AGAR KIDS REPORT
2020 AND 2021

Surveillance Outcome Programs – Bloodstream infections
from patients <18 years, January 2020 – December 2021

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Contents

Acronyms

AGAR	Australian Group on Antimicrobial Resistance
ACT	Australian Capital Territory
AESOP	Australian Enterococcal Surveillance Outcome Program
ASSOP	Australian Staphylococcus aureus Surveillance Outcome Program
AST	Antimicrobial Susceptibility Testing
AURA	Antimicrobial Use and Resistance in Australia
CNS	Central nervous system
ESBL	Extended-spectrum beta lactamase
EUCAST	European Committee on Antimicrobial Susceptibility Testing
GnSOP	Gram-negative Surveillance Outcome Program
IQR	Interquartile range
LoS	Length of stay
MDR	Multi-drug resistant/resistance
MIC	Minimum inhibitory concentration
MLST	Multi-locus sequence typing
MRSA	Methicillin-resistant *Staphylococcus aureus*
MSSA	Methicillin-sensitive *Staphylococcus aureus*
NSW	New South Wales
NT	Northern Territory
PCR	Polymerase chain reaction
SA	South Australia
ST	Sequence type
UTI	Urinary tract infection
VREfm	Vancomycin resistant *Enterococcus faecium*
WA	Western Australia
WGS	Whole genome sequencing
WSPID	World Society for Paediatric Infectious Diseases

Definitions

Term	Definition
All-cause mortality	All-cause mortality refers to outcome at 7- and 30-days from blood culture date of collection.
Child/Paediatric	A patient reported to AGAR who at the time of infection was <18 years of age.
Community-onset	An infection that is present on admission to hospital or within 48 hours
Device-related infection	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 bacteraemia associated with biliary stents.
Hospital-onset	An infection that was not present on admission to hospital and manifested after 48 hours of admission.
Increased exposure (I)*	A microorganism is categorised as "Susceptible, Increased exposure*" when there is a high likelihood of therapeutic success because exposure to the agent is increased by adjusting the dosing regimen or by its concentration at the site of infection.
Multi-drug resistant (MDR)	A bacterial isolate that to resistant to one or more antimicrobial agents in three or more antimicrobial classes
MRSA	Methicillin (oxacillin) resistant *Staphylococcus aureus* were classified as MRSA if cefoxitin screen positive (Vitek®) or cefoxitin MIC > 4 mg/L (Phoenix™) and *mecA* was detected. Cefoxitin screen negative isolates that were oxacillin-resistant underwent *mecA/nuc* PCR. If *mecA* was detected, the isolate was reported as MRSA.
Neonate	A child less than 29 days old
Resistant (R)*	A microorganism is categorised as "Resistant" when there is a high likelihood of therapeutic failure even when there is increased exposure to the agent.
Susceptible (S)*	A microorganism is categorised as "Susceptible, standard dosing regimen", when there is a high likelihood of therapeutic success using a standard dosing regimen of the agent.

* As per EUCAST [1]

1. Summary

There were 25,958 bloodstream isolates from 24,711 patients of all ages reported to the Australian Group on Antimicrobial Resistance (AGAR) from 1 January 2020 to 31 December 2021: 12,725 isolates in 2020 and 13,233 isolates in 2021. Of these, 1,679 isolates were reported from 1,611 paediatric patients (6.5%; aged <18 years): 856 isolates from 826 patients in 2020, and 823 isolates from 785 patients in 2021. Thirty-eight laboratories reported data from patients <18 years to AGAR in 2020-2021; 35 laboratories in each year respectively. Reports came from all states and mainland territories, with the greatest number of reports coming from the most populous states, New South Wales and Victoria.

The most frequently reported bacteraemic species in paediatric patients were *Staphylococcus aureus* and *Escherichia coli*. In all states, *S. aureus* was the most frequently reported isolate. *E. coli* was the second most frequently reported isolate in all states except Queensland where non-Typhoidal *Salmonella* spp. was more frequent. For patients aged <1 year, the most frequent isolate was *E. coli*, whereas in patients aged ≥1 year, the most frequent isolate was *S. aureus*. There were more males than females reported, and an over-representation of patients aged <1 year.

Most patients had a community-onset bacteraemia, but enterococcal bacteraemia in children was more often hospital-onset. The most frequently reported clinical manifestations observed were osteomyelitis/septic arthritis and device-related infections without metastatic focus. A quarter of patients had a bacteraemia that was device-related with the proportion of patients with a device-related bacteraemia higher in 2021 than in 2020. Overall, 10.8% of patients had more than one isolate identified within the same bacteraemic episode. The majority of polymicrobial episodes were reported in children <1 year. Seven- or 30-day mortality was uncommon in paediatric patients with bacteraemia (2.6% and 3.3% respectively).

Overall, there were 902 gram-negative isolates reported from 867 patients aged <18 years in 2020-2021; 800 Enterobacterales, 61 *Pseudomonas aeruginosa* and 41 *Acinetobacter* spp. The most frequently identified Enterobacterales were *E. coli* and the *Klebsiella pneumoniae* complex. A higher number of Enterobacterales episodes were reported in males and patients aged <1 year, and 14.1% of Enterobacterales isolates were from polymicrobial events. Of the Enterobacterales, 12.9% were resistant to third generation cephalosporins, 11.6% to gentamicin/tobramycin and 11.2% to piperacillin-tazobactam. Although only 0.3% of Enterobacterales were resistant to the carbapenems, 14.5% were considered multi-drug resistant (MDR). Twenty percent of *Salmonella* spp. were resistant to the fluroquinolones, whilst only two isolates (2.2%,) were resistant to ceftriaxone. No *Shigella* isolates were reported antimicrobial resistant. For *P. aeruginosa*, although no isolates were gentamicin/tobramycin resistant, 19.7% were resistant to piperacillin-tazobactam, and 13.1% were resistant to antipseudomonal cephalosporins. Only 3.3% (2/61) of *P. aeruginosa* were resistant to the carbapenems and 4.9% were considered MDR. Resistance in paediatric *Acinetobacter* spp bacteraemia was uncommon in children.

Of the 777 gram-positive isolates, 607 were *S. aureus* and 170 were enterococci. There were more *S. aureus* episodes reported in 2020 than in 2021. Overall, 12.9% of *S. aureus* were identified as methicillin-resistant *S. aureus* (MRSA); almost half of the *S. aureus* isolated in the Northern Territory were MRSA. The majority of *S. aureus* episodes were community-onset and from monomicrobial events. Resistance to erythromycin was 13.2%, 12.4% to clindamycin and 5.3% to ciprofloxacin. No

isolates were resistant to trimethoprim/sulfamethoxazole or reported with reduced susceptibility or resistance to vancomycin. Resistance to all antibiotics tested was higher in MRSA than methicillin-sensitive isolates. Overall, 6.5% of *S. aureus* were MDR, of which 65% were MRSA.

Almost three-quarters of all enterococci reported over the two years were *E. faecalis*, with half of reports from patients <1 year old. Enterococcal bacteraemia in patients <1 year were mostly associated with intra-abdominal infections, and febrile neutropenia in patients >1 year old. Ampicillin resistance in enterococci was 19.6%. Eight isolates were reported as vancomycin resistant and three isolates were reported as teicoplanin resistant. Five *E. faecium* isolates were classified as MDR.

From this report we see clear differences in the geographic distribution of pathogens and resistance profiles; gram-negative resistance was more frequently reported in Victoria whilst MRSA was more prevalent in the Northern Territory (NT). Vancomycin resistant *Enterococcus* was uncommon in paediatric bacteraemia. The report aims to be a baseline for understanding paediatric antimicrobial resistance (AMR) across Australia.

2. Background

The AGAR, founded in 1986, performs targeted AMR surveillance on *S. aureus*, *Enterococcus* and key gram-negative bacteraemia episodes across all Australian states and mainland territories. As of 2020, 49 hospitals from all Australian states and mainland territories were reporting data to AGAR [2–4].

AGAR commenced *S. aureus* surveillance in 1986 and for the gram-negative pathogens, *E. coli* and *Klebsiella* species, in 1992. Surveys were conducted biennially until 2008 when annual surveys commenced, alternating between community- and hospital-onset infections. In 2004, *Enterobacter* species was included. In 2013, AGAR commenced the Australian *S. aureus* Surveillance Outcome Program (ASSOP), the Australian Enterococcal Surveillance Outcome Program (AESOP) and the *Enterobacteriaceae* Surveillance Outcome Program (EnSOP) which focused on the AMR and some demographic data on all isolates prospectively collected from patients with bacteraemia. In 2015, *P. aeruginosa* and *Acinetobacter* species were added to the EnSOP, with the program subsequently referred to as the Gram-negative Surveillance Outcome Program (GnSOP) [2–4].

The AGAR reports feed into the key pillar objective #5 "Integrated Surveillance and Response to Resistance and Usage" of the National Antimicrobial Resistance Strategy of Australia [5]. The AGAR reports allow healthcare professionals and policy makers to "use evidence-based surveillance and monitoring data to inform actions and responses to contain antimicrobial resistance" [page 11][5].

Annual reports of the whole population of AGAR are produced. However previous analysis of the AGAR data comparing adult (>18 years) and paediatric (≤18 years) bacteraemia suggests there are lower rates of resistant organisms isolated in children, with different phenotypes and lower mortality rates. In 2018, the World Society for Paediatric Infectious Diseases (WSPID) declared AMR surveillance programs should present neonatal- and paediatric-specific data to assist with strengthening knowledge [6]. Currently age-specific data are not routinely reported in the majority of AMR surveillance programs, making focused paediatric specific interventions difficult [7]. By monitoring paediatric bacteraemia, we are able to provide insight not only into the dynamic

aetiology of bloodstream infection, but the impact of vaccine programs and inform strategies aimed at targeting invasive infections [8].

The key influences on bacteraemia incidence are age, vaccination coverage and exposure to invasive procedures [8]. In previous studies, neonates were often over-represented, reflecting the immaturity of the immune system and the use of invasive devices (e.g., intravenous catheters). Various reports from Australia and Europe suggest there are differences in the AMR burden of various organisms, not only between adults and children, but within different age groups among children. For example, gram-negative MDR organisms were previously found to disproportionately impact children, as demonstrated by a higher odds of death in children with bacteraemia secondary to an extended spectrum beta-lactamase (ESBL) containing organism vs non-ESBL bacteraemia when compared to the same ratio in adults [9]. In a European study, isolates from children <1 year had less AMR than those isolated from children ≥1 year old [7]. In a Scottish study, bacteraemia in children <1 year were more likely to be healthcare associated, whilst bacteraemia in children aged 1-15 years were more often community associated [10]. These findings impact the empiric treatment guidelines and stewardship initiatives, thereby highlighting the value of paediatric-specific reporting of bacteraemia.

3. Methods

3.1. Study Design

Forty-eight hospitals, with representation from each Australian state and mainland territory, were enrolled in the AGAR programs. In the 2020 and 2021 programs, 38 laboratories reported data from patients <18 years; 35 laboratories in each year respectively. From 1 January 2020 to 31 December 2021, laboratories that serviced hospitals participating in AGAR collected all isolates from unique patient episodes of bacteraemia for ASSOP and AESOP, and either all or up to 200 isolates per year for GnSOP. Approval to conduct the prospective data collection, including de-identified demographic data, was given by the research ethics committees associated with each participating hospital.

An episode was defined as a clinical event associated with a positive blood culture irrespective of the number of bacterial species identified. A new episode of bacteraemia in the same patient was recorded if the blood culture was collected more than two weeks after the initial positive culture. An episode was defined as community-onset if the first positive blood culture of the episode was collected 48 hours or less after hospital admission, and as hospital-onset if collected more than 48 hours after admission.

AGAR meets the data security requirements of the Antimicrobial Use and Resistance in Australia (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 unauthorized access, alteration, or loss,
- Ensuring compliance with relevant legislation and policies regarding administration, quality assurance, and data access and release.

3.2. Data collection

Data collected in the AGAR surveillance system from the laboratory for each episode included the patient's date of birth, sex, postcode of residence, date of sample collected, the organism isolated (genus and species), and the antimicrobial susceptibility test (AST) results (minimum inhibitory concentrations [MICs]). If the patient was admitted to hospital, the dates of admission and discharge were recorded. Depending on the level of participation by the healthcare facility, limited clinical and outcome data were also provided, and included the principal clinical manifestation, device-related infection (yes or no), polymicrobial infection (yes or no) and the outcome (died or survived) at seven- and 30-days post bacteraemia (see Appendix 9.1).

For this report, data from AGAR were filtered for patients <18 years (0 – 17 years inclusive).

3.3. Laboratory methods

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

For this report, the following organism complexes were defined:

- *Acinetobacter baumannii* complex: *A. baumannii, A. calcoaceticus, A. dijkshoorniae, A. nosocomialis, A. pittii,* and *A. seifertii*
- *Enterobacter cloacae* complex: *E. cloacae, E. asburiae, E. bugandensis, E. kobei, E. ludwigii, E. hormaechei* and *E. nimipressuralis*
- *Klebsiella pneumoniae* complex: *K. pneumoniae, K. quasipneumoniae* and *K. variicola*
- *Citrobacter freundii* complex: *C. freundii, C. braakii, C. gillenii, C. murliniae, C. rodenticum, C. sedlakii, C. werkmanii* and *C. youngae*

Klebsiella aerogenes was previously known as *Enterobacter aerogenes*.

AST was performed by two commercial semi-automated methods, Vitek® 2 (BioMérieux) or Phoenix™ (Becton Dickinson), which are calibrated to the ISO reference standard method of broth microdilution. Commercially available Vitek® 2 (AST-N246, AST-N410, AST-P612, AST-P643, or AST-P656) or Phoenix™ (NMIC-422, or PMIC-84) cards were used by all participants throughout the survey period.

Additional AST was performed on gram-negative organisms when the following conditions were met:

- *Escherichia coli*, *Klebsiella* spp., *Proteus* spp. or *Salmonella* spp. with ceftazidime or ceftriaxone MIC >1 mg/L, or cefoxitin MIC >8 mg/L,
- any Enterobacterales with cefepime MIC >1 mg/L,
- *Salmonella* spp. with ciprofloxacin MIC >0.25 mg/L,
- Enterobacterales with meropenem MIC >0.125 mg/L (> 0.25 mg/L if tested using Vitek®),
- *P. aeruginosa* or *Acinetobacter* spp. with meropenem MIC > 4 mg/L,
- any isolate with amikacin MIC >32 mg/L
- any isolate with colistin MIC > 4 mg/L

Gram-negative isolates were referred to a central laboratory (Centre for Infectious Diseases and Microbiology, The Westmead Institute for Medical Research). Whole genome sequencing (WGS) was performed on all referred GnSOP isolates at the Antimicrobial Resistance Laboratory, Microbial Genomics Reference Laboratory, Centre for Infectious Diseases and Microbiology and Microbiology Laboratory Services [CIDMLS], Institute of Clinical Pathology and Medical Research [ICPMR], Westmead Hospital using the Illumina NextSeq™ 500 platform. Data were analysed using a modified version of the Nullarbor bioinformatic pipeline.

WGS using the Illumina NextSeq™ 500 platform was performed on all *E. faecium* and MRSA referred to the Antimicrobial Resistance and Infectious Diseases Research Laboratory (AMRID), Murdoch University, WA. Genomic data were analysed using the Nullarbor bioinformatic pipeline. The pipeline was used to identify the multi-locus sequence type (ST) of all isolates, the SCC*mec* type of all MRSA isolates, and the presence of Panton-Valentine leucocidin (PVL) associated genes and *van* gene(s), in the MRSA and *E. faecium* isolates, respectively.

3.4. Data Analysis

The AMR for R package (v2.0) was used to transform MIC data as per EUCAST 2022 (v12) breakpoints [11,12]. Descriptive statistics for description of population and isolates for the overall population and per year were stratified by age, sex, and state/territory where appropriate. Categorical data was assessed using the chi-square or Fisher's exact test. Continuous data was assessed using the Student t-test or the Mann-Whitney U test. In this report, proportions are reported with a decimal point if <10% but not if >10%.

Population variables used the number of patients reported to AGAR for the time period of the report as the denominator when reporting numbers and proportions. Prevalence of resistance to various antibacterial agents are reported overall and by bacterial species and presented as proportions of susceptible (S), susceptible increased exposure (I) or resistant (R) [as is clinically relevant]. Where possible, the population used is reported below each table.

Episodes per 100,000 population were calculated by using the Estimated Resident Population (ERP) from the Australian Bureau of Statistics (ABS) at the mid-point of the three-year time period as the denominator [13].

The definitions used by Magiorakos *et. al.* were applied in this survey for the determination of MDR status, where MDR was defined as resistance to one or more agents in three or more antimicrobial categories [14]. For each species, antimicrobials were excluded from the count if affected by natural resistance mechanisms. Key indicator antibiotics were used for antimicrobial classes in determining MDR status; see Appendix 9.2 for a full list of antibiotics and antimicrobial classes used in this report[1].

When combining results for antimicrobial agents representing an antimicrobial group, the outcome was based on the most resistant result. For example, if the AST result of a bacterial species for imipenem was I and AST result for meropenem was R, then the AST result for the group carbapenems, which comprises imipenem and meropenem, was set as R. Combined AMR was

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[1] Please note the classes used for MDR determination (as per Appendix 9.2) are not the same as those reported in the Drug/Bug combination tables (Appendix 9.10) but are determined especially for AGAR

determined as R to at least one antimicrobial agent in each of the antimicrobial groups in the definition of combined AMR.

Proportions of AMR for a state or territory were only displayed on a map where the number of isolates tested in that state or territory for that drug/microorganism combination was greater than 10. Where the number tested in that state or territory was less than 10, the area is shaded grey on the map, and the proportion is displayed in the table.

When analysing the data for polymicrobial infections, a patient that had a polymicrobial infection reported by the laboratory but for which only one isolate was reported to AGAR, the episode was considered polymicrobial; it is possible the patient was infected with another organism that was not collected in the AGAR programs.

4. Characteristics

4.1. Reports

In 2020-2021, 25,958 isolates from 24,711 bacteraemic episodes were reported to AGAR: 12,725 isolates in 2020 and 13,233 isolates in 2021. Overall, 1,679 isolates were from 1,611 episodes in children: 826 episodes with 856 isolates in 2020, and 785 episodes with 823 isolates in 2021 [Table 1].

Table 1. Number and rate per 100,000 population of isolates and episodes reported per AGAR survey for 2020 and 2021.

	Adults			Children			Total		
	Isolates	Episodes	Episodes/ 100,000	Isolates	Episodes	Episodes/ 100,000	Total isolates	Total Episodes	Episodes/ 100,000
2020									
AESOP	1,135	1,115	5.6	95	93	1.6	1,230	1,208	4.7
ASSOP	2,431	2,408	12.0	303	300	5.3	2,734	2,708	10.5
GnSOP	8,336	7,801	39.0	425	392	6.9	8,761	8,193	31.9
Total	11,902	11,325	56.5	823	785	13.9	12,725	12,110	47.2
2021									
AESOP	1,225	1,209	6.0	75	74	1.3	1,300	1,283	5.0
ASSOP	2,643	2,612	13.0	304	301	5.3	2,947	2,913	11.3
GnSOP	8,509	7,953	39.7	477	451	8.0	8,986	8,404	32.7
Total	12,377	11,775	58.8	856	826	14.6	13,233	12,601	49.1
2020 – 2021									
AESOP	2,360	2,327	11.6	170	167	3.0	2,530	2,493	9.7
ASSOP	5,074	5,064	25.3	607	606	10.7	5,681	5,670	22.1
GnSOP	17,474	16,072	80.3	902	867	15.4	17,747	16,939	66.0
Total	24,279	23,100	115.3	1,679	1,611	28.5	25,958	24,711	96.3

Adults: ≥18 years, Paediatrics: <18 years. AESOP: Australian Enterococcal Surveillance Outcome Program; ASSOP: Australian Staphylococcus aureus Surveillance Outcome Program; GnSOP: Gram-negative Surveillance Outcome Program, Note: the numbers in each survey may not add up to the total column, as some patients are reported across different surveys and thus only counted once in the total. Population data were obtained from the Australian Bureau of Statistics.

Overall, 38 hospitals reported to AGAR Kids in 2020-2021; 35 hospitals in each year respectively. Reports of isolates came from all states and mainland territories, with the greatest number of reports from New South Wales (NSW) (n: 548) and Victoria (n: 456) [Figure 1]. Appendix 9.3 lists reports per hospital/laboratory in 2020-2021.
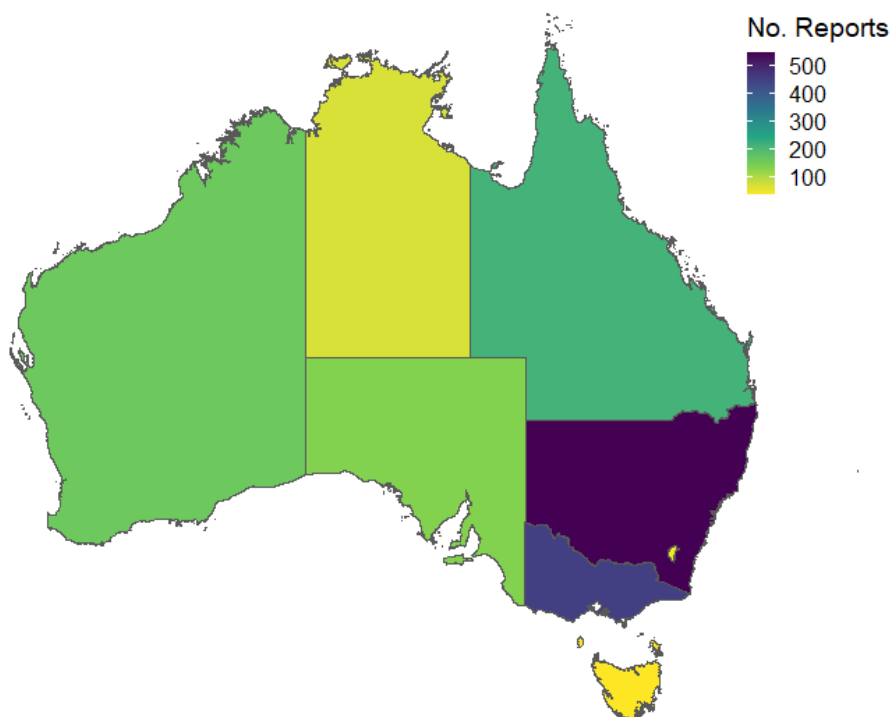
Figure 1. Number of reports in patients <18 years to AGAR, 2020-2021

The most frequently reported species were *S. aureus* (n: 607, 36.2%) and *E. coli* (n: 378, 22.5%) [Table 2]. Whilst in 2020 there were 14 reports of *Salmonella* Typhi, in 2021 there were no reports of *Salmonella* Typhi, presumably due to the closure of the Australian borders during COVID and no endogenous Typhi transmission occurs within Australia. There was an increase in the number of *Salmonella* non-Typhi (22 in 2020, 52 in 2021) and the number of *Serratia marcescens* (six in 2020, 12 in 2021) reported in 2021. A complete list of species reported per year is available in Appendix 9.4.

Table 2. Ten most common organisms reported to AGAR in patients aged <18 years, 2020-2021

Organism	2020	2021	Total [n (%)]	
Staphylococcus aureus	303	304	607	(36.2)
Escherichia coli	163	215	378	(22.5)
Enterococcus faecalis	60	62	122	(7.3)
Klebsiella pneumoniae complex	61	61	122	(7.3)
Enterobacter cloacae complex	60	46	106	(6.3)
Salmonella (non-Typhi)	22	52	74	(4.4)
Pseudomonas aeruginosa	31	30	61	(3.6)
Enterococcus faecium	32	9	41	(2.4)
Klebsiella oxytoca	13	17	30	(1.8)
Acinetobacter baumannii complex	10	8	18	(1.1)

For most jurisdictions, the largest proportion of reports to AGAR in 2020-2021 were the Enterobacterales, except in Western Australia (WA) which reported more *S. aureus* [Table 3]. In all states and mainland territories, *S. aureus* was the most frequently reported species, followed by *E. coli*, except in Queensland where *Salmonella* non-Typhi was more frequently reported. A complete list of organisms per state and territory is provided in Appendix 9.5.

Table 3. Number and proportion of key isolates reported per state and territory in patients <18 years to AGAR, 2020-2021

	Enterobacterales n (%)	*P. aeruginosa* n (%)	*Acinetobacter* n (%)	*S. aureus* n (%)	*Enterococcus* n (%)	Total Reports
ACT	23 (50.0)	0	0	20 (43.5)	3 (6.5)	46
NSW	264 (48.2)	27 (4.9)	16 (2.9)	173 (31.6)	68 (12.4)	548
NT	37 (51.4)	1 (1.4)	3 (4.2)	29 (40.3)	2 (2.8)	72
Qld	99 (45.6)	13 (6.0)	7 (3.2)	88 (40.6)	10 (4.6)	217
SA	56 (41.2)	5 (3.7)	4 (2.9)	57 (41.9)	14 (10.3)	136
Tas	17 (42.5)	1 (2.5)	3 (7.5)	15 (37.5)	4 (10.0)	40
Vic	238 (52.2)	5 (1.1)	3 (0.7)	152 (33.3)	58 (12.7)	456
WA	66 (40.2)	9 (5.5)	5 (3.0)	73 (44.5)	11 (6.7)	164
Total	800 (47.6)	61 (3.6)	41 (2.4)	607 (36.2)	170 (10.1)	1,679

The data in this table is at isolate level. ACT, Australian Capital Territory; NSW, New South Wales; NT, Northern Territory; Qld, Queensland; SA, South Australia; Tas, Tasmania; Vic, Victoria; WA, Western Australia.

For reports from patients aged <1 year, the most common species was *E. coli*, whereas in patients aged ≥1 year, the most common species was *S. aureus* [Table 4]. A complete breakdown of species reported per age group is reported in Appendix 9.6.

Table 4. Five most reported isolates in children <12 months and ≥1 year to AGAR, 2020-2021

Organism	No. reported	% of reports from age group
< 12 months		
Escherichia coli	238	36.7%
Staphylococcus aureus	148	22.8%
Enterococcus faecalis	78	12.0%
Klebsiella pneumoniae complex	43	6.6%
Enterobacter cloacae complex	37	5.7%
1-17 years		
Staphylococcus aureus	459	44.6%
Escherichia coli	140	13.6%
Klebsiella pneumoniae complex	79	7.7%
Enterobacter cloacae complex	69	6.7%
Pseudomonas aeruginosa	50	4.9%

The data in this table is at isolate level

4.2. Age and Sex

There was an over-representation of patients aged <1 year (n: 623; 38.7%) [Figure 2], and overall, 15.2% of episodes were from neonates (n: 244). There were more bacteraemia episodes from males (n:976, 60.6%) than females (n: 635, 39.4%) [Figure 2].
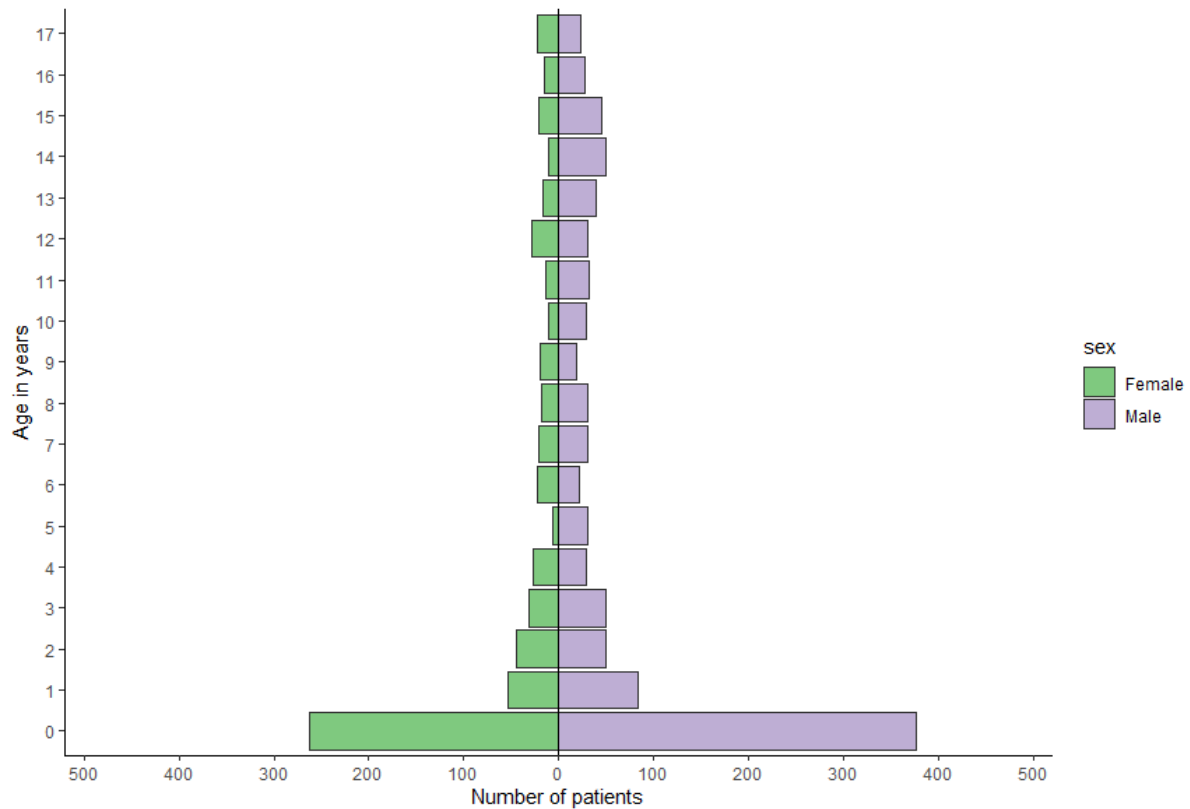
Figure 2. Age and sex of patients aged <18 years with episodes reported to AGAR, 2020-2021

The median age for patients was higher in patients with *S. aureus* than those with enterococcal or gram-negative bacteraemia [Table 5]. For patients with an enterococcal or gram-negative bacteraemia, the majority of episodes were from patients aged <1 year, whereas for *S. aureus* there was an even distribution of episodes over the age groups. In all programs, there were more bacteraemia episodes from male patients [Table 5].

Table 5. Age and sex distribution of patients per survey, AGAR 2020-2021

Characteristic	AESOP	ASSOP	GnSOP	Overall
	n = 167	*n = 601*	*n = 843*	*n = 1,611*
Age *median*	<12 months	6 years	1 year	2 years
IQR	(0, 4)	(1, 11.8)	(0, 7)	(0, 10)
Age group				
0 years	88 (52.7)	147 (23.8)	403 (46.5)	623 (38.7)
≤28 days	38 (22.8)	51 (8.4)	160 (18.5)	244 (15.1)
29-90 days	26 (15.6)	51 (8.4)	104 (11.7)	173 (10.7)
91-364 days	24 (14.4)	45 (7.4)	139 (16.3)	206 (12.8)
1-4 years	38 (22.8)	133 (22.0)	198 (22.4)	359 (22.3)
5-17 years	41 (24.6)	326 (54.2)	266 (31.1)	629 (39.0)
5-11 years	14 (8.4)	174 (29.0)	116 (13.6)	303 (18.8)
12-17 years	27 (16.2)	152 (25.3)	150 (17.4)	326 (20.2)
Sex				
Female	60 (35.9)	208 (34.4)	377 (43.7)	635 (39.4)
Male	107 (64.1)	398 (65.6)	490 (56.3)	976 (60.6)

AESOP: Australian Enterococcal Surveillance Outcome Program; ASSOP: Australian Staphylococcus aureus Surveillance Outcome Program; GnSOP: Gram-negative Surveillance Outcome Program. The data in this table is at patient level.

The mean age per state and territory ranged from 3.2 years in the Australian Capital Territory (ACT), to 5.7 years in Queensland [Table 6]. In the ACT all patients 0 – 364 days old are reported <1 year old [Figure 3].

Table 6. Mean age and age group distribution per state and territory, AGAR 2020-2021

State	Mean	Median age	<12 months	1 – 4 years	5 – 11 years	12+ years
	(SD)	*(IQR)*	*% (n)*	*% (n)*	*% (n)*	*% (n)*
ACT	3.2 (5.2)	0 (5)	56.5 (26)	17.4 (8)	10.9 (5)	15.2 (7)
NSW	4.7 (5.6)	2 (9)	39.2 (215)	24.6 (135)	18.2 (100)	17.9 (98)
NT	5.6 (6.2)	3 (11)	37.5 (27)	18.1 (13)	20.8 (15)	23.6 (17)
Qld	5.7 (5.8)	4 (11)	33.2 (72)	20.3 (44)	22.1 (48)	24.4 (53)
SA	5 (5.7)	2.5 (9.75)	38.2 (52)	21.3 (29)	20.6 (28)	19.9 (27)
Tas	5.5 (5.9)	3 (11)	37.5 (15)	17.5 (7)	22.5 (9)	22.5 (9)
Vic	4.5 (5.7)	1 (9)	41.2 (188)	24.6 (112)	14.5 (66)	19.7 (90)
WA	5.5 (5.7)	3 (11)	32.9 (54)	22.6 (37)	23.2 (38)	21.3 (35)

The data in this table is at patient level. ACT, Australian Capital Territory; NSW, New South Wales; NT, Northern Territory; Qld, Queensland; SA, South Australia; Tas, Tasmania; Vic, Victoria; WA, Western Australia.
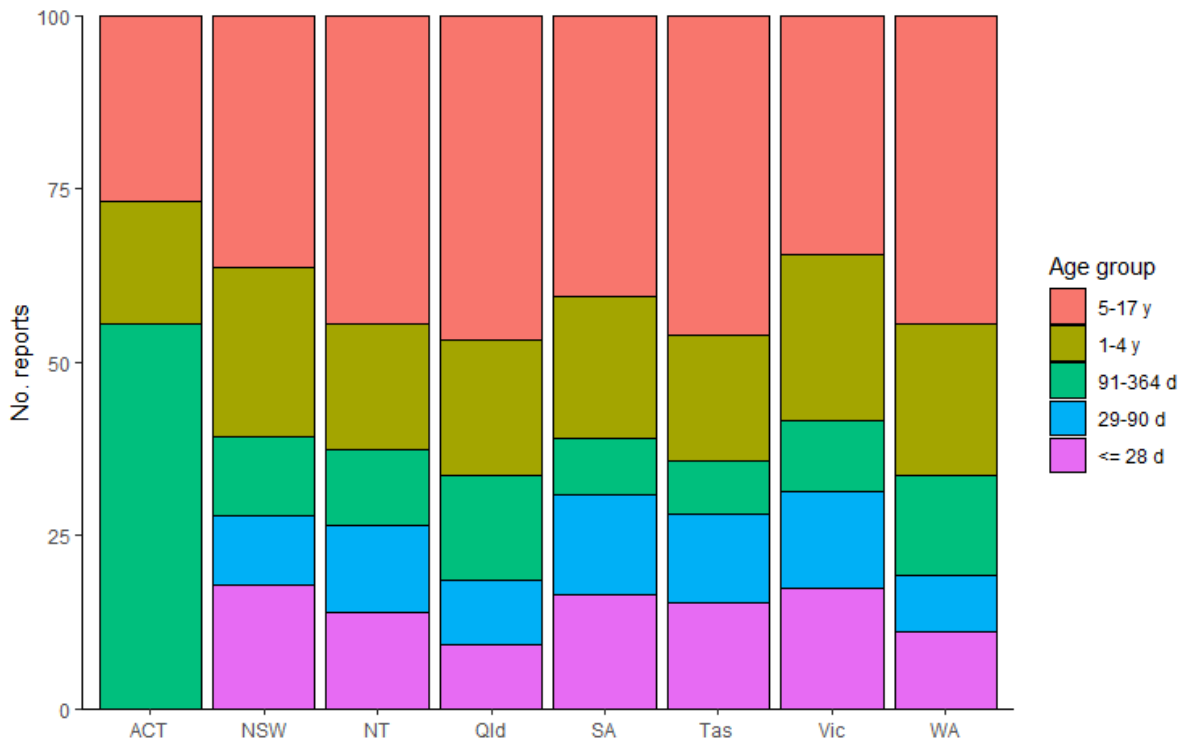
Figure 3. Age group distribution per state and territory, AGAR 2020-2021. Note: ACT does not report age <12 months.

4.3. Onset

Most bacteraemic episodes were community-onset (68.7% overall), however enterococcal episodes were more often hospital-onset [Table 7]. The proportion of hospital-onset episodes was highest in the neonatal age group and decreased with age; the median age for community-onset was three years (IQR: 0 – 10 years), whereas the median age for hospital-onset was <12 months years (IQR: 0 – 5 years). Tasmania had the highest proportion of community-onset episodes (85% of all episodes) with Victoria having the lowest proportion (58% of episodes).

