Communicable Diseases Intelligence

2025 Volume 49

cdc.gov.au/cdi • Electronic publication date: 18.11.2025 • doi.org/10.33321/cdi.2025.49.052

Australian Group on Antimicrobial Resistance (AGAR) surveillance outcome programs – bloodstream infections and antimicrobial resistance patterns in Australian children and adolescents, January 2022 – December 2023

Anita Williams, Geoffrey W Coombs, Jan M Bell, Denise A Daley, Shakeel Mowlaboccus, Penelope A Bryant, Anita J Campbell, Louise Cooley, Annaleise R Howard-Jones, Jon Iredell, Adam D Irwin, Brendan McMullan, Morgyn S Warner, Phoebe CM Williams, Christopher C Blyth

Australian Government
Department of Health, Disability and Ageing

Interim Australian Centre for Disease Control

Communicable Diseases Intelligence

Communicable Diseases Intelligence (CDI) is a peer-reviewed scientific journal published by the interim Australian Centre for Disease Control within the Department of Health, Disability and Ageing.

The journal aims to disseminate information on the epidemiology, surveillance, prevention and control of communicable diseases of relevance to Australia and the near region.

Submit an Article

Submit your next communicable disease related article to CDI for consideration.

Guidelines for authors and details on how to submit your publication is available on our website, or by email to the CDI Editor.

Contact us

Communicable Diseases Intelligence (CDI)

interim Australian Centre for Disease Control, Department of Health, Disability and Ageing

GPO Box 9848, Canberra ACT 2601

Website: **cdc.gov.au/cdi**

Email: **cdi.editor@health.gov.au**

ISSN: 2209-6051 Online

This journal is indexed by Index Medicus and Medline.

Contents

List of tables

Abstract

Between January 2022 and December 2023, there were 1,827 bloodstream infection (BSI) isolates in 1,745 children and adolescents reported to the Australian Group on Antimicrobial Resistance (AGAR) surveillance outcome programs, with 40% of episodes in children aged < 12 months. Two-thirds of BSIs were community-onset.

Of 1,034 gram-negative isolates, 932 (90%) were Enterobacterales. Gram-negative BSI episodes were more commonly community-onset and in children < 12 months of age. Of Enterobacterales isolates, 17.9% were ciprofloxacin resistant; 14.0% were ceftriaxone and/or ceftazidime resistant; 9.5% were gentamicin and/or tobramycin resistant; and 8.9% were piperacillin-tazobactam resistant. Increasing ciprofloxacin resistance was noted, primarily due to the increase in *Salmonella* Typhi BSI. Overall, 13% of Enterobacterales were extended spectrum β-lactamase producers, and 18.5% were multi-drug resistant (MDR).

Of 601 *Staphylococcus aureus* isolates, 13.6% were methicillin-resistant (MRSA), and 5.5% were MDR. Overall, 14.4% of *S. aureus* isolates were erythromycin resistant; 10.3% were clindamycin resistant; and 5.0% were ciprofloxacin resistant. Erythromycin, clindamycin, and ciprofloxacin resistance in MRSA were significantly higher than in methicillin-sensitive isolates. No co-trimoxazole resistant *S. aureus* was isolated.

There were 192 enterococcal isolates reported; 70.8% were *E. faecalis* and 17.2% were *E. faecium*. All ampicillin-resistant, vancomycin-resistant, and MDR enterococci were *E. faecium*.

The 2022–2023 AGAR Kids Biennial Report shows relative stability in the antimicrobial resistance landscape within the Australian paediatric population, with few significant differences detected when compared to the 2020–2021 report. Small increases in the proportion of resistant Enterobacterales and *Enterococcus* spp. isolates highlight the importance of ongoing surveillance to inform stewardship and infection prevention interventions.

Keywords: Australian Group on Antimicrobial Resistance (AGAR); antimicrobial resistance surveillance; paediatrics; bacteraemia; Enterobacterales; *Staphylococcus aureus*; *Enterococcus*

Introduction

The Australian Group on Antimicrobial Resistance (AGAR) performs targeted whole-of-population antimicrobial resistance (AMR) surveillance in *Staphylococcus aureus*, *Enterococcus* spp., and key gram-negative bloodstream isolates. In 2023, a total of 51 hospitals reported bloodstream infection (BSI) data to AGAR, with all Australian states and mainland territories represented and all tertiary paediatric hospitals participating.

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.[1] The reports allow healthcare professionals and policy makers to 'use evidence-based surveillance and monitoring data to inform actions and responses to contain antimicrobial resistance'.[1]

The AGAR Kids committee, formed in 2022, was established to investigate and present neonatal- and paediatric-specific AMR data from the AGAR programs. As called for by the World Society for Paediatric Infectious Diseases (WSPID),[2,3] accessible neonatal and paediatric data is required to optimise prescribing and antimicrobial stewardship efforts. The first AGAR Kids Biennial report described the epidemiology of AMR in bacterial isolates, reported to the AGAR programs from children and adolescents < 18 years of age, in 2020 and 2021.[4,5] A subsequent report from the AGAR Kids committee described the trends and shifts in AMR across nine years (2013–2021).[6–8]

This second biennial AGAR Kids report describes the epidemiology, antimicrobial susceptibility patterns and antimicrobial resistance trends of bacterial isolates, and the patient outcomes of children and adolescents < 18 years old with bacterial BSIs as reported to AGAR in 2022–2023.

Methods

From 1 January 2022 to 31 December 2023, participating laboratories submitted unique BSI episodes of *S. aureus*, *Enterococcus* spp., Enterobacterales, *Pseudomonas aeruginosa*, and *Acinetobacter* spp.

Participants

Forty-one laboratories processing blood cultures from 53 hospitals submitted data from patients < 18 years old to the AGAR surveillance outcome programs: 52 hospitals in 2022 and 51 hospitals in 2023. All tertiary paediatric hospitals (n = 8), and 25 of the 29 principal referral centres in Australia, reported data during the two years, as well as five public acute group A hospitals, three private group A hospitals, two private group B hospitals and all public group C hospitals in the north-west of Western Australia.

Data collection

A BSI 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 14 days 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 after hospital admission, and as hospital-onset if collected > 48 hours after admission.

The data submitted by each laboratory to AGAR for each episode included a laboratory accession number; the date of collection; the organism isolated (genus and species); and the antimicrobial susceptibility test results (minimum inhibitory concentrations [MICs]). The patient's age, sex and jurisdiction of residence were also provided. If the patient was admitted to hospital, the dates of admission and discharge were reported. Depending on the laboratory's level of participation in AGAR, limited clinical and outcome data were also provided, including the principal clinical manifestation, device related infection (yes or no), and the outcome (died, all-cause or survived) at seven and 30 days. For the AGAR Kids Biennial Report, data from AGAR were restricted to patients aged < 18 years (0–17 years inclusive).

Laboratory methods

Where possible, isolates were identified to species level by each laboratory, using the laboratory's routine method. Species 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). Antimicrobial susceptibility testing was performed using one of two commercial semi-automated systems: the Vitek® 2 (bioMérieux) or BD Phoenix™ (BD), both of which are calibrated to the ISO (International Organization for Standardization) reference standard method of broth microdilution.

All methicillin-resistant *S. aureus* (MRSA) isolates, all *E. faecium* isolates, and select gram-negative isolates with specific antimicrobial resistant profiles underwent whole genome sequencing (WGS) to determine the presence of specific antimicrobial resistant determinants, including cefotaximases (e.g. CTX-15); plasmid mediated AmpC β-lactamases; and carbapenemases such as New Delhi metallo-β-lactamases (NDMs). A detailed description of the molecular laboratory methods employed by AGAR is available in previously published reports.[6,7,9]

Data analysis

The AMR for R package (v2.0) was used to transform MIC data as per European Committee on Antimicrobial Susceptibility Testing (EUCAST) 2024 (v14) breakpoints.[10,11] Multi-drug resistance was defined as resistance to one or more agents in three or more antimicrobial classes. Intrinsic resistance mechanisms were not included in determining if an organism was multi-drug resistant (MDR). Apart from *Enterobacter* spp., Enterobacterales were phenotypically classified as an extended spectrum β-lactamase (ESBL) producer if the organism had a ceftriaxone and/or ceftazidime MIC ≥ 2 mg/L. For *Enterobacter* spp., isolates with a cefepime MIC ≥ 1 mg/L were classified as ESBL-producing.

Descriptive statistics for the overall population and per year were stratified by age, sex, and state/territory. Proportions were only calculated when the total number for a category was > 10. Categorical data were compared using the chi-square or Fisher's exact test. Continuous data were compared using the Mann-Whitney U-test. Associations between exposure and outcome were estimated using odds ratios (OR). Proportions for the organisms classified in the World Health Organisation (WHO) Bacterial Priority Pathogen List (BPPL) were calculated with 95% confidence intervals (95% CI).[12]

Ethics

Approval to conduct the prospective data collection was given by the research ethics committee associated with each participating healthcare facility.

