*	n	152	78	65	41	98	9	37	14	494
	%R	18.4, 32.2	0.0, 6.4	1.5, 7.7	14.6, 17.1	3.1, 4.1	n/a, n/a	0.0, 10.8	14.3, 42.9	8.1, 16.2
Methicillin-susceptible *S. aureus*	n	617	537	430	188	415	105	49	88	2,429
	%R	1.3, 2.8	0.6, 3.4	0.5, 2.1	1.6, 1.6	0.7, 2.4	0.0, 1.0	4.1, 10.2	0.0, 1.1	0.9, 2.6
Linezolid										
Staphylococcus aureus	n	770	615	494	232	513	115	86	102	2,927
	%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	152	78	65	42	98	9	37	14	495
	%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	0.0, 0.0	0.0, 0.0
Methicillin-susceptible *S. aureus*	n	618	537	429	190	415	106	49	88	2,432
	%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	409	363	495	229	513	68	0	102	2,179
	%R	0.2, 0.2	0.8, 0.8	3.2, 3.2	0.4, 0.4	0.8, 0.8	0.0, 0.0	n/a, n/a	0.0, 0.0	1.1, 1.1
Methicillin-resistant *S. aureus*	n	68	41	65	41	98	3	0	14	330
	%R	0.0, 0.0	0.0, 0.0	3.1, 3.1	2.4, 2.4	0.0, 0.0	n/a, n/a	n/a, n/a	0.0, 0.0	0.9, 0.9
Methicillin-susceptible *S. aureus*	n	341	322	430	188	415	65	0	88	1,849
	%R	0.3, 0.3	0.9, 0.9	3.3, 3.3	0.0, 0.0	1.0, 1.0	0.0, 0.0	n/a, n/a	0.0, 0.0	1.2, 1.2
Oxacillin/methicillin										
Staphylococcus aureus	n	770	615	495	232	513	115	86	102	2,928
	%R	19.7, 19.7	12.7, 12.7	13.1, 13.1	18.1, 18.1	19.1, 19.1	7.8, 7.8	43.0, 43.0	13.7, 13.7	16.9, 16.9
Rifampicin										

Antimicrobial agent and species	Category*	CLSI and EUCAST percentage susceptibility at indicated category								
		NSW	Vic	Qld	SA	WA	Tas	NT	ACT	Australia
Staphylococcus aureus	n	769	615	495	226	513	114	86	102	2,920
	%R	0.1, 0.4	0.0, 0.2	0.4, 0.4	0.0, 0.4	0.2, 0.4	0.0, 0.0	0.0, 0.0	1.0, 1.0	0.2, 0.3
Methicillin-resistant *S. aureus*	n	152	78	65	41	98	9	37	14	494
	%R	0.7, 1.3	0.0, 0.0	1.5, 1.5	0.0, 0.0	0.0, 1.0	n/a, n/a	0.0, 0.0	0.0, 0.0	0.4, 0.8
Methicillin-susceptible *S. aureus*	n	617	537	430	185	415	105	49	88	2,426
	%R	0.0, 0.2	0.0, 0.2	0.2, 0.2	0.0, 0.5	0.2, 0.2	0.0, 0.0	0.0, 0.0	1.1, 1.1	0.1, 0.2
Teicoplanin										
Staphylococcus aureus	n	770	615	481	231	513	115	86	102	2,913
	%R	0.0, 0.1	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.4	0.0, 0.0	0.0, 0.0	0.0, 0.0	0.0, 0.1
Tetracycline/doxycycline‡										
Staphylococcus aureus	n	769	615	495	229	513	114	86	102	2,923
	%NS/R	6.2, 7.5	5.0, 5.0	3.4, 3.4	0.4, 2.6	2.5, 2.5	2.6, 2.6	0.0, 0.0	3.9, 3.9	4.0, 4.5
Methicillin-resistant *S. aureus*	n	152	78	65	41	98	9	37	14	494
	%NS/R	24.3, 28.9	16.7, 16.7	9.2, 9.2	0.0, 7.3	3.1, 3.1	n/a, n/a	0.0, 0.0	21.4, 21.4	12.8, 14.8
Methicillin-susceptible *S. aureus*	n	617	537	430	188	415	105	49	88	2,429
	%NS/R	1.8, 2.3	3.4, 3.4	2.6, 2.6	0.5, 1.6	2.4, 2.4	1.9, 1.9	0.0, 0.0	1.1, 1.1	2.2, 2.4
Trimethoprim–sulfamethoxazole										
Staphylococcus aureus	n	766	615	487	224	513	114	85	102	2,906
	%R	1.2, 1.2	0.2, 0.2	0.0, 0.0	0.9, 0.9	0.4, 0.4	0.0, 0.0	4.7, 4.7	1.0, 1.0	0.7, 0.7
Methicillin-resistant *S. aureus*	n	149	78	65	39	98	9	36	14	488
	%R	4.0, 4.0	0.0, 0.0	0.0, 0.0	2.6, 2.6	2.0, 2.0	n/a, n/a	8.3, 8.3	7.1, 7.1	2.7, 2.7
Methicillin-susceptible *S. aureus*	n	617	537	422	185	415	105	49	88	2,418
	%R	0.5, 1.0	0.2, 0.0	0.0, 0.0	0.5, 0.5	0.0, 0.5	0.0, 0.0	2.0, 6.1	0.0, 1.1	0.2, 0.5
Vancomycin										
Staphylococcus aureus	n	770	615	495	231	513	115	86	102	2,927
	%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; ECOFF = epidemiological cut-off value; 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 doxycycline concentration range available on the Phoenix card used restricts the ability to accurately identify intermediate and resistant (CLSI) categories