Table 7. Patient characteristics per onset location for bacteraemic episodes reported to AGAR, 2020-2021

Characteristic	Community	Hospital
	n = 1,112	*n = 499*
Age median	3 years	<12 months
(IQR)	(0, 10)	(0, 6)
Age Group	*n (%)*	*n (%)*
≤28 days	135 (55.3)	109 (44.7)
29-90 days	86 (49.7)	87 (50.3)
91-364 days	131 (63.6)	75 (36.4)
1-4 years	264 (73.5)	95 (26.5)
5-17 years	496 (78.9)	133 (21.1)
Sex		
Female	438 (69.0)	197 (31.0)
Male	674 (69.1)	302 (30.9)
Survey*		
AESOP	72 (42.3)	98 (57.7)
ASSOP	478 (78.7)	129 (21.3)
GnSOP	605 (67.1)	297 (32.9)
State		
ACT	34 (75.6)	11 (24.4)
NSW	367 (71.5)	149 (28.9)
NT	59 (81.9)	13 (18.1)
Qld	153 (71.8)	60 (28.2)
SA	93 (71.5)	37 (28.5)
Tas	33 (84.6)	6 (15.4)
Vic	252 (57.5)	186 (42.5)
WA	121 (76.6)	37 (23.4)
Outcome**		
Died	21 (39.6)	32 (60.4)
Survived	895 (66.8)	445 (33.2)
Unknown	196 (89.9)	22 (10.1)

The data in this table is at patient level. AESOP: Australian Enterococcal Surveillance Outcome Program; ASSOP: Australian Staphylococcus aureus Surveillance Outcome Program; GnSOP: Gram-negative Surveillance Outcome Program. *Note: column for survey will not add to count of onset due to polymicrobial patients **at 30 days. ACT, Australian Capital Territory; NSW, New South Wales; NT, Northern Territory; Qld, Queensland; SA, South Australia; Tas, Tasmania; Vic, Victoria; WA, Western Australia.

4.4. Length of stay following blood culture collection

To describe the clinical significance of bacteraemia, the length of stay was reported as the number of days after the blood culture was collected and the date the patient was discharged or died

Overall, the mean length of stay following blood culture collection was 17.0 days (SD: 21.5) and the median was 10 days (IQR: 15). The minimum reported duration was 0 days, whilst the longest reported length of stay was 386 days. Children aged 29 – 90 days old had the longest reported length of stays. Children in Victoria had the longest mean length of stay [Table 8].

Table 8. Summary statistics for length of stay (LoS) in days for bacteraemia episode, AGAR 2020-2021

	Mean	SD	Median	IQR	Min	Max
Overall LoS	17.0	21.5	10	15	0	386
Age group						
≤28 days	20.4	23.8	12	22	0	191
29-90 days	23.7	24.3	16	29	0	108
91-364 days	18.4	23.9	9	17	0	163
1 – 4 years	16.1	18.5	11	11	0	154
5 – 17 years	14.3	20.2	10	10	0	386
Sex						
Male	16.7	25.7	9	15	0	386
Female	17.3	18.4	11	14	0	191
State						
ACT	11.9	8.5	9.5	12.5	0	29
NSW	13.7	13.1	10	9.25	0	110
NT	16.6	26.5	9	11.5	0	191
Qld	19.8	37.5	10	12	0	386
SA	17.2	16.4	11	15.2	0	88
Tas	13.8	14.7	8	13	1	67
Vic	21.8	20.0	15	25	0	108
WA	12.3	15.3	8	10.8	0	104
Outcome*						
Died	4.5	6.9	1	5	0	29
Survived	18.8	22.6	11	15	0	386
Unknown	7.8	6.1	7	7	0	29

The data in this table is at patient level. *Outcome at 30 days. ACT, Australian Capital Territory; NSW, New South Wales; NT, Northern Territory; Qld, Queensland; SA, South Australia; Tas, Tasmania; Vic, Victoria; WA, Western Australia.

4.5. Still admitted at 30 days post-blood culture collection

At 30 days, 21.7% (n: 350) of all children with a reported bacteraemia were still admitted to hospital. Victoria reported the highest proportion of patients still in hospital at 30 days [Table 9]. Patients with *Enterococcus* spp., *A. baumannii* complex, *S. marcescens* or *K. oxytoca* were more often reported to be in hospital at 30 days post-sample collection; a complete list of organisms and the proportion of patients still in hospital at 30 days is available in Appendix 9.7.

Table 9. Proportion of patients admitted at 30 days for a bacteraemia episode, AGAR 2020-2021

Characteristic	Still in n = 350 n (%)	Discharged n = 1,173 n (%)	Never admitted n = 50 n (%)	Unknown n = 38 n (%)
Age group				
≤28 days	73 (29.9)	156 (63.9)	1 (0.4)	14 (5.7)
29-90 days	64 (37)	100 (57.8)	7 (4)	2 (1.2)
91-364 days	65 (31.6)	126 (61.2)	8 (3.9)	7 (3.4)
1-4 years	57 (15.9)	287 (79.9)	9 (2.5)	6 (1.7)
5-17 years	91 (14.5)	504 (80.1)	25 (4)	9 (1.4)
Sex				
Female	140 (22)	452 (71.2)	23 (3.6)	20 (3.1)
Male	210 (21.5)	721 (73.9)	27 (2.8)	18 (1.8)
State				
ACT	9 (20)	36 (80)	0	0
NSW	95 (18.4)	368 (71.3)	36 (7)	17 (3.3)
NT	11 (15.3)	61 (84.7)	0	0
Qld	41 (19.2)	164 (77)	8 (3.8)	0
SA	25 (19.2)	92 (70.8)	0	13 (10)
Tas	4 (10.3)	35 (89.7)	0	0
Vic	151 (34.5)	284 (64.8)	3 (0.7)	0
WA	14 (8.9)	133 (84.2)	3 (1.9)	8 (5.1)
Outcome				
Died	0	53 (100)	0	0
Survived	350 (26.1)	970 (72.4)	20 (1.5)	0
Unknown	0	150 (68.8)	30 (13.8)	38 (17.4)

The data in this table is at patient level. ACT, Australian Capital Territory; NSW, New South Wales; NT, Northern Territory; Qld, Queensland; SA, South Australia; Tas, Tasmania; Vic, Victoria; WA, Western Australia.

4.6. Principal clinical manifestation

Over the two-year period, the most frequently reported clinical manifestations were osteomyelitis/septic arthritis (n: 255; 15.2%), and device-related infections without metastatic focus (n: 210; 12.5%) [Table 10].

Table 10. Reported principal clinical manifestations per survey, AGAR 2020-2021

Characteristic	AESOP n = 167 n (%)	ASSOP n = 606 n (%)	GnSOP n = 843 n (%)
Biliary tract infection (including cholangitis)	1 (0.6)	–	14 (1.7)
CNS infection (meningitis, abscess(es))	–	4 (0.7)	–
Deep abscess(es) excluding those in the CNS	–	13 (2.1)	–
Device-related infection with metastatic focus	1 (0.6)	12 (2.0)	9 (1.1)
Device-related infection without metastatic focus	38 (22.8)	64 (10.5)	93 (11.0)
Endocarditis		3 (0.5)	–
Febrile neutropenia	31 (18.6)	30 (5.0)	154 (18.3)
Intra-abdominal infection other than biliary tract	21 (12.6)	–	122 (14.5)
Osteomyelitis/septic arthritis	–	249 (41.4)	6 (0.7)
Pneumonia/empyema	–	13 (2.1)	–
Skin and skin structure infection	3 (1.8)	79 (13.0)	3 (0.6)
Urinary tract infection	11 (6.6)	–	170 (20.2)
Other clinical syndrome	30 (18.0)	64 (10.3)	155 (18.4)
No identifiable focus	26 (15.6)	55 (9.1)	65 (7.7)
Not recorded	5 (3.0)	20 (3.3)	52 (6.2)

AESOP: Australian Enterococcal Surveillance Outcome Program; ASSOP: Australian Staphylococcus aureus Surveillance Outcome Program; GnSOP: Gram-negative Surveillance Outcome Program. The population data for this table is at patient level per survey. A dash indicates that this clinical manifestation is not collected for this survey.

The principal clinical manifestation was different per age group and was dependent upon the organism (Appendix 9.8). However, for some clinical manifestations the numbers are very small and therefore should be interpreted with caution.

For enterococcal bacteraemia:
- Neonates: infections with no identifiable focus
- <3 months: intra-abdominal infections (other than biliary tract)
- 3 – 11 months: Other clinical syndromes or no identifiable focus
- 1 – 4 years: Device-related infections without metastatic focus
- 5 – 17 years: Febrile neutropenia

For *S. aureus* bacteraemia:
- Neonates: other clinical syndromes
- <3 months: Device-related infections without metastatic focus
- 3 – 11 months: Skin and skin structure infection
- 1 – 4 years: Osteomyelitis/septic arthritis
- 5 – 17 years: Osteomyelitis/septic arthritis

For Gram-negative bacteraemia:

- Neonates: Other clinical syndromes and urinary tract infections
- <3 months: Urinary tract infections
- 3 – 11 months: Urinary tract infections
- 1 – 4 years: Febrile neutropenia
- 5 – 17 years: Febrile neutropenia

Community-onset bacteraemic episodes were more frequently associated with an osteoarticular focus, whereas hospital-onset episodes were more frequently device-related or in patients with febrile neutropenia [Table 11].

Table 11. Reported principal clinical manifestations by onset type in per bacteraemia episode in children <18 years, AGAR 2020-2021

	Community (n = 1,115)		Hospital (n = 499)	
	n	%	n	%
Biliary tract infection (including cholangitis)	10	0.9	5	1.0
CNS infection (meningitis, abscess(es))	3	0.3	1	0.2
Deep abscess(es) excluding those in the CNS	12	1.1	1	0.2
Device-related infection with metastatic focus	12	1.1	10	2.0
Device-related infection without metastatic focus	94	8.4	100	20.0
Endocarditis	2	0.2	1	0.2
Febrile neutropenia	107	9.6	108	21.6
Intra-abdominal infection other than biliary tract	93	8.3	50	10.0
Osteomyelitis/septic arthritis	249	22.3	6	1.2
Pneumonia/empyema	9	0.8	4	0.8
Skin and skin structure infection	70	6.3	14	2.8
Urinary tract infection	166	14.9	15	3.0
Other clinical syndrome	143	12.8	104	20.8
No identifiable focus	80	7.2	68	13.6
Not recorded	65	5.8	12	2.4

The data in this table is at patient level

4.7. Device-related infections

Overall, 24.8% of patients had a bacteraemic episode that was device-related (n: 379). The proportion was higher in 2021 [27.4%, n:213] than in 2020 [22.2%, n:166]. The median length of stay was longer for patients with a device-related episode, compared to those patients without a device-related episode [Table 12].

Table 12. Patient characteristics for episodes related to device-related infections, AGAR 2020-2021

Characteristic	Device related n = 379 n (%)	Not device related n = 1,147 n (%)	Unknown n = 85 n (%)
Age *(median)*	2 years	2 years	2 years
(IQR)	(0, 8)	(0, 10)	(0, 11)
Age Group			
≤ 28 days	30 (12.3)	195 (79.9)	19 (7.8)
29-90 days	33 (19.1)	131 (75.7)	9 (5.2)
91-364 days	49 (23.8)	149 (72.3)	8 (3.9)
1-4 years	125 (34.8)	219 (61.0)	15 (4.2)
5-17 years	142 (22.6)	453 (72.0)	34 (5.4)
Sex			
Female	155 (24.4)	437 (68.8)	43 (6.8)
Male	224 (23)	710 (72.7)	42 (4.3)
State			
ACT	3 (6.7)	42 (93.3)	0
NSW	165 (32)	328 (63.6)	23 (4.5)
NT	2 (2.8)	48 (66.7)	22 (30.6)
Qld	29 (13.6)	184 (86.4)	0
SA	13 (10.0)	104 (80.0)	13 (10)
Tas	6 (15.4)	33 (84.6)	0
Vic	142 (32.4)	296 (67.6)	0
WA	19 (12.0)	112 (70.9)	27 (17.1)
Onset			
Community	188 (16.9)	851 (76.5)	73 (6.6)
Hospital	191 (38.3)	296 (59.3)	12 (2.4)
Length of Stay *(median)*	13 days	10 days	8 days
(IQR)	(8, 25)	(5, 19)	(4, 15)
Outcome			
Died	13 (24.5)	39 (73.6)	1 (1.9)
Survived	356 (26.6)	952 (71)	32 (2.4)
Unknown	10 (4.6)	156 (71.6)	52 (23.9)

*The population data for this table is at patient level

More device-related episodes were reported with gram-negative isolates. Overall, 13% of episodes that were MDR were associated with a device-related infection [Table 13].

Table 13. Isolate characteristics for device-related infections, AGAR 2020-2021.

Characteristic	Yes n = 412* n (%)	No n = 1,182* n (%)	Unknown n = 85* n (%)
Survey			
AESOP	74 (18.0)	91 (7.7)	5 (5.9)
ASSOP	108 (26.2)	474 (40.1)	25 (29.4)
GnSOP	230 (55.8)	617 (52.2)	55 (64.7)
MDR			
MDR	54 (13.1)	91 (7.7)	13 (15.3)
Not MDR	358 (86.9)	1,091 (92.3)	72 (84.7)

*The population data for this table is at isolate level

4.8. All-cause mortality

At seven days after blood culture collection, 2.6% of patients had died (n: 42); the proportion of patients who died increased to 3.3% at 30 days (n: 53). The median age of patients that died was younger to patients who survived (X^2: 12.5, p: <0.001). Whilst 49% of patients who died were from NSW (26/53, 49.1%), the highest proportion of patients who died within a jurisdiction was in Tasmania (3/39, 7.7%) [Table 14].

More than half of the deaths occurred in patients ≤28 days of age (27/53, 51%), of which 37% presented with community-onset bacteraemia and 63% with hospital-onset. Some neonates may not have left the hospital following birth, and therefore would only have been at risk of a hospital-onset infection.

Table 14. Patient characteristics of those who died within 30-days of sample collection, AGAR 20-21

Characteristic	Died	Survived	Unknown
	n = 53	*n = 1,340*	*n = 218*
	n (%)	*n (%)*	*n (%)*
Age *median (IQR)*	<12 months (0, 1)	2 years (0, 10)	2 years (0, 9.8)
Age Group			
≤28 days	27 (50.9)	182 (13.6)	35 (16.1)
29-90 days	9 (17)	151 (11.3)	13 (6)
91-364 days	3 (5.7)	161 (12)	42 (19.3)
1-4 years	6 (11.3)	317 (23.7)	36 (16.5)
5-17 years	8 (15.1)	529 (39.5)	92 (42.2)
Sex			
Female	25 (47.2)	509 (38)	101 (46.3)
Male	28 (52.8)	831 (62)	117 (53.7)
State			
ACT	1 (1.9)	19 (1.4)	25 (11.5)
NSW	26 (49.1)	398 (29.7)	92 (42.2)
NT	3 (5.7)	69 (5.1)	0
Qld	4 (7.5)	154 (11.5)	55 (25.2)
SA	1 (1.9)	116 (8.7)	13 (6)
Tas	3 (5.7)	36 (2.7)	0
Vic	11 (20.8)	410 (30.6)	17 (7.8)
WA	4 (7.5)	138 (10.3)	16 (7.3)
Onset			
Community	21 (39.6)	895 (66.8)	196 (89.9)
Hospital	32 (60.4)	445 (33.2)	22 (10.1)
Polymicrobial	8 (15.1)	149 (11.1)	17 (7.8)
Yes	27 (50.9)	182 (13.6)	35 (16.1)
No	45 (3.1)	1,191 (82.9)	201 (14.0)

*The population data for this table is at patient level. ACT, Australian Capital Territory; NSW, New South Wales; NT, Northern Territory; Qld, Queensland; SA, South Australia; Tas, Tasmania; Vic, Victoria; WA, Western Australia.

Table 15 outlines the organisms reported from patients who died within 30 days. It should be noted eight patients had polymicrobial infections and are discussed further in Section 4.9.

Table 15. Organisms reported to AGAR from patients <18 years who died within 30 days

	≤28 d	29 - 90 d	91 - 364 d	1 - 4 y	5 -17 y
MDR					
Enterobacter cloacae complex		1			
Escherichia coli	3	1			1
Klebsiella pneumoniae complex					2
Staphylococcus aureus				1	
Not MDR					
Acinetobacter baumannii complex		1			
Citrobacter koseri				1	
Enterobacter cloacae complex	3	3		3	
Enterococcus faecalis	4		1	1	
Escherichia coli	8	2	1		1
Klebsiella oxytoca	3				
Klebsiella pneumoniae complex	3	1	1	1	
Morganella morganii	1				
Proteus mirabilis	1				
Pseudomonas aeruginosa	3				2
Staphylococcus aureus	1		1	1	2

4.9. Polymicrobial bacteraemia

Overall, 10.8% of patients had more than one isolate reported in a bacteraemia episode. The majority of polymicrobial episodes were reported in children <12 months (72/174, 41.4%) [Table 16]. The complete list of reported polymicrobial organism combinations is available in Appendix 9.9.

Table 16. Patient characteristics of those with polymicrobial bacteraemia, AGAR 2020-2021

Characteristic	Polymicrobial	Monomicrobial
	n = 174	*n = 1,437*
	n (%)	*n (%)*
Age *median*	1 year	2 years
(IQR)	(0, 5)	(0, 10)
Age Group		
≤28 days	28 (11.5)	216 (88.5)
29-90 days	22 (12.7)	151 (87.3)
91-364 days	22 (10.7)	184 (89.3)
1-4 years	57 (15.9)	302 (84.1)
5-17 years	45 (7.2)	584 (92.8)
Sex		
Female	64 (10.1)	571 (89.9)
Male	110 (11.3)	866 (88.7)
State		
ACT	4 (8.9)	41 (91.1)
NSW	64 (12.4)	452 (87.6)
NT	5 (6.9)	67 (93.1)
Qld	9 (4.2)	204 (95.8)
SA	10 (7.7)	120 (92.3)
Tas	3 (7.7)	36 (92.3)
Vic	56 (12.8)	382 (87.2)
WA	23 (14.6)	135 (85.4)
Onset		
Community	107 (9.6)	1,005 (90.4)
Hospital	67 (13.4)	432 (86.6)
Outcome		
Died	8 (15.1)	45 (84.9)
Survived	149 (11.1)	1,191 (88.9)
Unknown	17 (7.8)	201 (92.2)

*The population data for this table is at patient level

5. Gram-negatives

Overall, there were 902 gram-negative isolates reported from 867 bacteraemia episodes in patients aged <18 years in 2020-2021; 800 Enterobacterales (88.7%), 61 *Pseudomonas aeruginosa* (6.8%) and 41 (4.5%) *Acinetobacter* spp.

Table 17. Number of Gram-negative isolates and patients <18 years to AGAR 2020-2021

	2020		2021		Overall	
	Isolates	**Episodes**	**Isolates**	**Episodes**	**Isolates**	**Episodes**
Gram negatives	425	407	477	460	902	867
Enterobacterales	367	350	433	416	800	766
Pseudomonas aeruginosa	31	31	30	30	61	61
Acinetobacter spp	27	26	14	14	41	40

5.1. Enterobacterales

There were 800 Enterobacterales[2] reported to AGAR; 367 in 2020 and 433 in 2021. The most frequently reported were *E. coli* and *K. pneumoniae* complex [Table 18].

Table 18. Species and number of reports of Enterobacterales reported to AGAR 2020-2021 from patients <18 years

Organism	2020 n = 367 n (%)	2021 n = 433 n (%)	Overall n = 800 n (%)
Citrobacter farmeri	1 (0.3)	0	1 (0.1)
Citrobacter freundii complex[1]	6 (1.6)	5 (1.2)	11 (1.4)
Citrobacter koseri	1 (0.3)	1 (0.2)	2 (0.3)
Enterobacter cloacae complex[2]	60 (16.3)	46 (10.6)	106 (13.3)
Enterobacter species	0	1 (0.2)	1 (0.1)
Escherichia coli	163 (44.4)	215 (49.7)	378 (47.3)
Escherichia hermanii	0	1 (0.2)	1 (0.1)
Franconibacter helveticus	0	1 (0.2)	1 (0.1)
Hafnia alvei	0	1 (0.2)	1 (0.1)
Klebsiella aerogenes	3 (0.8)	2 (0.5)	5 (0.6)
Klebsiella oxytoca	13 (3.5)	17 (3.9)	30 (3.8)
Klebsiella pneumoniae complex[3]	61 (16.6)	61 (14.1)	122 (15.3)
Klebsiella species	1 (0.3)	2 (0.5)	3 (0.4)
Morganella morganii	1 (0.3)	2 (0.5)	3 (0.4)
Pantoea agglomerans	3 (0.8)	1 (0.2)	4 (0.5)
Pantoea eucrina	0	1 (0.2)	1 (0.1)
Pantoea septica	1 (0.3)	0	1 (0.1)
Pantoea species	2 (0.5)	2 (0.5)	4 (0.5)
Pantoea vagans	0	1 (0.2)	1 (0.1)
Proteus mirabilis	5 (1.4)	3 (0.7)	8 (1.0)
Proteus penneri	0	1 (0.2)	1 (0.1)
Raoultella ornithinolytica	2 (0.5)	2 (0.5)	4 (0.5)
Salmonella (non-typhoidal)	22 (6.0)	52 (12.0)	74 (9.2)
Salmonella (typhoidal)	16 (4.4)	0	16 (2.0)
Serratia liquefaciens	0	2 (0.5)	2 (0.3)
Serratia marcescens	6 (1.6)	12 (2.8)	18 (2.2)
Shigella sonnei	0	1 (0.2)	1 (0.1)

*Population data for this table is at isolate level

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[2] Please note, *Salmonella* spp. are included in the analysis for Enterobacterales; the analyses of *Salmonella* spp further on are for specific antimicrobial-organism combinations that are of clinical importance and the authors believe should be highlighted separately.

The largest proportion of Enterobacterales were from NSW (264 isolates, 33%), followed by Victoria (238 isolates, 30%). The highest proportion of isolates were from patients <12 months old (391 isolates, 49%), and from males (447 isolates, 56%). Enterobacterales episodes were more frequently community-onset, and 14% of episodes were polymicrobial. Overall, 14.5% of the Enterobacterales were MDR [Table 19].

Table 19. Characteristics of patients <18 years reported to AGAR in 2020-2021 with an Enterobacterales

Characteristic	2020 n = 367 n (%)	2021 n = 433 n (%)	Overall n = 800* n (%)
Age *median*	1 year	<12 months	1 year
(IQR)	(0, 7)	(0, 7)	(0, 7)
Age Group			
≤ 28 days	60 (16.3)	97 (22.4)	157 (19.6)
29-90 days	43 (11.7)	56 (12.9)	99 (12.4)
91-364 days	62 (16.9)	73 (16.9)	135 (16.9)
1-4 years	94 (25.6)	79 (18.2)	173 (21.6)
5-17 years	108 (29.4)	128 (29.6)	236 (29.5)
Sex			
Female	156 (42.5)	197 (45.5)	353 (44.1)
Male	211 (57.5)	236 (54.5)	447 (55.9)
State			
ACT	6 (1.6)	17 (3.9)	23 (2.9)
NSW	124 (33.8)	140 (32.3)	264 (33)
NT	10 (2.7)	27 (6.2)	37 (4.6)
Qld	39 (10.6)	60 (13.9)	99 (12.4)
SA	24 (6.5)	32 (7.4)	56 (7)
Tas	10 (2.7)	7 (1.6)	17 (2.1)
Vic	118 (32.2)	120 (27.7)	238 (29.8)
WA	36 (9.8)	30 (6.9)	66 (8.3)
Onset			
Community	245 (66.8)	300 (69.3)	545 (68.1)
Hospital	122 (33.2)	133 (30.7)	255 (31.9)
Length of Stay *(median)*	10 days	10 days	10 days
(IQR)	(4, 21)	(5, 19)	(5, 21)
Polymicrobial			
Yes	48 (13.1)	65 (15.0)	113 (14.1)
No	319 (86.9)	368 (85.0)	687 (85.9)
MDR			
MDR	68 (18.5)	48 (11.1)	116 (14.5)
Not MDR	299 (81.5)	385 (88.9)	684 (85.5)

*Population data for this table is at isolate level. ACT, Australian Capital Territory; NSW, New South Wales; NT, Northern Territory; Qld, Queensland; SA, South Australia; Tas, Tasmania; Vic, Victoria; WA, Western Australia.

5.1.1. Susceptibility testing results

Gentamicin/Tobramycin

The proportion of Enterobacterales resistant to the aminoglycosides (gentamicin/tobramycin) was 11.6% (n: 92/793; 95%CI: 9.5–14.0%). Victoria reported the highest proportion of aminoglycoside resistant isolates (16.8%; 95%CI: 12.3-22.2), followed by South Australia (SA) (14.5%; 95%CI: 6.5-26.7) and NSW (11.9%; 95%CI: 8.2-16.5%). No aminoglycoside resistant isolates were reported in Tasmania [Figure 4]. Resistant isolates were more frequently reported in children aged 1-4 years of age. Isolates from patients with a hospital-onset episode were more frequently reported as resistant than those with a community-onset episode [Table 20]. Most isolates had an MIC of ≤1mg/L to gentamicin and tobramycin [Figure 4].

Table 20. Proportion of gentamicin/tobramycin resistance per state and territory and age group in isolates reported to AGAR 2020-2021 from patients aged <18 years

	No. isolates	No. resistant	% R	95% CI	
State					
ACT	23	1	4.3	0.1	21.9
NSW	264	31	11.9	8.2	16.5
NT	37	3	8.3	1.8	22.5
Qld	99	6	6.1	2.3	12.7
SA	56	8	14.5	6.5	26.7
Tas	17	0	0		
Vic	238	40	16.8	12.3	22.2
WA	66	3	4.6	1.0	12.9
Age group					
≤28 days	157	21	13.5	8.5	19.8
29-90 days	102	10	9.9	4.9	17.5
91-364 days	132	9	6.9	3.2	12.6
1-4 years	173	30	17.4	12.1	24.0
5-17 years	236	22	9.4	6.0	13.9
Onset					
Community	540	39	7.2	5.2	9.7
Hospital	253	53	20.9	16.1	26.5

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

Figure 4. Proportion of gentamicin/tobramycin resistance per state and territory in isolates reported to AGAR in 2020-2021 from patients aged <18 years
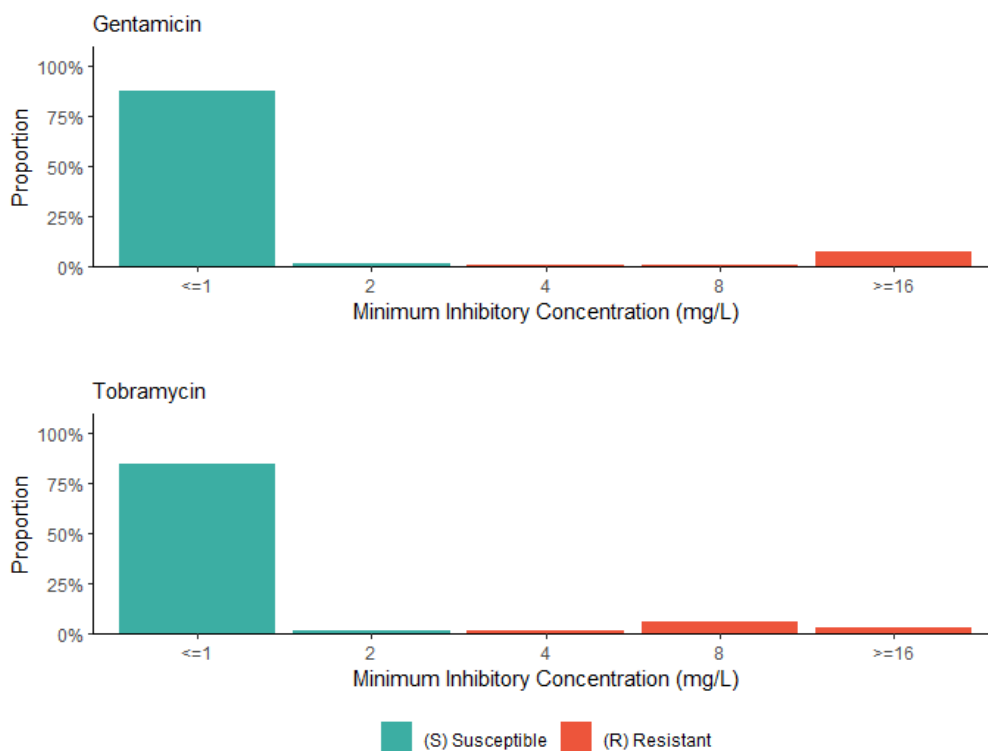
Figure 5. Distribution of MICs against gentamicin and tobramycin reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoints for gentamicin and tobramycin in Enterobacterales are both at 2mg/L for systemic infections according to EUCAST 2022.

Piperacillin-tazobactam

The proportion of Enterobacterales resistant to piperacillin-tazobactam was 11.2% (88/784; 95%CI: 9.1–13.6). Victoria reported the highest proportion of resistant isolates (15.3%; 95%CI: 11.0-20.6%), followed by NSW (13.1%; 95%CI: 9.2-17.8%). No piperacillin-tazobactam resistant isolates were reported in Tasmania and the ACT [Figure 6]. Isolates from children aged over 1 year were more often resistant. Isolates from patients with a hospital-onset episode were more frequently reported as piperacillin-tazobactam resistant than those with a community-onset episode [Table 21]. Most isolates had a MIC of ≤4 mg/L to piperacillin-tazobactam [Figure 7].

Table 21. Proportion of piperacillin-tazobactam resistance per state and territory in isolates reported to AGAR in 2020-2021 from patients aged <18 years

	No. isolates	No. resistant	% R	95% CI	
State					
ACT	23	0	0.0		
NSW	260	34	13.1	9.2	17.8
NT	36	3	8.3	1.8	22.5
Qld	97	8	8.2	3.6	15.6
SA	55	1	1.8	0.0	9.7
Tas	17	0	0.0		
Vic	235	36	15.3	11.0	20.6
WA	61	6	9.8	3.7	20.2
Age group					
≤28 days	155	2	1.3	0.2	4.6
29-90 days	97	12	12.0	6.4	20.0
91-364 days	132	9	7.0	3.2	12.8
1-4 years	170	27	15.9	10.7	22.3
5-17 years	230	38	16.5	12.0	22.0
Onset					
Community	534	38	7.1	5.1	9.6
Hospital	250	50	20.0	15.2	25.5

ACT, Australian Capital Territory; NSW, New South Wales; NT, Northern Territory; Qld, Queensland; SA, South Australia; Tas, Tasmania; Vic, Victoria; WA, Western Australia.
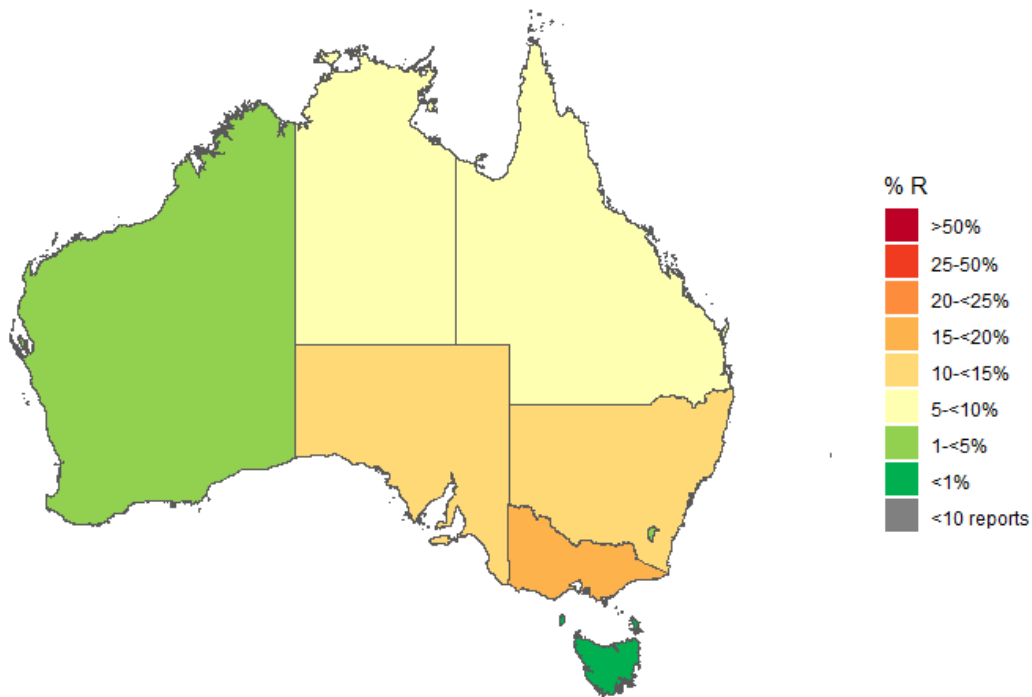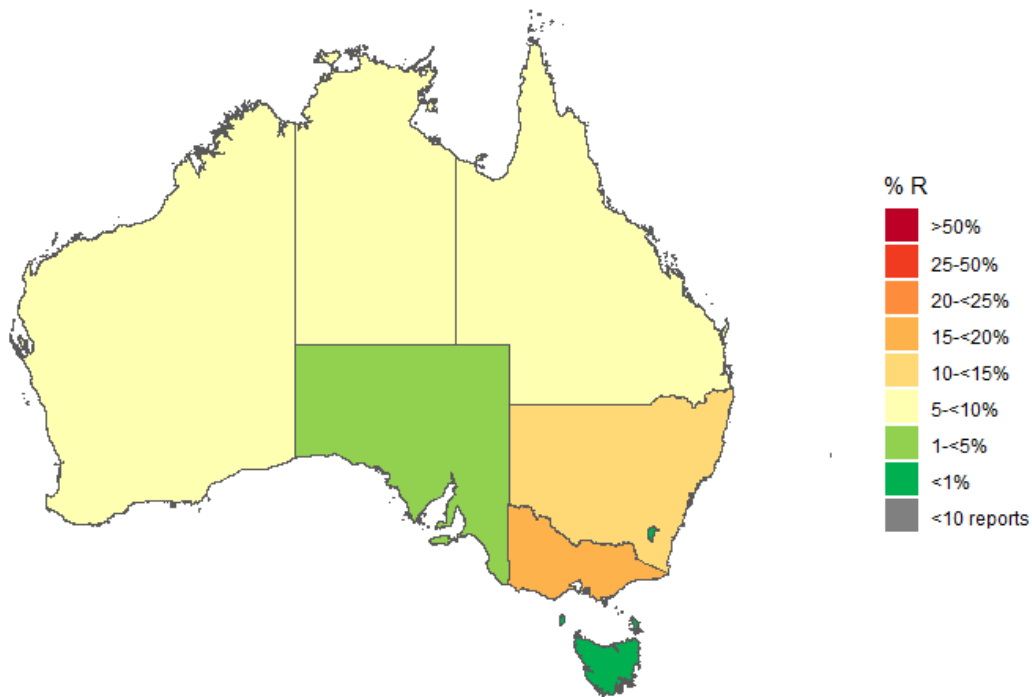
Figure 6. Proportion of piperacillin-tazobactam resistance per state and territory in isolates reported to AGAR in 2020-2021 from patients aged <18 years
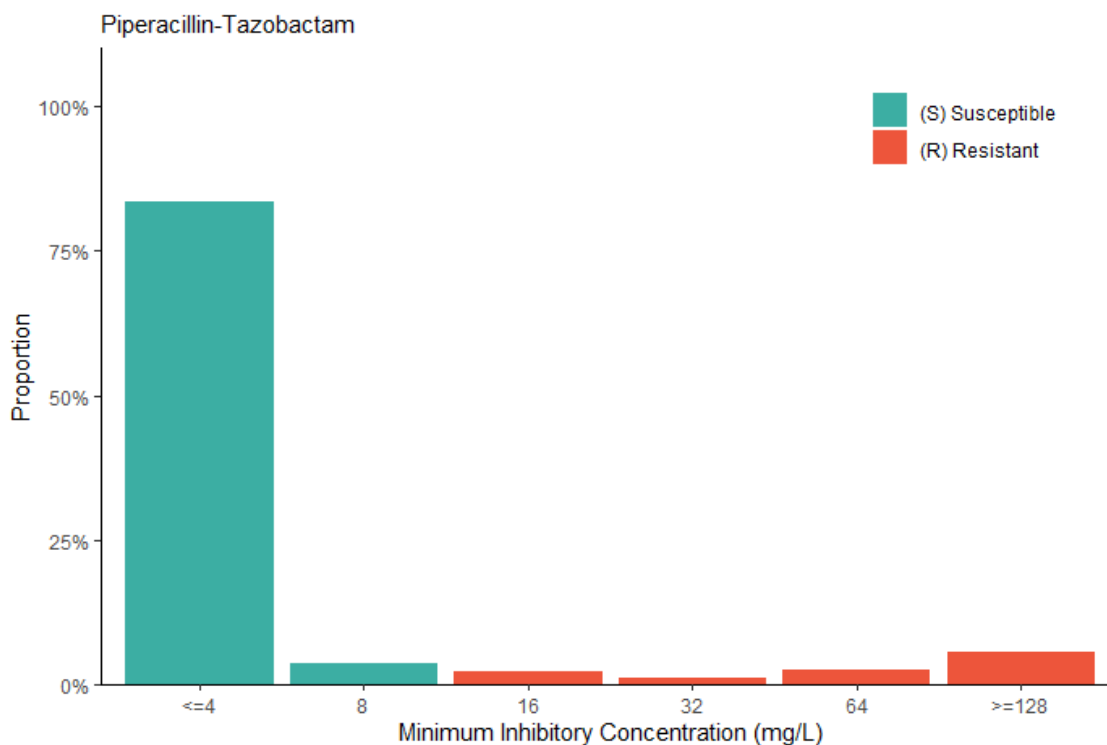
Figure 7. Distribution of MICs against piperacillin-tazobactam reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoint for piperacillin-tazobactam in Enterobacterales is 8mg/L, with the concentration of tazobactam fixed at 4mg/L, according to EUCAST 2022.