Results

Patient characteristics

Between 1 January 2022 and 31 December 2023, there were 1,827 isolates, from 1,745 children and adolescents < 18 years old, reported to the AGAR surveillance outcome programs. Across all Australian states and mainland territories, Enterobacterales were the most frequently reported isolates (n = 932; 51.0%). Over the two years, *Staphylococcus aureus* (n: 601) and *Escherichia coli* (n: 457) comprised more than half of all isolates reported to AGAR (57.9%; 1,058/1,827). The commonest isolates remained unchanged between 2020–2021 and 2022–2023, with the exception of *Salmonella* Typhi for which significantly more isolates were reported in 2022–2023 than in 2020–2021 (50 vs 14 isolates; χ^2: 17; $p < 0.001$; 95% CI: 1.0–2.8) (see Appendix A, Tables A.1.1 and A.1.2).[4] Approximately half of the *S*. Typhi isolates were from children aged 5–11 years (n = 23; 46.0%); a similar proportion were from those living in Victoria (24/50; 48.0%).

Over the two years, 40.5% of episodes were in children aged < 12 months (n = 706/1,745), with a quarter of all episodes occurring in children ≤ 90 days old. Two-thirds of all episodes were community-onset (n = 1,184; 67.8%). However, as observed in 2020–2021, *Enterococcus* spp. BSIs were more frequently hospital-onset than were BSIs involving *S. aureus* or Enterbacterales (67.6% vs 27.9%; χ^2: 117, $p < 0.001$). As a proportion of total BSIs, hospital-onset infections were highest in Victoria (41.7%) and New South Wales (36.4%), in children < 12 months old (44.1%), in device-related infections (60.1%), and in BSIs involving at least one MDR isolate (87.5%) (Table 1).

The most frequently reported primary clinical manifestations were febrile neutropenia (n = 218; 12.5%), osteomyelitis/septic arthritis (n = 213; 12.2%), and urinary tract infections (UTI; n = 204; 11.7%). Episodes with at least one MDR isolate were most frequently reported in children and adolescents with febrile neutropenia (53/213; 24.3%) or UTIs (26/204; 12.7%) reported as the principal clinical manifestation.

Overall, 19.3% of episodes were device-related; a decrease from the 23.5% of episodes in the previous report χ^2: 9; $p = 0.003$). This decrease was primarily observed in Victoria, which decreased from 32.4% in 2020–2021 to 20.7% in 2022–2023 (χ^2: 16; $p < 0.001$). Thirteen percent of BSI episodes were polymicrobial (227/1,745); such episodes were more commonly observed in hospital-onset infections ($p = 0.001$) (Table 1).

The median length of stay (LoS) following blood culture collection was 11 days (interquartile range, IQR: 6–22 days) (Table 1). Children and adolescents with an episode involving at least one MDR isolate remained in hospital longer than did patients who did not have a MDR isolate (14 days vs 9 days; χ^2: 16; $p < 0.001$).

One in five patients were still admitted to hospital at thirty days post-blood culture collection (380/1,745; 21.8%) (Table 1). Remaining in hospital thirty days post-collection was more frequent in children and adolescents with either an enterococcal BSI (OR: 2.7; 95% CI: 1.9–3.8), aged < 12 months (OR: 2.6; 95% CI: 2.0–3.2), a hospital-onset infection (OR: 11.2; 95% CI: 8.6–14.6), or a device-related infection (OR: 2.3; 95% CI: 1.7–2.9).

Over the two years, 46 children and adolescents died with a BSI (2.6%). *E. coli* was reported in a quarter of patients who died (n = 13/46; 28.3%). Seven of the patients who died had an MDR isolate (15.2%) (Table 2).

Table 1: Characteristics of patients aged < 18 years with a bacteraemic event reported to the Australian Group on Antimicrobial Resistance, per survey, January 2022 – December 2023

		Enterococcus spp. (N = 185)		*S. aureus* (N = 593)		Gram-negative bacteria (N = 967)		Total patients (N = 1,745)[a]	
Category	**Characteristic**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
Age (years)	Median	< 1	—	6	—	1	—	2	—
	IQR[b]	0–5	—	0–12	—	0–9	—	0–10	—
Age group	≤ 28 days	46	24.9	50	8.4	194	20.1	290	16.6
	29–90 days	29	15.7	47	7.9	105	10.9	181	10.4
	91–364 days	32	17.3	59	9.9	144	14.9	235	13.5
	1– 4 years	30	16.2	110	18.5	186	19.2	326	18.7
	5–11 years	16	8.6	174	29.3	168	17.4	358	20.5
	12–17 years	32	17.3	153	25.8	170	17.6	355	20.3
Sex	Female	75	40.5	237	40.0	411	42.5	723	41.4
	Male	110	59.5	356	60.0	556	57.5	1,022	58.6
Jurisdiction[c]	ACT	5	2.7	19	3.2	30	3.1	54	3.1
	NSW	70	37.8	209	35.2	336	34.7	615	35.2
	NT	4	2.2	36	6.1	32	3.3	72	4.1
	Qld	10	5.4	70	11.8	102	10.5	182	10.4
	SA	17	9.2	36	6.1	68	7.0	121	6.9
	Tas.	5	2.7	16	2.7	29	3.0	50	2.9
	Vic.	53	28.6	135	22.8	260	26.9	448	25.7
	WA	21	11.4	72	12.1	110	11.4	203	11.6
Onset location	Community	60	32.4	466	78.6	658	68.0	1,184	67.8
	Hospital	125	67.6	127	21.4	309	32.0	561	32.2
Device-related BSI[d]	Yes	72	39.6	95	16.5	170	19.4	337	19.3
	No	111	59.4	460	77.2	733	74.0	1,304	74.7
	Unknown	2	1.0	38	6.3	64	6.6	104	6.0

Category	Characteristic	*Enterococcus* spp. (N = 185)		*S. aureus* (N = 593)		Gram-negative bacteria (N = 967)		Total patients (N = 1,745)[a]	
		n	%	n	%	n	%	n	%
Polymicrobial BSI[d]	—	72	38.9	54	9.1	101	10.4	227	13.0
Length of stay (days)	Median	16.5	—	12	—	10	—	11	—
	IQR	7–35.2	—	7–23	—	5–20	—	6–22	—
All-cause mortality at 30 days	Died	7	3.8	7	1.2	32	3.3	46	2.6
	Survived	151	81.6	435	73.4	681	70.4	1,267	72.6
	Unknown	27	14.6	151	25.5	254	26.3	432	24.8

a The total column may not equate to the sum of each organism group, as some patients have polymicrobial bacteraemic episodes and are reported in each respective column to their episode but only counted once in the total number of patients.

b IQR: interquartile range.

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

d BSI: bloodstream infection.

Table 2: Characteristics of patients aged < 18 years with a bacteraemic event reported to the Australian Group on Antimicrobial Resistance for which one or more isolate was multidrug resistant, *Enterobacterales* isolates that produced extended-spectrum β-lactamases, or *Staphylococcus aureus* isolates that were methicillin-resistant, January 2022 – December 2023