Third generation Cephalosporins

Overall, resistance to the third generation cephalosporins (ceftriaxone and/or ceftazidime) in the Enterobacterales was 12.9% (102/793; 95%CI: 10.6–15.4%). Whilst all states reported isolates resistant to the third generation cephalosporins, Victoria had the highest proportion of resistant isolates (19.3%; 95%CI: 14.5-24.9%) [Figure 8]. Isolates from children aged 1-4 years reported the highest proportion of resistant isolates (20.3; 95%CI: 14.6-27.1%). Isolates from patients with a hospital-onset episode were more frequently reported resistant to the third generation cephalosporins than those with a community-onset episodes [Table 22]. The majority of isolates had MICs of ≤1 mg/L to ceftazidime and ceftriaxone [Figure 9].

Table 22. Proportion of third generation cephalosporin resistance per state and territory and age group in isolates reported to AGAR in 2020-2021 from patients aged <18 years

|	No. isolates	No. Resistant	% R	95%CI	
State					
ACT	23	1	4.3	0.1	21.9
NSW	264	37	14.2	10.2	19.1
NT	37	2	5.6	0.7	18.7
Qld	99	6	6.1	2.3	12.7
SA	56	4	7.3	2.0	17.6
Tas	17	1	5.9	0.1	28.7
Vic	238	46	19.3	14.5	24.9
WA	66	5	7.7	2.5	17.0
Age group					
≤28 days	157	13	8.3	4.5	13.8
29-90 days	102	11	10.9	5.6	18.7
91-364 days	132	12	9.2	4.8	15.5
1-4 years	173	35	20.3	14.6	27.1
5-17 years	236	31	13.3	9.2	18.4
Onset					
Community	540	44	8.1	6.0	10.8
Hospital	253	58	22.9	17.9	28.6

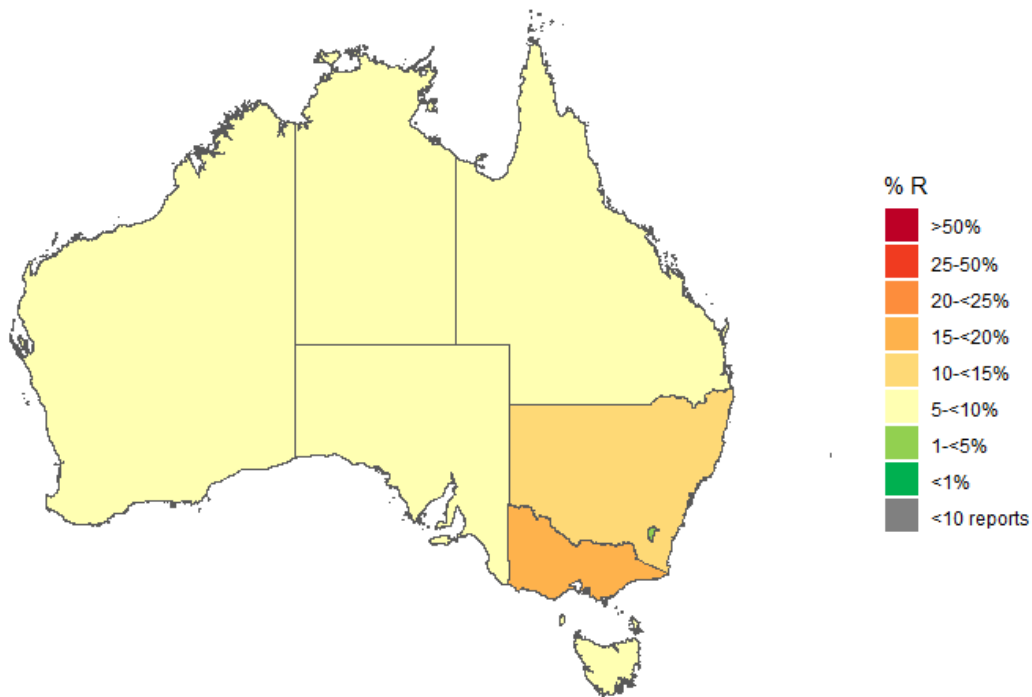*Figure 8. Proportion of third generation cephalosporins resistance per state and territory in isolates reported to AGAR in 2020-2021 from patients aged <18 years*
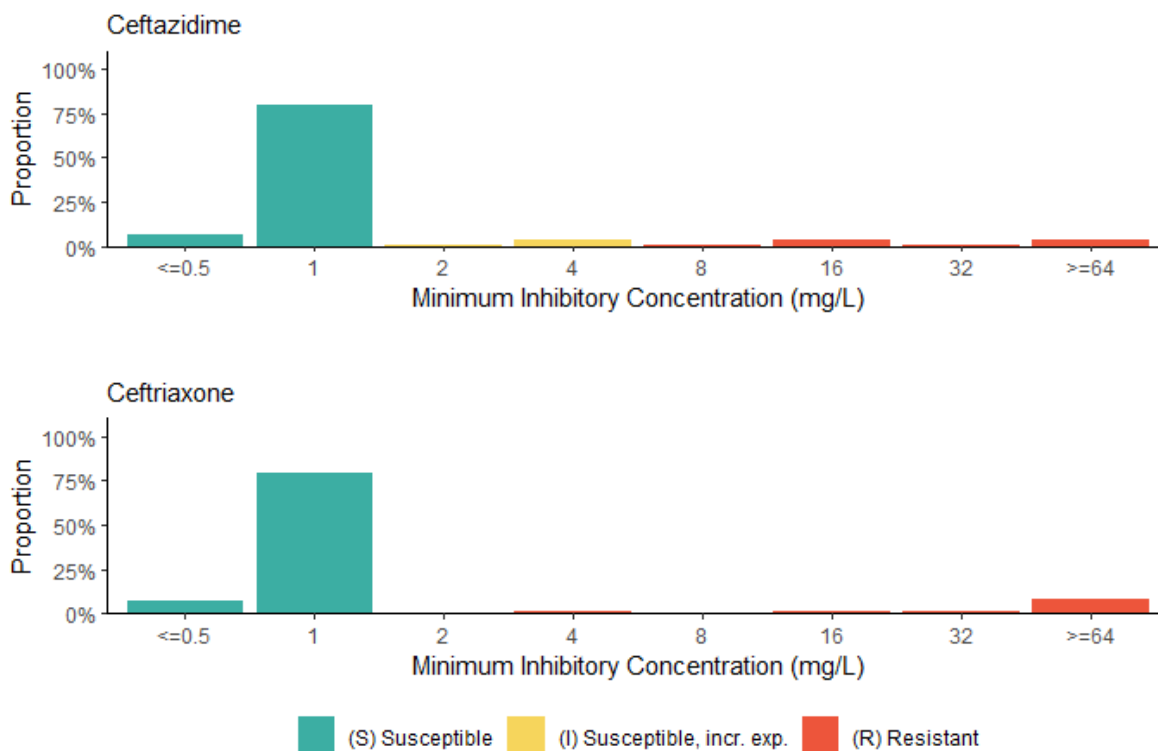

Figure 9. Distribution of MICs against ceftazidime and ceftriaxone reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoint of ceftazidime in Enterobacterales is 4mg/L and 2mg/L for ceftriaxone according to EUCAST 2022.

Ciprofloxacin

Overall, 13.2% of Enterobacterales were reported as ciprofloxacin resistant (101/766; 95%CI: 10.9-15.8). Isolates from patients with a hospital-onset episode were more frequently reported as ciprofloxacin resistant than those with a community-onset bacteraemia [Table 23]. Isolates from children aged over 1 year were more frequently resistant (19.4%; 95%CI: 13.6-26.4). Victoria reported the highest proportion of resistant isolates (20.3%; 95%CI: 15.4-26.0) [Figure 10]. Most isolates had an MIC value of ≤0.5mg/L to ciprofloxacin [Figure 11].

Table 23. Proportion of ciprofloxacin resistance per state and territory and age group in isolates reported to AGAR in 2020-2021 from patients aged <18 years

	No. isolates	No. resistant	%R	95% CI	
State					
ACT	23	2	8.7	1.1	28.0
NSW	264	27	10.8	7.2	15.3
NT	37	0	0.0	0.0	10.0
Qld	99	10	11.8	5.8	20.6
SA	56	8	14.5	6.5	26.7
Tas	17	2	11.8	1.5	36.4
Vic	238	48	20.3	15.4	26.0
WA	66	4	6.2	1.7	15.0
Age group					
≤28 days	157	16	10.3	6.0	16.1
29-90 days	102	10	9.9	4.9	17.5
91-364 days	132	10	8.1	4.0	14.4
1-4 years	173	31	19.4	13.6	26.4
5-17 years	236	34	15.0	10.6	20.4
Onset					
Community	513	52	10.1	7.7	13.1
Hospital	253	49	19.4	14.7	24.8

ACT, Australian Capital Territory; NSW, New South Wales; NT, Northern Territory; Qld, Queensland; SA, South Australia; Tas, Tasmania; Vic, Victoria; WA, Western Australia.
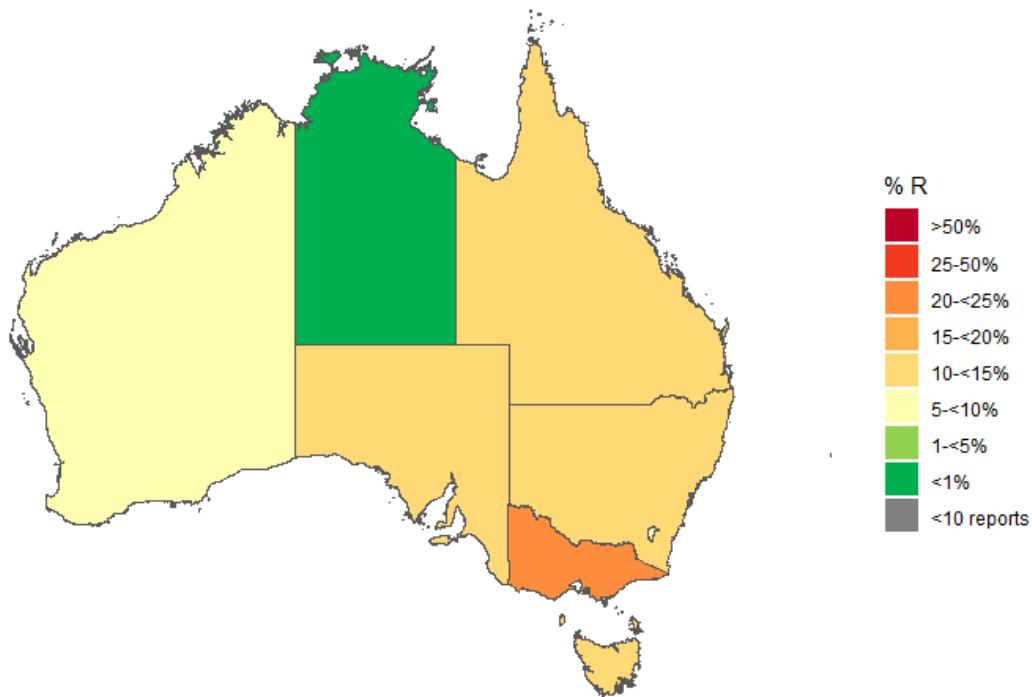
Figure 10. Proportion of ciprofloxacin resistance per state and territory in isolates reported to AGAR in 2020-2021 from patients aged <18 years
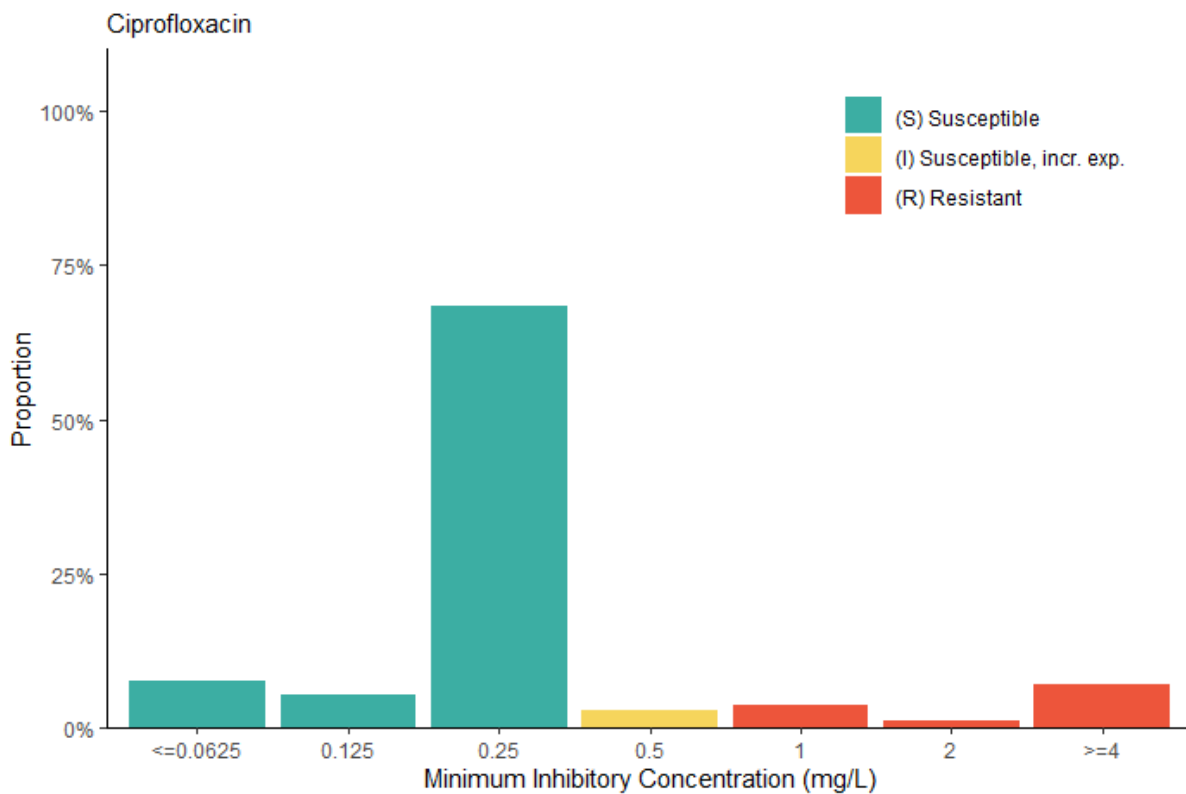
Figure 11. Distribution of MICs against ciprofloxacin reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoint for ciprofloxacin in Enterobacterales is 0.5mg/L except for Salmonella spp. which is at 0.06mg/L, according to EUCAST 2022.

Meropenem

Of the 792 Enterobacterales that had meropenem susceptibility testing performed, only two *Enterobacter cloacae* complex isolates were resistant (0.3%; 95% CI: 0.0 – 0.9). The isolates reported were a community-onset bacteraemia from Queensland and a hospital-onset bacteraemia from Victoria, both in patients aged 5-17 years. The majority of Enterobacterales isolates had an meropenem MIC of ≤0.25mg/L [Figure 12].

Figure 12. Distribution of MICs against meropenem reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoint for meropenem in Enterobacterales is 8mg/L according to EUCAST 2022.

5.1.2. Multi-drug resistance

Overall, 116 (14.5%) of the 800 Enterobacterales were identified as MDR. The most frequent species with a MDR phenotype were *E. coli*, the *K. pneumoniae* complex and the *E. cloacae* complex [Table 24]. Victoria had the highest proportion of Enterobacterales resistant to three or more classes of antimicrobials [Table 25].
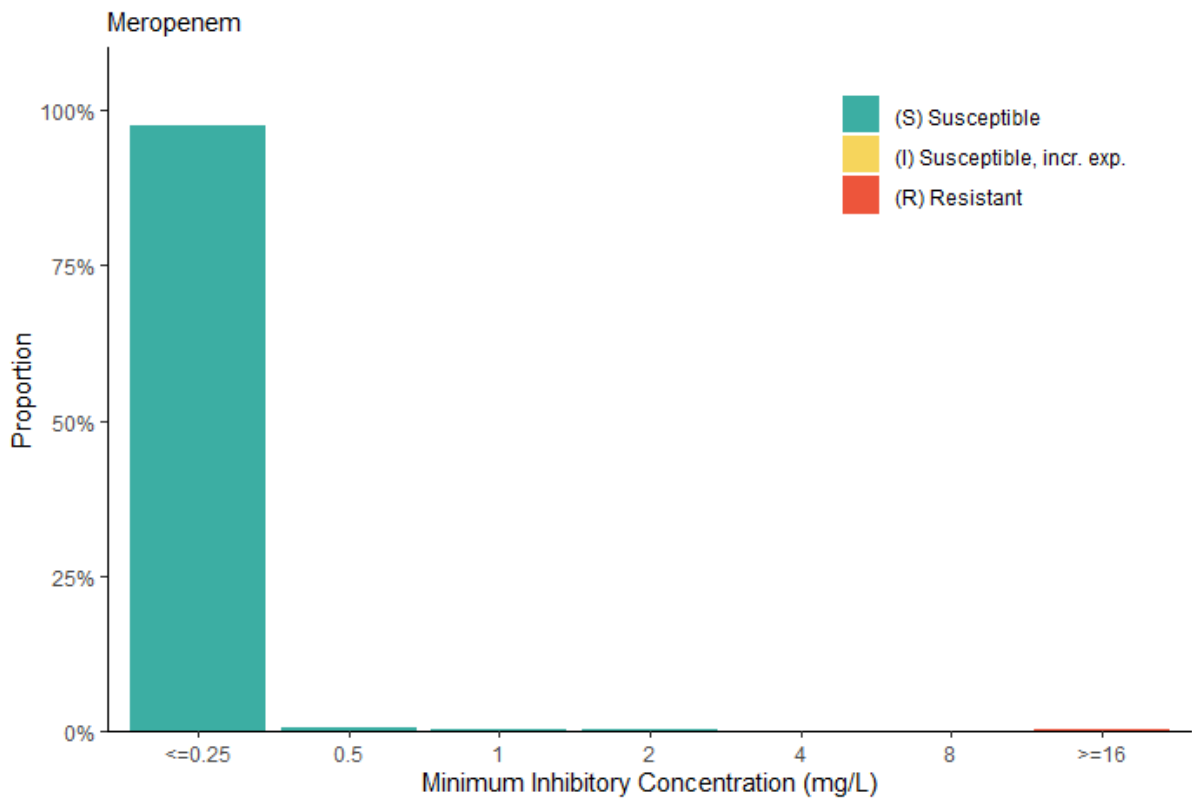
Table 24. Proportion of Enterobacterales isolates reported that are categorised as multidrug resistant (MDR).

	MDR n (%)	Not MDR n (%)
Citrobacter farmeri	1 (100)	0
Citrobacter freundii complex	1 (9.1)	10 (90.9)
Enterobacter cloacae complex	15 (14.2)	91 (85.8)
Escherichia coli	70 (18.5)	308 (81.5)
Klebsiella oxytoca	1 (3.3)	29 (96.7)
Klebsiella pneumoniae complex	22 (18.0)	100 (82.0)
Proteus mirabilis	2 (25.0)	6 (75.0)
Salmonella species (typhoidal)	4 (25.0)	12 (75.0)

Species not listed did not have any MDR isolates reported in 2020-2021

Table 25. Number of Enterobacterales isolates resistant to how many antimicrobial classes[3]

	Number of antimicrobial classes resistant									
	Not multidrug resistant					**Multidrug resistant**				
	0	*1*	*2*	*%*		*3*	*4*	*5*	*6*	*%*
ACT	10	10	2	95.7		0	0	1	0	4.3
NSW	126	63	36	85.2		20	11	7	1	14.8
NT	19	7	9	94.6		1	1	0	0	5.4
Qld	63	17	10	90.9		4	3	1	1	9.1
SA	23	20	7	89.3		3	2	0	1	10.7
Tas	12	2	1	88.2		2	0	0	0	11.8
Vic	103	53	32	79.0		15	12	22	1	21.0
WA	35	13	11	89.4		4	2	1	0	10.6

MDR Enterobacterales isolates were more likely to be hospital-onset (*p*: <0.01) and associated with a device-related infection (*p*: <0.01). MDR Enterobacterales isolates were more frequent in patients with febrile neutropenia. Of the 41 patients who died with an Enterobacterales episode, 19.5% of the isolates were MDR.

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[3] Antimicrobial classes (agents) were aminoglycosides (amikacin, gentamicin, tobramycin), anti-pseudomonal penicllins + β-lactamase inhibitors (piperacillin-tazobactam), Carbapenems (meropenem), non-extended spectrum cephalosporins (cefazolin, cefuroxime), extended spectrum cephalosporins (cefepime, ceftazidime, ceftriaxone), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim-sulfamethoxazole), penicllins (ampicillin) and penicllins + β-lactamase inhibitors (amoxicillin-clavulanic acid).

Table 26. Characteristics of patients with an Enterobacterales isolate and multidrug resistance

Characteristic	MDR n = 161 (%)	Not MDR n = 684 (%)
Age *[median, (IQR)]*	2 years (0, 8)	<12 months (0, 7)
Age Group		
≤ 28 days	18 (11.5)	139 (88.5)
29-90 days	12 (12.1)	87 (87.9)
91-364 days	9 (6.7)	126 (93.3)
1-4 years	40 (23.1)	133 (76.9)
5-17 years	37 (15.7)	199 (84.3)
Sex		
Female	48 (13.6)	305 (86.4)
Male	68 (15.2)	379 (84.8)
Onset		
Community	55 (10.1)	490 (89.9)
Hospital	61 (23.9)	194 (76.1)
State		
ACT	1 (4.3)	22 (95.7)
NSW	39 (14.8)	225 (85.2)
NT	2 (5.4)	35 (94.6)
Qld	9 (9.1)	90 (90.9)
SA	6 (10.7)	50 (89.3)
Tas	2 (11.8)	15 (88.2)
Vic	50 (21)	188 (79)
WA	7 (10.6)	59 (89.4)
Device-related		
Yes	66 (11.8)	493 (88.2)
No	9 (16.7)	45 (83.3)
Unknown	41 (21.9)	146 (78.1)
Principal manifestation		
Biliary tract infection (including cholangitis)	0 (0)	12 (100)
Device-related infection with metastatic focus	3 (33.3)	6 (66.7)
Device-related infection without metastatic focus	20 (22.7)	68 (77.3)
Febrile neutropenia	41 (29.9)	96 (70.1)
Intra-abdominal infection other than biliary tract	9 (7.1)	117 (92.9)
Osteomyelitis/septic arthritis	0 (0)	5 (100)
Skin and skin structure infection	1 (33.3)	2 (66.7)
Urinary tract infection	12 (7.2)	154 (92.8)
Other clinical syndrome	16 (10.9)	131 (89.1)
No identifiable focus	5 (8.8)	52 (91.2)
Not recorded	9 (18)	41 (82)
Length of Stay *(median)*	13 days	9 days
(IQR)	(8, 25)	(4, 20)
30-day all-cause mortality	8 (19.5)	33 (80.5)

*The population data of this table is at isolate level. ACT, Australian Capital Territory; NSW, New South Wales; NT, Northern Territory; Qld, Queensland; SA, South Australia; Tas, Tasmania; Vic, Victoria; WA, Western Australia.

The highest proportion of MDR Enterobacterales isolates were from Victoria (n: 59, 39.6%) and NSW (n: 53, 35.6%). [Figure 13.A]. Victoria had the highest proportion of Enterobacterales isolates that were MDR (24.8%), followed by NSW (20.1%) [Figure 13.B].
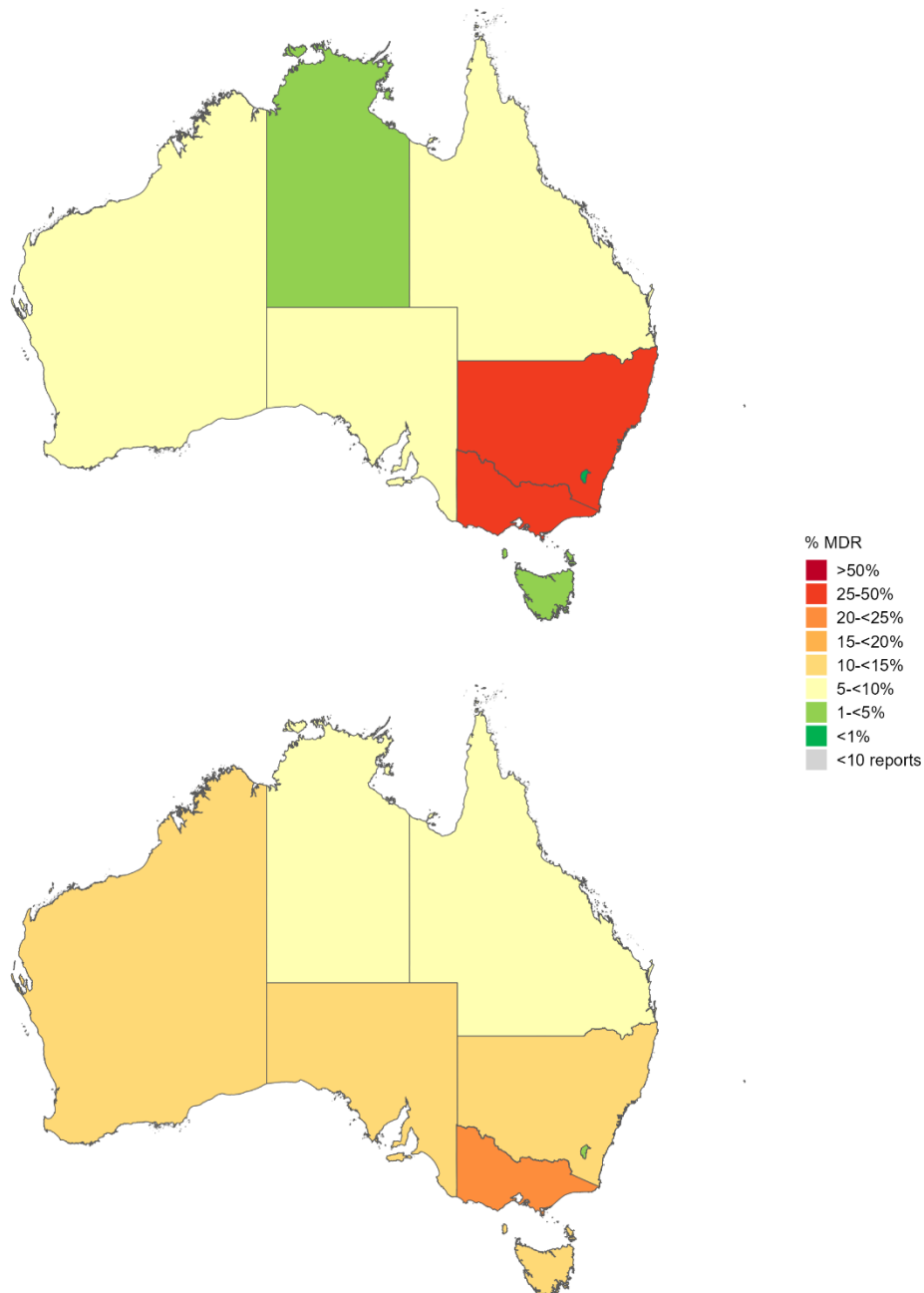

Figure 13. A) Proportion of MDR Enterobacterales isolates reported to AGAR overall, B) proportion of Enterobacterales isolates reported per state and territory that were MDR

5.2. *Salmonella* spp

There were 90 isolates of *Salmonella* reported to AGAR: 38 isolates in 2020 and 52 isolates in 2021. Two isolates in 2020 were *Salmonella* Paratyphi A, and 14 isolates were *Salmonella* Typhi; neither serotypes were reported in 2021 [Table 27].

Table 27. Number and type of Salmonella isolates reported to AGAR from patients <18 years in 2020 and 2021

Subspecies/Serovar	2020 n = 38 (%)	2021 n = 52 (%)	Overall n = 90 (%)
Salmonella (non-Typhi)	22.0 (57.9)	52.0 (100)	74.0 (82.2)
Paratyphi A	2 (5.3)	0	2 (2.2)
Typhi	14 (36.8)	0	14 (15.6)
MDR			
MDR	4 (10.5)	0	4 (4.4)
Not MDR	34 (89.5)	52 (100)	86 (95.6)

Four *Salmonella* Typhi isolates were MDR – two isolates from Tasmania, and one isolate each from NSW and Queensland. None of the MDR isolates were *Salmonella* non-Typhi, or reported in children <12 months.

The largest proportion of *Salmonella* isolates were reported from Queensland (36%) and NSW (24%). *Salmonella* isolates were more frequently reported in female patients. More than half of *Salmonella* isolates were reported in patients <5 years of age. All *Salmonella* infections were community-onset, and only one patient had a polymicrobial bacteraemia. No patients were reported to have died with a *Salmonella* bacteraemia in 2020-2021 [Table 28].

Table 28. Age, sex, clinical characteristics of Salmonella *species in patients aged <18 years reported to AGAR in 2020 and 2021.*

	2020	2021	Overall
	n = 38 (%)	n = 52 (%)	n = 90 (%)
Age *(median)*	3.5 years	1.5 years	2.5 years
(IQR)	(1, 7.8)	(0, 7)	(0, 7)
Age Group			
≤ 28 days	0	1 (1.9)	1 (1.1)
29-90 days	0	3 (5.8)	3 (3.3)
91-364 days	9 (23.7)	15 (28.8)	24 (26.7)
1-4 years	15 (39.5)	15 (28.8)	30 (33.3)
5-17 years	14 (36.8)	18 (34.6)	32 (35.6)
Sex			
Female	16 (42.1)	33 (63.5)	49 (54.4)
Male	22 (57.9)	19 (36.5)	41 (45.6)
State			
ACT	0	2 (3.8)	2 (2.2)
NSW	12 (31.6)	10 (19.2)	22 (24.4)
NT	2 (5.3)	5 (9.6)	7 (7.8)
Qld	9 (23.7)	23 (44.2)	32 (35.6)
SA	2 (5.3)	0	2 (2.2)
Tas	2 (5.3)	2 (3.8)	4 (4.4)
Vic	5 (13.2)	7 (13.5)	12 (13.3)
WA	6 (15.8)	3 (5.8)	9 (10.0)
Onset			
Community	38 (100)	52 (100)	90 (100)
Length of Stay *(median)*	4 days	5 days	5 days
(IQR)	(3, 6)	(3, 8)	(3, 7)
Polymicrobial			
Yes	0	1 (1.9)	1 (1.1)
No	38 (100)	51 (98.1)	90 (98.9)

*Population data for this table is at isolate level. ACT, Australian Capital Territory; NSW, New South Wales; NT, Northern Territory; Qld, Queensland; SA, South Australia; Tas, Tasmania; Vic, Victoria; WA, Western Australia.

5.2.1. Susceptibility test results

Ceftriaxone

Only two salmonella isolates (2.2%, 95%CI: 0.3-7.8%) were ceftriaxone resistant; one *S.* Typhi isolated in 2020 in NSW and one *Salmonella* species isolated in 2021 in Queensland, both from patients aged 5-17 years and both community-onset. Most *Salmonella* isolates had a ceftriaxone MIC of ≤1mg/L [Figure 14].
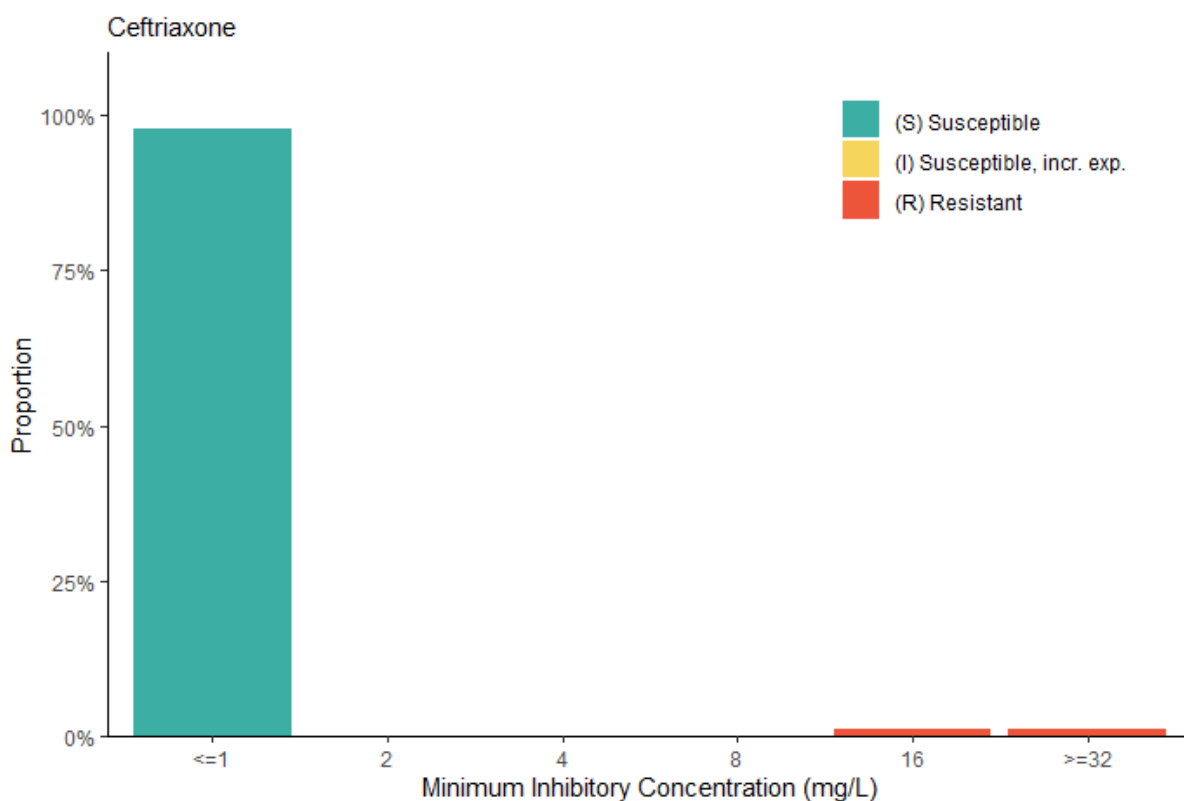

Figure 14. Distribution of MICs against ceftriaxone in Salmonella isolates reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoint for ceftriaxone in Salmonella species is 2mg/L for indications other than meningitis, according to EUCAST 2022.

Ciprofloxacin

Of the 63 *Salmonella* isolates tested, 13 were ciprofloxacin resistant (20.6%, 95% CI: 8.8–24.7%); nine were *Salmonella* Typhi, two were *Salmonella* Paratyphi A and two were *Salmonella* spp. Whilst NSW and Queensland reported the most isolates, Tasmania reported the highest proportion of ciprofloxacin resistant isolates [Figure 15]. All ciprofloxacin resistant isolates were from children aged >1 year old [Table 29].