		Enterobacterales[a,b]								*Enterococcus*[a]				*Staphylococcus aureus*[a,c]							
		MDR		Not MDR		ESBL		Not ESBL		MDR		Not MDR		MRSA		MSSA		MDR		Not MDR	
Category	Characteristic	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
Overall	—	172	18.5	760	81.5	125	13.4	807	86.6	33	5.5	568	94.5	82	13.6	519	86.4	15	7.8	177	92.2
Age (years)	Median	2	—	1	—	1	—	1	—	1	—	6	—	5	—	6	—	13	—	< 1	—
	IQR[d]	0–11	—	0–8	—	0–11	—	0–8	—	0–4	—	0–12	—	1–10	—	0–12	—	1–15	—	0–4	—
Age group	≤ 28 days	40	20.7	153	79.3	32	16.6	161	83.4	9	17.3	43	82.7	5	9.6	47	90.4	1	2.1	46	97.9
	29–90 days	12	11.1	96	88.9	10	9.3	98	90.7	2	4	48	96	5	10	45	90	1	3.4	28	96.6
	91–364 days	20	14	123	86	18	12.6	125	87.4	5	8.3	55	91.7	8	13.3	52	86.7	1	2.9	33	97.1
	1–4 years	35	21	132	79	23	13.8	144	86.2	9	8.1	102	91.9	23	20.7	88	79.3	1	3.1	31	96.9
	5–11 years	26	17.1	126	82.9	15	9.9	137	90.1	7	4	167	96	26	14.9	148	85.1	1	6.3	15	93.7
	12–17 years	39	23.1	130	76.9	27	16	142	84	1	0.6	153	99.4	15	9.7	139	90.3	10	29.4	24	70.6
Sex	Female	62	15.7	334	84.3	47	11.9	349	88.1	16	6.6	226	93.4	37	15.3	205	84.7	5	6.4	73	93.6
	Male	110	20.5	426	79.5	78	14.6	458	85.4	17	4.7	342	95.3	45	12.5	314	87.5	10	8.8	104	91.2
Jurisdiction[e]	ACT	6	18.8	26	81.3	6	18.8	26	81.2	0	—	19	100	1	5.3	18	94.7	0	—	5	—
	NSW	69	21.3	255	78.7	60	18.5	264	81.5	12	5.7	200	94.3	22	10.4	190	89.6	6	8.1	68	91.9
	NT	5	16.1	26	83.9	3	9.7	28	90.3	4	11.1	32	88.9	19	52.8	17	47.2	1	—	3	—
	Qld	6	6.1	92	93.9	4	4.1	94	95.9	3	4.3	67	95.7	4	5.7	66	94.3	1	10	18	90
	SA	14	23	47	77	10	16.4	51	83.6	1	2.6	38	97.4	4	10.3	35	89.7	0	—	5	—
	Tas.	4	13.3	26	86.7	2	6.7	28	93.3	0	—	16	100	0	—	16	100	0	—	46	100
	Vic.	53	21	199	79	33	13.1	219	86.9	13	9.6	123	90.4	18	13.2	118	86.8	7	13.2	23	86.8
	WA	15	14.4	89	85.6	7	6.7	97	93.3	0	—	73	100	14	19.2	59	80.8	0	—	23	100
Onset location	Community	105	16.3	539	83.7	70	10.9	574	89.1	19	4.1	450	95.9	68	14.5	401	85.5	1	1.6	61	98.4
	Hospital	67	23.3	221	76.7	55	19.1	233	80.9	14	10.6	118	89.4	14	10.6	118	89.4	14	10.8	116	89.2

Category	Characteristic	*Enterobacterales*[a,b]								*Enterococcus*[a]				*Staphylococcus aureus*[a,c]							
		MDR		Not MDR		ESBL		Not ESBL		MDR		Not MDR		MRSA		MSSA		MDR		Not MDR	
		n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%
Device-related BSI[f]	Yes	34	20	136	80	29	17.1	141	82.9	7	7.1	92	92.9	8	8.1	91	91.9	5	6.6	71	93.4
	No	126	18.1	569	81.9	88	12.7	607	87.3	22	4.7	442	95.3	65	14	399	86	10	9.6	104	90.4
	Unknown	12	17.9	55	82.1	8	11.9	59	88.1	3	8.1	34	91.9	9	23.7	29	76.3	0	—	2	100
Polymicrobial BSI[f]	—	26	18.8	112	81.2	16	11.6	122	88.4	2	3.2	60	96.8	5	8.1	57	91.9	4	5.1	75	94.9
Length of stay (days)	Median	14	—	9	—	15	—	9	—	17	—	11	—	16	—	11	—	17	—	17	—
	IQR[d]	8–24	—	4–17	—	8–28	—	4–18	—	8–39	—	7–22	—	8–29	—	7–22	—	9–24	—	7–36	—
All-cause mortality at 30 days	Died	5	17.9	23	82.1	5	17.9	23	82.1	0	—	7	100	3	—	4	—	1	14.3	6	85.7
	Survived	134	20.7	512	79.3	98	15.2	548	84.8	26	5.9	414	94.1	64	14.5	376	85.5	14	8.9	144	91.1
	Unknown	33	12.8	225	87.2	22	8.5	236	91.5	7	4.5	147	95.5	15	9.7	139	90.3	0	—	27	100

a MDR: multidrug resistant.

b ESBL: extended-spectrum β-lactamase.

c. MRSA: methicillin-resistant *Staphylococcus aureus*. MSSA: methicillin-susceptible *Staphylococcus aureus*.

d IQR: interquartile range.

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

f BSI: bloodstream infection.

Gram negatives

There were 1,034 gram-negative bacterial isolates from 967 episodes reported in children and adolescents to AGAR in 2022–2023; this was more than the 902 isolates from 867 episodes reported in 2020–2021. Ninety percent of gram-negative isolates were identified as Enterobacterales (n = 932/1,034, 90.1%); 6.6% were *Pseudomonas aeruginosa* (n = 68/1,034); and 3.3% were *Acinetobacter* spp. (n = 34/1,034). A majority of BSI episodes with gram-negative bacteria were community-onset (68.0%) and in males (57.5%); infants < 12 months of age accounted for the highest proportion of gram-negative BSI episodes (48.4%) (Table 1).

Enterobacterales

Overall, 17.9% of Enterobacterales were ciprofloxacin resistant; 14.0% were ceftriaxone and/or ceftazidime resistant; 9.5% were gentamicin and/or tobramycin resistant; and 8.9% were piperacillin-tazobactam resistant. Only seven Enterobacterales isolates were meropenem resistant (0.8%). No meropenem-resistant isolates were reported in infants < 12 months old (Table 3).

The proportion of ciprofloxacin-resistant Enterobacterales was significantly higher than reported in 2020–2021 (17.9% vs 13.2%; χ^2: 7; $p = 0.009$). However, if *Salmonella* spp. were excluded from the analysis, the ciprofloxacin-resistant proportion of isolates was similar in 2022–2023 to the proportions reported in 2020–2021 (12.7% vs 12.5%). Similarly, if *Salmonella* spp. were removed from the analysis, the proportions of ciprofloxacin-resistant Enterobacterales in Victoria (27.1% including *Salmonella* spp. vs 19.3% excluding *Salmonella* spp.; χ^2: 4; $p = 0.05$), in neonates (17.2% vs 8.3%; χ^2: 5; $p = 0.02$), and in community-onset BSIs (19.3% vs 8.1%, χ^2: 29, $p < 0.001$) were all similar to the 2021–2022 reporting period.

For *Salmonella* spp., almost half of the isolates reported were ciprofloxacin resistant (67/143; 46.9%; 95% CI: 38.5–55.4); a significant increase when compared to 2020–2021 (46.9% vs 20.6%; χ^2: 12; $p = 0.007$). The increase was primarily attributed to the increase in *S*. Typhi reported as a proportion of all *Salmonella* isolates during the reporting period (34.0% vs 15.6% of all *Salmonella* isolates were *S*. Typhi), given that 70.1% of ciprofloxacin-resistant *Salmonella* isolates in 2022–2023 were *S*. Typhi (47/67). Of the *S*. Typhi isolates, 94% were ciprofloxacin resistant (47/50), compared with only 9.9% of non-typhoidal *Salmonella* (8/81; χ^2: 86.4; $p < 0.001$). There were only three ceftriaxone-resistant *Salmonella* spp. reported in 2022–2023, including one *S*. Typhi.

One hundred and twenty-five (13.4%) of the 932 Enterobacterales had an ESBL phenotype. In the neonatal population there was a significant increase in the proportion of Enterobacterales with an ESBL phenotype, from 8.3% in 2020–2021 to 16.6% in 2022–2023 (χ^2: 5, p: 0.03). Additionally, an ESBL phenotype was identified more frequently in patients with a hospital-onset BSI than in patients with a community-onset BSI (OR: 1.9; 95% CI: 1.3–2.8; $p < 0.001$) (Table 2).

The proportion of MDR Enterobacterales increased from 14.5% in 2020–2021 to 18.5% in 2022–2023 (n = 172/932; χ^2: 5; $p = 0.03$). Over two thirds of MDR Enterobacterales were identified as *E. coli* (69.8%; 120/172), and one in four *E. coli* were MDR (26.3%; n= 120/457). The likelihood of an Enterobacterales isolate being MDR was greater for hospital-onset BSIs (OR: 1.6; 95% CI: 1.1–2.2; $p = 0.01$). The median length of stay for patients with an MDR Enterobacterales BSI was significantly longer than for those with a non-MDR Enterobacterales BSI (14 days vs 9 days; $p < 0.001$) (Table 2).

Table 3: Number of *Enterobacterales* isolates tested and proportion of isolates resistant to gentamicin/tobramycin, ceftriaxone/ceftazidime, piperacillin–tazobactam, and ciprofloxacin from patients aged < 18 years as reported to the Australian Group on Antimicrobial Resistance, January 2022 – December 2023

		Gentamicin/tobramycin[a]				Ceftriaxone/ceftazidime[a]				Piperacillin–tazobactam[a]				Ciprofloxacin[a]			
Category	Characteristic	N	n	R%	95% CI	N	n	R%	95% CI	N	n	R%	95% CI	N	n	R%	95% CI
Overall	—	927	88	9.5	7.7–11.6	927	130	14.0	11.9–16.4	917	82	8.9	7.2–11.0	927	166	17.9	15.5–20.6
Jurisdiction[b]	ACT	32	3	9.4	2.0–25.0	32	6	18.8	7.2–36.4	32	3	9.4	2.0–25	32	7	21.9	9.3–40.0
	NSW	322	34	10.6	7.4–14.4	322	62	19.3	15.1–24	321	42	13.1	9.6–17.3	321	52	16.2	12.3–20.7
	NT	31	2	6.5	0.8–21.4	31	3	9.7	2.0–25.8	31	0	0	—	30	2	6.7	0.8–22.1
	Qld	97	5	5.2	1.7–11.6	97	4	4.1	1.1–10.2	97	5	5.2	1.7–11.6	98	6	6.1	2.3–12.9
	SA	60	7	11.7	4.8–22.6	60	11	18.3	9.5–30.4	60	5	8.3	2.8–18.4	60	10	16.7	8.3–28.5
	Tas.	29	1	3.4	0.1–17.8	29	2	6.9	0.8–22.8	29	0	0	—	29	3	10.3	2.2–27.4
	Vic.	252	32	12.7	8.9–17.5	252	35	13.9	9.9–18.8	245	23	9.4	6.0–13.8	251	68	27.1	21.7–33.0
	WA	104	4	3.8	1.1–9.6	104	7	6.7	2.7–13.4	102	4	3.9	1.1–9.7	104	18	17.3	10.6–26.0
Age group	≤ 28 days	192	18	9.4	5.7–14.4	192	30	15.6	10.8–21.5	192	10	5.2	2.5–9.4	192	33	17.2	12.1–23.3
	29–90 days	108	9	8.3	3.9–15.2	108	11	10.2	5.2–17.5	105	8	7.6	3.3–14.5	107	4	3.7	1.0–9.3
	91–364 days	141	13	9.2	5.0–15.3	141	21	14.9	9.5–21.9	136	12	8.8	4.6–14.9	142	11	7.7	3.9–13.4
	1–4 years	166	15	9	5.1–14.5	166	25	15.1	10.0–21.4	165	16	9.7	5.6–15.3	165	37	22.4	16.3–29.6
	5–11 years	152	10	6.6	3.2–11.8	152	16	10.5	6.1–16.5	151	14	9.3	5.2–15.1	151	52	34.4	26.9–42.6
	12–17 years	168	23	13.7	8.9–19.8	168	27	16.1	10.9–22.5	168	22	13.1	8.4–19.2	168	29	17.3	11.9–23.8
Onset location	Community	641	47	7.3	5.4–9.6	641	71	11.1	8.8–13.8	636	29	4.6	3.1–6.5	639	123	19.3	16.3–22.5
	Hospital	286	41	14.3	10.5–18.9	286	59	20.6	16.1–25.8	281	53	18.9	14.5–23.9	286	43	15	11.1–19.7

a N: number of isolates tested; n: number of resistant isolates; R%: proportion of resistant isolates; 95% CI: 95% confidence interval.

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

Pseudomonas aeruginosa

Over the two years, 64 *P. aeruginosa* isolates were reported: 36 in 2022 and 28 in 2023. No *P. aeruginosa* isolates were reported from the Northern Territory (as in 2020–2021) or from Tasmania. Thirteen *P. aeruginosa* isolates were piperacillin-tazobactam resistant (13/68; 19.1%; 95% CI: 10.6–30.5); nine were cefepime and/or ceftazidime resistant (13.2%; 95% CI: 6.2–23.6); seven were ciprofloxacin resistant (10.3%; 95% CI: 4.2–20.1). One isolate was meropenem resistant (1.5%; 95% CI: 0.0–7.9) and no *P. aeruginosa* isolates were tobramycin resistant. The two MDR *P. aeruginosa* isolates reported (3.1%) reported were from children aged 5–11 years old with hospital-onset BSIs.

Acinetobacter spp.

In total, 34 *Acinetobacter* spp. isolates from 30 patients were reported over the two years; however, 71% of such isolates were reported in 2023 (24/34; 70.6%). One *Acinetobacter* isolate, identified as *A. lwoffii*, was ciprofloxacin and co-trimoxazole resistant. No other *Acinetobacter* isolates were resistant to the antimicrobials tested, including meropenem or amikacin.

Molecular analysis

One in four gram-negative isolates were referred for molecular analysis of resistance genes in 2022-2023 (266/1,034; 25.7%), with results available for 264 at the time of analysis. In approximately 40% of the isolates referred for WGS, a β-lactamase resistance gene was detected (38.3%; 101/264), including the majority of *E. coli* (73/81) and *Klebsiella pneumoniae* complex (22/26) isolates. More detailed genomic analysis is available in the 2022 and 2023 AGAR amalgam reports.[9,13] The proportion of ESBL gene detection in referred isolates was not significantly different to that seen in previous years (37.5% in 2018–2019 and 38.7% in 2020–2021).

Genes conferring resistance to the carbapenems were detected in seven gram-negative isolates: $bla_{\text{OXA-23}}$ was detected in an *A. baumanii* isolate, bla_{NDM} in two *E. coli* isolates, and $bla_{\text{IMP-4}}$ in four isolates: an *E. coli*, an *Enterobacter cloacae* complex isolate, a *K. pneumoniae* complex and a *Serratia marcescens*.

Gram positives

Staphylococcus aureus

There were 601 *S. aureus* isolates reported from 593 children and adolescents in 2022–2023; 13.6% were MRSA and 5.5% were MDR. The median age of patients with *S. aureus* bacteraemia (SAB) was 6 years, and 60.0% of patients were male (356/593). Most SABs were community-onset (78.6%; 466/593) and monomicrobial (90.1%; 539/593). Only 16.0% of SABs were device-related. One in five SAB patients remained in hospital after 30 days (120/593; 20.2%) (Table 1).

Overall, 14.4% of *S. aureus* were erythromycin resistant; 10.3% were clindamycin resistant; and 5.0% were ciprofloxacin resistant. Proportions of resistance in MRSA were significantly higher for erythromycin ($p = 0.02$), clindamycin ($p = 0.04$) and ciprofloxacin ($p < 0.001$). No *S. aureus* was resistant to co-trimoxazole (Table 4). Five percent of *S. aureus* were MDR; two-thirds of all MDR *S. aureus* were MRSA (21/33; 63.6%). More than half of MDR SABs were community-onset (19/33; 57.5%) (Table 2).

Although the proportion of *S. aureus* that were methicillin resistant in the Northern Territory was higher in 2022–2023 than in 2020–2021, the difference was not statistically significant (52.8% vs 48.3%; $p = 0.9$). Of the total 82 MRSA isolates, WGS results were available for 72 isolates at the time of analysis. The most frequently identified MRSA clone was ST93-IV (29/72; 40.3%). The Panton-Valentine Leucocidin (PVL) toxin associated-genes were detected in 71.0% of MRSA (54/72), with the Northern Territory having the highest proportion of MRSA that were PVL positive (17/18; 94.4%).

Table 4: Number of *Staphylococcus aureus* isolates tested and proportion of isolates resistant to clindamycin, ciprofloxacin, and erythromycin from patients aged < 18 years as reported to the Australian Group on Antimicrobial Resistance, January 2022 – December 2023

		Clindamycin[a]				Ciprofloxacin[a]				Erythromycin[a]			
Category	Characteristic	N	n	R%	95% CI	N	n	R%	95% CI	N	n	R%	95% CI
Overall	—	600	62	10.3	8.0–13.1	600	30	5.0	3.4–7.1	584	84	14.4	11.6–17.5
Jurisdiction[b]	ACT	19	3	15.8	3.4–39.6	19	0	0	—	19	3	15.8	3.4–39.6
	NSW	211	22	10.4	6.7–15.4	211	13	6.2	3.3–10.3	195	25	12.8	8.5–18.3
	NT	36	5	13.9	4.7–29.5	36	3	8.3	1.8–22.5	36	5	13.9	4.7–29.5
	Qld	70	9	12.9	6.1–23	70	1	1.4	0.0–7.7	70	9	12.9	6.1–23.0
	SA	39	1	2.6	0.1–13.5	39	1	2.6	0.1–13.5	39	12	30.8	17.0–47.6
	Tas.	16	2	12.5	1.6–38.3	16	0	0	—	16	2	12.5	1.6–38.3
	Vic.	136	14	10.3	5.7–16.7	136	12	8.8	4.6–14.9	136	22	16.2	10.4–23.5
	WA	73	6	8.2	3.1–17	73	0	0	—	73	6	8.2	3.1–17.0
Age group	≤ 28 days	52	12	23.1	12.5–36.8	52	3	5.8	1.2–15.9	52	17	32.7	20.3–47.1
	29–90 days	50	3	6.0	1.3–16.5	50	3	6	1.3–16.5	48	6	12.5	4.7–25.2
	91–364 days	60	13	21.7	12.1–34.2	60	4	6.7	1.8–16.2	58	13	22.4	12.5–35.3
	1–4 years	110	12	10.9	5.8–18.3	110	9	8.2	3.8–15	106	19	17.9	11.2–26.6
	5–11 years	174	12	6.9	3.6–11.7	174	6	3.4	1.3–7.4	169	17	10.1	6.0–15.6
	12–17 years	154	10	6.5	3.2–11.6	154	5	3.2	1.1–7.4	151	12	7.9	4.2–13.5
Onset location	Community	468	43	9.2	6.7–12.2	468	20	4.3	2.6–6.5	458	60	13.1	10.1–16.5
	Hospital	132	19	14.4	8.9–21.6	132	10	7.6	3.7–13.5	126	24	19.0	12.6–27.0
Methicillin resistance[c]	MRSA	82	13	15.9	8.7–25.6	82	18	22	13.6–32.5	82	18	22.0	13.6–32.5
	MSSA	518	49	9.5	7.1–12.3	518	12	2.3	1.2–4.0	502	66	13.1	10.3–16.4

a N: number of isolates tested; n: number of resistant isolates; R%: proportion of resistant isolates; 95% CI: 95% confidence interval.