Table 29. Proportion of resistance to ciprofloxacin per state and territory in Salmonella isolates reported to AGAR in 2020-2021 from patients aged <18 years

	No. isolates	No. Resistant	% R	95% CI	
State					
ACT	2	0	0.0		
NSW	12	4	33.3	9.9	65.1
NT	6	0	0.0		
Qld	18	2	11.1	1.4	34.7
SA	2	0	0.0		
Tas	4	2	50.0	6.8	93.2
Vic	10	4	40.0	12.2	73.8
WA	9	1	11.1	0.3	48.2
Age group					
≤28 days	1	0	0.0		
29-90 days	3	0	0.0		
91-364 days	16	0	0.0		
1-4 years	18	5	27.8	9.7	53.5
5-17 years	25	8	32.0	14.9	53.5
Onset					
Community	63	13	20.6	11.5	32.7

ACT, Australian Capital Territory; NSW, New South Wales; NT, Northern Territory; Qld, Queensland; SA, South Australia; Tas, Tasmania; Vic, Victoria; WA, Western Australia.
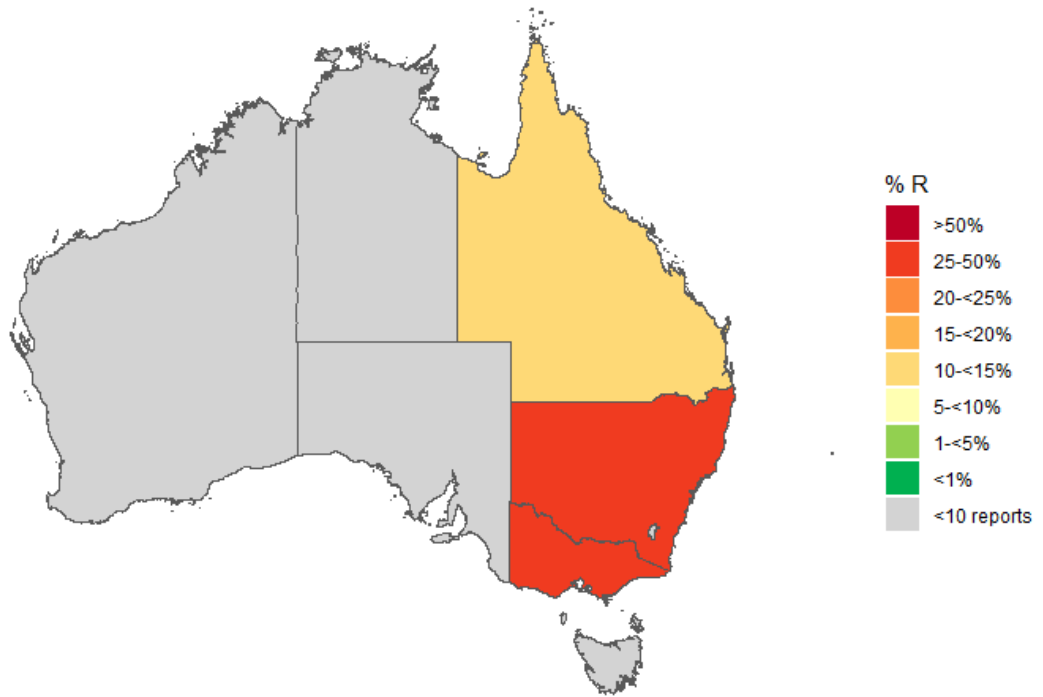
Figure 15. Proportion of ciprofloxacin resistance per state and territory in Salmonella isolates reported to AGAR in 2020-2021 from patients aged <18 years
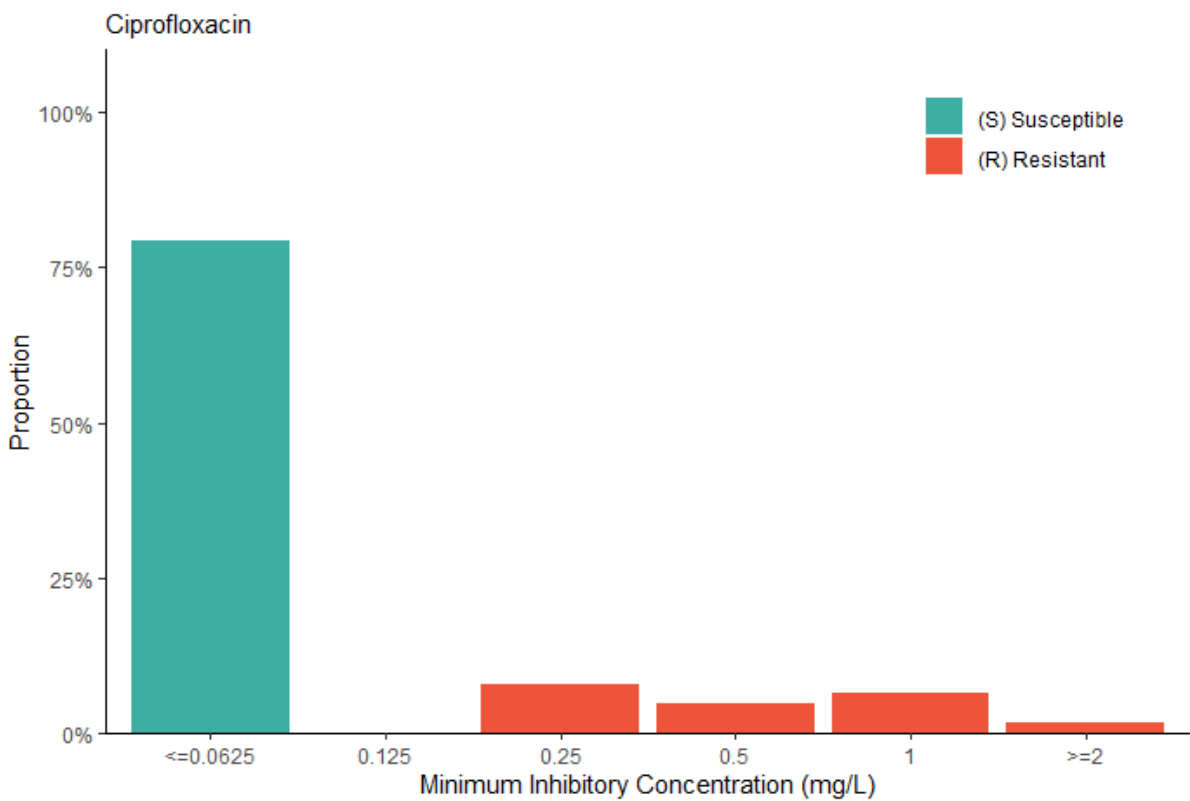
Figure 16. Distribution of MICs against ciprofloxacin in Salmonella isolates reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoint for ciprofloxacin in Salmonella species is 0.06mg/L according to EUCAST 2022.

5.3. Pseudomonas aeruginosa

There were 61 *Pseudomonas aeruginosa* reported to AGAR: 31 isolates in 2020 and 30 isolates in 2021. No isolates were reported from the ACT, and only one isolate was reported from Tasmania. Overall, 4.9% of isolates were MDR, and two isolates were carbapenem resistant (3.3%) [WHO priority pathogen].

Table 30. Characteristics of patients <18 years reported to AGAR in 2020-2021 with P. aeruginosa

	2020 n = 31 (%)	2021 n = 30 (%)	Overall n = 61 (%)
Age *median*	4 years	5 years	4 years
(IQR)	(2, 6.5)	(2, 9)	(2, 9)
Age Group			
≤ 28 days	1 (3.2)	4 (13.3)	5 (8.2)
29-90 days	2 (6.5)	0	2 (3.3)
91-364 days	3 (9.7)	1 (3.3)	4 (6.6)
1-4 years	12 (38.7)	8 (26.7)	20 (32.8)
5-17 years	13 (41.9)	17 (56.7)	30 (49.2)
Sex			
Female	14 (45.2)	6 (20)	20 (32.8)
Male	17 (54.8)	24 (80)	41 (67.2)
State			
ACT	0	0	0
NSW	14 (45.2)	13 (43.3)	27 (44.3)
NT	1 (3.2)	0	1 (1.6)
Qld	9 (29)	4 (13.3)	13 (21.3)
SA	4 (12.9)	1 (3.3)	5 (8.2)
Tas	0	1 (3.3)	1 (1.6)
Vic	1 (3.2)	4 (13.3)	5 (8.2)
WA	2 (6.5)	7 (23.3)	9 (14.8)
Onset			
Community	20 (64.5)	17 (56.7)	37 (60.7)
Hospital	11 (35.5)	13 (43.3)	24 (39.3)
Length of Stay	14 days	12 days	12 days
(IQR)	(8, 19)	(9, 20)	(8, 20)
Polymicrobial			
Yes	5 (16.1)	3 (10.0)	8 (13.1)
No	26 (83.9)	27 (90.0)	53 (86.9)
MDR			
MDR	2 (6.5)	1 (3.3)	3 (4.9)
Not MDR	29 (93.5)	29 (96.7)	58 (95.1)

*Population data for this table is at isolate level. ACT, Australian Capital Territory; NSW, New South Wales; NT, Northern Territory; Qld, Queensland; SA, South Australia; Tas, Tasmania; Vic, Victoria; WA, Western Australia.

5.3.1. Susceptibility testing results

Gentamicin/Tobramycin

For *P. aeruginosa* there are no EUCAST clinical breakpoints for gentamicin. No *P. aeruginosa* isolates were reported tobramycin resistant. The distribution of gentamicin and tobramycin MICs are shown in Figure 17.
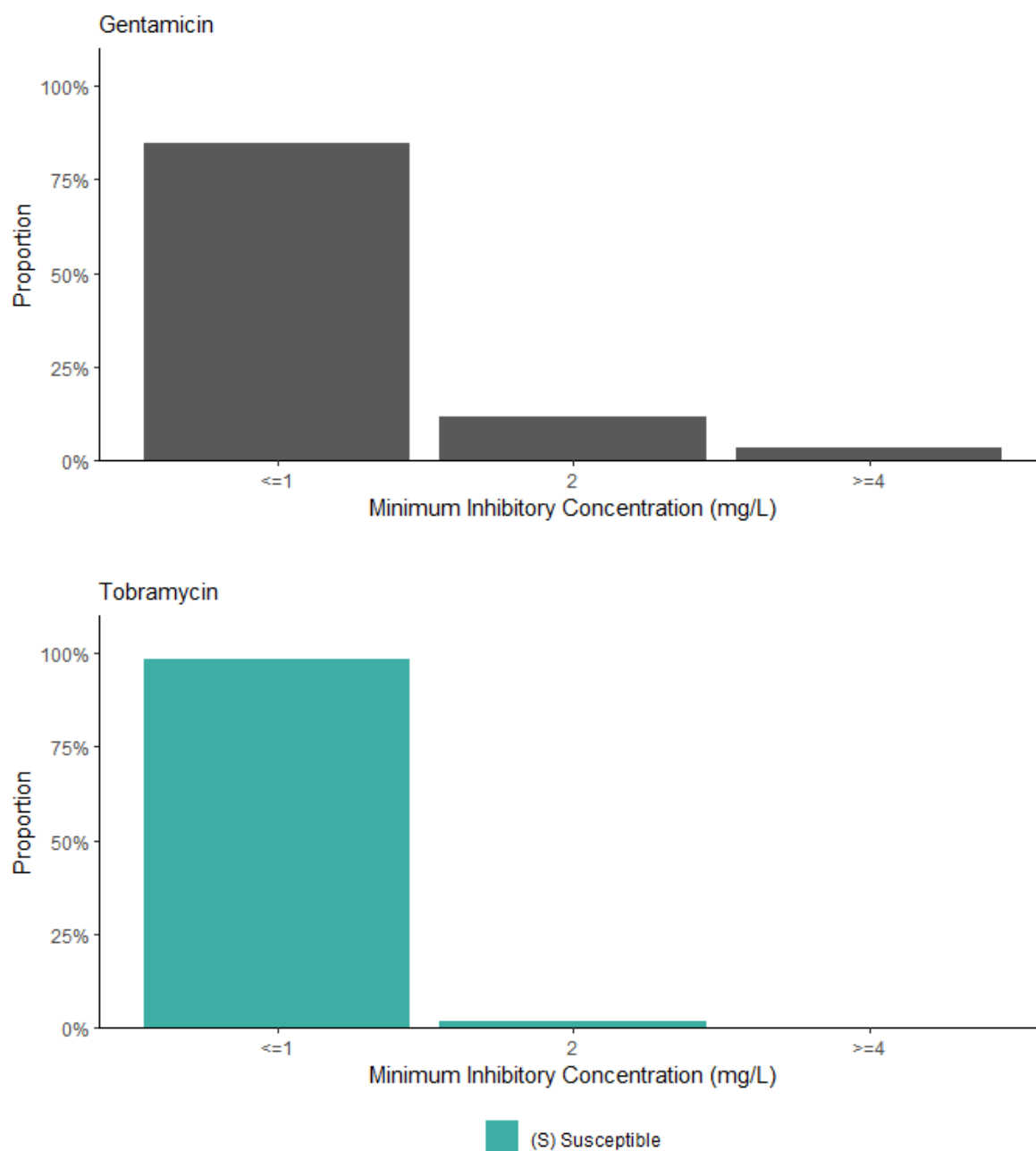

Figure 17. Distribution of MICs against gentamicin and tobramycin for P. aeruginosa isolates reported to AGAR 2020-2021 from patients aged <18 years. The breakpoint for tobramycin in P. aeruginosa is 2mg/L for systemic infections according to EUCAST 2022; there is no prescribed cut-off for gentamicin and P. aeruginosa.

Piperacillin-tazobactam

Overall, 19.7% of *P. aeruginosa* were piperacillin-tazobactam resistant [n: 12; 95%CI: 10.6–31.8%]; 22.6% of isolates in 2020 (n: 7) and 16.7% in 2021 (n: 5). Whilst SA reported the highest proportion of isolates as piperacillin-tazobactam resistant, only three isolates were identified in the state [Figure 18; Table 31]. More community-onset isolates were reported piperacillin-tazobactam resistant than hospital-onset isolates [Table 31]. The piperacillin-tazobactam MICs are shown in Figure 19.

Table 31. Proportion of piperacillin-tazobactam resistance per state and territory and per age group in P. aeruginosa isolates reported to AGAR in 2020-2021 from patients aged <18 years

	No. isolates	No. Resistant	% R	95% CI	
State					
ACT	0				
NSW	27	7	25.9	11.1	46.3
NT	1	0	0		
Qld	13	2	15.4	1.9	45.4
SA	5	3	60.0	14.7	94.7
Tas	4	0	0		
Vic	5	0	0		
WA	9	0	0		
Age group					
≤28 days	5	1	20.0	0.5	71.6
29-90 days	2	0	0		
91-364 days	4	0	0		
1-4 years	20	5	25.0	8.7	49.1
5-17 years	30	6	20.0	7.7	38.6
Onset					
Community	37	8	21.6	9.8	38.2
Hospital	24	4	16.7	4.7	37.4

ACT, Australian Capital Territory; NSW, New South Wales; NT, Northern Territory; Qld, Queensland; SA, South Australia; Tas, Tasmania; Vic, Victoria; WA, Western Australia.
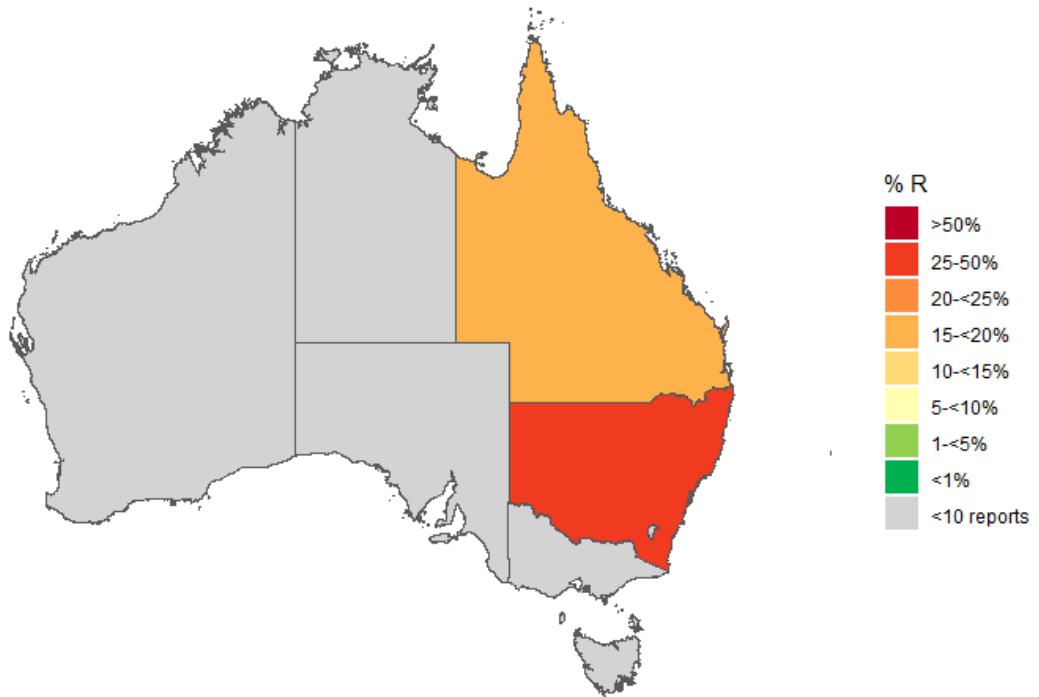
Figure 18. Proportion of piperacillin-tazobactam resistance per state and territory in P. aeruginosa isolates reported to AGAR in 2020-2021 from patients aged <18 years
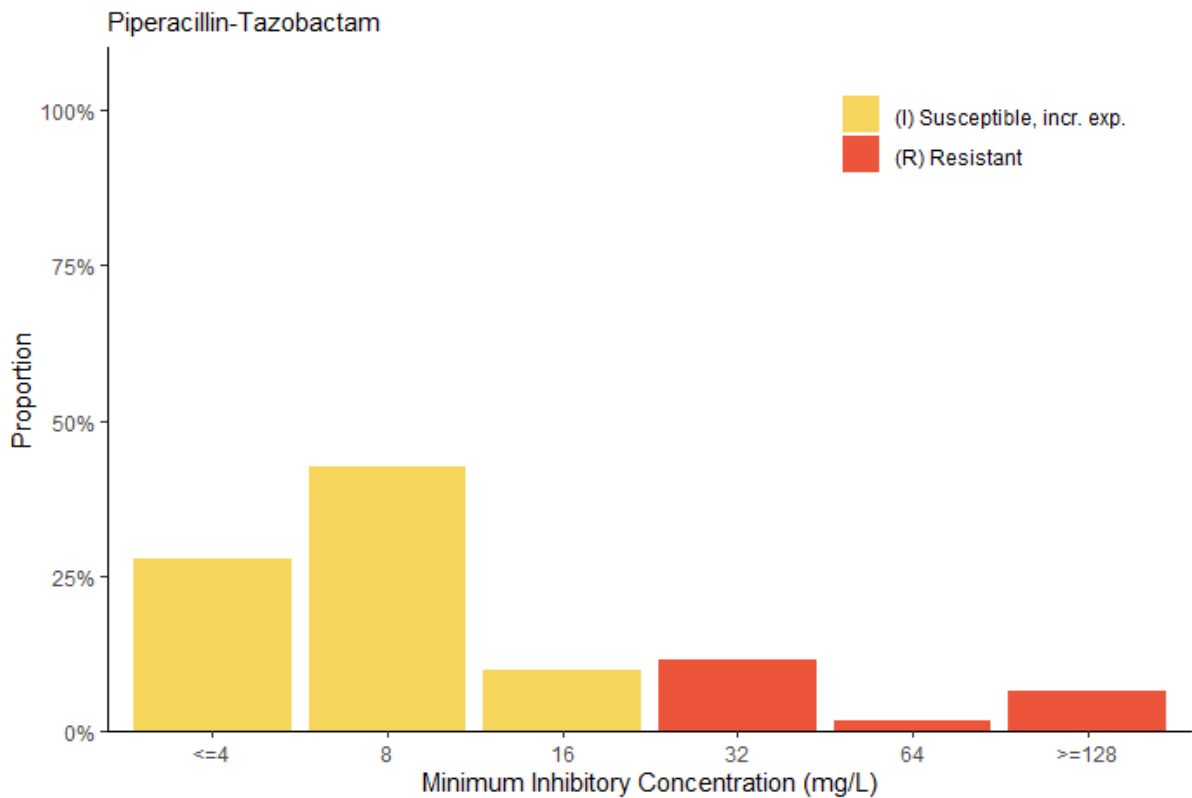
Figure 19. Distribution of MICs against piperacillin-tazobactam in P. aeruginosa isolates reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoint for piperacillin-tazobactam in P. aeruginosa is 16mg/L, with the concentration of tazobactam fixed at 4mg/L, according to EUCAST 2022.

Third/Fourth generation Cephalosporins

Of the 61 *P. aeruginosa* tested, eight (13.1%, 95%CI: 5.8-24.2%) were resistant to either ceftazidime and/or cefepime. Although NSW had the highest number of resistant isolates, SA had the highest proportion of isolates that were resistant to the third/fourth generation cephalosporins [Figure 20, Table 32]. All susceptible isolates were of increased exposure susceptibility [Figure 21].

Table 32. Proportion of resistance to cefepime and/or ceftazidime resistance per state and territory in P. aeruginosa isolates reported to AGAR in 2020-2021 from patients aged <18 years

|	No. isolates	No. Resistant	% R	95%CI	
State					
ACT	0				
NSW	27	5	18.5	6.3	38.1
NT	1	0	0		
Qld	13	1	7.7	0.2	36.0
SA	5	2	40	5.3	85.3
Tas	1	0	0		
Vic	5	0	0		
WA	9	0	0		
Age group					
≤ 28 days	5	1	20	0.5	71.6
29-90 days	2	0	0		
91-364 days	4	0	0		
1-4 years	20	2	10	1.2	31.7
5-17 years	30	5	16.7	5.6	34.7
Onset					
Community	37	5	13.5	4.5	28.8
Hospital	24	3	12.5	2.7	32.4

Figure 20. Proportion of cefepime and/or ceftazidime resistance per state and territory in P. aeruginosa isolates reported to AGAR in 2020-2021 from patients aged <18 years

Figure 21. Distribution of MICs against cefepime and ceftazidime in P. aeruginosa isolates reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoint for cefepime and ceftazidime in P. aeruginosa is 8mg/L respectively, according to EUCAST 2022.

Ciprofloxacin

Overall, 9.8% of *P. aeruginosa* were ciprofloxacin resistant (n: 6; 95%CI: 3.7-20.2%). All resistant isolates were reported from patients aged 5-17 years. SA had the highest number of ciprofloxacin resistant isolates [Figure 22; Table 33]. More community-onset isolates were reported resistant to ciprofloxacin than hospital-onset isolates [Table 33]. Most isolates had a ciprofloxacin MIC of ≤0.25mg/L [Figure 23].

Table 33. Proportion of resistance to ciprofloxacin resistance per state and territory in P. aeruginosa isolates reported to AGAR in 2020-2021 from patients aged <18 years

	No. isolates	No. Resistant	% R	95%CI	
State					
ACT	0				
NSW	27	2	7.4	0.9	24.3
NT	1	0	0.0		
Qld	13	1	7.7	0.2	36.0
SA	5	3	60.0	14.7	94.7
Tas	1	0	0.0		
Vic	5	0	0.0		
WA	9	0	0.0		
Age group					
≤ 28 days	5	0	0.0		
29-90 days	2	0	0.0		
91-364 days	4	0	0.0		
1-4 years	20	0	0.0		
5-17 years	30	6	20.0	7.7	38.6
Age group					
Community	37	5	13.4	4.5	28.8
Hospital	24	1	4.2	0.1	21.1

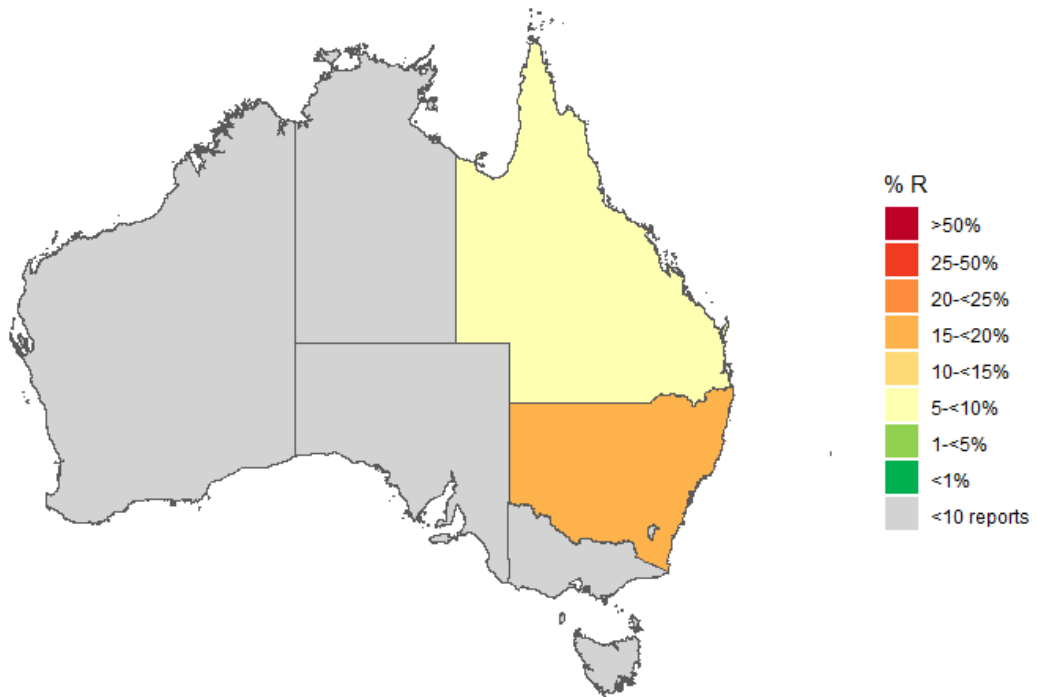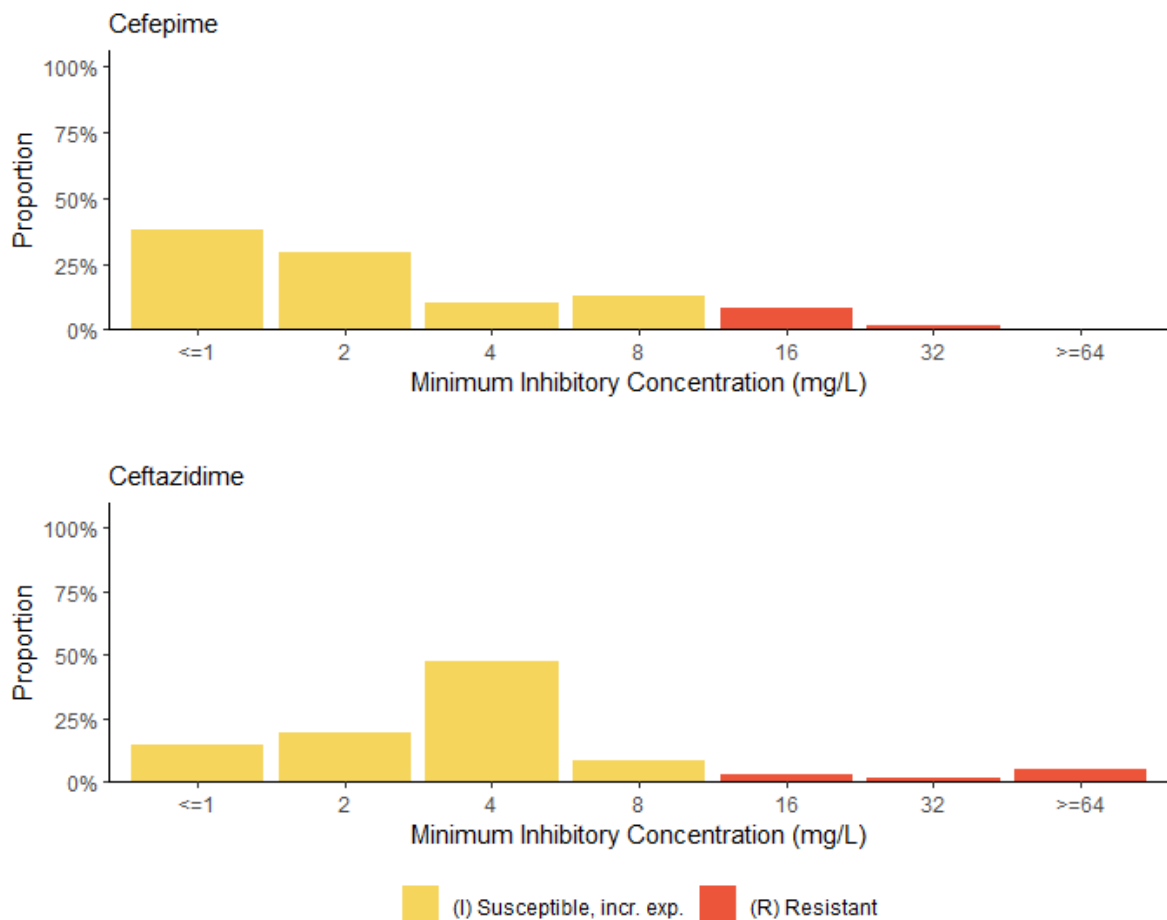*Figure 22. Proportion of ciprofloxacin resistance per state and territory in P. aeruginosa isolates reported to AGAR in 2020-2021 from patients aged <18 years*

Figure 23. Distribution of MICs against ciprofloxacin in P. aeruginosa isolates reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoint for ciprofloxacin in P. aeruginosa is 0.5mg/L, according to EUCAST 2022.

Meropenem

Only two *P. aeruginosa* were reported meropenem resistant (3.3%; 95%CI: 0.4-11.3%) – one isolate from Queensland (1/13, 7.7%), and one isolate from Victoria (1/5, 20%). The two isolates were reported in children aged 1-4 years. Most isolates had a meropenem MIC of ≤0.25 mg/L [Figure 25].
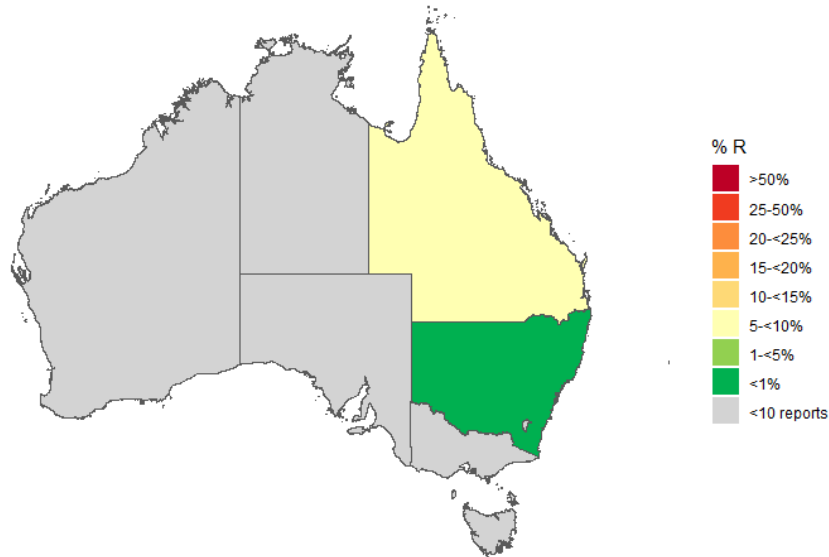
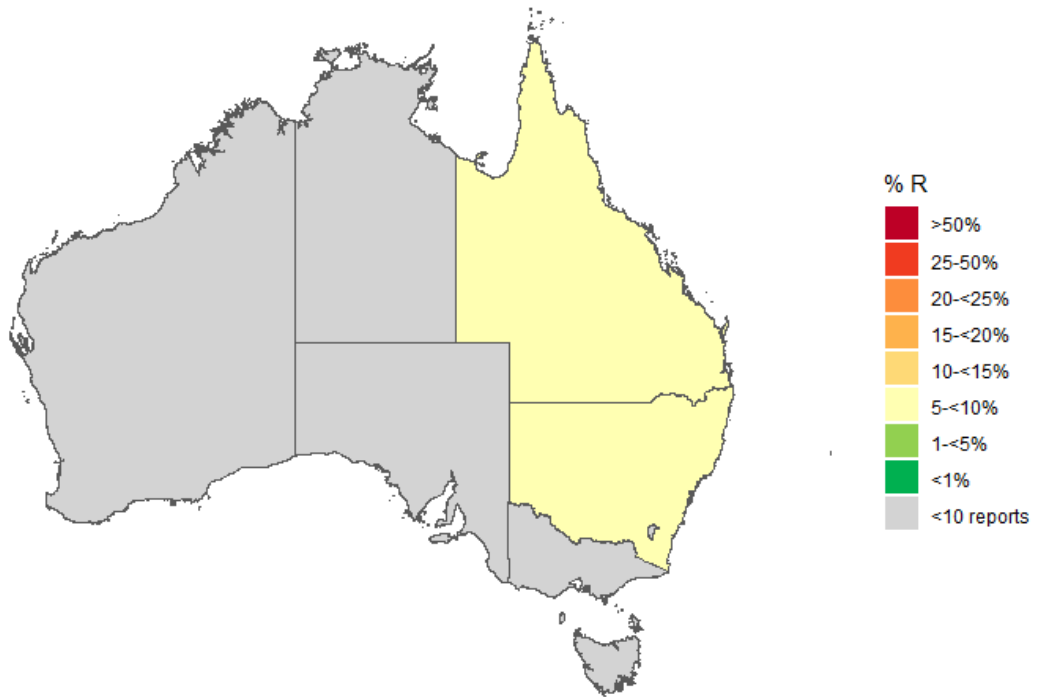*Figure 24. Proportion of meropenem resistance per state and territory in P. aeruginosa isolates reported to AGAR in 2020-2021 from patients aged <18 years*
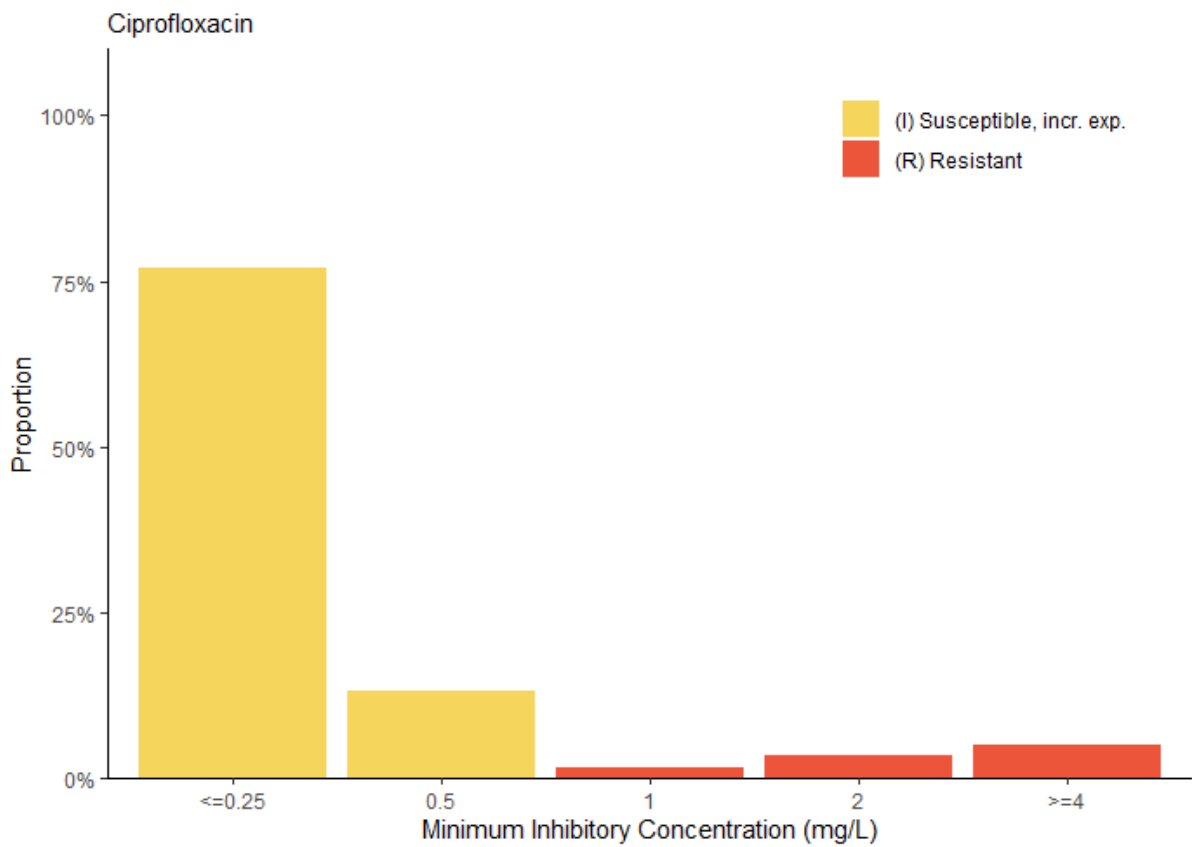

Figure 25. Distribution of MICs against meropenem in P. aeruginosa isolates reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoint for meropenem in P. aeruginosa for infections other than meningitis is 8mg/L, according to EUCAST 2022.

5.3.2. Multi-drug resistance

Only three *P. aeruginosa* were identified as MDR – one from NSW and two from SA [Table 34].

Table 34. Number of Pseudomonas aeruginosa isolates resistant to number of antimicrobial classes[4]

	Number of antimicrobial classes resistant						
	Not multidrug resistant					Multidrug resistant	
	0	*1*	*2*	*%*		*3*	*%*
ACT	0	0	0			0	
NSW	19	3	4	96.3		1	3.7
NT	1	0	0	100		0	
Qld	10	1	2	100		0	
SA	2	0	1	60		2	40
Tas	1	0	0	100		0	
Vic	4	1	0	100		0	
WA	9	0	0	100		0	

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[4] Antimicrobial classes (agents) were aminoglycosides (amikacin, gentamicin, tobramycin), anti-pseudomonal penicllins + β-lactamase inhibitors (piperacillin-tazobactam), Carbapenems (meropenem), extended spectrum cephalosporins (cefepime, ceftazidime, ceftriaxone), and fluoroquinolones (ciprofloxacin)

5.4. *Acinetobacter* spp.

Forty-one *Acinetobacter* spp. isolates were reported to AGAR; 27 in 2020, and 14 in 2021. The most reported species/complex was *A. baumannii* complex. No *Acinetobacter* isolates were MDR [Table 35].