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

c MRSA: methicillin-resistant *Staphylococcus aureus*; MSSA: methicillin-susceptible *Staphylococcus aureus*.

Enterococcus spp.

Over the two years there were 192 *Enterococcus* spp. isolates reported from 182 patients. The majority of isolates were *E. faecalis* (70.8%; 136/192), and 17.2% of enterococci were *E. faecium* (33/192). More than half of all *E. faecium* isolates were isolated in New South Wales (19/33; 57.6%). *E. faecium* BSI episodes were more frequently hospital-onset (χ^2: 5.3; $p = 0.02$), and most neonatal enterococcal BSIs were caused by *E. faecalis* (41/46, 89.1%).

Although only 14.2% of *Enterococcus* isolates were ampicillin resistant (26/183), all ampicillin-resistant isolates were identified as *E. faecium*. Overall, 81.3% of *E. faecium* were ampicillin resistant (26/32). Ampicillin-resistant enterococcal BSIs were primarily hospital-onset or in adolescents 12–17 years of age (Table 5).

Vancomycin resistance was only detected in *E. faecium* isolates; 40.6% of *E. faecium* isolates were vancomycin resistant (13/32). While there was an increase in the proportion of vancomycin-resistant *E. faecium* in 2022–2023 compared to 2020–2021, this increase did not attain statistical significance because of the small numbers of isolates reported (40.6% vs 19.5%; χ^2: 3; $p = 0.09$). Vancomycin-resistant enterococci (VRE) were 21.5% of all hospital-onset enterococcal infections; most VRE occurred in adolescents aged 12–17 years (61.5%; 8/13). Significant differences were also noted between different jurisdictions (Table 5). Of the 13 *E. faecium* isolates phenotypically resistant to vancomycin, 12 were *vanB* positive, and one was *vanA* positive. Only one *E. faecium* isolate was teicoplanin resistant (Table 5).

Fifteen *E. faecium* isolates (45.5%) were MDR, of which 14 were hospital-onset (14/15; 93.3%) (Table 3). Of the 44 *E. faecium* isolates were referred for WGS, there were 23 different sequence types (ST) identified, with ST78 the most frequent (11/44; 25.0%).

WHO Priority Pathogens

From the WHO Bacterial Priority Pathogens List (BPPL), two of the three 'critical priority' group pathogens were detected in children and adolescents over the two years: 14.6% of Enterobacterales were third-generation cephalosporin resistant and 1.2% of Enterobacterales were carbapenem resistant. No carbapenem-resistant *A. baumanii* were reported. Five of the six 'high priority' group resistant isolates surveyed by AGAR were detected (Table 6).

Table 5: Number of *Enterococcus* spp. isolates tested and proportion of isolates resistant to ampicillin and vancomycin from patients aged < 18 years as reported to the Australian Group on Antimicrobial Resistance, January 2022 – December 2023

		Ampicillin[a]				Vancomycin[a]			
Category	Characteristic	N	n	R%	95% CI	N	n	R%	95% CI
Overall	—	183	26	14.2	9.5–20.1	187	13	7.0	3.8–11.6
Species	*E. faecalis*	131	0	0	—	133	0	0	—
	E. faecium	32	26	81.3	63.6–92.8	32	13	40.6	23.7–59.4
	Other *Enterococcus*	20	0	0	—	22	0	0	—
Jurisdiction[b]	ACT	5	0	0	—	5	0	0	—
	NSW	65	17	26.2	16–38.5	69	4	5.8	1.6–14.2
	NT	4	1	25	—	4	1	25	—
	Qld	10	1	10	0.3–44.5	10	1	10	0.3–44.5
	SA	18	0	0	—	18	0	0	—
	Tas	5	0	0	—	5	0	0	—
	Vic	53	7	13.2	5.5–25.3	53	7	13.2	5.5–25.3
	WA	23	0	0	—	23	0	0	—
Age group	≤ 28 days	46	2	4.3	0.5–14.8	46	1	2.2	0.1–11.5
	29–90 days	26	1	3.8	0.1–19.6	28	1	3.6	0.1–18.3
	91–364 days	34	3	8.8	1.9–23.7	34	1	2.9	0.1–15.3
	1–4 years	28	5	17.9	6.1–36.9	30	1	3.3	0.1–17.2
	5–11 years	16	4	25	7.3–52.4	16	1	6.3	0.2–30.2
	12–17 years	33	11	33.3	18–51.8	33	8	24.2	11.1–42.3
Onset location	Community	58	2	3.4	0.4–11.9	59	0	0	—
	Hospital	125	24	19.2	12.7–27.2	128	13	10.2	5.5–16.7

a N: number of isolates tested; n: number of resistant isolates; R%: proportion of resistant isolates; 95% CI: 95% confidence interval.

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

Table 6: Number and proportion of World Health Organization (WHO) priority pathogens and resistance profiles detected in patients aged < 18 years within the Australian Group on Antimicrobial Resistance (AGAR) surveillance outcomes programs, January 2022 – December 2023

			Resistance characteristics[a]			
Priority	**Organism**	**Resistance to[b]**	**N**	**n**	**R%**	**95% CI**
Critical	Enterobacterales	Carbapenems	932	11	1.2	0.5–1.9
	Enterobacterales	3GC	932	130	13.9	11.7–16.2
	A. baumannii complex	Carbapenems	15	0	0	—
High	*Salmonella* Typhi	Fluroquinolones	50	47	94.0	87.4–100
	Shigella spp.	Fluroquinolones	1	0	0	—
	E. faecium	Vancomycin	32	13	40.6	23.7–59.4
	P. aeruginosa	Carbapenems	68	1	1.5	0–4.3
	Non-typhoidal *Salmonella*	Fluroquinolones	85	8	9.4	3.2–15.6
	S. aureus	Methicillin	601	82	13.6	10.9–16.4
	Neisseria gonorrhoeae[c]	3GC and/or fluroquinolones	—	—	—	—
Medium	Group A *Streptococcus*[c]	Macrolides	—	—	—	—
	Streptococcus pneumoniae[c]	Macrolides	—	—	—	—
	Haemophilus influenzae[c]	Ampicillin	—	—	—	—
	Group B *Streptococcus*[c]	Penicillin	—	—	—	—

a N: number of isolates tested; n: number of resistant isolates; R%: proportion of resistant isolates; 95% CI: 95% confidence interval.

b Carbapenems: meropenem, ertapenem, imipenem; 3GC (third-generation cephalosporins): ceftazidime, ceftriaxone; fluoroquinolones: ciprofloxacin, levofloxacin, moxifloxacin, norfloxacin.

c Organisms not collected within AGAR surveillance outcome programs, but listed here to provide context of the full WHO pathogen list.

Discussion

The 2022–2023 AGAR Kids Biennial Report shows stability in the AMR landscape within the Australian paediatric population, with few significant differences detected when compared to the 2020–2021 report. Minor variations observed between the two reporting periods were possibly due to the easing of coronavirus disease 2019 (COVID-19) public health measures across Australia in 2022.