Table 35. Acinetobacter spp. reported and characteristics of patients <18 years reported to AGAR in 2020-2021

Characteristic	2020 n = 27 (%)	2021 n = 14 (%)	Overall n = 41 (%)
Species			
Acinetobacter baumannii complex	10 (37)	8 (57.1)	18 (43.9)
Acinetobacter johnsonii	1 (3.7)	0	1 (2.4)
Acinetobacter lwoffii	6 (22.2)	4 (28.6)	10 (24.4)
Acinetobacter soli	0	1 (7.1)	1 (2.4)
Acinetobacter species	4 (14.8)	1 (7.1)	5 (12.2)
Acinetobacter ursingii	6 (22.2)	0	6 (14.6)
Age *(median)*	2 years	3.5 years	2 years
(IQR)	(0, 3.5)	(1, 5.8)	(0, 5)
Age Group			
≤28 days	2 (7.4)	0	2 (4.9)
29-90 days	3 (11.1)	1 (7.1)	4 (9.8)
91-364 days	3 (11.1)	2 (14.3)	5 (12.2)
1-4 years	13 (48.1)	5 (35.7)	18 (43.9)
5-17 years	6 (22.2)	6 (42.9)	12 (29.3)
Sex			
Female	12 (44.4)	5 (35.7)	17 (41.5)
Male	15 (55.6)	9 (64.3)	24 (58.5)
State			
ACT	0	0	0
NSW	10 (37)	6 (42.9)	16 (39)
NT	2 (7.4)	1 (7.1)	3 (7.3)
Qld	4 (14.8)	3 (21.4)	7 (17.1)
SA	4 (14.8)	0	4 (9.8)
Tas	2 (7.4)	1 (7.1)	3 (7.3)
Vic	2 (7.4)	1 (7.1)	3 (7.3)
WA	3 (11.1)	2 (14.3)	5 (12.2)
Onset			
Community	13 (48.1)	10 (71.4)	23 (56.1)
Hospital	14 (51.9)	4 (28.6)	18 (43.9)
Length of Stay *median*	17 days	12 days	12 days
(IQR)	(5, 32)	(8, 16)	(6, 28)
Polymicrobial	10 (37.0)	4 (28.6)	14 (34.1)
MDR			
Not MDR	27 (100)	14 (100)	41 (100)
Mortality*	0	1 (7.1)	1 (2.4)

*As reported by 30 days. Population data for this table is at isolate level.

5.4.1. Susceptibility testing results

Meropenem

All *Acinetobacter* isolates were meropenem susceptible [Figure 32].

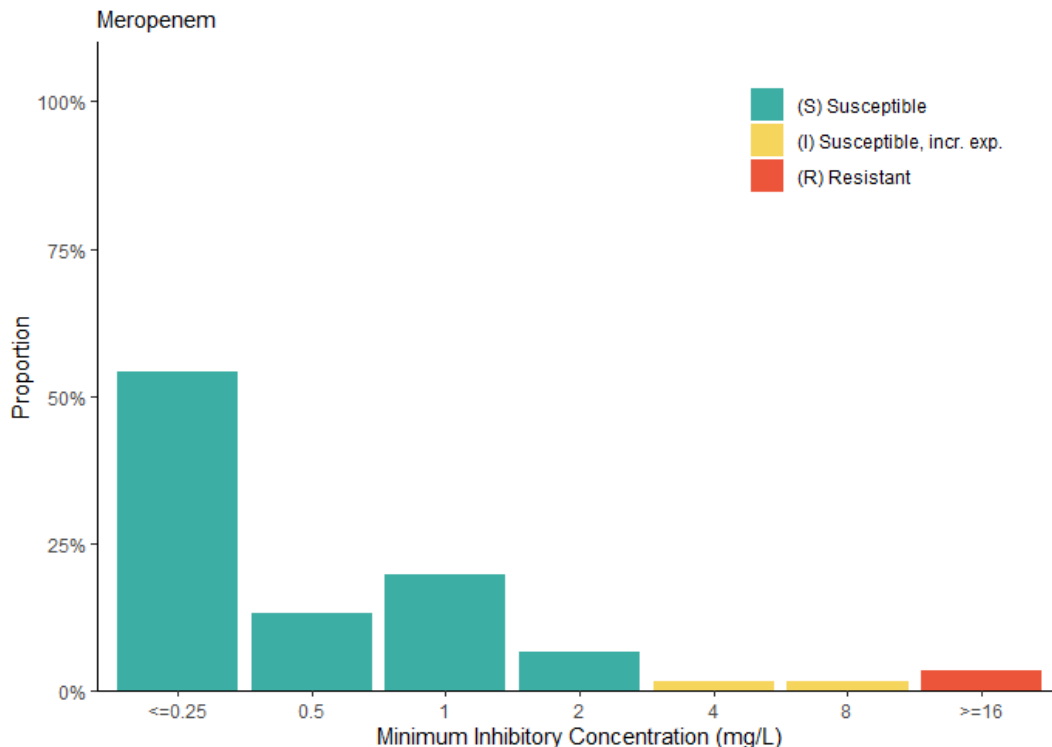*Figure 26. Distribution of MICs against meropenem in Acinetobacter isolates reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoint for meropenem in Acinetobacter species for indications other than meningitis is 8mg/L according to EUCAST 2022.*

Ciprofloxacin

One *Acinetobacter* isolate was reported as ciprofloxacin resistant [Figure 27]. The isolate, from WA, was not speciated and came from a child aged 91-364 days old with a hospital-onset infection.

Figure 27. Distribution of MICs against ciprofloxacin in Acinetobacter isolates reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoint for ciprofloxacin in Acinetobacter species is 1mg/L according to EUCAST 2022.

Amikacin

One Acinetobacter isolate was reported amikacin resistant [Figure 28]; an isolate, identified as A. *ursingii*, from Tasmania was from a child aged 5-17 years with a hospital-onset infection.
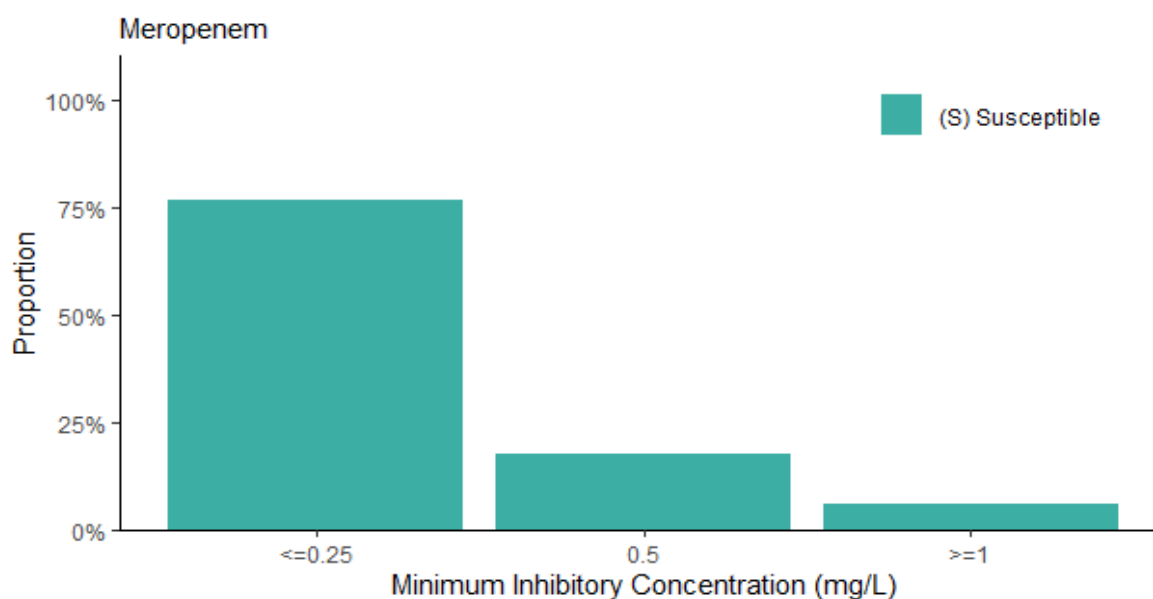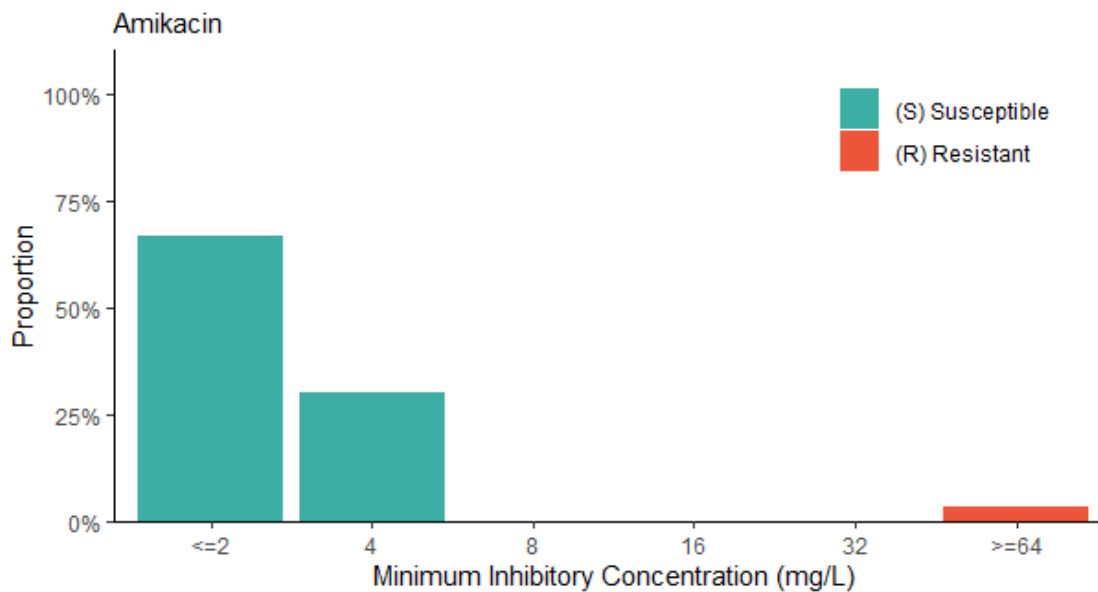

Figure 28. Distribution of MICs against amikacin in Acinetobacter isolates reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoint for amikacin in Acinetobacter species is 4mg/L according to EUCAST 2022.

Trimethoprim/Sulfamethoxazole

Three isolates were resistant to co-trimoxazole (8.6%; 95%CI: 1.8 – 23.1%) [Figure 29]. All resistant isolates were reported from patients ages 1-4 years. Two resistant isolates were from WA, and one resistant isolate was from Victoria.
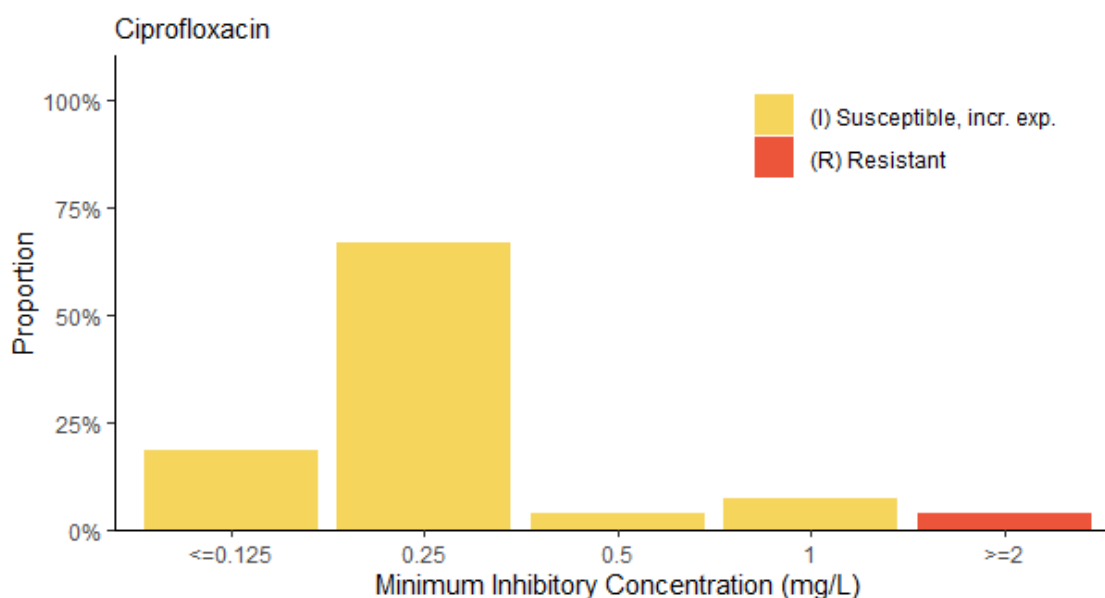

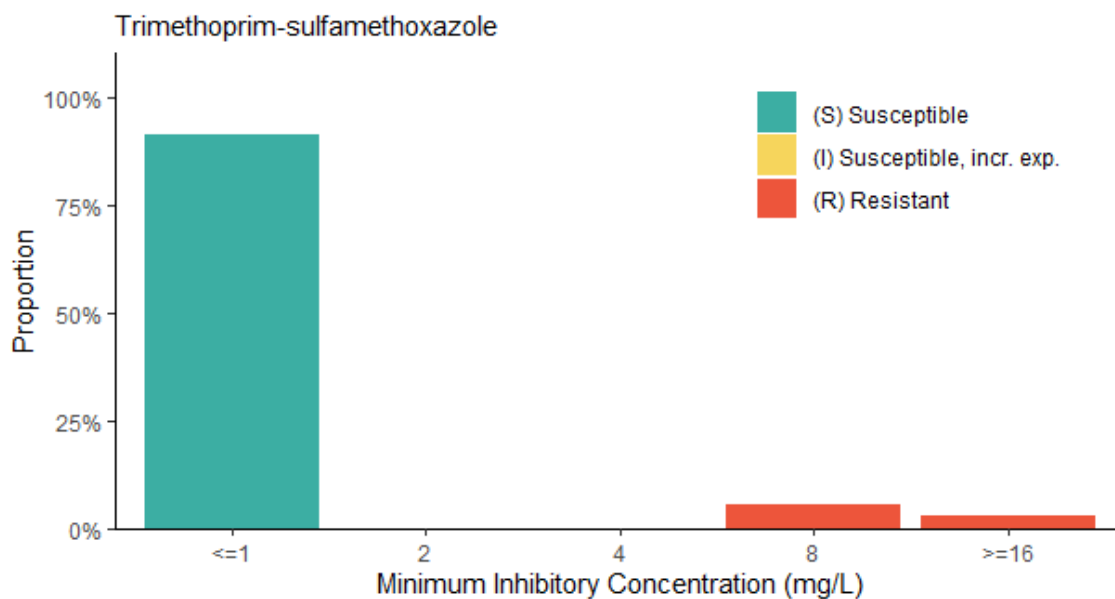*Figure 29. Distribution of MICs against trimethoprim/sulfamethoxazole in Acinetobacter isolates reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoint for trimethoprim/sulfamethoxazole in Acinetobacter species is 4mg/L according to EUCAST 2022.*

5.5. Molecular epidemiology

5.5.1. Extended Spectrum β-Lactamases (ESBLs)

Resistances conferred by ESBL-containing gram-negative organisms are clinically important, particularly in the hospital environment, and are an increasing challenge in the community.

ESBLs are clinically important as they compromise the efficacy of third generation cephalosporins, which have been an important therapeutic alternative for infections in patients presenting from the community. ESBL-producing isolates are often co-resistant to other non-β-lactam agents. The lack of available oral options for treatment can result in unnecessary hospitalisation and, in the setting of bacteraemia, increased risk of mortality.

Most ESBL-producing isolates will be detected using the CLSI/EUCAST ceftriaxone 'susceptible' breakpoint of 1 mg/L. The CLSI 'susceptible' breakpoint of 4 mg/L for ceftazidime is less reliable for ESBL detection. Isolates with either ceftriaxone or ceftazidime MICs above 1 mg/L were referred for further investigation including sequencing. Neither ceftriaxone nor ceftazidime testing will identify ESBL production in *Enterobacter* species because of their intrinsic chromosomal AmpC β-lactamase. In *Enterobacter*, cefepime MICs of greater than 0.25 mg/L suggest the isolate harbours an ESBL. However, due to the cefepime concentration range available on the susceptibility cards, isolates with a cefepime MIC of greater than 1 mg/L were referred and underwent sequencing.

Overall, 99 Enterobacterales expressed an ESBL phenotype including 48 *E. coli*, 26 *K. pneumoniae* complex and 14 *E. cloacae* complex isolates. The proportion of all *Enterobacterales* isolates with an ESBL phenotype was highest in Victoria and this is true also for *E. coli* and *K. pneumonia* complex isolates [Table 36/Figure 30].

Table 36. Number and proportion of Gram-negative isolates with a phenotype suggestive of extended spectrum β-lactamase producing in 2020-2021

	ACT	NSW	NT	Qld	SA	Tas	Vic	WA	AUS
ESBL	1	35	3	5	5	0	44	6	99
%	4.6	13.3	8.1	5.1	8.9	0	18.5	9.1	12.4
Not ESBL	22	229	34	94	51	17	194	60	701

Table 37 Number and proportion of E. coli and K. pneumoniae complex isolates that had an MIC of ≥2 mg/L for either ceftazidime and/or ceftriaxone.

		ACT	NSW	NT	Qld	SA	Tas	Vic	WA	AUS
E. coli	**ESBL**	1	18	2	1	4	0	17	5	48
	%	5.6	14.3	8.3	3.8	11.8	--	15.5	15.2	12.7
	Not ESBL	17	108	22	25	30	7	93	28	330
***K. pneumoniae* complex**	**ESBL**	0	7	1	0	0	0	18	0	26
	%	--	17.5	--	0.0	--	--	40.0	--	21.3
	Not ESBL	2	33	1	17	6	3	27	7	96
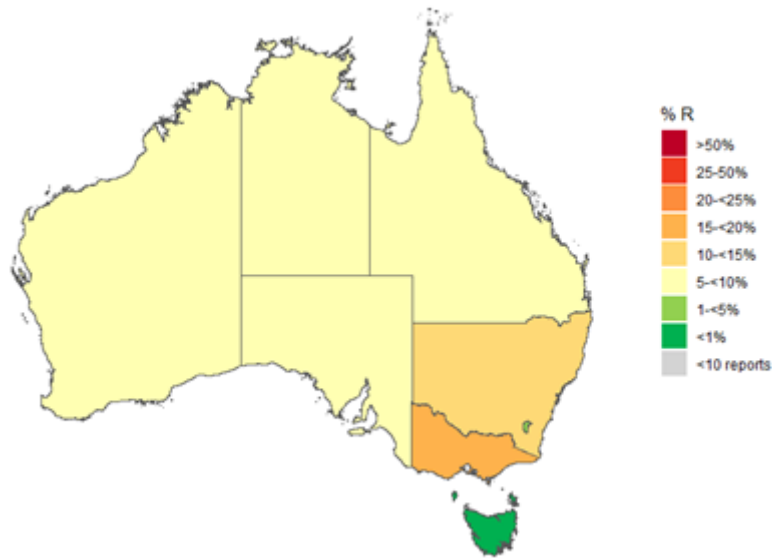
Figure 30. Proportion of Enterobacterales isolates reported in each state which had an MIC of ≥2 mg/L for either ceftazidime and/or ceftriaxone.

Table 38. Minimum inhibitory concentrations for K. pneumoniae complex, E. coli and P. aeruginosa to ceftazidime and ceftriaxone, and the number of isolates that exhibit the extended-spectrum β-lactamase phenotype. The dotted line indicates the breakpoint for the respective organism and antimicrobial agent.

	MIC (mg/L)	*K. pneumoniae complex*	*E. coli*	*P. aeruginosa*
Ceftazidime	≤0.12	2	5	
	≤0.5	8	24	
	≤1	87	299	9
	2	2	1	12
	4	2	21	29
	8	3		5
	16	6	15	2
	≥32	4	1	1
	≥64	8	8	3
	N/A		4	
Ceftriaxone	≤0.25	2	5	
	≤0.5	8	25	
	≤1	87	301	
	2		1	
	≥4	2	3	
	8	1	1	
	16	3	1	12
	≥32	3	2	9
	≥64	16	35	13
	N/A		4	23

Note: Extended spectrum β-lactamase phenotype defined as ceftriaxone or ceftazidime MIC > 1 mg/L
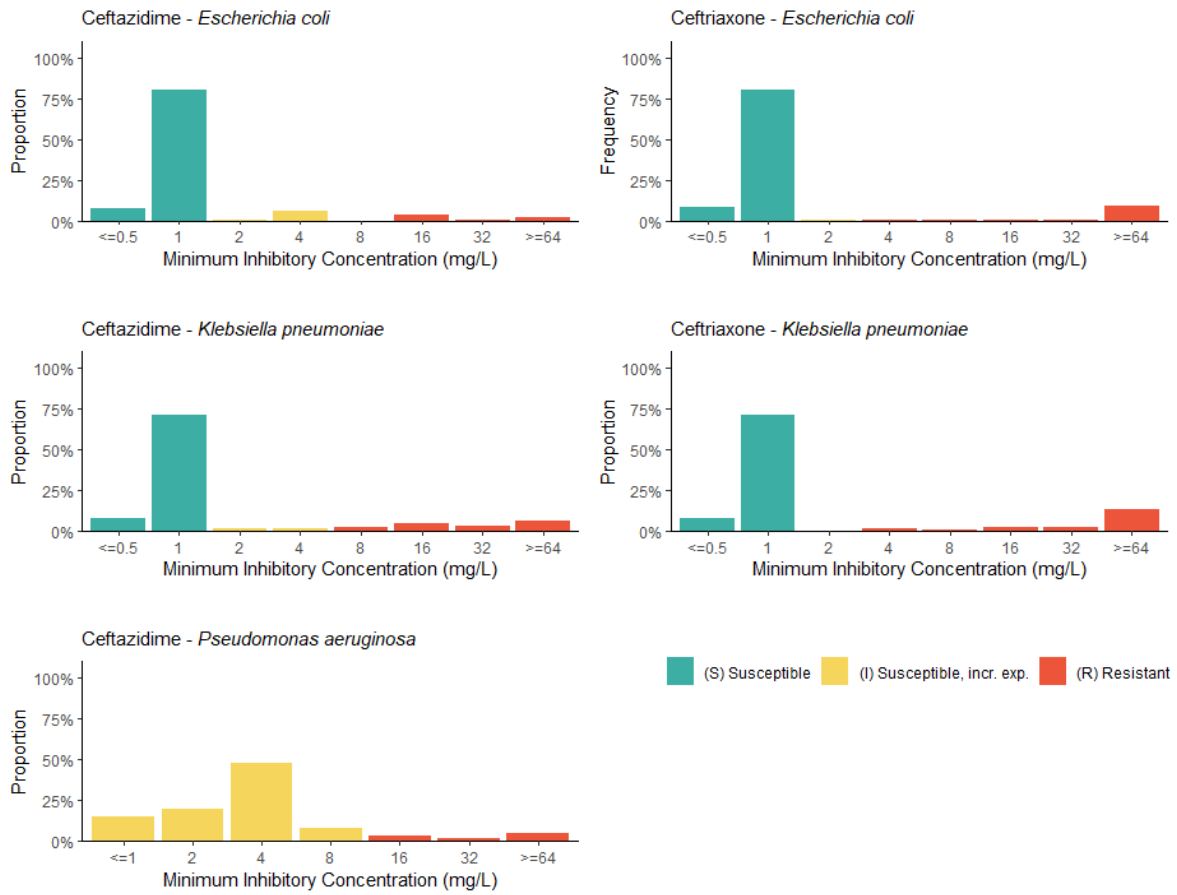
Figure 31. Minimum inhibitory concentrations for E. coli, K. pneumoniae complex and P. aeruginosa for ceftazidime and ceftriaxone

Table 39. Minimum inhibitory concentrations for Enterobacterales to ceftazidime and ceftriaxone, and the number of isolates that exhibit the extended-spectrum β-lactamase phenotype, per state and territory. The dotted line indicates the breakpoint for the respective antimicrobial agent.

	MIC (mg/L)	ACT	NSW	NT	Qld	SA	Tas	Vic	WA
Ceftazidime	≤0.12		11						
	≤0.5		12			33			
	≤1	22	21	33	93	17	17	193	6
	2					1		3	
	4	1	8	1		2		12	4
	8		1	1				2	
	16		1	1	3	2		9	1
	≥32		5		1			2	
	≥64		12		2			17	
Ceftriaxone	≤0.25		12						
	≤0.5		11			36			
	≤1	22	21	34	93	14	16	194	59
	2					1			1
	≥4		4			2	1		
	8		2					4	
	16		2	1	2			2	
	≥32		1						
	≥64	1	18	1	4	2		38	5

Note: Extended spectrum β-lactamase phenotype defined as ceftriaxone or ceftazidime MIC > 1 mg/L.

β-lactamase resistance genes were detected in 74 isolates across eight different species; *E. coli* was the most common species to have an ESBL detected. Victoria had the highest number of isolates with a β-lactamase resistance gene detected. The majority of isolates were from children under five years [Table 40].

Table 40. β-lactamase resistance genes detected in gram-negative organisms from patients <18 years as reported to AGAR, 2020-2021

	ESBL	AmpC	Carb	ESBL, AmpC	ESBL, Carb	Not Detected	N/A*
Total detected	*60*	*8*	*2*	*3*	*1*	*108*	*9*
Organism							
Acinetobacter lwoffii						2	
Acinetobacter ursingii						2	
Enterobacter cloacae complex	4		2		1	7	
Escherichia coli	34	4		2		11	4
Hafnia alvei						1	
Klebsiella oxytoca						3	
Klebsiella pneumoniae complex	19	3		1		8	1
Pantoea agglomerans						1	
Proteus mirabilis	2						
Pseudomonas aeruginosa						3	
Salmonella (non-Typhi)		1				56	3
Salmonella Paratyphi A						2	
Salmonella Typhi	1					12	1
State							
ACT	1					2	
NSW	18	7	1			36	2
NT				2		8	
Qld	2	1	1			17	2
SA	3					6	1
Tas						5	
Vic	32			1	1	22	3
WA	4					12	1
Age group							
<12 months	23	2	1	1	0	37	1
1-4 years	22	4	0	0	0	34	2
5-11 years	6	1	1	1	0	18	2
>12 years	9	1	0	1	1	19	4

*N/A: not available for sequencing

5.5.2. Carbapenemases

The phenotype for carbapenemase resistance in Enterobacterales is a meropenem MIC >2mg/L, and an MIC of >8mg/L in *P. aeruginosa* and *Acinetobacter* spp.

Three Enterobacterales and three *P. aeruginosa* had MICs above their meropenem breakpoint; no *Acinetobacter* isolates had a MIC above the breakpoint. The three Enterobacterales isolates had a Class B carbapenemase gene, two isolates with IMP-4, and one isolate with an NDM-1. Carbapenemase genes were not detected in the three *P. aeruginosa* isolates with a meropenem MIC >8mg/L [Table 41].

Table 41. Number of isolates with carbapenemase genes, organism group, meropenem MIC, AGAR, 2020-2021

MIC mg/L	Enterobacterales	*P. aeruginosa*	*Acinetobacter* spp.
≤0.125	47		3
≤0.25	734	33	23
≤0.5	4	8	6
1	2	12	2
2	2	4	
4		1	
≥8	1[a]	1	
≥16	2[a,b]	2	

a) IMP-4 detected b) NDM-1 detected. Note: the dotted line indicates the threshold for meropenem for phenotypic determination of carbapenemase for each respective organism.

Of the two isolates with an IMP-4 gene, one was isolated from a child in NSW aged 5-17 years, and the other from a Queensland infant aged <1 year The NDM-1 *Enterobacter cloacae* complex isolate, detected in a child aged 5-17 years from Victoria, was also an EBSL-producer.

5.5.3. Fluoroquinolone resistance

Ciprofloxacin resistance (MIC > 0.06 mg/L) in non-typhoidal *Salmonella* was 4.2% (2/48 isolates). The two Paratyphi isolates were ciprofloxacin resistant, whilst 69.2% of Typhi isolates were resistant (9/13). One *Salmonella* non-Typhi isolate had AmpC detected, and one *Salmonella* Typhi isolate had ESBL detected [Table 42].

E. coli ciprofloxacin resistance (MIC>0.25mg/L) was 17.2% (66/374 isolates). For 28 of the isolates three harboured AmpC, 24 an ESBL, and one isolate AmpC and ESBL.

K. pneumoniae complex ciprofloxacin resistance (MIC>0.25mg/L) was 27.9% (31/111 isolates). For 20 of the isolates three harboured AmpC, and 17 an ESBL.

Table 42. Salmonella, E. coli and K. pneumoniae complex minimum inhibitory concentrations to ciprofloxacin. The dotted line indicates the breakpoint threshold for each respective organism.

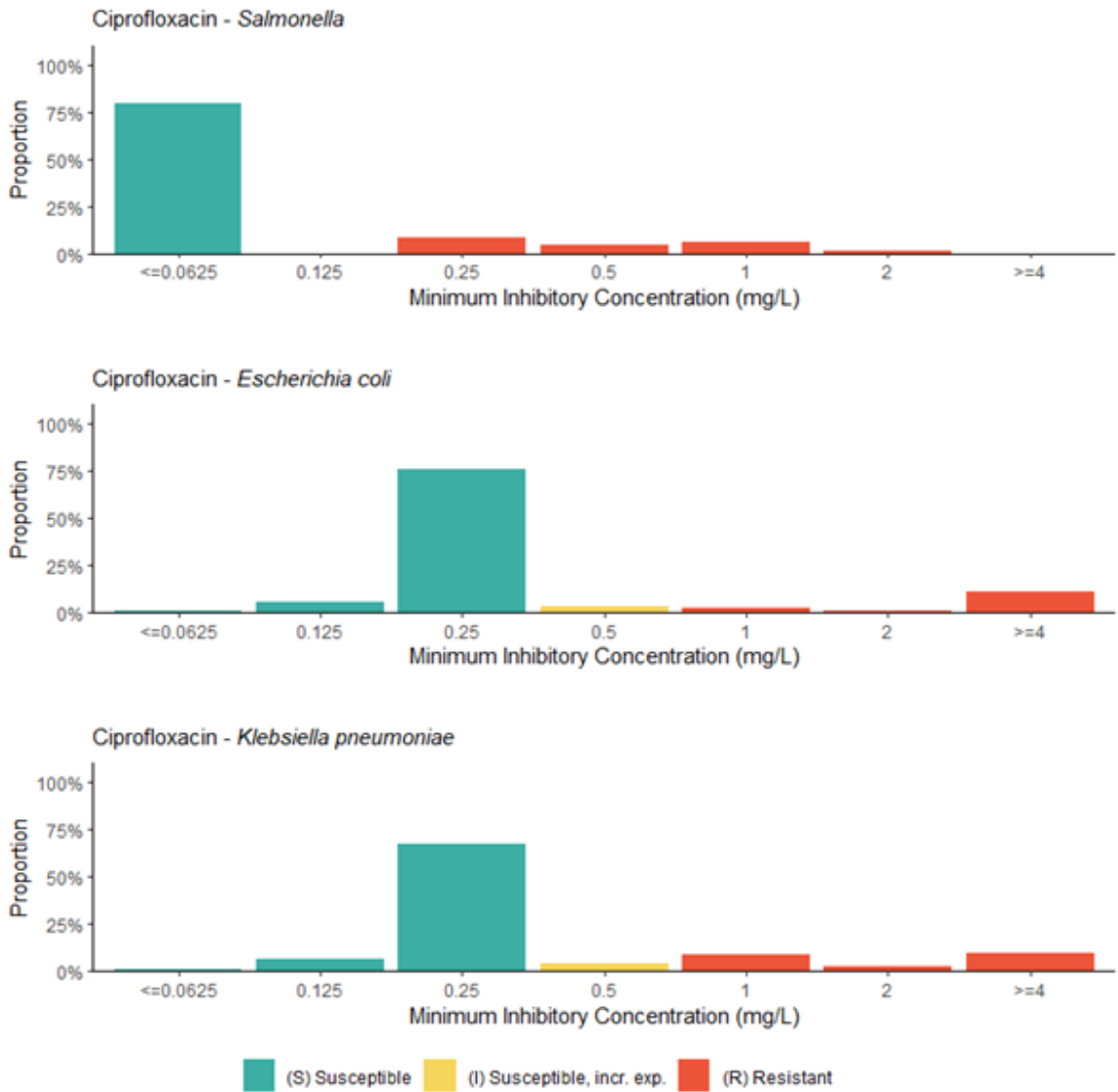|	*E. coli*	*K. pneumoniae*	*Salmonella* (non-Typhi)	*Salmonella* Paratyphi A	*Salmonella* Typhi
≤0.06	4	1	46[a]		4
≤0.125	21[b]	8			
≤0.25	283[a,b,c]	82[b,c]	2		3
0.5	13[b]	5[a,b]			3
1	10[b]	11[b]		2	2[b]
≥2	3[b]	3			1
≥4	40[a,b,c]	12[b]			

a) AmpC isolate b) ESBL isolate c) AmpC/ESBL isolate

Figure 32. Minimum inhibitory concentration frequency charts for Salmonella, E. coli and K. pneumoniae complex

6. Gram-positives

6.1. Staphylococcus aureus

There were 607 *S. aureus* reported to AGAR: 303 in 2020 and 304 in 2021. Overall, 12.9% of *S. aureus* were methicillin resistant (n: 78) and 5.6% of isolates were MDR (n: 34). The patient's median age was six years, and the number of episodes reported across the different age groups was relatively equal. The majority of isolates were reported from NSW (29%) and Victoria (25%). The majority of episodes were community-onset (79%) and were not polymicrobial (93%) [Table 43].

Table 43. Characteristics of patients <18 years reported to AGAR in 2020-2021 with an S. aureus.

	2020, n = 303	**2021, n = 304**	**Overall, n = 607**
Age *median*	6 years	6 years	6 years
(IQR)	(1, 12)	(0, 11)	(1, 11.5)
Age Group			
≤ 28 days	26 (8.6)	25 (8.2)	51 (8.4)
29-90 days	22 (7.3)	29 (9.5)	51 (8.4)
91-364 days	22 (7.3)	24 (7.9)	46 (7.6)
1-4 years	68 (22.4)	65 (21.4)	133 (21.9)
5-17 years	165 (54.5)	161 (53)	326 (53.7)
Sex			
Female	112 (37)	96 (31.6)	208 (34.3)
Male	191 (63)	208 (68.4)	399 (65.7)
State			
ACT	12 (4)	8 (2.6)	20 (3.3)
NSW	83 (27.4)	90 (29.6)	173 (28.5)
NT	12 (4)	17 (5.6)	29 (4.8)
Qld	49 (16.2)	39 (12.8)	88 (14.5)
SA	35 (11.6)	22 (7.2)	57 (9.4)
Tas	10 (3.3)	5 (1.6)	15 (2.5)
Vic	74 (24.4)	78 (25.7)	152 (25)
WA	28 (9.2)	45 (14.8)	73 (12)
Onset			
Community	241 (79.5)	237 (78)	478 (78.7)
Hospital	62 (20.5)	67 (22)	129 (21.3)
Length of Stay *(median)*	10 days	12 days	11 days
(IQR)	(7, 17)	(7, 19)	(7, 18)
Polymicrobial			
Yes	19 (6.3)	25 (8.2)	44 (7.2)
No	284 (93.7)	279 (91.8)	563 (92.8)
30-day all-cause mortality	4 (1.3)	2 (0.7)	6 (1.0)
MDR			
MDR	14 (4.6)	20 (6.6)	34 (5.6)
Not MDR	289 (95.4)	284 (93.4)	573 (94.4)
MRSA			
MRSA	43 (14.5)	35 (11.8)	78 (13.2)
MSSA	259 (85.5)	268 (88.2)	527 (86.8)

*Population data for this table is at isolate level

6.1.1. Susceptibility testing results

MRSA

The NT reported the highest proportion of *S. aureus* isolates that were MRSA (45%). MRSA was not reported in the ACT or Tasmania [Figure 33, Figure 34].

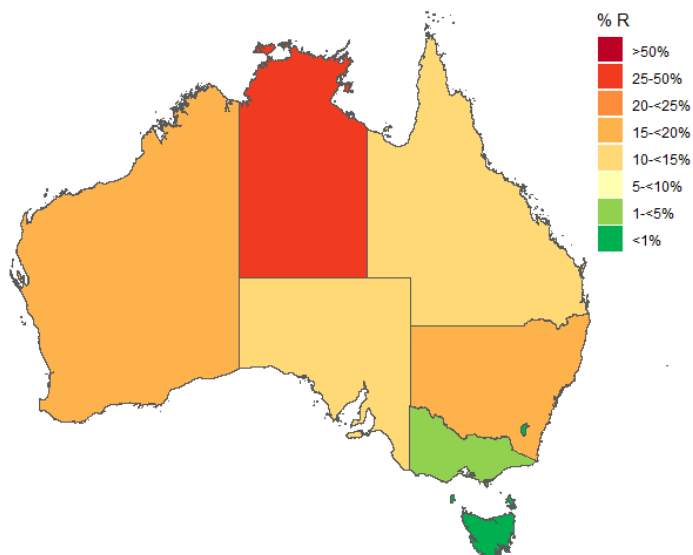*Figure 33. Proportion of S. aureus isolates reported as MRSA to AGAR in patients aged <18 years, 2020-2021*
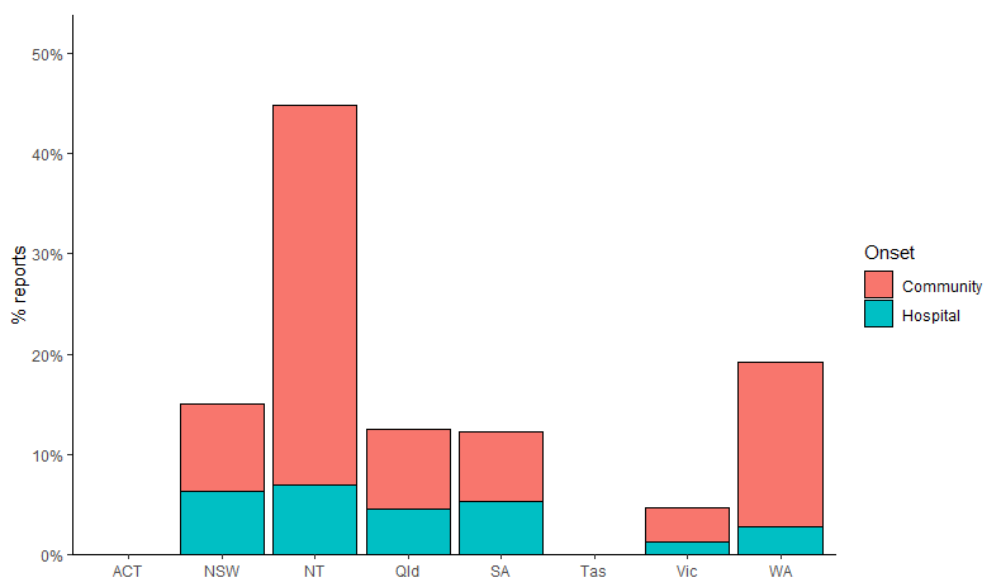
Figure 34. Methicillin-resistant Staphylococcus aureus as a percentage of all S. aureus isolates per infection onset type, by state and territory, AGAR, 2021

MRSA isolates were most frequently reported in patients aged 1-4 years, as well as those that were hospital-onset, and MDR [Table 44].

Table 44. Number and proportion of MRSA and MSSA isolates per state and territory and age group reported to AGAR from patients aged <18 years, 2020-2021

Characteristic	MRSA, n = 78	MSSA, n = 529
Age *(median)*	4 years	6 years
(IQR)	(0.3, 10)	(1, 12)
Age Group		
≤28 days	7 (13.7)	44 (86.3)
29-90 days	9 (17.6)	42 (82.4)
91-364 days	4 (8.7)	42 (91.3)
1-4 years	25 (18.8)	108 (81.2)
5-17 years	35 (10.7)	291 (89.3)
Sex		
Female	34 (16.3)	174 (83.7)
Male	46 (11.5)	353 (88.5)
State		
ACT	0	20 (100)
NSW	27 (15.6)	146 (84.4)
NT	14 (48.3)	15 (51.7)
Qld	11 (12.5)	77 (87.5)
SA	7 (12.3)	50 (87.7)
Tas	0	15 (100)
Vic	7 (4.6)	145 (95.4)
WA	14 (19.2)	59 (80.8)
Onset		
Community	56 (11.7)	422 (88.3)
Hospital	24 (18.6)	105 (81.4)
Length of Stay *(median)*	14 days	10 days
(IQR)	(9, 23)	(7, 18)
Still in at 30 days		
Yes	16 (15.8)	85 (84.2)
No	62 (12.9)	420 (87.1)
Not admitted	0	14 (100)
Unknown	2 (20)	8 (80)
MDR		
MDR	22 (64.7)	12 (35.3)
Not MDR	58 (10.1)	515 (89.9)

*Population data for this table is at isolate level

Clindamycin

Overall, 12.4% of *S. aureus* were clindamycin resistant (n: 75; 95%CI: 9.8-15.2). The NT had the highest proportion of clindamycin resistant isolates. No clindamycin resistant isolates were reported in Tasmania [Figure 35/Table 45]. All age groups <5 years reported ~15% of isolates resistant to clindamycin [Table 45]. Most isolates had an MIC of ≤0.25mg/L [Figure 36]. Resistance to clindamycin was higher in MRSA than in MSSA.

Table 45. Proportion of clindamycin resistance per state and territory and age group in S. aureus isolates reported to AGAR in 2020-2021 from patients aged <18 years

	No. tested	No. Resistant	%R	95% CI	
State					
ACT	20	3	15.0	3.2	37.9
NSW	173	29	16.8	11.5	23.2
NT	29	6	20.7	8.0	39.7
Qld	88	13	14.8	8.1	23.9
SA	57	3	5.3	1.1	14.6
Tas	15	0			
Vic	152	15	9.9	5.6	15.8
WA	73	6	8.2	3.1	17.0
Age group					
≤28 days	51	9	17.6	8.4	30.9
29-90 days	51	8	15.7	7.0	28.6
91-364 days	46	7	15.2	6.3	28.9
1-4 years	133	21	15.8	1.0	23.1
5-17 years	326	30	9.2	6.3	12.9
Onset					
Community	478	55	11.5	8.8	14.7
Hospital	129	20	15.5	9.7	22.9
Overall					
MRSA	78	15	19.2	11.2	29.7
MSSA	529	60	11.3	8.8	14.4

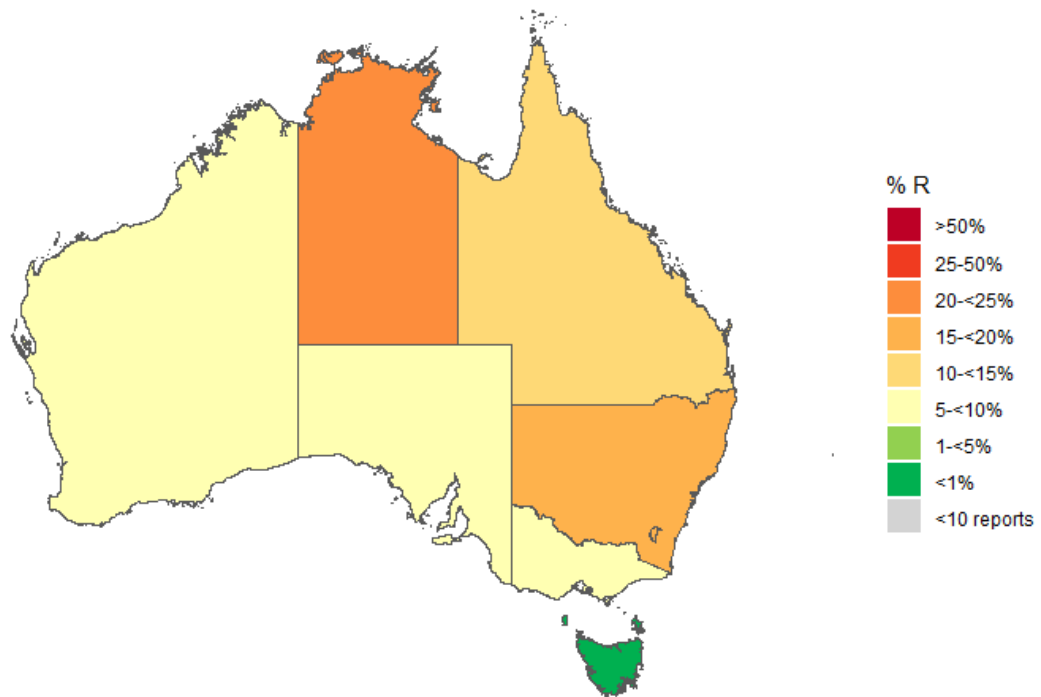*Figure 35. Proportion of clindamycin resistance per state and territory in S. aureus isolates reported to AGAR in 2020-2021 from patients aged <18 years*

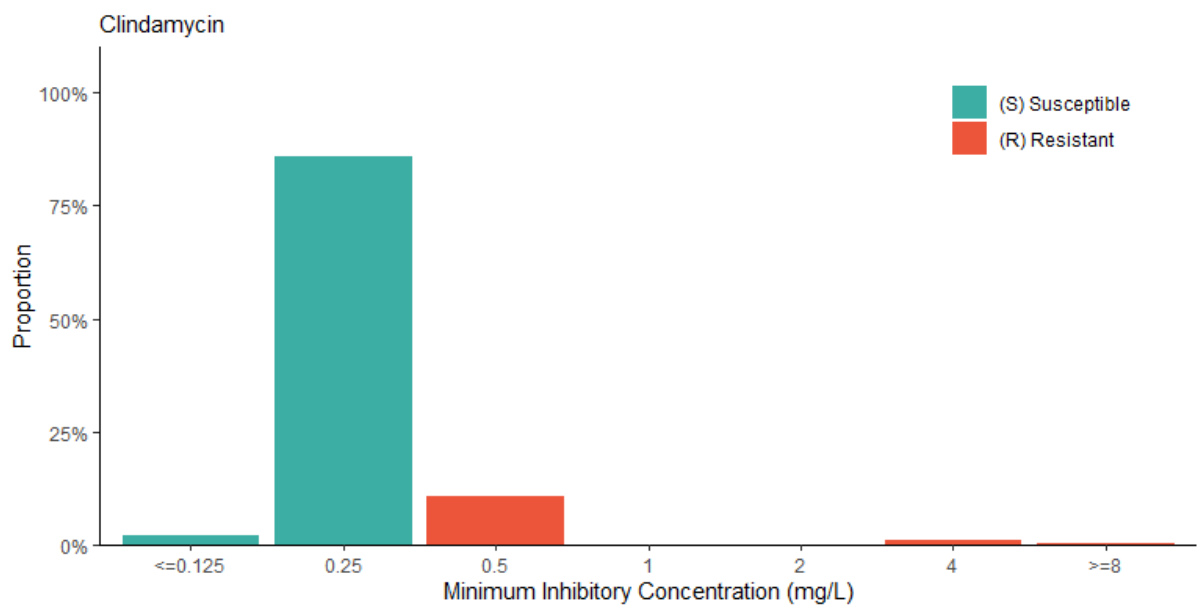*Figure 36. Distribution of MICs against clindamycin reported to AGAR 2020-2021 from S. aureus isolates in patients aged <18 years. The breakpoint for meropenem in Staphylococci is 0.25mg/L according to EUCAST 2022.*

Ciprofloxacin

Overall, 5.3% of *S. aureus* were ciprofloxacin resistant (n: 32; 95%CI: 3.6 – 7.4%); 3.6% of *S. aureus* isolates were reported as resistant in 2020 (n: 11), and 6.9% in 2021 (n: 21). The highest proportion of isolates reported as ciprofloxacin resistance was in NSW (9.8%, n: 17). No isolates were ciprofloxacin resistant in Tasmania [Figure 37]. Resistant isolates were most frequently reported in patients aged 91 – 364 days [Table 46]. Most *S. aureus* had a ciprofloxacin MIC of ≤0.5mg/L [Figure 38]. Resistance to ciprofloxacin was higher in MRSA isolates than MSSA isolates.

Table 46. Proportion of clindamycin resistance per state and territory and age group in S. aureus isolates reported to AGAR in 2020-2021 from patients aged <18 years

	No. isolates	No. resistant	% R	95%CI	
State					
ACT	20	1	5.0	0.1	24.9
NSW	173	17	9.8	5.8	15.3
NT	29	1	3.4	0.1	17.8
Qld	88	4	4.5	1.3	11.2
SA	57	3	5.3	1.1	14.6
Tas	15	0			
Vic	152	4	2.6	0.7	6.6
WA	73	2	2.7	0.3	9.5
Age group					
≤28 days	51	4	7.8	2.2	18.9
29-90 days	51	2	3.9	0.5	13.5
91-364 days	46	6	13.0	4.9	26.3
1-4 years	133	8	6.0	2.6	11.5
5-17 years	326	12	3.7	1.9	6.3
Onset					
Community	478	22	4.6	2.9	6.9
Hospital	129	10	7.8	3.8	13.8
Overall					
MRSA	78	13	16.7	9.2	26.8
MSSA	529	19	3.6	2.2	5.6

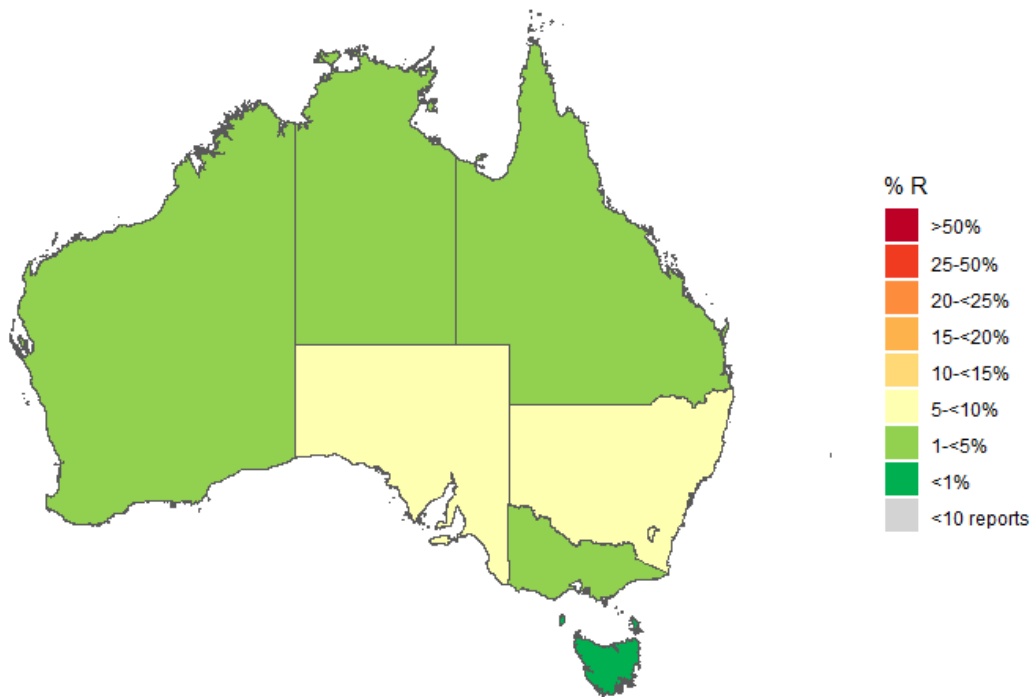*Figure 37. Proportion of ciprofloxacin resistance per state and territory in S. aureus isolates reported to AGAR in 2020-2021 from patients aged <18 years*
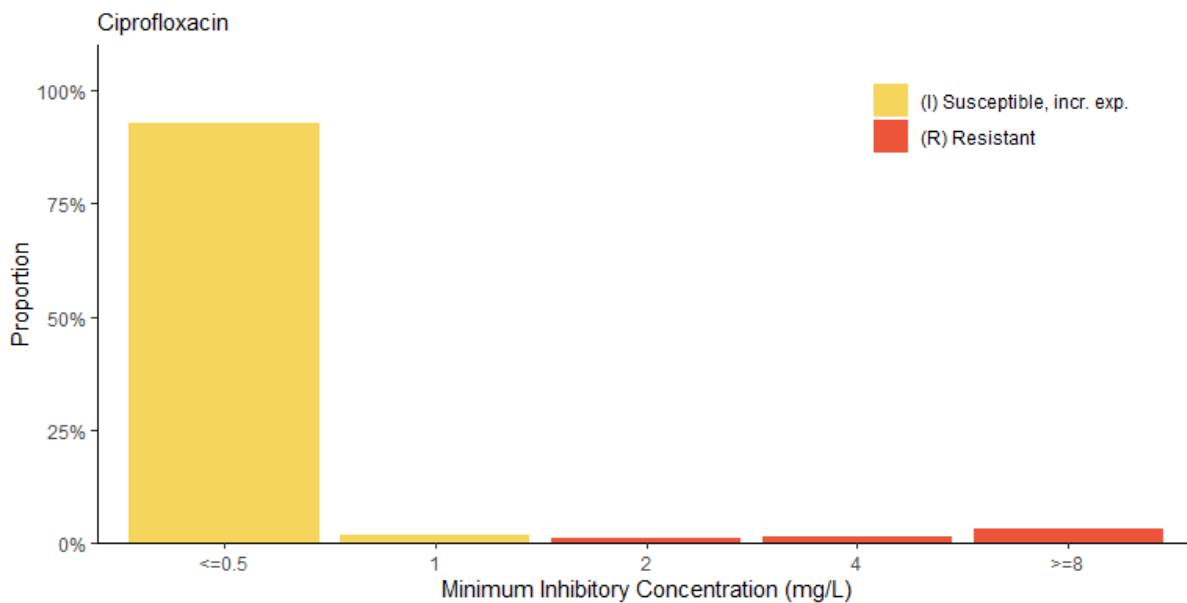

Figure 38. Distribution of MICs against ciprofloxacin reported to AGAR 2020-2021 from S. aureus isolates in patients aged <18 years. The breakpoint for meropenem in S. aureus is 1mg/L according to EUCAST 2022.

Erythromycin

Overall, 13.2% of *S. aureus* were erythromycin resistant (n: 80; 95%CI: 10.6-16.1%): 11.2% of isolates in 2020 were resistant (n: 34), whilst 15.1% of isolates were resistant in 2021 (n: 46). The highest proportion of erythromycin resistant isolates were reported in the NT (20.7%, n: 6), and from neonatal patients (19.6%, n: 10) [Figure 39/Table 47]. Most isolates had an erythromycin MIC ≤1mg/L [Figure 40].

Table 47. Proportion of erythromycin resistance per state and territory and age group in S. aureus isolates reported to AGAR in 2020-2021 from patients aged <18 years

	No. isolates	No. resistant	% R	95%CI	
State					
ACT	20	2	10.0	1.7	29.3
NSW	173	28	16.2	11.3	22.2
NT	29	6	20.7	8.8	38.2
Qld	88	14	15.9	9.4	24.7
SA	57	7	12.3	5.5	22.8
Tas	15	0	0.0		
Vic	152	17	11.2	6.9	17.0
WA	73	6	8.2	3.4	16.3
Age group					
≤ 28 days	51	10	19.6	9.8	33.1
29-90 days	51	9	17.6	8.4	30.9
91-364 days	46	5	10.9	3.6	23.6
1-4 years	133	24	18.0	11.9	25.6
5-17 years	326	32	9.8	6.8	13.6
Onset					
Community	478	59	12.3	9.5	15.6
Hospital	129	21	16.3	10.4	23.8
Overall					
MRSA	78	18	23.1	14.3	34.0
MSSA	529	62	11.7	9.1	14.8
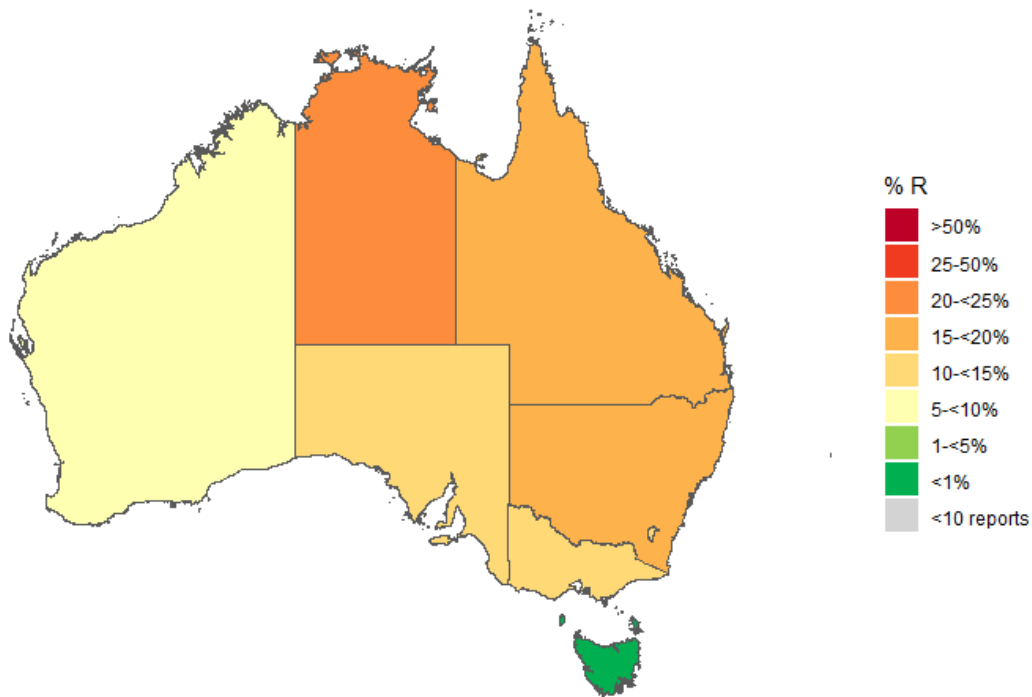
Figure 39. Proportion of erythromycin resistance per state and territory in S. aureus isolates reported to AGAR in 2020-2021 from patients aged <18 years

Figure 40. Distribution of MICs against ciprofloxacin reported to AGAR 2020-2021 from S. aureus isolates in patients aged <18 years. The breakpoint for meropenem in S. aureus is 2mg/L according to EUCAST 2022.

Trimethoprim/Sulfamethoxazole

No *S. aureus* isolates were reported trimethoprim-sulfamethoxazole, with most isolates having a MIC ≤0.5 (n: 574, 95.5%). Of the six isolates reported with an increased exposure (I), three were MRSA. All six isolates were from community-onset episodes, and one isolate was reported from each jurisdiction except the ACT or Tasmania.

Figure 41. Distribution of MICs against trimethoprim-sulfamethoxazole reported to AGAR 2020-2021 from S. aureus isolates in patients aged <18 years. The breakpoint for meropenem in S. aureus is 4mg/L according to EUCAST 2022.

Vancomycin

No *S. aureus* were reported with increased exposure (I) or resistant to vancomycin. Most isolates had a vancomycin MIC of 1 mg/L [Figure 42].

Figure 42. Distribution of MICs against vancomycin reported to AGAR 2020-2021 from S. aureus isolates in patients aged <18 years. The breakpoint for vancomycin in S. aureus is 2mg/L according to EUCAST 2022.

Mupirocin

For *S. aureus* there are no EUCAST clinical breakpoints for mupirocin. Of the 59 isolates that were tested against mupirocin, most were reported with an MIC ≤0.5mg/L (43 isolates, 73%). Nine isolates were reported to have a MIC ≥512mg/L (15.3%) [Figure 43].

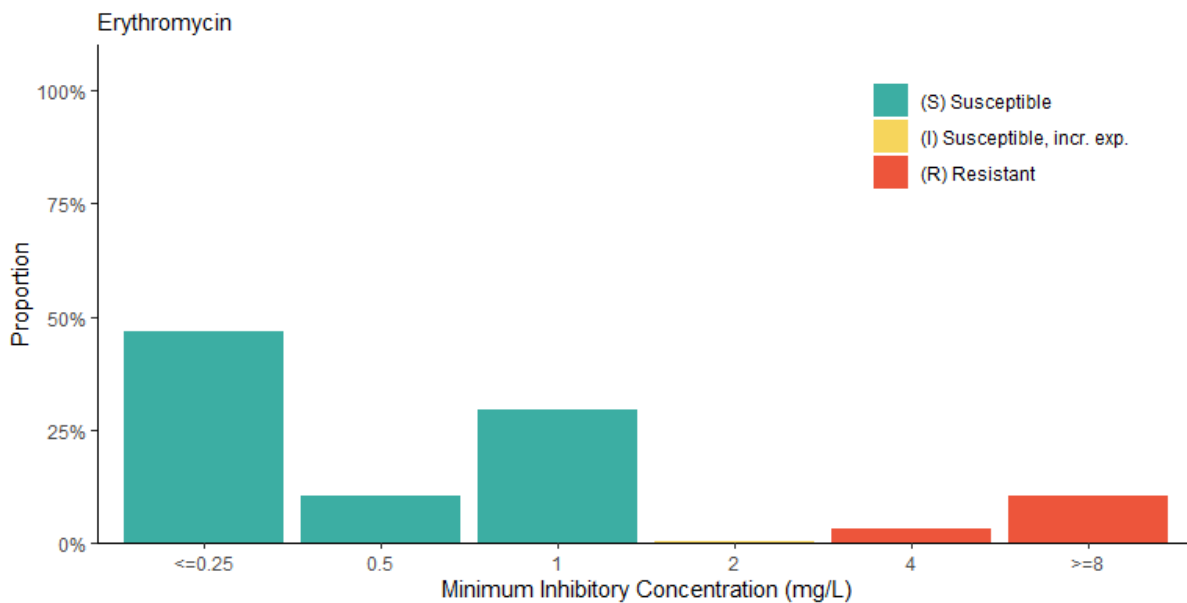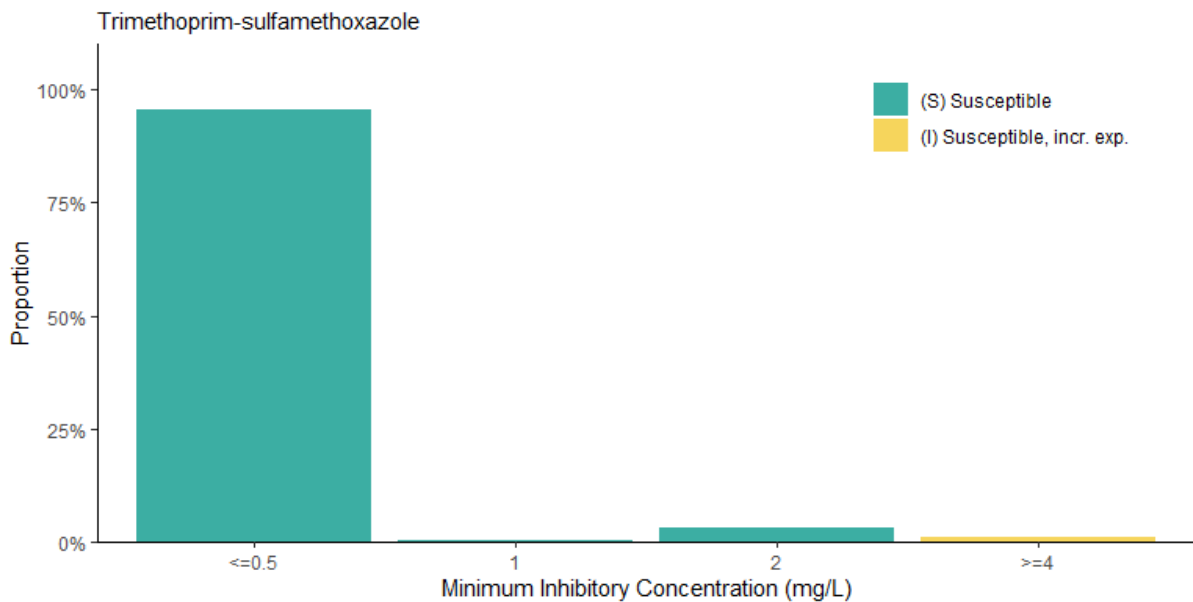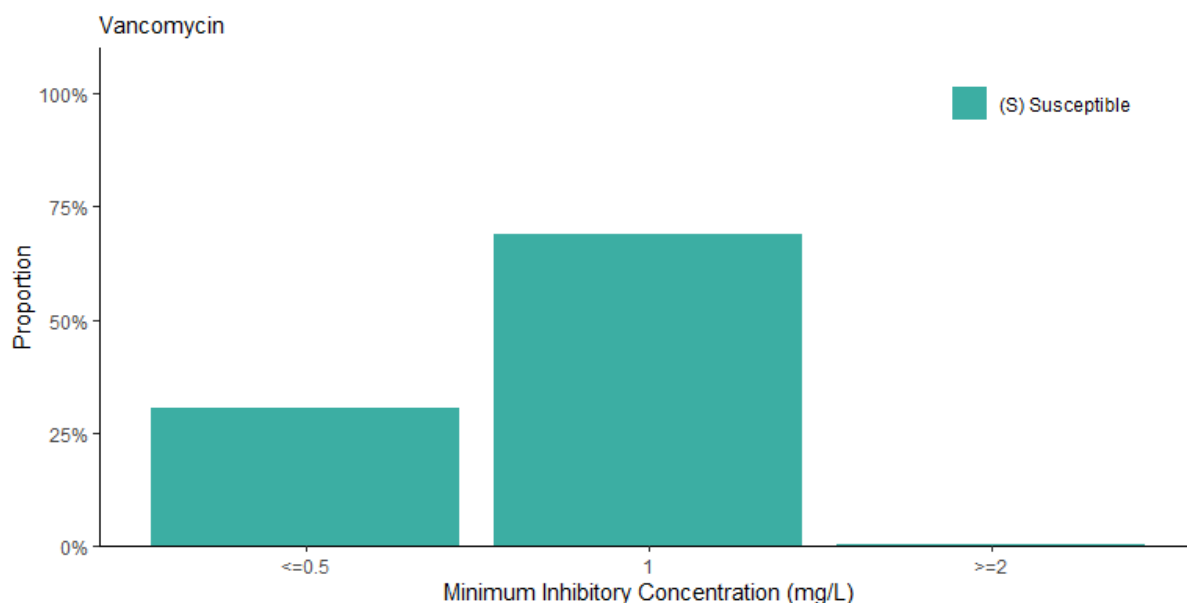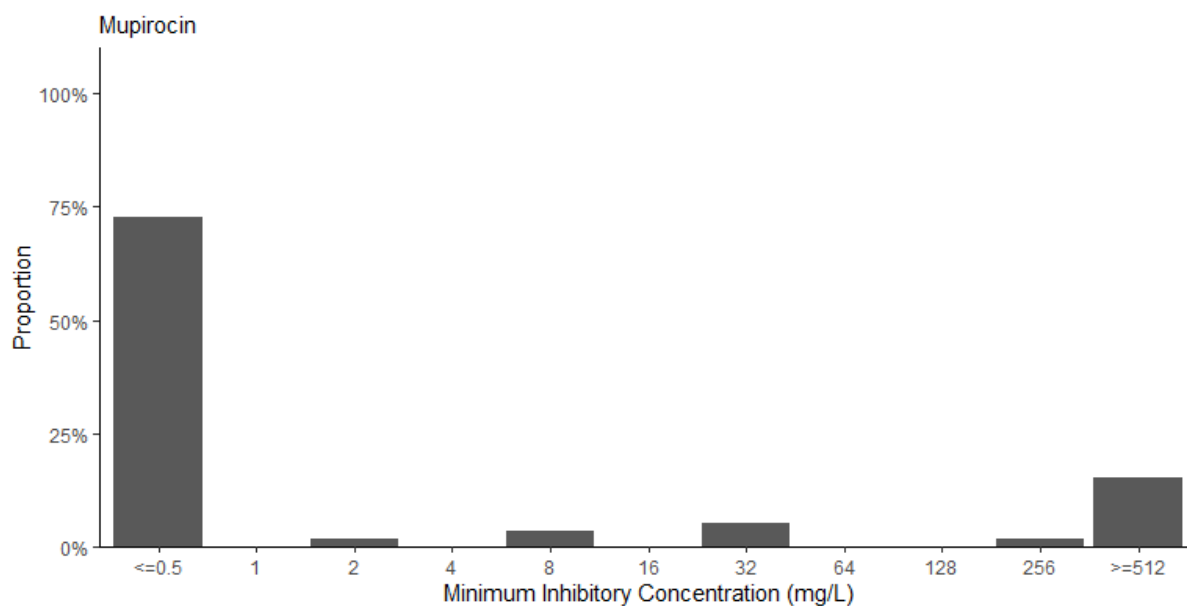*Figure 43. Distribution of MICs against mupirocin reported to AGAR 2020-2021 from S. aureus isolates in patients aged <18 years. There are no breakpoints for mupirocin reported in EUCAST 2022.*

6.1.2. Multi-drug resistance

Overall, 5.6% of all *S. aureus* were MDR (n: 34); 64.7% were MRSA (n: 22) [Table 48].

Table 48. Proportion of S. aureus isolates that are multidrug resistant, by methicillin resistance.

	MDR *% (n)*	Not MDR *% (n)*
MRSA	28.2% (22)	71.8% (56)
MSSA	2.3% (12)	97.7% (517)

NSW had the highest proportion of MRSA isolates that were MDR, and the ACT had the highest proportion of MSSA isolates that were classified as MDR. Queensland had no MRSA isolates that were MDR and Tasmania had no MDR MSSA or MRSA [Table 49].

Table 49. Number of S. aureus isolates resistant to number of antimicrobial classes, by methicillin resistance status[5]

	MRSA: Number of antimicrobial classes resistant							
	Not multidrug resistant				Multidrug resistant			
	0	*1*	*2*	*%*	*3*	*4*	*5*	*%*
ACT	0	0	0		0	0	0	
NSW	0	9	6	55.6	6	3	3	44.4
NT	0	11	0	78.6	3	0	0	21.4
Qld	0	10	1	100.0	0	0	0	
SA	0	4	1	71.4	1	1	0	28.6
Tas	0	0	0		0	0	0	
Vic	0	5	0	71.4	1	1	0	28.6
WA	0	11	0	78.6	2	0	1	21.4
	MSSA: Number of antimicrobial classes resistant							
ACT	15	3	0	90.0	2	0	0	10.0
NSW	118	8	17	97.9	1	1	1	2.1
NT	10	1	3	93.3	1	0	0	6.7
Qld	51	14	11	98.7	1	0	0	1.3
SA	40	6	3	98.0	1	0	0	2.0
Tas	15	0	0	100.0	0	0	0	
Vic	119	10	13	97.9	3	0	0	2.1
WA	51	5	2	98.3	1	0	0	1.7

A statistically significant difference in the age was identified in patients with a MDR *S. aureus* episode compared to patients with a non-MDR *S. aureus* (*p*: <0.001). MDR *S. aureus* episodes are more likely to be hospital-onset (*p*: <0.001), however MDR infections were not more device-related (*p*: 0.06) [Table 50].

---

[5] Antimicrobial classes (agents) were aminoglycosides (amikacin, gentamicin, tobramycin), ansamycins (rifampicin), cephamycins/anti-staphylococcal β-lactams (cefoxitin), fluoroquinolones (ciprofloxacin), folate pathway inhibitors (trimethoprim-sulfamethoxazole), fusidic acid, glycopeptides (vancomycin, teicoplanin), lincosamides (clindamycin), lipopeptides (daptomycin), macrolides (erythromycin), oxazolidinones (linezolid), phenicols (chloramphenicol) and tetracyclines (tetracycline, doxycycline)

Table 50. Characteristics of patients with an S. aureus isolate and multidrug resistance.