Although the WHO BPPL was updated in 2024 and thus is different to the list reported against in the 2020–2021 AGAR Kids report, when compared to global estimates, the proportion of resistant isolates detected in the Australian paediatric population is limited. Whilst the global median resistance of *A. baumannii* to carbapenems was 69.0–73.4% in 2022, no resistant isolates were reported in AGAR Kids. Conversely, whilst the global median resistance to ciprofloxacin for *Salmonella* spp. was 16.7% (5.4–30.4%), the proportion in Australian children and adolescents was 46.9%. Though this result is higher than the global median estimates, the majority of ciprofloxacin-resistant *Salmonella* observed in this report were *S*. Typhi, cases of which in Australia are almost always acquired whilst travelling to endemic regions.[14] This is reflected by the significant reduction of salmonellosis notifications across the population to the National Notifiable Disease Surveillance System (NNDSS) during the Australian border lockdown period, and by the absence of any cases of *S*. Typhi or *S*. Paratyphi reported in the 2020–2021 AGAR Kids report.[4,15] Considering children and adolescents have increased risk to Typhi acquisition when travelling overseas, increased messaging around *S*. Typhi vaccine uptake before overseas travel may be helpful in reducing the number of typhoid infections.[14,16] The Australian Immunisation Handbook recommends typhoid vaccination for all travellers aged ≥ 2 years to endemic regions.[17]

Whilst most ciprofloxacin-resistant *Salmonella* were identified as *S*. Typhi or *S*. Paratyphi, ~10% of non-typhoidal *Salmonella* were also ciprofloxacin resistant, which is similar to other Australian AMR surveillance reports.[18] Although ciprofloxacin-resistant *Salmonella* BSIs are associated with overseas travel, several papers have described endogenous fluoroquinolone resistance in Australian *Salmonella* isolates, as well as concordant resistance to third-generation cephalosporins or azithromycin.[19–21] Monitoring fluoroquinolone resistance in animal *Salmonella* isolates, particularly by surveillance of plasmid-mediated quinolone resistance (PMQR) genes, may provide oversight of endogenous ciprofloxacin resistance transmission in the circumstances of low numbers in humans.[22]

Although not statistically significant, the proportion of third-generation cephalosporin resistant Enterobacterales has continued to increase, with 15.9% of Enterobacterales resistant to third-generation cephalosporins in 2023; this is the highest proportion observed in the paediatric population across 11 years of AGAR surveillance.[6] Research conducted from five Australian children's hospitals during 2019–2021 indicates a slightly higher proportion of third-generation cephalosporin resistant Enterobacterales BSIs at 21.9%.[23] As was observed in this report, children with third-generation cephalosporin resistant Enterobacterales BSIs, as well as those with MDR Enterobacterales BSIs, had longer hospital stays and higher mortality.[23] In recent years, penicillins with extended-spectrum (J01CA), first-generation cephalosporins (J01DB), and β-lactam/β-lactamase inhibitor combinations (J01CR) were some of the more frequently dispensed systemic antibacterial classes under the Pharmaceutical Benefits Scheme (PBS) and Repatriation PBS (RPBS).[18] As third-generation cephalosporins are often used as first-line empirical treatment for paediatric sepsis and meningitis, ongoing strategies to combat increasing resistance must include antimicrobial stewardship and ongoing attention to the appropriateness of third-generation cephalosporin use.

Over the past 10 years there has been a small but clinically important increase in the number of carbapenem-resistant Enterobacterales (CPE) in the AGAR paediatric population; from one isolate in 2014–2015 to 11 isolates in 2022–2023 (χ^2: 5; p = 0.02). A similar increase of CPE has been observed in the AGAR adult population. This trend has occurred in parallel with an increase in meropenem use since 2017.[18] However, there has been no similar increase of carbapenem resistance observed in the *Acinetobacter* spp. or *P. aeruginosa* in either the paediatric or adult population. A more detailed analysis of CPE BSIs in Australia indicates that most isolates were locally acquired (endemic) rather than overseas.[18,24]

There was no change in the proportion of antimicrobial resistance reported in *P. aeruginosa* isolates during 2022–2023 in the paediatric AGAR populations, despite a national increase in piperacillin-tazobactam use from 2018–2022.[18,24,25] In a recent analysis of paediatric *P. aeruginosa* BSIs in Queensland, Slack et al. observed increases in piperacillin-tazobactam and ciprofloxacin resistances between 2015–2019.[26] The piperacillin-tazobactam resistant proportions observed by Slack et al. are similar to those in the paediatric AGAR population, both during the same time frame (2015–2019) and in 2022–2023. Conversely, the proportion of ciprofloxacin resistance in the paediatric AGAR population is greater than that observed in the Queensland report.[6] Resistance in *P. aeruginosa* should be monitored carefully, as *P. aeruginosa* BSIs are more frequent in patients with serious underlying comorbidities or frequent healthcare contact.

There were no statistically significant changes in the proportions of *S. aureus* resistance when compared to the previous AGAR Kids Biennial report. As previously observed, the Northern Territory had the highest proportion of *S. aureus* that were methicillin resistant, as was observed in the adult population.[4,7,27] In a recent analysis of MRSA data across the north of Australia (2016–2021), an increase in MRSA infection was associated with remoteness index; i.e., the more remote, the higher the odds of an MRSA infection. However, no significant association between socio-economic indexes and MRSA infection was observed.[28] Using Bayesian modelling, Wozniak et. al., found the remote regions of east and west Pilbara (Western Australia), Daly-West Arnhem and Alice Springs (Northern Territory), and the Outback North (Queensland) had the highest predicted prevalence of MRSA across all age groups and sexes, whilst urban settings had the lowest predicted prevalence.[28] Future geographic analysis of AGAR Kids data using similar methods across a national dataset are planned, with results expected to mirror these findings.

Although there was an increase in the proportion of *E. faecium* resistant to vancomycin in the paediatric population between the two biennial reports, the total number of vancomycin-resistant *E. faecium* (VREfm) was small and should be interpreted with caution. It should be noted, however, that during the same time period the proportion of VREfm reported in the adult population increased significantly, from 37.2% in 2020–2021 to 48.9% in 2022–2023 (χ^2: 29; $p < 0.001$). As observed in children and adolescents, all VRE reported in adults in 2022–2023 were *E. faecium*.[9] When compared internationally, Australia continues to have higher proportions of *E. faecium* that are vancomycin resistant: over the past five years, the United Kingdom observed increases in VREfm from 20.6% in 2019 to 22.4% in 2023 ($p = 0.07$), and the EU/EEA population-weighted mean percentage of VREfm was 19.8% in 2023; however, national percentages of VRE across the EU/EEA ranged from 0.0% to 60.9%.[29,30] As well as increasing resistance to vancomycin, there was an increase in the proportion of MDR enterococci in both adults and children in Australia. As *Enterococcus* spp. have intrinsic resistance to several antimicrobial classes, increasing resistance to the few antimicrobial agents available to treat enterococcal BSIs poses a critical threat.

Conclusions

The 2022–2023 AGAR Kids Biennial Report shows relative stability in the AMR landscape within the Australian paediatric population, with few significant differences detected when compared to the 2020–2021 report. From BSIs in children and adolescents during 2022–2023, there have been small increases in the proportions of resistant Enterobacterales and *Enterococcus* spp. isolates reported, whilst resistance in *S. aureus* has remained stable. The lifting of public health restrictions and the increase in international travel may have impacted the epidemiology of BSIs and antimicrobial resistance patterns in the paediatric AGAR population during 2022–2023. The second edition of the AGAR Kids Biennial report reiterates the importance of reporting age-delimited data in AMR surveillance reports, with distinct differences observed not only between adults and children, but amid age groups.

Acknowledgments

This report was the work of the AGAR Kids committee and was funded by the Australian Government Department of Health, Disability and Ageing. The AGAR Kids committee would like to thank the participants to the AGAR surveillance program in 2022/2023:

Australian Capital Territory

Peter Collignon and Susan Bradbury – The Canberra Hospital

New South Wales

Alison Kesson and Andrew Jarrett – Children's Hospital Westmead

Thomas Gottlieb and John Huynh – Concord Hospital

Gabrielle O'Kane and Nola Hitchick – Gosford Hospital

Hemalatha Varadhan and Bree Harris – John Hunter Hospital

Michael Maley and Helen Ziochos – Liverpool Hospital

James Branley and Linda Douglass – Nepean Hospital

Monica Lahra and Peter Huntington – Prince of Wales Hospital

Angela Wong – Royal North Shore Hospital

Sebastiaan van Hal and Thomas Le – Royal Prince Alfred Hospital

David Lorenz – St Vincent's Hospital

Monica Lahra and Peter Huntington – Sydney Children's Hospital

Jon Iredell and Andrew Ginn – Westmead Hospital

Peter Newton and Melissa Hoddle – Wollongong Hospital

Northern Territory

James McLeod – Alice Springs Hospital

Rob Baird and Jann Hennessy – Royal Darwin Hospital

Queensland

Enzo Binotto and Annika Klein – Cairns Base Hospital

Petra Derrington and Cheryl Curtis – Gold Coast University Hospital

Jennifer Robson and Marianne Allen – Greenslopes Private Hospital and Mater Private Hospital

Robert Horvath – Prince Charles Hospital

Naomi Runnegar and Joel Douglas – Princess Alexandra Hospital

Clare Nourse and Narelle George – Queensland Children's Hospital

Claire Heney and Narelle George – Royal Brisbane and Women's Hospital

South Australia

Kelly Papanaoum and Xiao Ming Chen – Flinders Medical Centre

Morgyn Warner and Kija Smith – Royal Adelaide Hospital and Women's and Children's Hospital