	MDR, n = 34	Not MDR, n = 573
Age *median*	<12 months	6 years
(IQR)	(0, 3.8)	(1, 12)
Age Group		
<12 months	18 (12)	130 (88)
1-4 years	12 (9.0)	121 (91)
5-11 years	2 (1.1)	172 (99)
> 12 years	2 (1.3)	150 (99)
Sex		
Female	15 (7.2)	193 (93)
Male	19 (4.8)	380 (95)
Onset		
Community	18 (3.8)	460 (96)
Hospital	16 (12)	113 (88)
State		
ACT	2 (10)	18 (90)
NSW	15 (8.7)	158 (91)
NT	4 (14)	25 (86)
Qld	1 (1.1)	87 (99)
SA	3 (5.3)	54 (95)
Tas	0	15 (100)
Vic	5 (3.3)	147 (97)
WA	4 (5.5)	69 (95)
Device-related		
Yes	7 (6.5)	101 (94)
No	23 (4.9)	451 (95)
Unknown	4 (16)	21 (84)
Principal manifestation		
CNS infection (meningitis, abscess(es))	0	4 (100)
Deep abscess(es) excluding those in the CNS	1 (7.7)	12 (92)
Device-related infection with metastatic focus	0	12 (100)
Device-related infection without metastatic focus	4 (6.2)	60 (94)
Endocarditis	0	3 (100)
Febrile neutropenia	1 (3.3)	29 (97)
Osteomyelitis/septic arthritis	6 (2.4)	243 (98)
Pneumonia/empyema	2 (15)	11 (85)
Skin and skin structure infection	5 (6.3)	74 (94)
Other clinical syndrome	9 (14)	56 (86)
No identifiable focus	2 (3.6)	53 (96)
Not recorded	4 (20)	16 (80)
Length of Stay *(median)*	14 days	10 days
(IQR)	(10, 20)	(7, 18)
30-day all-cause mortality	1 (17)	5 (83)

The highest proportion of all MDR *S. aureus* were from NSW (44.1%) [Figure 44.A], whilst the NT and ACT had the highest proportion of *S. aureus* that were MDR (13.8% and 10.0% respectively) [Figure 44.B].
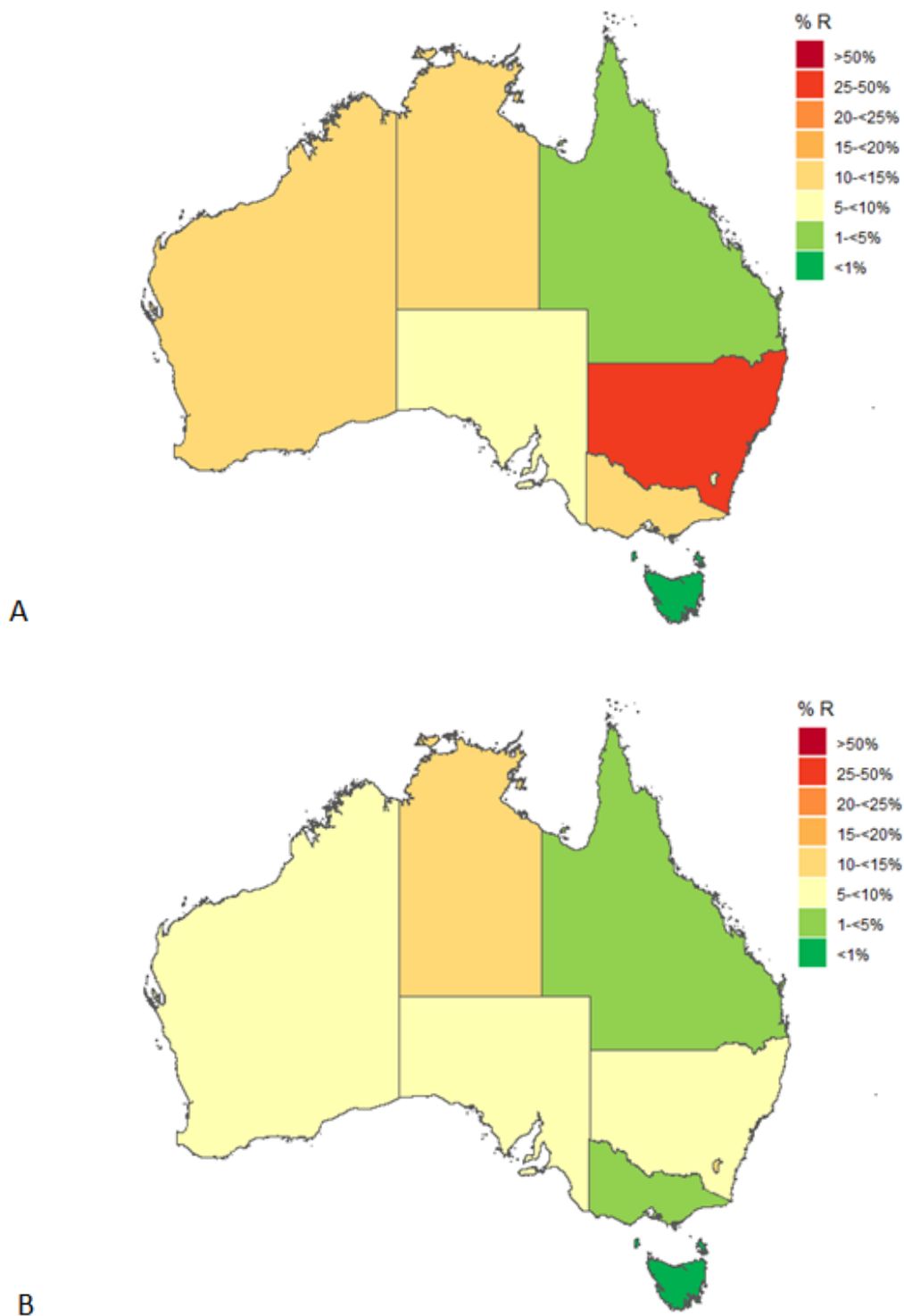
Figure 44. Proportion of MDR S. aureus isolates reported to AGAR overall, B) proportion of S. aureus isolates reported per state and territory that were MDR

6.1.3. Molecular epidemiology

WGS was performed on 71 MRSA isolates. Twenty-five multi-locus sequence types were identified, of which ST93-IV (n: 25, 32.1%), was the most frequently identified, for both community-onset and hospital-onset episodes [Table 51].

Table 51. Number and proportion of clone types of S. aureus isolates and the infection onset type as reported to AGAR in 2020-2021 from patients <18 years

Characteristic	Community, n = 49 (%)	Hospital, n = 22 (%)
ST1-IV	2 (4.1)	1 (4.5)
ST121-V	1 (2.0)	0
ST1232-V	1 (2.0)	0
ST149-IV	1 (2.0)	0
ST1524-IV	1 (2.0)	0
ST22-IV	2 (4.1)	3 (13.6)
ST22-IV (pvl positive)	2 (4.1)	2 (9.1)
ST2884-V	1 (2.0)	0
ST30-IV	3 (6.1)	1 (4.5)
ST4301-IV	1 (2.0)	0
ST45-IV	0	1 (4.5)
ST45-V	0	1 (4.5)
ST5-IV	6 (12.2)	1 (4.5)
ST5-unk	0	1 (4.5)
ST5-VI	1 (2.0)	0
ST508-IV	0	1 (4.5)
ST6-IV	3 (6.1)	2 (9.1)
ST6145-V	1 (2.0)	0
ST6156-IV	1 (2.0)	0
ST7708-IV	1 (2.0)	0
ST8-IV	1 (2.0)	0
ST834-IV	0	1 (4.5)
ST872-IV	0	1 (4.5)
ST93-IV	19 (38.8)	6 (27.3)
ST953-IV	1 (2.0)	0

The Panton-Valentine leucocidin (PVL) associated genes was tested for in 71 isolates and detected in 41 (57.8%) [Table 52].

Table 52. Number and proportion of S. aureus isolates that had Panton-Valentine leucocidin (PVL) toxin genes detected, and the respective infection onset type, in isolates reported to AGAR in 2020-2021 from patients <18 years

	Community n = 49 (%)	Hospital n = 22 (%)
Detected	33 (67.3)	8 (36.3)
Not detected	16 (32.7)	14 (63.7)
Sequence type of PVL positive isolates		
ST1232-V	1	
ST1524-IV	1	
ST22-IV	2	2
ST2884-V	1	
ST30-IV	3	
ST4301-IV	1	
ST5-IV	3	
ST7708-IV	1	
ST8-IV	1	
ST93-IV	19	6

The highest proportion of isolates that were PVL-positive originated from the NT and WA [Table 53].

Table 53. Location of where S. aureus isolates for PVL testing were detected

	No. isolates tested	Detected		Not detected	
		n	*%*	*n*	*%*
ACT	0				
NSW	26	9	34.6	17	65.4
NT	12	11	91.7	1	8.3
Qld	6	4	66.7	2	33.3
SA	6	3	50.0	3	50.0
Tas	0				
Vic	7	4	57.1	3	42.9
WA	14	10	71.4	4	28.6

6.2. *Enterococcus* spp.

Overall, 170 enterococci were reported to AGAR, 95 isolates in 2020 and 75 isolates in 2021. Of the 170 isolates, 122 were *Enterococcus. faecalis.* Five *E. faecium* isolates were MDR (2.9%) [Table 54].

Table 54. Number and proportions of species and multidrug resistance of Enterococcus isolates in patients <18 years reported to AGAR, 2020-2021

	2020 n = 95 (%)	2021 n = 75 (%)	Overall n = 170 (%)
Species			
E. casseliflavus	0	1 (1.3)	1 (0.6)
E. faecalis	60 (63.2)	62 (82.7)	122 (71.8)
E. faecium	32 (33.7)	9 (12)	41 (24.1)
E. gallinarum	3 (3.2)	0	3 (1.8)
E. lactis	0	3 (4)	3 (1.8)
MDR			
MDR	2 (2.1)	3 (4.0)	5 (2.9)
Not MDR	93 (97.9)	72 (96.0)	165 (97.1)

Isolates were most frequently reported from patients <1 years old and were mostly neonates (43%). The largest proportion of episodes were from NSW and Victoria. The proportion of patients still in hospital at 30 days was higher in patients who had an enterococcal infection [Table 55].

Table 55. Characteristics of patients with Enterococcus spp. reported in children aged <18 years reported to AGAR in 2020 and 2021.

Characteristic	2020 n = 95 (%)	2021 n = 75 (%)	Overall n = 170 (%)
Age *(median)*	<12 months	<12 months	<12 months
(IQR)	(0, 7)	(0, 2)	(0, 3.8)
Age Group			
≤ 28 days	21 (22.1)	17 (22.7)	38 (22.4)
29-90 days	14 (14.7)	12 (16)	26 (15.3)
91-364 days	14 (14.7)	10 (13.3)	24 (14.1)
1-4 years	19 (20)	22 (29.3)	41 (24.1)
5-17 years	27 (28.4)	14 (18.7)	41 (24.1)
Sex			
Female	33 (34.7)	27 (36)	60 (35.3)
Male	62 (65.3)	48 (64)	110 (64.7)
State			
ACT	2 (2.1)	1 (1.3)	3 (1.8)
NSW	35 (36.8)	33 (44)	68 (40)
NT	1 (1.1)	1 (1.3)	2 (1.2)
Qld	7 (7.4)	3 (4)	10 (5.9)
SA	13 (13.7)	1 (1.3)	14 (8.2)
Tas	3 (3.2)	1 (1.3)	4 (2.4)
Vic	29 (30.5)	29 (38.7)	58 (34.1)
WA	5 (5.3)	6 (8)	11 (6.5)
Onset			
Community	48 (50.5)	24 (32)	72 (42.4)
Hospital	47 (49.5)	51 (68)	98 (57.6)
Device-related infection			
Yes	37 (39%)	37 (49%)	74 (44%)
No	54 (57%)	37 (49%)	91 (54%)
Unknown	4 (4.2%)	1 (1.3%)	5 (2.9%)
Length of Stay *(median)*	9 days	16 days	12 days
(IQR)	(4, 28)	(9, 42)	(8, 34)
Still in at 30 days			
Yes	35 (36.8)	32 (42.7)	67 (39.4)
No	54 (56.8)	41 (54.7)	95 (55.9)
Not admitted	3 (3.2)	2 (2.7)	5 (2.9)
Unknown	3 (3.2)	0	3 (1.8)
Polymicrobial	38 (40)	25 (33.3)	63 (37.1)

*Population data for this table is at isolate level

6.2.1. Susceptibility testing results

Ampicillin

Overall, 19.6% of isolates were ampicillin resistant (n: 33; 95%CI: 13.9–26.5%); one isolate was *E. faecalis*, whilst the rest were *E. faecium* (n: 32). Over 70% of ampicillin resistant isolates were hospital-onset (n: 24). Most isolates were reported in patients aged 5-17 years, and from patients living in NSW [Figure 45/Table 56]. Enterococci from hospital-onset episodes were more frequently ampicillin resistant compared to community-onset enterococcal episodes [Table 56]. Most isolates had an ampicillin MIC ≤2 mg/L [Figure 45]

Table 56. Proportion of resistance to ampicillin in Enterococcus spp. per state and territory reported to AGAR in 2020-2021 from patients aged <18 years.

	No. isolates	No. Resistant	% R	95% CI	
State					
ACT	3	1	33.3	0.8	90.6
NSW	68	15	22.7	13.3	34.7
NT	2	1	50.0	1.3	98.7
Qld	10	0	0.0		
SA	14	7	50.0	23.0	77.0
Tas	4	1	25.0	0.6	80.6
Vic	58	8	13.8	6.1	25.4
WA	11	0	0.0		
Age group					
≤28 days	37	2	5.4	0.7	18.2
29-90 days	26	2	7.7	0.9	25.1
91-364 days	23	3	13.0	2.8	33.6
1-4 years	41	7	17.1	7.2	32.1
5-17 years	41	19	46.3	30.7	62.6
Onset					
Community	71	9	12.7	6.0	22.7
Hospital	97	24	24.7	16.5	34.5

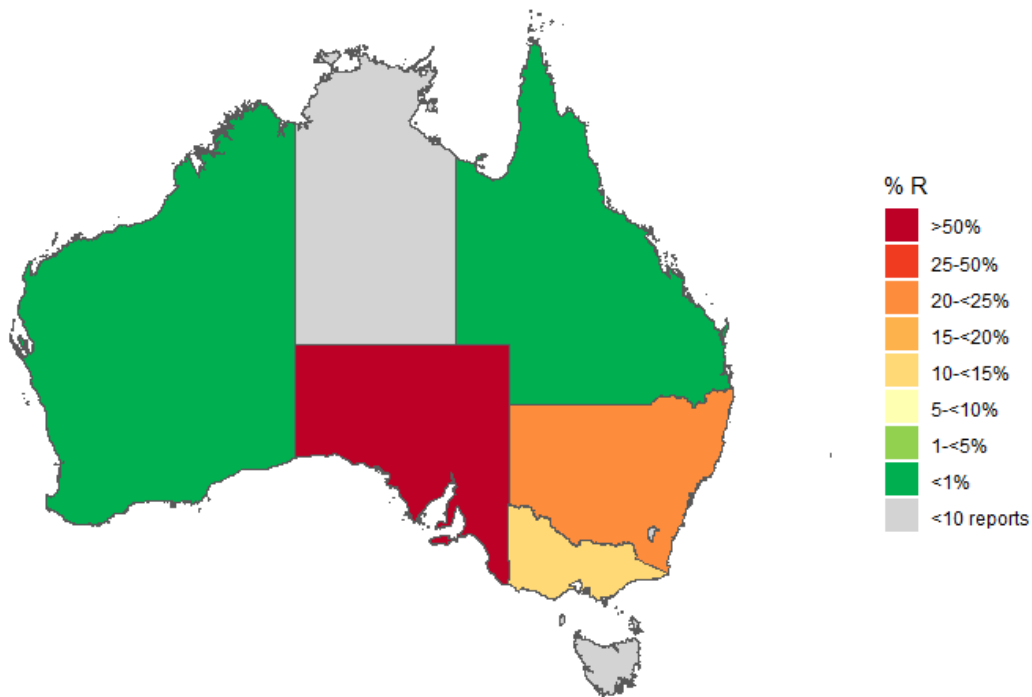*Figure 45. Proportion of ampicillin resistance in Enterococcus spp. per state and territory reported to AGAR in 2020-2021 from patients aged <18 years.*

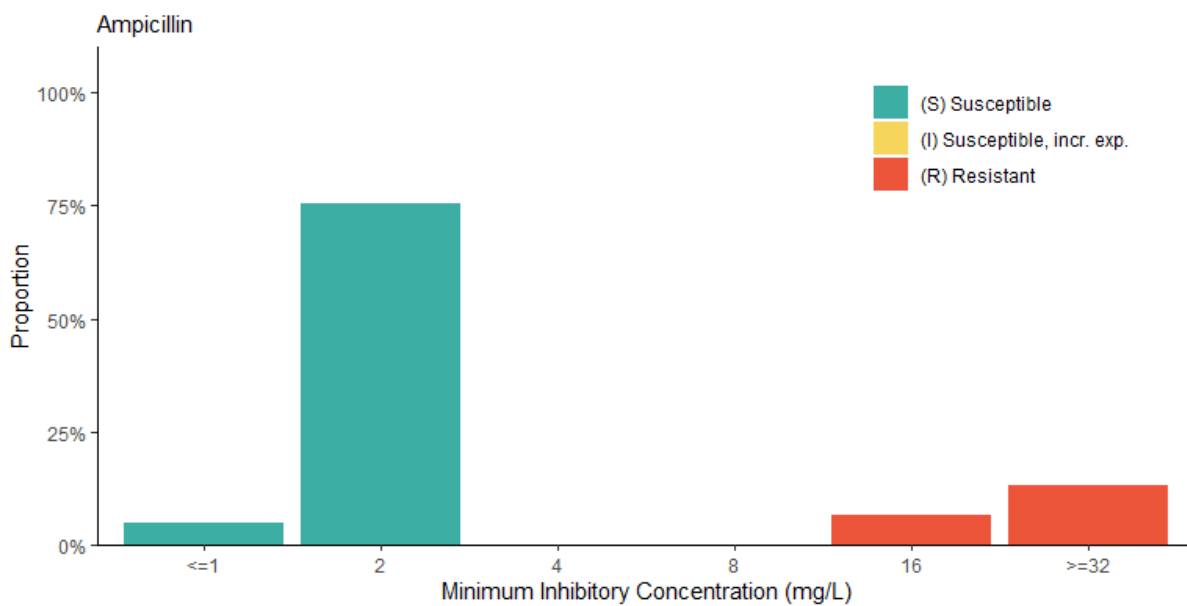*Figure 46. Distribution of MICs against ampicillin in Enterococcus spp. reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoint for ampicillin in Enterococcal spp. is 8mg/L intravenous administration, according to EUCAST 2022.*

Vancomycin

Eight vancomycin resistant *E. faecium* (VREfm) were identified (4.7%; 95%CI: 2.1 – 9.1%); all from hospital-onset episodes [Table 57]. VREfm were identified in Queensland, Victoria, and NSW [Figure 47]. Most enterococci had a vancomycin MIC ≤4mg/L [Figure 48].

Table 57. Proportion of resistance to vancomycin per state and territory in Enterococcus spp. reported to AGAR in 2020-2021 from patients aged <18 years.

	No. isolates	No. Resistant	% R	95% CI	
State					
ACT	3	0	0.0		
NSW	68	2	2.9	0.4	10.2
NT	2	0	0.0		
Qld	10	0	0.0		
SA	14	2	14.3	1.8	42.8
Tas	4	0	0.0		
Vic	58	4	6.9	1.9	16.7
WA	11	0	0.0		
Age group					
≤28 days	38	1	2.6	0.1	13.8
29-90 days	26	1	3.8	0.1	19.6
91-364 days	24	1	4.2	0.1	21.1
1-4 years	41	3	7.3	1.5	19.9
5-17 years	41	2	4.9	0.6	16.5
Onset					
Community	71	0	0		
Hospital	98	8	8.2	3.6	15.5

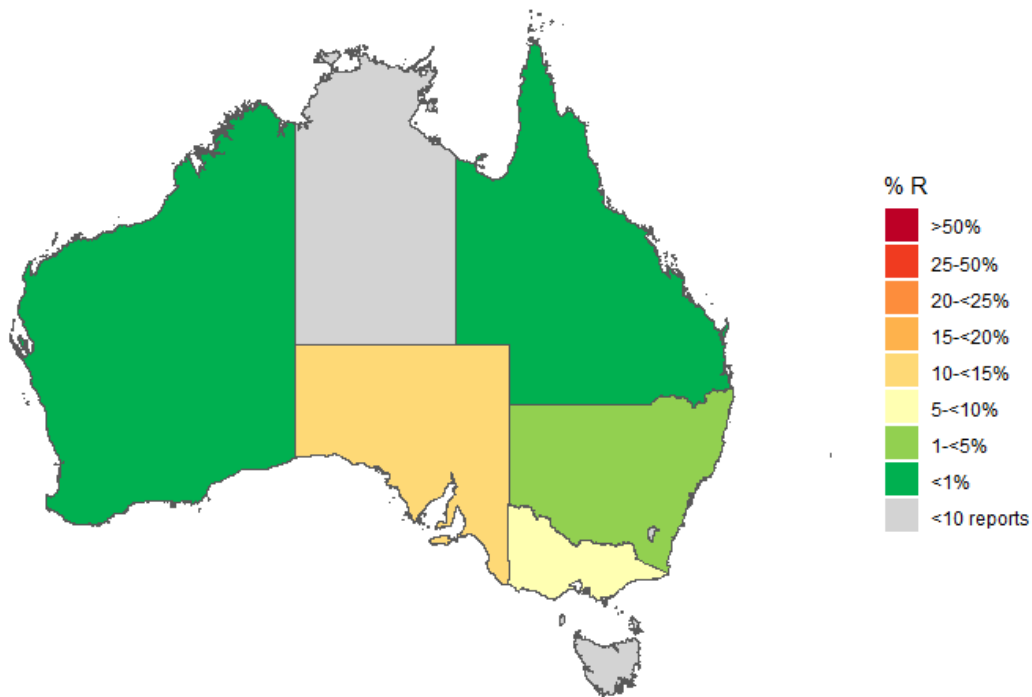*Figure 47. Proportion of vancomycin resistance per state and territory in Enterococcus spp. reported to AGAR in 2020-2021 from patients aged <18 years.*
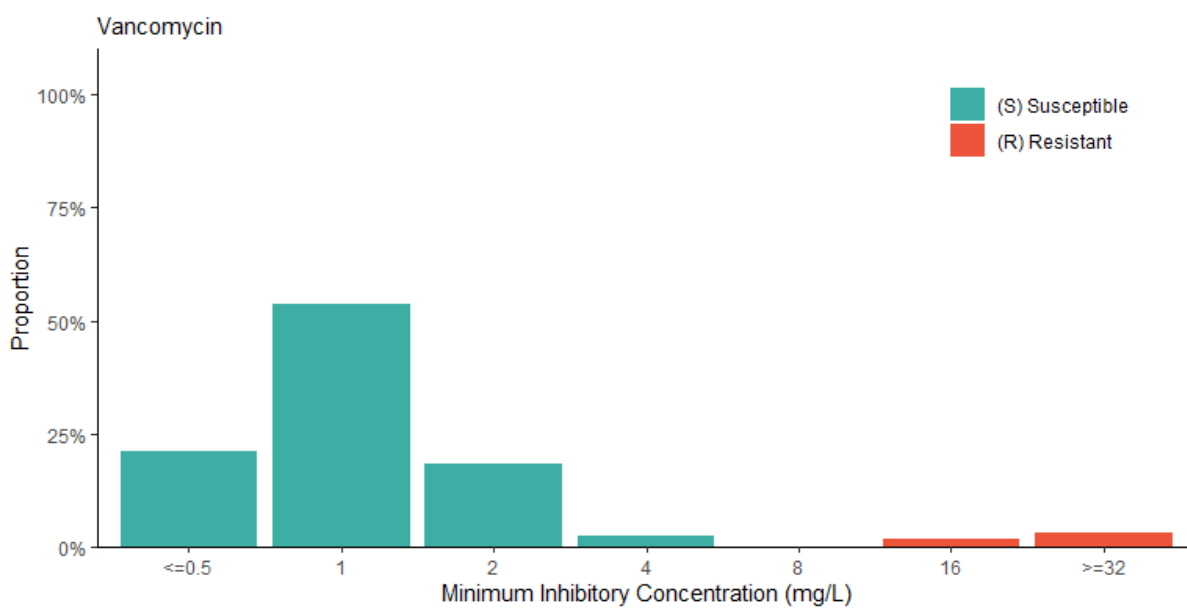

Figure 48. Distribution of MICs against vancomycin in Enterococcus spp. reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoint for vancomycin in Enterococcus spp. is 4mg/L, according to EUCAST 2022.

Teicoplanin

Three *E. faecium* were identified as teicoplanin (1.8%; 95%CI: 0.4 – 5.1%); all were from hospital-onset episodes. Teicoplanin resistant isolates were identified in NSW and Victoria [Table 58/Figure 49]. The majority of enterococci had a teicoplanin MIC ≤2mg/L [Figure 50].

Table 58. Proportion of resistance to vancomycin in Enterococcus spp. per state and territory reported to AGAR in 2020-2021 from patients aged <18 years.

	No. isolates	No. Resistant	% R	95% CI	
State					
ACT	3	0	0.0		
NSW	68	2	2.9	0.4	10.2
NT	2	0	0.0		
Qld	10	0	0.0		
SA	14	0	0.0		
Tas	4	0	0.0		
Vic	58	1	1.7	0.0	9.2
WA	11	0	0.0		
Age group					
≤28 days	38	0	0.0		
29-90 days	26	0	0.0		
91-364 days	24	0	0.0		
1-4 years	41	2	4.9	0.6	16.5
5-17 years	41	1	2.4	0.1	12.9
Onset					
Community	72	0	0		
Hospital	98	3	3.1	0.6	8.7

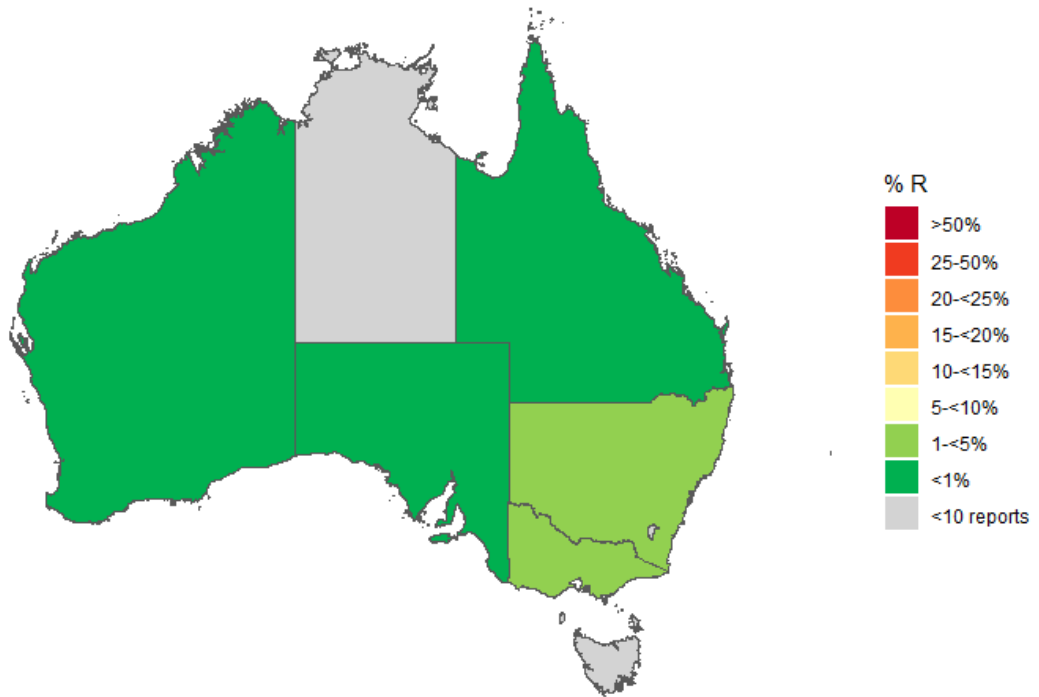*Figure 49. Proportion of teicoplanin resistance in Enterococcus spp. per state and territory reported to AGAR in 2020-2021 from patients aged <18 years.*
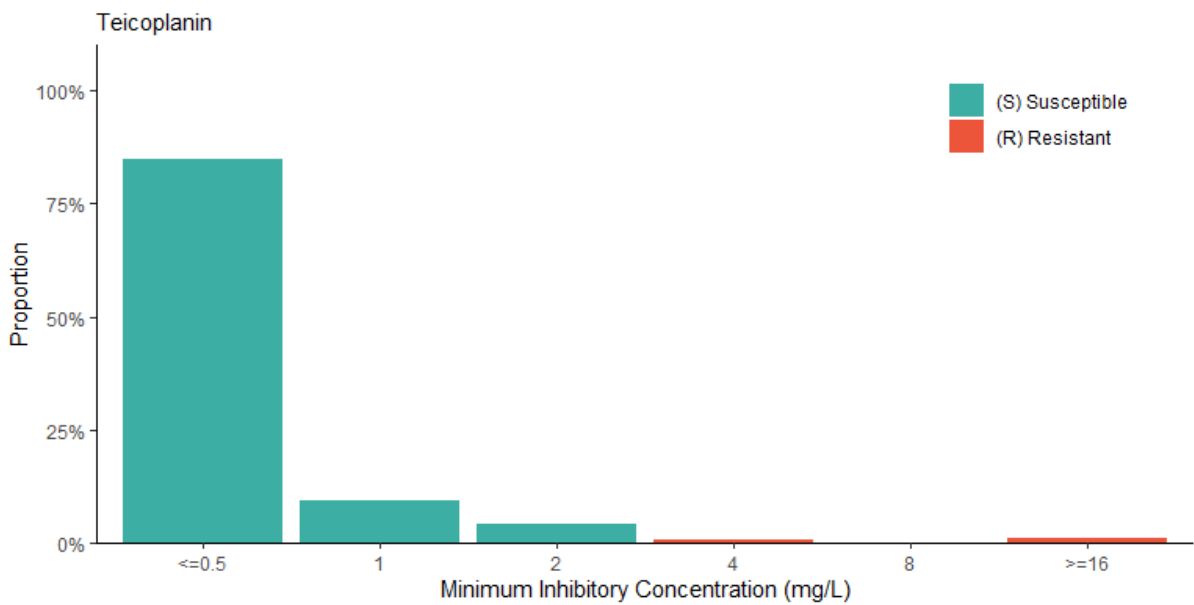

Figure 50. Distribution of MICs against teicoplanin in Enterococcus spp. reported to AGAR 2020-2021 from isolates in patients aged <18 years. The breakpoint for teicoplanin in Enterococcus spp. is 2mg/L, according to EUCAST 2022.

6.2.2. Multi-drug resistance

Five *E. faecium* were MDR (2.9%) [Table 59]. Four of the five MDR *Enterococcus* were identified in Victoria; the remaining isolate in SA [Figure 51]. The majority of *Enterococcus* spp. were not resistant to any classes of antimicrobials (72.9%) [Table 60].

Table 59. Number of Enterococcus spp. reported that are categorised as multidrug resistant (MDR).

Species	MDR	Not MDR
casseliflavus	0	1
faecalis	0	121
faecium	5	36
gallinarum	0	3
lactis	0	3

Table 60. Number of Enterococcus spp. resistant to how many antimicrobial classes[6]

	Number of antimicrobial classes resistant					
	Not multidrug resistant				Multidrug resistant	
	0	*1*	*2*	*%*	*3*	*%*
ACT	2	1	0	100	0	
NSW	49	9	10	100	0	
NT	1	0	1	100	0	
Qld	9	1	0	100	0	
SA	7	5	1	92.9	1	7.1
Tas	3	0	1	100	0	
Vic	46	6	2	93.1	4	6.9
WA	10	1	0	100	0	

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[6] Antimicrobial classes (agents) were aminoglycosides (gentamicin high level), streptomycin (high level), fluoroquinolones (ciprofloxacin), glycopeptides (vancomycin, teicoplanin), lipopeptides (daptomycin), oxazolidinones (linezolid), penicllins (ampicillin), and tetracyclines (tetracycline, doxycycline)
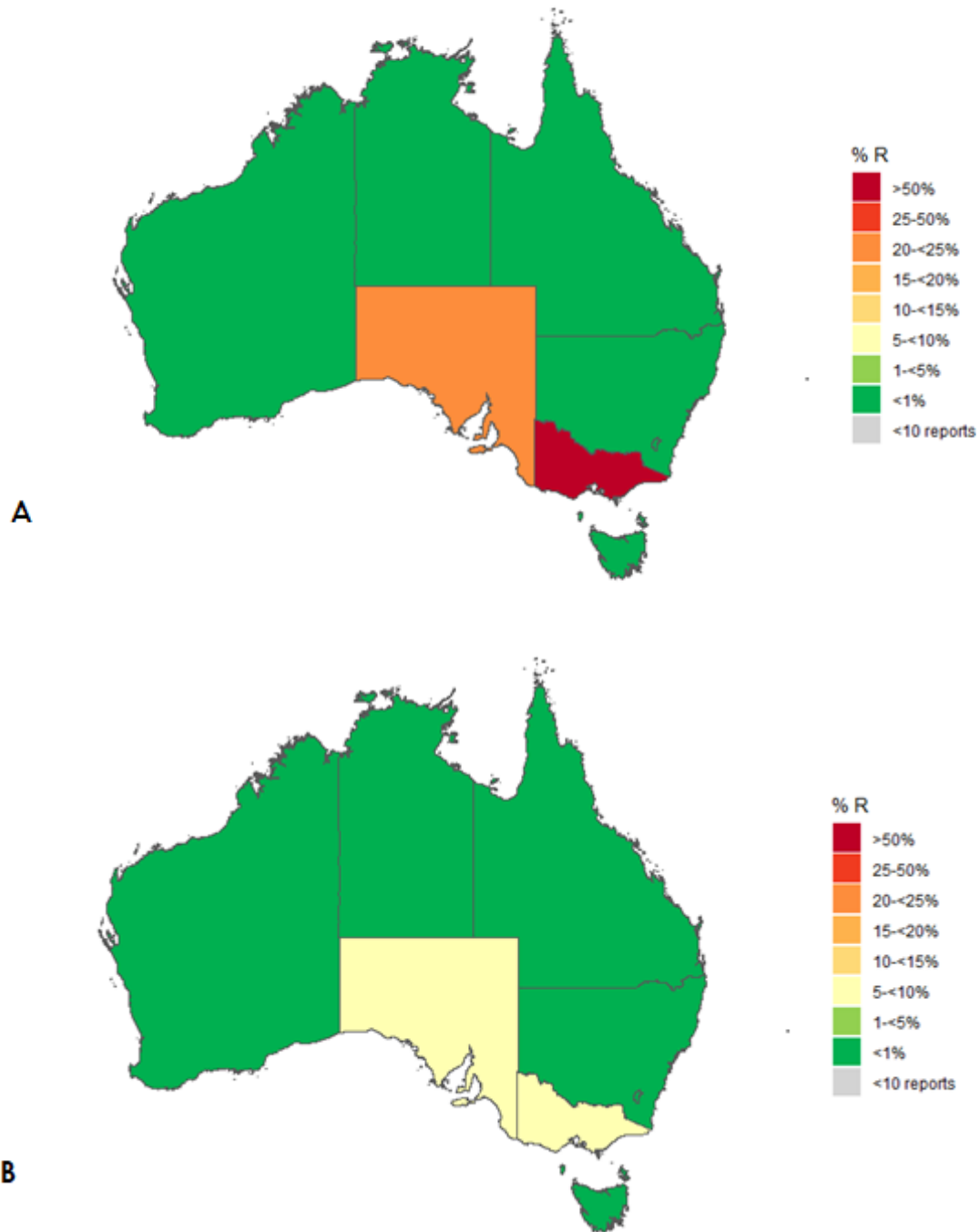
Figure 51. A) Proportion of MDR Enterococcus spp. reported to AGAR overall, B) proportion of Enterococcus spp. reported per state and territory that were MDR

6.2.3. Molecular epidemiology

van genes

Of the 41 *E. faecium* identified, two isolates harboured *vanA* (both from NSW) and six harboured *vanB* (two from SA, and four from Victoria). No *E. faecium* isolates harboured both *vanA* and *vanB* genes. All vanA or *vanB* positive isolates were phenotypically vancomycin (MIC >4mg/L) [Table 61].

Table 61. Vancomycin minimum inhibitory concentration results by van gene detection for E. faecium isolates

MIC (mg/L)	*vanA*	*vanB*	Not detected
≤0.5			29
1			3
2			
4			
>16	2	1	
≥32		5	

Multi-locus sequence type (MLST)

For the 41 *E. faecium* isolates, the most frequent sequence types (STs) were ST17 (n: 9, 22.0%), which was the most prevalent ST in SA, and ST1421 (n: 7, 17.1%), which was the most frequent ST in NSW [Table 62].

Table 62. Enterococcus faecium MLST detected per state and territory in patients <18 years, 2020-2021

	ACT	NSW	NT	Qld	SA	Tas	Vic	WA	Total
ST17		2			6		1		9
ST1421		7							7
ST796							4		4
ST80	1	1					2		4
ST1424		2				1			3
Other STs*	0	4	2	0	2	0	3	1	14
No result		1					1		

*Other STs include 1 of each of the following: ST117, ST1974, ST2028, ST2043, ST21, ST253, ST55, ST555, ST60, ST612, ST867, ST92.

7. Discussion

This is the first comprehensive AGAR report describing the epidemiology of AMR in the Australian paediatric population. The AGAR AMR surveillance programs provide the opportunity to specifically analyse and report on bacteraemia from Australian children, thereby informing Australian policy and prescribing practice. The programs also provide an opportunity to compare paediatric data with the Australian adult population. Although there are some similarities, numerous differences warrant ongoing paediatric reporting.

AMR surveillance of paediatric bacteraemia is a powerful tool, providing an understanding of the aetiology of disease, susceptibility patterns, and the impact of infection prevention and control strategies [8,15]. There are few reports on paediatric populations from similar AMR national surveillance systems. Whilst the European system (EARS-Net) requests age to the nearest year, the data point is not mandatory and thus EARS-Net data are not routinely stratified by age [7]. In the UK, the English Surveillance Programme for Antimicrobial Utilisation and Resistance (ESPAUR) does stratify patient age, but paediatric specific reports are not available [16]. The Canadian AMR surveillance program presents key highlights of age-stratified data [17]. One-off epidemiological reports have been produced from different regions and countries, yet interpretation and comparison to AGAR Kids is difficult because of differences in the organisms selected for surveillance [7,9,15,18–26]. In addition, limited clinical and resistance data over time reduce the ability to track AMR over time and assess the impact of changes in prescription recommendations.

In Australian children (excluding neonates), the most frequently reported organism in the AGAR 2020 and 2021 programs was *S. aureus* (36% of isolates) and *E. coli* (23%) – in neonates and the adult population this is reversed, with *E. coli* being the most frequent (43.1% and 39% respectively) followed by *S. aureus* (20.2% and 20.9% respectively). A similar observation has been identified in Japan by Kusama *et. al.,* [25], and likely reflects the commonality of UTIs as the source of bacteraemia in the neonatal and adult population [4] and bone and joint infection in children. Several papers globally have demonstrated *E. coli* bacteraemia is more frequent in children <1 year and *S. aureus* more frequent in children with increasing age [15,19,22,27–30]. In enterococcal bacteraemia, differences in the predominant species in adults and children were identified. In paediatrics, whilst approximately 25% of enterococci were identified as *E. faecium,* in adults almost 40% of episodes were due to *E. faecium*. Similarly, in several studies assessing paediatric bacteraemia, *E. faecalis* was more frequently identified than *E. faecium* [18,31]. Interestingly, on a population level, the UK has reported a shift in enterococcal bacteraemia, with more *E. faecium* and less *E. faecalis* reported during the COVID-19 pandemic; future AGAR Kids reports will be needed to investigate if a similar trend occurs in the Australian paediatric population [16].

In the AGAR Kids dataset, most paediatric bacteraemia, overall, were community-onset (69% overall). Although community-onset bacteraemia was most frequent for gram-negative (67%) and *S. aureus* (79%) episodes, enterococcal episodes were more often hospital-onset (58%). In the Australian adult population, 76% of episodes were community-onset representing 78% of gram-negative, 79% of *S. aureus* and 56% of enterococcal episodes (55.6%). There have been similar reports of higher proportion of community-onset *S. aureus* infections in children with a predominance of osteomyelitis/septic arthritis [9,22,32–34]. It is also worth noting that a large proportion of our paediatric population with hospital-onset enterococcal bacteraemia were

neonates and therefore may not have had a risk of a community onset infection. Enterococcal bacteraemia was found to be more commonly associated with device-related infections without metastatic infection (23%), whereas in adults, enterococcal bacteraemia was more frequently associated with a UTI (15.1%); in our study only 6.6% of paediatric enterococcal bacteraemia were associated with a UTI.

Regional differences were noted in the pathogens causing paediatric bacteraemia. The increased proportion of *Salmonella* bacteraemia in Queensland is consistent with previous Australian reports [20,28], and is consistent with the literature of bacteraemia in tropical environments [35–37]. Significant differences in the antimicrobial susceptibility patterns were also observed between jurisdictions. A higher proportion of resistant Enterobacterales was observed in Victoria compared to other jurisdictions. The proportion of Enterobacterales in Victoria resistant to gentamicin/tobramycin and 3rd generation cephalosporins was significantly higher than the national average; 16.8% compared to 11.6% for gentamicin/tobramycin (*p*: 0.04), and 19.3% compared to 12.9% for 3rd generation cephalosporins (*p:* 0.01). Similarly, Victoria reported the highest proportion of ESBL phenotypes (18.5%) in Enterobacterales, significantly higher than the national average of 12.4%. In Victorian children with an ESBL, the episode was frequently hospital-onset, and was associated with an increased length of stay, and more often device-related. Whether there are differences in the population sampled or true differences in the prevalence of resistant pathogens in Victorian children requires further investigation.

Similar to gram-negative bacteraemia, regional differences in *S. aureus* were noted; there was clear disproportion in the geographic distribution of MRSA episodes reported across Australia, and the over representation from the NT is found in both adults and children. The higher proportions of resistance in MRSA compared to MSSA and an older age group is aligned with the literature [16]. A more detailed investigation in the geographic distribution of MRSA in paediatrics is proposed and it is hypothesised that there will be a higher proportion of MRSA across the north of Australia which has been reported in the literature [34,38–40].

As per the WHO-defined priority list of pathogens [41], only four critical priority isolates were identified: two *P. aeruginosa* and two *E. cloacae* complex carbapenem-resistant (CRE). However, 21 WHO-defined high priority pathogens were identified other than MRSA: eight VREfm and 13 fluroquinolone-resistant *Salmonella*. These findings suggest that despite the increasing levels of AMR, WHO priority pathogens are rarely detected in the Australian paediatric population. This also demonstrates the benefit of using local paediatric data to strengthen antimicrobial stewardship programs and inform antibiotic guidelines.

Additional data analysis will be undertaken on a regular basis to track the emergence of AMR in Australian children, investigate the differences in AMR between adults and paediatric bacteraemia isolates, and assess the trends in paediatric AMR across Australia.

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9. Appendices

9.1. Demographic data collected for the AGAR surveillance programs

Field Name	Permitted values	AESOP	ASSOP	GnSOP
Year	YYYY [2013 to 2021]	Yes	Yes	Yes
Survey	AESOP, ASSOP, GnSOP	Yes	Yes	Yes
LabCode	Refer to Table A1	Yes	Yes	Yes
State	NSW, VIC, QLD, WA, SA, TAS, NT, ACT	Yes	Yes	Yes
DOC	Date of collection (dd-mm-yyyy)	Yes	Yes	Yes
LabNo	Alphanumerical	Yes	Yes	Yes
Genus	Drop down list	Yes	Yes	Yes
Species	Drop down list	Yes	Yes	Yes
Organism	Identifies organisms within a complex (where known)	no	no	Yes
Polymicrobial	Yes, No	Yes	Yes	Yes
Age	Years	Yes	Yes	Yes
Age Groupings	≤28 d, 29-90 d, 91-364 d, 1-4 y, 5-17 y, 18+ y	Yes	Yes	Yes
Sex	Male, Female	Yes	Yes	Yes
Admitted	Yes, No	Yes	Yes	Yes
Onset *Calculated from date of admission and date of blood collection. Hospital-onset (HO) if > 48h; Community-onset (CO)*	CO, HO	Yes	Yes	Yes
DaysPostBact Length of hospital stay following bacteraemia. *Calculated from the date of blood culture collection to patient discharge or death*	Number, (if negative, patient recalled) Not admitted: Not admitted No dates: Admitted, but no dates or outcome Bronze: Admitted, extra data not required Unknown: no information provided	Yes	Yes	Yes
Stillin30D *Calculated if not provided*	Yes No Not admitted: Not admitted and death > 30 d Bronze: Admitted, extra data not required Unknown': Admitted, outcome unknown .: no information provided	Yes	Yes	Yes
Device-related Infection*	Yes, No	Yes	Yes	Yes
Principal Clinical Manifestation*	See Table 1	Yes	Yes	Yes
Updated 7D outcome*	Died, Survived, Unknown	Yes	Yes	Yes
Updated 30D outcome*	Died, Survived, Unknown	Yes	Yes	Yes

*   Not provided by all hospitals (requirement for Silver/Gold (2013-2015) level participation only)

Notes
1. *Enterococcus lactis* identified from 2021
2. Organism identifies species assigned to a complex (where known); *A. baumannii* complex, *E. cloacae* complex, *C. freundii* complex, *K. pneumoniae* complex)
3. Date of birth not provided by ACT

9.2. Antibiotics and Antimicrobial Classes

Antimicrobial	Class Code	AESOP	ASSOP	GnSOP
Amikacin	Aminoglycosides			x
Amoxicillin-Clavulanate	Penicillins + β-lactamase Inhibitor			x
Ampicillin	Penicillins	x		x
Aztreonam				x
Benzylpenicillin		x	x	
Cefalexin				x
Cefazolin	Non-Extended Spectrum Cephalosporin			x
Cefepime	Extended Spectrum Cephalosporin			x
Cefoxitin			x*	x
Ceftazidime	Extended Spectrum Cephalosporin			x
Ceftolozane-Tazobactam				x
Ceftriaxone	Extended Spectrum Cephalosporin			x
Cefuroxime	Non-Extended Spectrum Cephalosporin			x
Chloramphenicol		x	x	x
Ciprofloxacin	Fluoroquinolone	x	x	x
Clindamycin	Lincosamides		x	
Colistin				x
Daptomycin	Lipopeptides	x	x	
Doxycycline	Tetracyclines	x	x	
Ertapenem				x
Erythromycin	Macrolides	x	x	
Fosfomycin		x	x	x
Fusidic Acid	Fusidic Acid		x	
Gentamicin	Aminoglycosides		x	x
Gentamicin High	Aminoglycosides	x		
Imipenem		x		x
Levofloxacin		x		
Linezolid	Oxazolidinones	x	x	
Mecillinam				x
Meropenem	Carbapenems			x
Moxifloxacin			x	
Mupirocin			x	
Mupirocin High				
Nitrofurantoin		x	x	x
Norfloxacin		x	x	x
Piperacillin-Tazobactam	Anti-Pseudomonal Penicillin + β-lactamase Inhibitor			x
Quinupristin-Dalfopristin		x	x	
Rifampicin	Ansamycins		x	
Streptomycin Synergy		x		

Teicoplanin	Glycopeptides	x	x	
Tetracycline	Tetracyclines	x	x	x
Ticarcillin-Clavulanate				x
Tigecycline		x		x
Tobramycin	Aminoglycosides			x
Trimethoprim		x	x	x
Trimethoprim/ Sulfamethoxazole	Folate Pathway Inhibitors	x	x	x
Vancomycin	Glycopeptides	x	x	

S. aureus against cefoxitin is tested as a screening test with +/- result rather than an MIC result

As defined by Magiorakos *et., al.,*[14]:

Criteria for defining MDR, XDR and PDR

> MDR: non-susceptible to ≥1 agent in ≥3 antimicrobial categories.
> XDR: non-susceptible to ≥1 agent in all but ≤2 categories.
> PDR: non-susceptible to all antimicrobial agents listed.

When a species has intrinsic resistance to an antimicrobial agent or to the whole category, that agent or category must be removed from the list in this table prior to applying the criteria for the definitions and should not be counted when calculating the number of agents or categories to which the bacterial isolate is non-susceptible.

9.3. Reports per Hospital and State

Jurisdiction	Lab code		No. reports
ACT	TCH	Canberra Health Services	46
NSW	CHW	Children's Hospital Westmead	255
	CRGH	Concord Repatriation General Hospital	4
	JHH	John Hunter Hospital	74
	LH	Liverpool Hospital	17
	NH	Nepean Hospital	24
	RNS	Royal North Shore Hospital	15
	RPAH	Royal Prince Alfred Hospital	9
	SCH	Sydney Children's Hospital	116
	SVHS	St Vincent's Hospital - Sydney	3
	WH	Westmead Hospital	16
	WoH	Wollongong Hospital	15
NT	ASH	Alice Springs Hospital	23
	RDH	Royal Darwin Hospital	49
Qld	GCH	Cairns Base Hospital	32
	GPH	Gold Coast Hospital	2
	QCH	Queensland Children's Hospital	141
	RBWH	Royal Brisbane and Women's Hospital	19
	TPCH	The Prince Charles Hospital	23
SA	FMC	Flinders Medical Centre	34
	RAH	Royal Adelaide Hospital	6
	WCH	Women's and Children's Hospital SA	96
Tas	LGH	Launceston General Hospital	17
	RHH	Royal Hobart Hospital	23
Vic	AH	Alfred Hospital	1
	AUH	Austin Hospital	6
	DH	Dandenong Hospital	6
	MCH	Monash Children's Hospital	110
	MMC	Monash Medical Centre, Clayton	4
	RMH	Royal Melbourne Hospital	4
	RWCH	Royal Children's Hospital, Parkville	324
	SVH	St Vincent's Hospital Melbourne	1
WA	FSH	Fiona Stanley Hospital	22
	JDP	Joondalup Health Campus	7
	PCH	Perth Children's Hospital	105
	RPH	Royal Perth Hospital	4
	RWA*	Regional north-west Western Australia	24
	SCGH	Sir Charles Gairdner Hospital	2

* RWA (Kimberley and Pilbara)
- Broome Hospital
- Derby Hospital
- Fitzroy Crossing Hospital
- Halls Creek Hospital
- Karratha Health Campus
- Kununurra Hospital
- Newman Hospital
- Onslow Hospital
- Paraburdoo Hospital
- Port Hedland
- Roebourne Hospital
- Tom Price Hospital
- Wyndham Hospital

9.4. Organisms reported per year

Name	2020	2021	Total	
			n	%
Staphylococcus aureus	303	304	607	36.2%
Escherichia coli	163	215	378	22.5%
Enterococcus faecalis	60	62	122	7.3%
Klebsiella pneumoniae complex	61	61	122	7.3%
Enterobacter cloacae complex	60	46	106	6.3%
Salmonella (non-Typhi)	22	52	74	4.4%
Pseudomonas aeruginosa	31	30	61	3.6%
Enterococcus faecium	32	9	41	2.4%
Klebsiella oxytoca	13	17	30	1.8%
Acinetobacter baumannii complex	10	8	18	1.1%
Serratia marcescens	6	12	18	1.1%
Salmonella Typhi	14		14	0.8%
Citrobacter freundii complex	6	5	11	0.7%
Acinetobacter lwoffii	6	4	10	0.6%
Proteus mirabilis	5	3	8	0.5%
Acinetobacter ursingii	6		6	0.4%
Acinetobacter	4	1	5	0.3%
Klebsiella aerogenes	3	2	5	0.3%
Pantoea spp.	2	2	4	0.2%
Pantoea agglomerans	3	1	4	0.2%
Raoultella ornithinolytica	2	2	4	0.2%
Enterococcus gallinarum	3		3	0.2%
Enterococcus lactis		3	3	0.2%
Klebsiella spp.	1	2	3	0.2%
Morganella morganii	1	2	3	0.2%
Citrobacter koseri	1	1	2	0.1%
Salmonella Paratyphi A	2		2	0.1%
Serratia liquefaciens complex		2	2	0.1%
Acinetobacter johnsonii	1		1	0.1%
Acinetobacter soli		1	1	0.1%
Citrobacter farmeri	1		1	0.1%
Enterobacter spp.		1	1	0.1%
Enterococcus casseliflavus		1	1	0.1%
Escherichia hermannii		1	1	0.1%
Franconibacter helveticus		1	1	0.1%
Hafnia alvei		1	1	0.1%
Pantoea eucrina		1	1	0.1%
Pantoea septica	1		1	0.1%
Pantoea vagans		1	1	0.1%
Proteus penneri		1	1	0.1%
Shigella sonnei		1	1	0.1%

9.5. Isolates reported per state and territory, 2020-2021

Organism	ACT	NSW	Qld	SA	Vic	WA	NT	Tas
Acinetobacter spp		1	1	1	1	1		
Acinetobacter baumannii complex		7	3	2	2	1	2	1
Acinetobacter johnsonii			1					
Acinetobacter lwoffii		4	2			2	1	1
Acinetobacter soli		1						
Acinetobacter ursingii		3		1		1		1
Citrobacter farmeri					1			
Citrobacter freundii complex		1	1	1	5	3		
Citrobacter koseri	1				1			
Enterobacter spp				1				
Enterobacter cloacae complex		45	17	3	33	4	1	3
Enterococcus casseliflavus						1		
Enterococcus faecalis	2	50	9	6	45	7		3
Enterococcus faecium	1	17		8	11	1	2	1
Enterococcus gallinarum		1	1			1		
Enterococcus lactis					2	1		
Escherichia coli	18	126	26	34	110	33	24	7
Escherichia hermannii				1				
Franconibacter helveticus		1						
Hafnia alvei					1			
Klebsiella spp		1			2			
Klebsiella aerogenes		4			1			
Klebsiella oxytoca		13	4	3	7	3		
Klebsiella pneumoniae complex	2	40	17	6	45	7	2	3
Morganella morganii					2		1	
Pantoea spp		1			1	1	1	
Pantoea agglomerans		2			2			
Pantoea eucrina						1		
Pantoea septica					1			
Pantoea vagans					1			
Proteus mirabilis		1	1	1	4	1		
Proteus penneri		1						
Pseudomonas aeruginosa		27	13	5	5	9	1	1
Raoultella ornithinolytica		2	1	1				
Salmonella (non-Typhi)	2	15	30	2	8	8	7	2
Salmonella Paratyphi A		2						
Salmonella Typhi		5	2		4	1		2
Serratia liquefaciens complex					2			
Serratia marcescens		4		3	7	4		
Shigella sonnei							1	
Staphylococcus aureus	20	173	88	57	152	73	29	15

9.6. Isolates reported per age group in 2020-2021

name	≤28 days	29-90 days	91-364 days	1-4 years	5-17 years
Acinetobacter spp	1		1	1	2
Acinetobacter baumannii complex		3	2	7	6
Acinetobacter johnsonii					1
Acinetobacter lwoffii	1		2	6	1
Acinetobacter soli				1	
Acinetobacter ursingii		1		3	2
Citrobacter farmeri				1	
Citrobacter freundii complex	1			4	6
Citrobacter koseri	1			1	
Enterobacter spp		1			
Enterobacter cloacae complex	14	13	10	40	29
Enterococcus casseliflavus				1	
Enterococcus faecalis	36	24	18	27	17
Enterococcus faecium	2	2	5	12	20
Enterococcus gallinarum				1	2
Enterococcus lactis				1	2
Escherichia coli	109	58	71	50	90
Escherichia hermannii					1
Franconibacter helveticus					1
Hafnia alvei				1	
Klebsiella spp		1	1	1	
Klebsiella aerogenes		2	2		1
Klebsiella oxytoca	8	3	4	6	9
Klebsiella pneumoniae complex	15	13	15	28	51
Morganella morganii	2				1
Pantoea spp	1	1		1	1
Pantoea agglomerans				2	2
Pantoea eucrina					1
Pantoea septica	1				
Pantoea vagans				1	
Proteus mirabilis	1		2	3	2
Proteus penneri					1
Pseudomonas aeruginosa	5	2	4	20	30
Raoultella ornithinolytica		1		1	2
Salmonella (non-Typhi)	1	3	24	24	22
Salmonella Paratyphi A				1	1
Salmonella Typhi				5	9
Serratia liquefaciens complex		1		1	
Serratia marcescens	3	5	3	2	5
Shigella sonnei					1
Staphylococcus aureus	51	51	46	133	326

9.7. Admission status of isolates at 30 days post-sample collection

Characteristic	Yes n = 366	No n = 1,22	Not admitted n = 51	Unknown n = 38
Acinetobacter	2 (40)	3 (60)	0	0
Acinetobacter baumannii complex	7 (39)	10 (56)	1 (5.6)	0
Acinetobacter johnsonii	0	1 (100)	0	0
Acinetobacter lwoffii	3 (30)	6 (60)	1 (10)	0
Acinetobacter soli	0	1 (100)	0	0
Acinetobacter ursingii	0	6 (100)	0	0
Citrobacter farmeri	1 (100)	0	0	0
Citrobacter freundii complex	0	11 (100)	0	0
Citrobacter koseri	1 (50)	1 (50)	0	0
Enterobacter	0	1 (100)	0	0
Enterobacter cloacae complex	34 (32)	70 (66)	2 (1.9)	0
Enterococcus casseliflavus	0	1 (100)	0	0
Enterococcus faecalis	47 (39)	70 (57)	2 (1.6)	3 (2.5)
Enterococcus faecium	16 (39)	22 (54)	3 (7.3)	0
Enterococcus gallinarum	3 (100)	0	0	0
Enterococcus lactis	1 (33)	2 (67)	0	0
Escherichia coli	68 (18)	278 (74)	12 (3.2)	20 (5.3)
Escherichia hermannii	0	1 (100)	0	0
Franconibacter helveticus	0	1 (100)	0	0
Hafnia alvei	0	1 (100)	0	0
Klebsiella	1 (33)	2 (67)	0	0
Klebsiella aerogenes	4 (80)	1 (20)	0	0
Klebsiella oxytoca	11 (37)	16 (53)	0	3 (10)
Klebsiella pneumoniae complex	32 (26)	88 (72)	1 (0.8)	1 (0.8)
Morganella morganii	1 (33)	2 (67)	0	0
Pantoea	0	3 (75)	1 (25)	0
Pantoea agglomerans	1 (25)	3 (75)	0	0
Pantoea eucrina	0	1 (100)	0	0
Pantoea septica	1 (100)	0	0	0
Pantoea vagans	0	1 (100)	0	0
Proteus mirabilis	1 (13)	7 (88)	0	0
Proteus penneri	0	1 (100)	0	0
Pseudomonas aeruginosa	17 (28)	43 (70)	1 (1.6)	0
Raoultella ornithinolytica	1 (25)	3 (75)	0	0
Salmonella (non-Typhi)	3 (4.1)	60 (81)	10 (14)	1 (1.4)
Salmonella Paratyphi A	0	1 (50)	1 (50)	0
Salmonella Typhi	1 (7.1)	11 (79)	2 (14)	0
Serratia liquefaciens complex	1 (50)	1 (50)	0	0
Serratia marcescens	7 (39)	11 (61)	0	0
Shigella sonnei	0	1 (100)	0	0
Staphylococcus aureus	101 (17)	482 (79)	14 (2.3)	10 (1.6)

*Percentages are calculated on the row, i.e. the denominator is the total number of that genus/species reported during 2020-2021

9.8. Principal Clinical Manifestation per age group

Survey	Principal clinical manifestation	28 d	29-90	91-364	1-4	5-17 y
AESOP	Biliary tract infection (including cholangitis)					1
	Device-related infection with metastatic focus				1	
	Device-related infection without metastatic focus	4	6	5	15	8
	Febrile neutropenia			1	12	18
	Intra-abdominal infection other than biliary tract	7	7	4	2	1
	Skin and skin structure infection		1		1	1
	Urinary tract infection	5	2	2	1	1
	Other clinical syndrome	8	6	6	2	8
	No identifiable focus	11	3	6	4	2
	Not recorded	3	1			1
ASSOP	CNS infection (meningitis, abscess(es))					4
	Deep abscess(es) excluding those in the CNS	2		2	2	7
	Device-related infection with metastatic focus		1	3	3	5
	Device-related infection without metastatic focus	8	13	9	17	17
	Endocarditis					3
	Febrile neutropenia	1		2	13	14
	Osteomyelitis/septic arthritis	5	8	1	46	189
	Pneumonia/empyema	1	2	1	5	4
	Skin and skin structure infection	6	8	13	23	29
	Other clinical syndrome	13	1	5	12	24
	No identifiable focus	11	9	8	7	2
	Not recorded	4		1	5	1
GNSOP	Biliary tract infection (including cholangitis)			7	2	5
	Device-related infection with metastatic focus		1	1	4	3
	Device-related infection without metastatic focus	9	7	11	38	35
	Febrile neutropenia		2	7	55	94
	Intra-abdominal infection other than biliary tract	18	14	24	31	37
	Osteomyelitis/septic arthritis			2	1	3
	Skin and skin structure infection		2		2	1
	Urinary tract infection	41	46	45	15	23
	Other clinical syndrome	54	17	26	32	33
	No identifiable focus	27	8	8	9	15
	Not recorded	11	7	8	9	17

9.9. Polymicrobial combinations reported

When cleaning the data for polymicrobial infections, those patients that had polymicrobial reported by the laboratory, but no other isolate was reported for the same patient in AGAR, were kept as reported; it is possible that the patient was infected with another organism that AGAR does not collect. This is why some combinations are reports of single isolates.

Combination	No. reports
A. baumannii complex	*4*
A. baumannii complex*, E. faecalis, S. aureus*	*1*
A. baumannii complex*, E. cloacae* complex*, E. coli*	*1*
A. baumannii complex*, S. aureus*	*1*
A. baumannii complex*, Acinetobacter spp.*	*1*
Acinetobacter spp.	*4*[7]
Acinetobacter spp, E. faecalis, K. oxytoca	*1*
C. freundii complex	*3*
C. freundii complex*, K. pneumoniae* complex	*2*
C. freundii complex*, S. marcescens*	*1*
E. cloacae complex	*7*
E. cloacae complex*, E. faecalis*	*3*
E. cloacae complex*, E. faecalis, S. aureus*	*1*
E. cloacae complex*, E. faecalis, K. pneumoniae* complex	*1*
E. cloacae complex*, E. faecalis, K. pneumoniae* complex*, E. faecium*	*1*
E. cloacae complex*, E. coli, P. mirabilis*	*1*
E. cloacae complex*, K. oxytoca*	*4*
E. cloacae complex*, K. pneumoniae* complex	*4*
E. cloacae complex*, Klebsiella spp.*	*1*
E. coli	*14*[8]
E. coli, K. pneumoniae complex	*4*
E. coli, K. pneumoniae complex *(2 isolates)*	*1*
E. coli, P. mirabilis	*1*
E. faecalis	*24*
E. faecalis, E. coli	*2*
E. faecalis, E. coli, K. oxytoca	*1*
E. faecalis, E. coli, S. aureus	*1*
E. faecalis, E. faecium, K. pneumoniae complex	*1*
E. faecalis, K. oxytoca	*3*
E. faecalis, K. pneumoniae complex	*4*
E. faecalis, K. pneumoniae complex*, P. aeruginosa*	*1*
E. faecalis, S. aureus	*2*
E. faecalis, S. liquefaciens	*1*
E. faecium	*8*[9]
Enterococcus spp	*4*[10]
H. alvei	*1*

[7] *johnsonii* (1), *soli* (1), *ursingii* (2)

[8] 1 patient with two *E. coli* isolates

[9] 1 patient with two *E. faecium* isolates

[10] *gallinarum* (1), *lactis* (2)

K. oxytoca	*2*
K. oxytoca, S. marcescens	*1*
K. pneumoniae complex	*8*
K. pneumoniae complex*, P. aeruginosa*	*1*
K. pneumoniae complex*, S. aureus*	*1*
K. pneumoniae complex*, S. marcescens*	*1*
P. aeruginosa	*6*
S. aureus	*36*[11]
S. marcescens	*1*
Salmonella non-Typhoidal	*1*

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[11] 1 patient with two *S. aureus* isolates

9.10. Bug-drug combination tables

9.10.1. Enterobacterales

Group	Drug	*C. freundii* complex	*E. cloacae* complex	*E. coli*	*K. oxytoca*
Aminoglycosides	Amikacin	0.0 (0/11)	4.7 (5/106)	1.6 (6/374)	0.0 (0/28)
	Gentamicin	0.0 (0/11)	10.4 (11/106)	12.0 (45/374)	0.0 (0/29)
	Tobramycin	0.0 (0/11)	11.5 (12/104)	11.7 (43/368)	0.0 (0/27)
Beta-lactams/penicillins	Amoxicillin/clavulanic acid	20.0 (2/10)	0.0 (0/106)	9.6 (36/374)	10.3 (3/29)
	Ampicillin	0.0 (0/10)	0.0 (0/69)	58.4 (216/370)	0.0 (0/29)
	Aztreonam			10.7 (3/28)	
	Piperacillin/tazobactam	18.2 (2/11)	21.7 (23/106)	6.7 (25/373)	13.8 (4/29)
	Ticarcillin/clavulanic acid	20.0 (2/10)	26.7 (27/101)	15.0 (51/339)	0.0 (0/23)
Carbapenems	Ertapenem			3.6 (1/28)	
	Imipenem			0.0 (0/28)	
	Meropenem	0.0 (0/11)	1.9 (2/105)	0.0 (0/374)	0.0 (0/29)
Cephalosporins – 2nd gen	Cefuroxime			17.6 (3/17)	
- 3rd gen	Ceftazidime	18.2 (2/11)	17.0 (18/106)	6.4 (24/374)	0.0 (0/29)
	Ceftriaxone	18.2 (2/11)	20.8 (22/106)	11.2 (42/374)	0.0 (0/29)
- 4th gen	Cefepime	0.0 (0/11)	6.6 (7/106)	4.5 (17/374)	0.0 (0/29)
- 5th gen	Cefdaloxime/tazobactam			5.9 (1/17)	
Other antibacterials	Fosfomycin		20.0 (1/5)	0.0 (0/33)	33.3 (2/6)
Polymyxins	Colistin			3.6 (1/28)	
Quinolones	Ciprofloxacin	0.0 (0/11)	5.7 (6/106)	14.2 (53/374)	3.4 (1/29)
Tetracyclines	Tigecycline			7.1 (2/28)	
Trimethoprims	Trimethoprim/sulfamethoxazole	36.4 (4/11)	44.3 (47/106)	34.8 (130/374)	6.9 (2/29)

Group	Drug	*K. pneumoniae* complex	*S. enterica*	*S. marcescens*	*Salmonella*
Aminoglycosides	Amikacin	3.3 (4/122)	0.0 (0/21)	0.0 (0/18)	0.0 (0/67)
	Gentamicin	13.9 (17/122)	0.0 (0/21)	0.0 (0/18)	0.0 (0/67)
	Tobramycin	15.8 (19/120)	0.0 (0/21)	41.2 (7/17)	0.0 (0/66)
Beta-lactams/penicillins	Amoxicillin/clavulanic acid	14.8 (18/122)	0.0 (0/21)	0.0 (0/16)	1.5 (1/67)
	Ampicillin	0.0 (0/120)	23.8 (5/21)	0.0 (0/16)	3.0 (2/66)
	Aztreonam	0.0 (0/8)			
	Piperacillin/tazobactam	23.0 (28/122)	0.0 (0/21)	0.0 (0/11)	0.0 (0/66)
	Ticarcillin/clavulanic acid	0.0 (0/112)	23.8 (5/21)	0.0 (0/13)	1.5 (1/66)
Carbapenems	Ertapenem	12.5 (1/8)			
	Imipenem	0.0 (0/8)			
	Meropenem	0.0 (0/122)	0.0 (0/21)	0.0 (0/18)	0.0 (0/67)
Cephalosporins – 2nd gen	Cefuroxime	0.0 (0/5)			
– 3rd gen	Ceftazidime	17.2 (21/122)	4.8 (1/21)	0.0 (0/18)	1.5 (1/67)
	Ceftriaxone	20.5 (25/122)	4.8 (1/21)	0.0 (0/18)	1.5 (1/67)
– 4th gen	Cefepime	7.4 (9/122)	4.8 (1/21)	0.0 (0/18)	0.0 (0/67)
– 5th gen	Ceftolozane/tazobactam	0.0 (0/5)			
Other antibacterials	Fosfomycin	0.0 (0/10)			
Polymyxins	Colistin	0.0 (0/8)			
Quinolones	Ciprofloxacin	21.3 (26/122)	47.4 (9/19)	0.0 (0/18)	4.8 (2/42)
Tetracyclines	Tigecycline				
Trimethoprims	Trimethoprim/sulfamethoxazole	31.3 (38/122)	23.8 (5/21)	0.0 (0/18)	0.0 (0/66)

9.10.2. Staphylococcus aureus

Group	Drug	*S. aureus*	MSSA	MRSA
Aminoglycosides	Gentamicin	3.5 (21/607)	2.3 (12/527)	11.3 (9/80)
Amphenicols	Chloramphenicol	1.5 (1/66)	1.7 (1/58)	0.0 (0/8)
Antimycobacterials	Rifampicin	0.0 (0/237)	0.0 (0/206)	0.0 (0/31)
Beta-lactams/penicillins	Benzylpenicillin	82.8 (501/605)	80.2 (421/525)	100.0 (80/80)
Glycopeptides	Teicoplanin	0.0 (0/606)	0.0 (0/526)	0.0 (0/80)
	Vancomycin	0.0 (0/607)	0.0 (0/527)	0.0 (0/80)
Macrolides/lincosamides	Clindamycin	12.4 (75/607)	11.4 (60/527)	18.8 (15/80)
	Erythromycin	13.2 (80/607)	11.8 (62/527)	22.5 (18/80)
	Quinupristin/Dalfopristin	0.0 (0/66)	0.0 (0/58)	0.0 (0/8)
Other antibacterials	Daptomycin	0.0 (0/607)	0.0 (0/527)	0.0 (0/80)
	Fosfomycin	0.0 (0/66)	0.0 (0/58)	0.0 (0/8)
	Fusidic acid	4.3 (26/607)	4.0 (21/527)	6.3 (5/80)
Oxazolidinones	Linezolid	0.0 (0/607)	0.0 (0/527)	0.0 (0/80)
Quinolones	Ciprofloxacin	5.3 (32/607)	3.6 (19/527)	16.3 (13/80)
	Moxifloxacin	0.0 (0/66)	0.0 (0/58)	0.0 (0/8)
Tetracyclines	Doxycycline	1.5 (1/66)	1.7 (1/58)	0.0 (0/8)
	Tetracycline	2.5 (14/563)	1.8 (9/488)	6.7 (5/75)
Trimethoprims	Trimethoprim/sulfamethoxazole	0.0 (0/601)	0.0 (0/524)	0.0 (0/77)

9.10.3. Pseudomonas aeruginosa

Group	Drug	*P. aeruginosa*
Aminoglycosides	Amikacin	0.0 (0/61)
	Tobramycin	0.0 (0/61)
Beta-lactams/penicillins	Piperacillin/tazobactam	19.7 (12/61)
	Ticarcillin/clavulanic acid	50.9 (29/57)
Carbapenems	Meropenem	3.3 (2/61)
Cephalosporins - 3rd gen.	Ceftazidime	9.8 (6/61)
- 4th gen.	Cefepime	9.8 (6/61)
	Cefepime/tazobactam	13.1 (8/61)
Quinolones	Ciprofloxacin	9.8 (6/61)

9.10.4. Enterococcus

Group	Drug	*E. faecalis*	*E. faecium*
Aminoglycosides	Gentamicin-high	10.8 (11/102)	41.0 (16/39)
Beta-lactams/penicillins	Ampicillin	0.8 (1/121)	78.0 (32/41)
Carbapenems	Imipenem	0.0 (0/12)	0.0 (0/7)
Glycopeptides	Teicoplanin	0.0 (0/122)	7.3 (3/41)
	Vancomycin	0.0 (0/122)	19.5 (8/41)
Macrolides/lincosamides	Quinupristin/Dalfopristin	0.0 (0/8)	0.0 (0/7)
Other antibacterials	Nitrofurantoin	0.8 (1/121)	
Oxazolidinones	Linezolid	0.0 (0/110)	0.0 (0/34)
Tetracyclines	Tigecycline	0.0 (0/12)	0.0 (0/7)
Trimethoprims	Trimethoprim/sulfamethoxazole	0.0 (0/39)	0.0 (0/11)

9.11. Overall antimicrobial resistance classes and proportions

Number of classes organisms are resistant to for all organisms reported to AGAR in patients <18 years of age, 2020-2021.

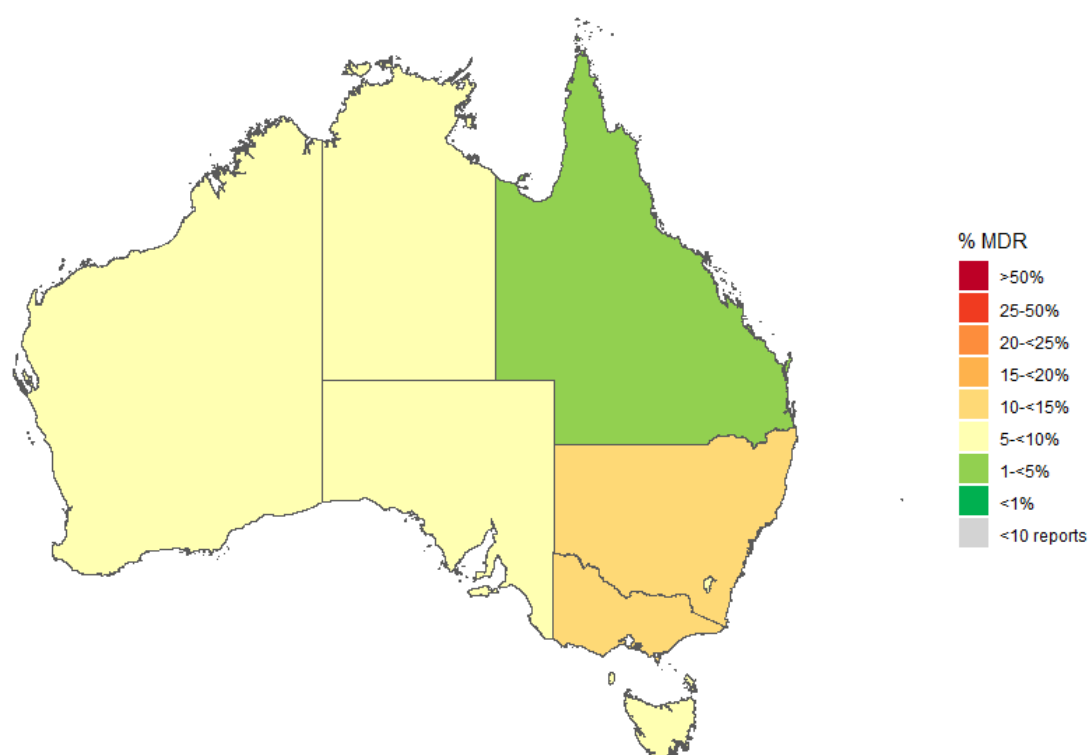|	Number of antimicrobial classes resistant								
	Not multidrug resistant				Multidrug resistant				
	0	1	2		3	4	5	6	
ACT	27	14	2	93.5	2	1	0	0	6.5
NSW	327	93	73	90.0	28	11	15	1	10.0
NT	34	19	13	91.7	5	0	1	0	8.3
Qld	140	43	24	95.4	5	1	3	1	4.6
SA	76	35	13	91.2	8	0	3	1	8.8
Tas	33	3	2	95.0	2	0	0	0	5.0
Vic	274	76	47	87.1	23	22	13	1	12.9
WA	107	33	13	93.3	7	2	2	0	6.7

Figure 52. Proportion of MDR isolates reported per state and territory to AGAR from patients <18 years, 2020-2021