Tasmania

Pankaja Kalukottege, Kathy Wilcox, and Brooke Woolley – Launceston General Hospital

Louise Cooley and David Jones – Royal Hobart Hospital

Victoria

Adam Jenney and Jacqueline Williams – The Alfred Hospital

Marcel Leroi and Elizabeth Grabsch – Austin Health

Tony Korman and Kathryn Cisera – Dandenong Hospital

Tony Korman and Despina Kotsanas – Monash Medical Centre and Monash Children's Hospital

Katherine Bond and Rose Cotronei – Royal Melbourne Hospital

Andrew Daley and Gena Gonis – Royal Women's Hospital

Amy Crowe and Lisa Brenton – St Vincent's Hospital

Western Australia

Denise Daley and Shakeel Mowlaboccus – Fiona Stanley Hospital

Shalinie Perera and Ian Meyer – Joondalup Hospital

Michael Leung and Jacinta Bowman – North-west WA Regional Hospitals

Christopher Blyth and Jacinta Bowman – Perth Children's Hospital

Owen Robinson and Geoffrey Coombs – Royal Perth Hospital

Ronan Murray and Jacinta Bowman – Sir Charles Gairdner Hospital

Sudha Pottumarthy-Boddu and Alicia Robinson – St John of God Hospital Murdoch

Author details

Anita Williams,[1,2]

Geoffrey W Coombs,[3,4,5]

Jan M Bell,[6]

Denise A Daley,[4,5]

Shakeel Mowlaboccus,[3,5]

Penelope A Bryant,[7,8]

Anita J Campbell,[1,10,11]

Louise Cooley,[12,13]

Annaleise R Howard-Jones,[14,15]

Jon Iredell,[15-18]

Adam D Irwin,[19,20]

Brendan McMullan,[21,22]

Morgyn S Warner,[23,24]

Phoebe CM Williams,[15,21,22,25]

Christopher C Blyth[1,10,11,26]

1. Wesfarmers Centre of Vaccines and Infectious Diseases, The Kids Research Institute Australia, Nedlands, WA
2. UWA Centre for Child Health Research, School of Medicine, University of Western Australia, Nedlands, WA
3. School of Medical, Molecular and Forensic Sciences, Murdoch University, Murdoch, WA
4. Department of Microbiology, PathWest Laboratory Medicine WA, Fiona Stanley Hospital, Murdoch, WA
5. Australian Group on Antimicrobial Resistance, Fiona Stanley Hospital, Murdoch, WA
6. Australian Group on Antimicrobial Resistance, Adelaide, SA
7. Infectious Diseases, The Royal Children's Hospital Melbourne, Parkville, Victoria
8. Department of Paediatrics, University of Melbourne, Parkville, Victoria
9. Clinical Paediatrics, Murdoch Children's Research Institute, Parkville, Victoria
10. Department of Infectious Diseases, Perth Children's Hospital, Nedlands, WA
11. Division of Paediatrics, School of Medicine, University of Western Australia, Nedlands, WA
12. Department of Microbiology and Infectious Diseases, Royal Hobart Hospital, Hobart, Tasmania
13. School of Medicine, University of Tasmania, Hobart, Tasmania
14. Department of Infectious Diseases & Microbiology, The Children's Hospital at Westmead, Westmead, NSW
15. Sydney Institute for Infectious Diseases (SydneyID), The University of Sydney, Camperdown, NSW
16. Centre for Infectious Diseases and Microbiology, The Westmead Institute for Medical Research, Westmead, NSW
17. Faculty of Medicine and Health, University of Sydney, Sydney, NSW
18. Westmead Hospital, Western Sydney Local Health District, Westmead, NSW
19. UQ Centre for Clinical Research, The University of Queensland, Brisbane, Queensland
20. Infection Management and Prevention Service, Queensland Children's Hospital, Brisbane, Queensland
21. School of Clinical Medicine, Faculty of Medicine and Health, University of New South Wales, Kensington, NSW
22. Department of Immunology and Infectious Diseases, Sydney Children's Hospital, Sydney Children's Hospitals Network, Randwick, NSW
23. Microbiology & Infectious Diseases Directorate, SA Pathology, Central Adelaide Local Health Network, Adelaide, SA
24. Faculty of Health and Medical Sciences, University of Adelaide, Adelaide, SA
25. School of Women and Children's Health, University of New South Wales, Kensington, NSW
26. Department of Microbiology, PathWest Laboratory Medicine WA, QEII Medical Centre, Nedlands, WA

Corresponding author

Ms Anita Williams

Address: The Kids Research Institute Australia, 15 Hospital Ave, Nedlands 6009 WA

Phone: +61 8 6319 1000

Email: anita.williams@thekids.org.au

References

1. Department of Health, Department of Agriculture, Water and the Environment. *Australia's National Antimicrobial Resistance Strategy – 2020 and Beyond*. Publication number 12589. Canberra: Australian Government Department of Health, Disability and Ageing; 2019. [Accessed on 24 May 2023.] Available from: https://www.amr.gov.au/sites/default/files/2022-11/australia-s-national-antimicrobial-resistance-strategy-2020-and-beyond_0.pdf.

2. Buttery J, Yang Y, Sharland M, World Society for Pediatric Infectious Diseases. World Society for Pediatric Infectious Diseases declaration on combating antimicrobial resistance in children. *World J Pediatr*. 2018;14(6):523–4. doi: https://doi.org/10.1007/s12519-018-0195-x.

3. World Society for Pediatric Infectious Diseases (WSPID). Declaration on Combating Antimicrobial Resistance in Children. [Media statement.] Geneva: WSPID; July 2020. [Accessed on 23 June 2025.] Available from: https://wspid.org/declaration-on-combating-antimicrobial-resistance-in-children/.

4. Williams A, Coombs GW, Bell J, Daley D, Mowlaboccus S, Bryant PA et al. Australian Group on Antimicrobial Research surveillance outcome programs – bloodstream infections and antimicrobial resistance patterns from patients less than 18 years of age, January 2020 – December 2021. *Commun Dis Intell (2018)*. 2024;48. doi: https://doi.org/10.33321/cdi.2024.48.32.

5. Williams A, Coombs GW, Bell JM, Daley DA, Mowlaboccus S, Bryant PA et al. *AGAR Kids Surveillance Outcome Programs – Bloodstream Infections from Patients <18 Years, January 2022 – December 2023*. Perth: Australian Group on Antimicrobial Resistance (AGAR); May 2025. Available from: https://agargroup.org.au/wp-content/uploads/2025/05/AGAR-Kids-2nd-Biennial_FINAL.pdf.

6. Williams A, Coombs GW, Bell JM, Daley DA, Mowlaboccus S, Bryant PA et al. Antimicrobial resistance in *Enterobacterales*, *Acinetobacter* spp. and *Pseudomonas aeruginosa* isolates from bloodstream infections in Australian children, 2013–2021. *J Pediatric Infect Dis Soc*. 2024;13(12):617–25. doi: https://doi.org/10.1093/jpids/piae111.

7. Williams A, Coombs GW, Bell JM, Daley DA, Mowlaboccus S, Bryant PA et al. Antimicrobial resistance in *Staphylococcus aureus* and *Enterococci* spp. isolates from bloodstream infections in Australian children, 2013–2021. *J Pediatric Infect Dis Soc*. 2025;14(2):piae110. doi: https://doi.org/10.1093/jpids/piae110.

8. Williams A, Coombs GW, Bell J, Daley DA, Mowlaboccus S, Bryant PA et al. *Antimicrobial resistance in bacteraemic isolates from paediatric patients in Australia, 2013–2021: an AGAR-Kids report*. Perth: AGAR; March 2024. Available from: https://agargroup.org.au/wp-content/uploads/2024/03/AGAR-Kids_nine-year-report-2013-2021_20240315.pdf.

9. Coombs G, Bell J, Blyth C, Bond K, Daley D, Cooley L et al. *Australian Group on Antimicrobial Resistance Surveillance Outcomes Programs: Bloodstream Infections 2023 Report*. Sydney: Australian Commission on Safety and Quality in Health Care (ACSQHC); November 2024. [Accessed on 8 January 2025.] Available from: https://www.safetyandquality.gov.au/sites/default/files/2024-12/agar_surveillance_outcome_programs_report_2023.pdf.

10. European Committee on Antimicrobial Susceptibility Testing (EUCAST). *Breakpoint tables for interpretation of MICs and zone diameters, Version 14.0*. Basel: EUCAST; January 2024. Available from: https://www.eucast.org/fileadmin/src/media/PDFs/EUCAST_files/Breakpoint_tables/v_14.0_Breakpoint_Tables.pdf.

11. Berends MS, Friedrich AW, Albers CJ, Luz CF, Sinha BNM, Glasner C. AMR—an R package for working with antimicrobial resistance data. *J Stat Softw*. 2022;104(3):1–31. doi: https://doi.org/10.18637/jss.v104.i03.

12. World Health Organization (WHO). *WHO Bacterial Priority Pathogens List, 2024: bacterial pathogens of public health importance to guide research, development and strategies to prevent and control antimicrobial resistance*. Geneva: WHO; 2024. [Accessed on 20 May 2024.] Available from: https://iris.who.int/bitstream/handle/10665/376776/9789240093461-eng.pdf.

13. Coombs G, Bell JM, Daley D, Collignon P, Cooley L, Gottlieb T et al. *Australian Group on Antimicrobial Resistance Surveillance Outcomes Programs: Bloodstream Infections 2022 Report*. Sydney: ACSQHC; December 2023. Available from: https://www.safetyandquality.gov.au/publications-and-resources/resource-library/agar-surveillance-outcome-programs-2022-report-0.

14. Forster DP, Leder K. Typhoid fever in travellers: estimating the risk of acquisition by country. *J Travel Med*. 2021;28(8):taab150. doi: https://doi.org/10.1093/jtm/taab150.

15. Davis BPF, Amin J, Franklin N, Beggs PJ. Salmonellosis in Australia in 2020: possible impacts of COVID-19 related public health measures. *Commun Dis Intell (2018)*. 2022;46. doi: https://doi.org/10.33321/cdi.2022.46.2.

16. Stanaway JD, Reiner RC, Blacker BF, Goldberg EM, Khalil IA, Troeger CE et al. The global burden of typhoid and paratyphoid fevers: a systematic analysis for the Global Burden of Disease Study 2017. *Lancet Infect Dis*. 2019;19(4):369–81. doi: https://doi.org/10.1016/S1473-3099(18)30685-6.

17. Australian Technical Advisory Group on Immunisation (ATAGI). *The Australian Immunisation Handbook*. Canberra: Australian Government Department of Health, Disability and Ageing; 2023. [Accessed on 20 April 2023.] Available from: https://immunisationhandbook.health.gov.au/.

18. ACSQHC. AURA 2023: *Fifth Australian report on antimicrobial use and resistance in human health*. Sydney: ACSQHC; 2023. Available from: https://www.safetyandquality.gov.au/publications-and-resources/resource-library/aura-2023-fifth-australian-report-antimicrobial-use-and-resistance-human-health-report.

19. Williamson DA, Lane CR, Easton M, Valcanis M, Strachan J, Veitch MG et al. Increasing antimicrobial resistance in nontyphoidal *Salmonella* isolates in Australia from 1979 to 2015. *Antimicrob Agents Chemother*. 2018;62(2):10.1128/aac.02012-17. doi: https://doi.org/10.1128/AAC.02012-17.

20. Sia CM, Baines SL, Valcanis M, Lee DYJ, Gonçalves da Silva A, Ballard SA et al. Genomic diversity of antimicrobial resistance in non-typhoidal *Salmonella* in Victoria, Australia. *Microb Genom*. 2021;7(12):000725. doi: https://doi.org/10.1099/mgen.0.000725.

21. Luo L, Payne M, Wang Q, Kaur S, Rathnayake IU, Graham R et al. Genomic epidemiology and multilevel genome typing of Australian *Salmonella enterica* serovar Enteritidis. *Microbiol Spectr*. 2023;11(1):e0301422. doi: https://doi.org/10.1128/spectrum.03014-22.

22. Cuypers WL, Jacobs J, Wong V, Klemm EJ, Deborggraeve S, Van Puyvelde S. Fluoroquinolone resistance in Salmonella: insights by whole-genome sequencing. *Microb Genom*. 2018;4(7):e000195. doi: https://doi.org/10.1099/mgen.0.000195.

23. Wen SCH, Harris PNA, Forde B, Permana B, Chatfield MD, Lau CL et al. Characterization of gram-negative bloodstream infections in hospitalized Australian children and their clinical outcomes. *Clin Infect Dis*. 2024;79(3):ciae341. doi: https://doi.org/10.1093/cid/ciae341.

24. Bell JM, Lubian AF, Partridge SR, Gottlieb T, Robson J, Iredell J et al. Australian Group on Antimicrobial Resistance (AGAR) Gram-negative Surveillance Outcome Program (GnSOP) Bloodstream Infection Annual Report 2023. *Commun Dis Intell (2018)*. 2025;49. doi: https://doi.org/10.33321/cdi.2025.49.003.

25. Bell JM, Lubian AF, Partridge SR, Gottlieb T, Robson J, Iredell JR et al. Australian Group on Antimicrobial Resistance (AGAR) Gram-negative Surveillance Outcome Program (GnSOP) Bloodstream Infection Annual Report 2022. *Commun Dis Intell (2018)*. 2023;47. doi: https://doi.org/10.33321/cdi.2023.47.69.

26. Slack MPE, Grimwood K, Tuzel E, Kim H, Edwards F, Laupland KB. *Pseudomonas aeruginosa* bloodstream infections in children in Queensland, Australia, 2000–2019. *J Paediatr Child Health*. 2025;61(2):241–8. doi: https://doi.org/10.1111/jpc.16745.

27. Coombs G, Daley D, Shoby P, Mowlaboccus S. Australian Group on Antimicrobial Resistance (AGAR) Australian *Staphylococcus aureus* Surveillance Outcome Program (ASSOP) Bloodstream Infection Annual Report 2023. *Commun Dis Intell (2018)*. 2024;48. doi: https://doi.org/10.33321/cdi.2024.48.57.

28. Wozniak TM, Young A, Conlan D, Shausan A, Dyda A, Sartorius B et al. Application of Bayesian spatial modelling to uncover geographical disparities and improve antimicrobial resistant surveillance. [Preprint.] *medRXiv*. 2024. [Accessed on 9 January 2025.] doi: https://doi.org/10.1101/2024.11.06.24316846.

29. UK Health Security Agency (UKHSA). *English surveillance programme for antimicrobial utilisation and resistance (ESPAUR) report 2023 to 2024*. London: UKHSA; November 2024. [Accessed on 20 December 2024.] Available from: https://www.gov.uk/government/publications/english-surveillance-programme-antimicrobial-utilisation-and-resistance-espaur-report.

30. European Centre for Disease Prevention and Control (ECDC). *Antimicrobial resistance in the EU/EEA (EARS-Net) – Annual epidemiological report for 2023*. Stockholm: ECDC; 18 November 2024. Available from: https://www.ecdc.europa.eu/en/publications-data/antimicrobial-resistance-eueea-ears-net-annual-epidemiological-report-2023.

Appendix A

Table A.1.1: Number and proportion of the ten most frequently reported isolates to the Australian Group on Antimicrobial Resistance in patients aged < 18 years, January 2020 – December 2021

	2020 N: 823		2021 N: 856		2020–2021 N: 1,679	
Organism	**n**	**%**	**n**	**%**	**n**	**%**
Staphylococcus aureus	303	36.8	304	35.5	607	36.2
Escherichia coli	163	19.8	215	25.1	378	22.5
Enterococcus faecalis	60	7.3	62	7.2	122	7.3
Klebsiella pneumoniae complex	61	7.4	61	7.1	122	7.3
Enterobacter cloacae complex	60	7.3	46	5.4	106	6.3
Salmonella (non-Typhi)	22	2.7	52	6.1	74	4.4
Pseudomonas aeruginosa	31	3.8	30	3.5	61	3.6
Enterococcus faecium	32	3.9	9	1.1	41	2.4
Klebsiella oxytoca	13	1.6	17	2.0	30	1.8
Acinetobacter baumannii complex	10	1.2	8	0.9	18	1.1

Table A.1.2: Number and proportion of the ten most frequently reported isolates to the Australian Group on Antimicrobial Resistance in patients aged < 18 years, January 2022 – December 2023

	2022 N: 791		2023 N: 1,036		2022–2023 N: 1,827	
Organism	**n**	**%**	**n**	**%**	**n**	**%**
Staphylococcus aureus	278	35.1	323	31.2	601	32.9
Escherichia coli	200	25.3	257	24.8	457	25.0
Enterococcus faecalis	67	8.5	69	6.7	136	7.4
Klebsiella pneumoniae complex	45	5.7	62	6.0	107	5.9
Enterobacter cloacae complex	37	4.7	54	5.2	91	5.0
Salmonella (non-Typhi)	34	4.3	51	4.9	85	4.7
Pseudomonas aeruginosa	38	4.8	30	2.9	68	3.7
Salmonella Typhi	15	1.9	35	3.4	50	2.7
Serratia marcescens	12	1.5	23	2.2	35	1.9
Enterococcus faecium	15	1.9	18	1.7	33	1.8